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GENETIC AND PHYSIOLOGICAL ANALYSES OF YIELD AND YIELD-RELATED TRAITS IN WEST AFRICA RICE GERMPLASM UNDER INDUCED DROUGHT STRESS

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GENETIC AND PHYSIOLOGICAL ANALYSES OF YIELD AND YIELD-RELATED TRAITS IN WEST AFRICA RICE GERMPLASM UNDER INDUCED DROUGHT STRESS

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This work has not been presented elsewhere for the award of a degree, or any other purpose.

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DEDICATION

This work is dedicated to the Almighty God for His love, protection and good health throughout the period of this study. I dedicated this work to my lovely wife Aku NYAMEDZOSSE, parents (Yawo A. ADJAH and Atsufoe GBOGBO) and my family for their unconditional support during this work.

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LIST OF ABBREVIATIONS AND ACRONYMS

^{o}C	Degree Celsius
11D	11 days after drought stress initiation
18D	18 days after drought stress initiation
27D	27 days after drought stress initiation
5D	Five days after drought stress initiation
A	Scale A
AGRA	Alliance for a Green Revolution in Africa
ANOVA	Analysis of variance
B	Scale B
BC	Backcross
BC_1	Backcross with the parent 1
BC_2	Backcross with the parent 2
C	Scale C
C.V	Coefficient of variation
cm	Centimetre
CRI1	Carotenoid reflectance Index 1
CRI2	Carotenoid reflectance Index 2
CSIR-CRI	Council of Scientific and Industrial Research – Crops Research Institute
D	Scale D
d	additive effect
D.F	Degree of freedom
DD	Degree of dominance
DRR	Recovery from drought
DTF	Days to flowering
E	Transpiration rate
ETR	Electron transport rate
F_1	F_1 generation of a cross from P_1 and P_2
F_2	F_2 generation from advancement of F_1
GA	Genetic advance
GAM (%)	Genetic advance as percent of mean
GL	Grain length
gsw	Stomatal conductance
GW	Grain width
GYP	Grain yield per plant
h	dominance effect
h^2_{bs}	Heritability in the broad-sense
h^2_{ns}	Heritability in the narrow-sense
HMP	Heterosis over mid-parent
i	additive × additive effect
IRRI	International Rice Research Institute
j	additive × dominance effect
l	dominance × dominance effect
LDS	Leaf drying score
LRS	leaf rolling score
m	mean effect

m^2	Square meter
MRH	Residual heterosis over mid-parent
NDVI	Normalized difference vegetative index
P_1	recipient parent
P_2	donor parent
PH	Plant height
PhiPS II	Quantum yield of fluorescence
PL	Panicle length
PN	Panicle number
r	coefficient of correlation
RDVI	Renormalized difference vegetative index
RICOWAS	Scaling-up climate-resilient rice production in West Africa
S.D.	Standard deviation
SES	standard evaluation system
t-cal.	calculated t value
TI	Transgressive index
TN	Tiller number
Var	Variance
Vg	Genetic variance

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RÉSUMÉ

La sécheresse est le facteur le plus important qui limite la production de riz pluvial en Afrique et elle est aggravée par les changements climatiques, ce qui constitue une menace sérieuse pour la sécurité alimentaire du continent. Cette étude visait à évaluer l'impact du stress de la sécheresse sur les traits morpho-physiologiques, biochimiques et sur l'abondance des transcrits des gènes répondant à la sécheresse parmi les génotypes de riz et à sélectionner des génotypes tolérants à la sécheresse. En outre, l'étude a cherché à comprendre la base génétique et l'héritage derrière l'expression de la tolérance des lignées de sélection de riz au stress de la sécheresse. Pour atteindre ces objectifs, 100 génotypes ont été criblés sous le stress de la sécheresse dans des conditions de terrain en utilisant un plan 10×10 α-lattice. Sur ces 100 génotypes, 14 ont été sélectionnés et criblés sous le stress de la sécheresse en serre en utilisant un plan en blocs complets randomisés. Sur les 14, quatre génotypes ont été choisis pour l'analyse de l'expression des gènes. En outre, deux génotypes sensibles à la sécheresse (CRI-Agrarice et Jasmine 85) ont été croisés avec un riz tolérant à la sécheresse (APO) pour développer six populations (F_1, F_2, BC_1, BC_2, P_1 et P_2) pour chacun des deux croisements parmi lesquels une analyse de la moyenne des générations a été effectuée. Des données ont été collectées sur le rendement en grains et les caractères liés au rendement, les échanges gazeux des feuilles (conductance stomatique, taux de transpiration), la teneur en eau relative, la réflectance des feuilles et les caractères biochimiques (teneur en malondialdéhyde et en proline). Le profilage QTL du rendement de la sécheresse a été utilisé pour faciliter la sélection. Dans le cadre du criblage au champ, pour tous les caractères étudiés, une réduction générale a été observée parmi les génotypes soumis à un stress de sécheresse par rapport à des conditions de non-sécheresse. Le rendement en grains était positivement corrélé avec la plupart des caractères liés au rendement dans les deux régimes hydriques. Dans le cadre du criblage en serre, en général, la performance moyenne de tous les génotypes a été réduite de manière significative sous un stress de sécheresse de 11, 18, 27 jours et au stade de la reproduction par rapport aux conditions de non-sécheresse pour la conductance stomatique, le taux de transpiration pour la plupart des génotypes sauf APO, UPLR-17 et Togo Marshall. Une augmentation du malondialdéhyde de >45% a été observée pour tous les génotypes, sauf pour CRI-Enapa (25,15%), APO (39,37%) et UPLR-17 (43,65%). Le rendement en grains présentait une corrélation négative significative avec le retard de floraison et une corrélation positive significative avec l'indice de différence végétative renormalisée (RDVI). Les gènes *osBHLH6* et *Cytokinin-O-glucosyltransferase-1* ont été régulés à la hausse dans tous les génotypes évalués dans des conditions de sécheresse

en chambre de croissance. Lors de l'évaluation en serre, parmi les croisements et les régimes hydriques, l'interaction génétique additive x additive était prédominante, même si les tests d'échelle n'étaient pas significatifs, ce qui indique l'efficacité de la sélection dans les premières générations. Sur la base de la corrélation et de l'indice de distance multitraits génotype-idéotype (MGIDI) utilisant les valeurs relatives des caractères : le rendement en grains, la biomasse, le score de fertilité des épillets, la longueur des grains, le malondialdéhyde et le RDVI sont recommandés pour le suivi lors de la sélection de génotypes tolérants à la sécheresse. Dans l'ensemble, Viwonor short, UPLR-17, APO et CRI-Enapa ont été sélectionnés par ordre chronologique comme génotypes présentant une tolérance accrue à la sécheresse et sont recommandés pour être utilisés comme donneurs des gènes tolérants à la sécheresse ou éventuellement relâchés à des fins commerciales.

Mots clés : Sécheresse, échanges gazeux, réflectance, action des gènes, ségrégation, proline, QTL, expression des gènes

ABSTRACT

Drought is the single most important factor limiting upland rice production in Africa and is aggravated by climate change leading to a serious food security threat in the continent. This study aimed to assess the impact of drought stress on morpho-physiological, biochemical traits and transcripts abundance of drought-responsive genes among the rice genotypes and select drought-tolerant genotypes. Furthermore, the study sought to understand the genetic basis and inheritance behind the expression of tolerance of the rice breeding lines to drought stress. To achieve these objectives, 100 genotypes were screened under drought stress in field conditions using 10×10 alpha-lattice design. Out of the 100, selected 14 genotypes were further screened under drought stress in the greenhouse using randomized complete-block design. Out of the 14, four genotypes were chosen for gene expression analysis. Furthermore, two drought-sensitive genotypes (CRI-Agrarice and Jasmine 85) were crossed with a drought-tolerant rice (APO) to develop six populations (F_1, F_2, BC_1, BC_2, P_1 and P_2) for each of the two crosses among which a generation mean analysis was conducted. Data were collected on grain yield and yield-related traits, leaf gas exchanges (stomatal conductance, transpiration rate), relative water content, leaf reflectance and biochemical traits (malondialdehyde and proline content). Drought yield-QTL profiling was used to assist in the selection. Under the field screening, for all the investigated traits, a general reduction was observed among the genotypes under drought stress compared to non-drought conditions. Grain yield was positively correlated with most yield-related traits under both water-regimes. Under the greenhouse screening, in general, the mean performance of all the genotypes was reduced notably under 11, 18, 27 days and reproductive stage drought stress compared to the non-drought conditions for stomatal conductance, transpiration rate for most genotypes except APO, UPLR-17 and Togo Marshall. Increase in malondialdehyde of >45% for all genotypes was observed, except in CRI-Enapa (25.15%), APO (39.37%) and UPLR-17 (43.65%). Grain yield had a significant negative correlation with delay-in-flowering and a significant positive correlation with renormalised difference vegetative index (RDVI). The genes os*BHLH6* and *Cytokinin-O-glucosyltransferase-1* were upregulated in all the genotypes evaluated under drought conditions in growth chambers. Under the screenhouse evaluation, among both crosses and water-regimes, additive x additive gene interaction was predominant even though the scaling tests were not significant indicating the effectiveness of selection in early generations. Based on the correlation and the multi-trait genotype-ideotype distance index (MGIDI) using relative trait values: grain yield, biomass, spikelet fertility score, grain length, malondialdehyde and

RDVI are recommended for monitoring during the selection of drought-tolerant genotypes. Overall, Viwonor short, UPLR-17, APO and CRI-Enapa were selected in chronological order as genotypes with enhanced tolerance to drought and are recommended to be used as drought-tolerant donors or possibly released for commercial purposes.

Key words: Drought, gas exchanges, reflectance, gene action, segregation, proline, QTL, gene expression

CHAPTER 1 INTRODUCTION

1.1 Problem statement

Forty percent (40%) of the overall area under rice cultivation in Africa is allocated to rainfed upland rice production, 38% for rainfed lowland, 12% for irrigated lowland, 6% for deep water and floating, and 4% for mangrove swamps (Bimpong et al., 2011). Upland and lowland rice production which constitute about 80% of the total rice production area in Africa are likely prone to be the most vulnerable to drought (Bimpong et al., 2011). Most of the severe droughts in the last ten years have been in Africa, the continent which already has the lowest level of crop production and drought adaptive capacity. Drought has adversely affected agriculture in different parts of the continent, with the production of rice declining in many parts of West Africa due to increasing water deficits (Bates et al., 2008). At the global level, agricultural drought frequency and area are predicted to increase by 50 to 200% in a relative sense during this 21st century (Zhao & Dai, 2017) causing rice yields loss by 25.4% (Zhang et al., 2018), as result of the unpredictable occurrence of drought as a result of the current changes in climate (Serraj et al., 2009), there is a need to develop improved crops tolerant to drought in order to satisfy the need of food of an increasing population in Africa especially in West Africa. Rice, which is one of the staple foods in West Africa, is an ideal crop to address the problem.

As projected by global climate models, recurrent drought events under future climate change may result in increased losses when droughts overlap with sensitive stages of crop growth (Kumar et al., 2014). When drought occurs the grain yield of rice severely decreases (Maisura et al., 2014). Singh et al. (2010) observed in six generations of six crosses of rice under drought and irrigated conditions a reduction in several characters including grain yield under drought conditions. Yield decreases are due to the detrimental effect of drought on plant height, number of tillers, leaf area, root length, root thickness and root depth, spikelet fertility, panicle exertion, leaf greenness, leaf temperature, days to flowering, days to maturity, leaf tip drying and leaf rolling (Bocco et al., 2012; Ndjiondjop et al., 2010).

The following questions are being addressed in this study: how importantly the rice grain yield and related traits are affected when drought stress occurs during vegetative and reproductive development stages of the rice plant? What is the effect of drought stress on the physiological and biochemical traits on our germplasm used in this study during vegetative and reproductive development stages of the rice plant? Does the known drought-tolerant QTLs used to genotype our population able to select for the drought-tolerant genotypes? And lastly, what are the

genetic bases and the inheritance of drought-tolerant traits in six generations of rice crosses evaluated under drought stress?

1.2 State of the knowledge

The worldwide overall paddy rice production is 787 million tons per annum, and it is grown on over 165 million hectares of land (FAOSTAT, 2023). Rice is one of the staple foods worldwide, since it provides 20% of dietary energy per capita and 13% of the dietary protein for human consumption. The dietary shares of rice in developing countries are about 29.1% dietary protein and 29.3% dietary energy (Sautter et al., 2006). Apart from its importance, rice is also the greatest consumer of water among all crops (Bouman et al., 2007). Climate variability greatly influences water resources while droughts and floods are projected to increase in future. Crop yield is highly affected by climatic variations since it depends on specific climate conditions. Ray et al. (2015) estimated the total rice yield variability due to climate variability over the last three decades and concluded that approximately 53% of rice harvesting regions experiences the influence of climate variability on yield at the rate of about 0.1 t/hm^2 per year and approximately 32% of rice yield variability is due to year-to-year climate variability.

With the current climate change patterns, extreme weather conditions especially water scarcity and drought are expected to be frequent in the near future (Turral et al., 2011; Wassmann et al., 2009). Water plays a major role in agricultural and food production (Wang et al., 2012), and its deficits threaten food security by reducing crop yields and increasing their year-to-year variability (Foley et al., 2011). Drought is defined as the difficulties of a plant exhibiting its normal physiological functions due to the deficit in water potential and turgor of the plant (Lisar et al., 2012). Forty percent (40%) of the overall area under rice cultivation in Africa is allocated to rainfed upland rice production, 38% for rainfed lowland, 12% for irrigated lowland, 6% for deep water and floating, and 4% for mangrove swamps. Upland and lowland rice production which constitute about 80% of the total rice production area in Africa is likely prone to be the most vulnerable to drought (Bimpong et al., 2011). Drought is the most significant abiotic constraint for rice production in sub-Saharan Africa (Reynolds et al., 2015), and it is one of the major abiotic stresses that constrains yield stability (Lanceras et al., 2004).

The grain yield of rice severely decreases under drought stress (Maisura et al., 2014). Singh et al. (2010) observed in six generations of six crosses of rice under drought and irrigated conditions a reduction in several characters including grain yield under drought conditions.

Yield decreases are due to the detrimental effect of drought on plant height, number of tillers, leaf area, root length, root thickness and root depth, spikelet fertility, panicle exertion, leaf greenness, leaf temperature, days to flowering, days to maturity, leaf tip drying and leaf rolling (Bocco et al., 2012; Ndjiondjop et al., 2010).

The first step in any crop improvement programme is the knowledge of the amount of genetic variability that exists among the genotypes, since the amount of variability is essential in the formulation of any efficient breeding methodology (Tiwari & Pandey, 2011). Several authors (Arifuzzaman et al., 2022; Ravindra Babu et al., 2012; Adjah et al., 2020; Asante et al., 2019) have studied variability through various genetic variability parameters. Even though several studies have reported wide ranges of genetic variability for grain quality traits, yield and its components under rainfed and normal irrigation, only a few works have been done to quantify drought effect on genetic variability parameters. The presence of wide variability among rice genotypes is imperative for yield and related traits improvement. Parameters such as coefficient of variation, heritability in broad-sense and narrow-sense, and genetic advance are important breeding tools to assess the variation.

Understanding the genetic dissection of loci underlying drought stress tolerance in rice will boost the development of new cultivars with improved grain yield under drought stress conditions. To this end, the identification of grain yield QTLs under drought with large and consistent effects across the genetic backgrounds and various environments is the most suitable step for its successful applicability in breeding programs (Yadav et al., 2019). To reverse the problem of yield losses due to drought stress, various tactics have been in use in plant breeding and the QTL approach is one of them. To date, QTLs that are linked to grain yield under drought stress have been reported in all chromosomes of rice. Robust grain yield QTLs under drought stress namely, $qDTY_{1.1}$, $qDTY_{2.1}$, $qDTY_{3.1}$, and $qDTY_{12.1}$ have been identified using SSR markers by Bernier et al. (2007), Ghimire et al. (2012),Venuprasad et al. (2009) and Vikram et al. (2011), respectively. Four stable QTLs namely $qDTY_{2.4}$, $qDTY_{3.3}$, $qDTY_{6.3}$, and $qDTY_{11.2}$ have been identified for rice grain yield under reproductive stage drought stress using SNPs markers through genotyping-by-sequencing (GBS) based high-density linkage map (Yadav et al., 2019).

Simple Sequence Repeats (SSR) markers have been successfully used to study QTL mapping (McCouch et al., 2002), also to construct genetic linkage maps in rice by linking genotype and phenotypic variation of various traits (Bazrkar-Khatibani et al., 2019; Wang et al., 2023; Fan

et al., 2020). But, the approach to using SSRs markers is somehow tedious, time-consuming and cost-ineffective due to laborious gel-based genotyping (Rasheed et al., 2017). To overcome the limitations of SSRs, next-generation sequencing markers such as SNPs have been developed. SNP markers have a lot of advantages over SSRs markers. SNP markers are more valuable and cost effective, informative markers due to high abundance and uniform distribution in genomes, high multiplexing and ease of automation (Varshney et al., 2018). Recently a next generation sequencing tool, a high-throughput SNP genotyping, has been developed with a rapid, precise and low-cost genotyping technique to boost the process of QTL mapping (Bhat & Yu, 2021; Nishimura et al., 2022; Scheben et al., 2017). In rice, different kinds of fixed SNP chips namely 6 K SNP chips, 44 K SNP chips, 50 K SNP chips and 700 K SNP arrays (Yu et al., 2014; Zhao et al., 2011) have been developed to find association between phenotype and genotype (Thomson et al., 2017).

Furthermore, a thorough understanding of physiological (leaf gas exchanges and leaf reflectance parameters) and biochemical (Malondialdehyde (MDA), proline content etc.) dissection of African indigenous ecotypes such as *Oryza glaberrima* types and other landraces can help to increase genetic gain in rice productivity in West Africa. These indigenous rice genotypes contain several drought-tolerant features such as drought-responsive genes, and metabolic and anti-oxidative response status which are useful in rice improvement programs. Limited works have been reported on the physiological characteristics of rice under drought stress in West African countries among which relative water content (Bimpong et al., 2018; Sangodele et al., 2014; Umego et al., 2020) and chlorophyll content (Adeboye et al., 2021) and transpiration efficiency (Affortit et al., 2022).

The future of development of drought-tolerant rice varieties is associated with the identification of genes associated with drought tolerance. Approximately 10% of rice genes are responsive to drought stress (Xiong, 2013). Potential candidate genes can be transcription factors, involved in cell protection through repairs, production of oxidative species (ROS), antioxidant activity. Several approaches can be used to identify potential drought responsive genes among which the use quantitative reverse transcription polymerase chain reaction, qRT-PCR (Rouf Mir et al., 2012). Up to date several drought responsive genes have been identified including CALCINEURIN B-LIKE PROTEIN-INTERACTING PROTEIN KINASE 12, *OsCIPK12* (Benjamins et al., 2001), Rice *WRKY* gene13 (Qiu et al., 2008; Xiao et al., 2013), dihydroorotate dehydrogenase 1, *OsDHODH1* (Liu et al., 2009), Drought-hypersensitive

mutant1, *DSM1* (Ning et al., 2010), Calcium dependent protein kinase, *OsCDPK7* (Saijo et al., 2000), basic leucine zipper (*b-ZIP*) transcription factor 72, *OsbZIP72* (Yang et al., 2019; Lu et al., 2009). Based on qRT-PCR, the expression profile of several drought responsive genes was upregulated in the drought-tolerant genotype Nagina 22, and down-regulated in the drought-sensitive genotype IR64 (Kaur et al., 2023).

Asides the chapter one which is the general introduction to this work, this thesis contained in the following order: the chapter two which covered the overall literature review; the chapter three talked about the research methodology, the chapter four is made of the results and discussions, while the chapter five of conclusion and recommendations.

1.3 Research hypothesis

The following hypothesis has been formulated for this study: West Africa Rice genotypes evaluated in this study display variations in the agronomic, physiological, biochemical traits and induced transcripts abundance when drought stress occurs during plant development stages; and additive × additive type of gene action is predominant in the segregating populations developed from a cross of two contrasting parents under drought stress.

1.4 OBJECTIVES

1.4.1 General objective

This study aims to contribute at designing a drought-resilient rice cultivar with high grain yield under drought stress conditions.

1.4.2 Specific objectives

Four objectives are being pursued in this study:

1. Demonstrate the effects of drought stress on morphological, physiological and biochemical traits among the rice genotypes.
2. Identify the genotypes that are tolerant to drought stress based on morpho-physiological, biochemical and molecular data.
3. Determine the transcripts abundance (gene expression) of known drought responsive genes in contrasting rice genotypes during the vegetative phase of rice growth.
4. Determine the genetic basis and inheritance behind the expression of tolerance of the rice breeding lines to drought stress.

CHAPTER 2 LITERATURE REVIEW

The literature review of this thesis has been published as a comprehensive review article in rice science as Adjah et al. (2022), https://doi.org/10.1016/j.rsci.2022.06.002.

2.1 Rice

Rice is the common name of the plant species belonging to the genus Oryza in the family Poaceae (Gramineae) (Kellogg, 2009). *Oryza sativa* and *Oryza glaberrima* Steud are the two cultivated species. Among the cultivated rice, *Oryza glaberrima* Steud is domesticated in West Africa whereas all Asian, American, and European rice varieties belong to *Oryza sativa* groups. Apart from the two cultivated species, the denomination wild rice refers to all other Oryza species. Several genetic studies have shown the wild-type *Oryza rufipogon* to be the wild ancestor of *Oryza sativa*, the Asian rice (Choi et al., 2019; Londo et al., 2006; Tong et al., 2023; Vigueira et al., 2019), while other studies have proposed *Oryza nivara*, an annual occurring type of *Oryza rufipogon* as the most recent ancestor of *Oryza sativa* (Yamanaka et al., 2003). Whereas *Oryza glaberrima* is evolved from the wild-type of *Oryza barthii* (Wang et al., 2014). The cultivated species is classified into two sub-species namely japonica and indica groups, characterized by short grain and long grain rice, respectively (Figure 1). Currently, there are more than 120000 different varieties of these cultivated rice classified based on their colour as white rice, red and black rice etc. Furthermore, Japonica rice has been classified into two ecotypes namely temperate and tropical japonica according to the ecosystems where they have been developed. On the other hand, indica sub-specie have been classified into ecotypes such as Aus, Boro, Amman and Rayada according to their growing ecosystems and time (Morinaga, 1968). The genome sequencing of 3010 accessions has shown that *Oryza sativa* species can be further classified into nine sub-populations namely four indica sub-populations, three japonica sub-populations and two single groups. Commonly called Asian rice, all these nine sub-populations could be related to geographic location and have been widely grown across the world with indica representing more than 80% and japonica 15%. On the other hand, *Oryza glaberrima*, which accounts for less than 5% of global rice production, is grown in some areas of Africa and is commonly called African rice (Wang et al., 2018).

The genus Oryza comprises 23 species, including both cultivated and wild species, and is divided into four major complexes (Table 1) as follows: the *sativa* Complex (eight species),

the *officinalis* Complex (11species), and the two remote relatives of *Oryza sativa* namely the *ridleyanae* Complex, and the *granulata* Complex (Joseph et al., 2008; Wing et al., 2018).

Figure 1. Two most cultivated rice species across the world: **(A)** *Oryza Sativa Japonica*, retrieved from *https://rice-genome-hub.southgreen.fr/data_search/organism*; **(B)** *Oryza Sativa Indica*, retrieved from https://www.vivacepanorama.com/food-crops-rice-oryza-sativa/

Table 1. Genus Oryza: Classification and distribution of 23 species

Class	Species	Chromosome number	Genome	Distribution
Section sativa	*Oryza sativa* L.	24	AA	Asia
	O. rufipogon sensu lato	24	AA	Asia, Oceania
	O. nivara	24	AA	Asia, Oceania
	O. glaberrima Steud.	24	AA	West Africa
	O. barthii A. Chev.	24	AA	Africa
	O. longistaminata Chev. et Roehr	24	AA	Africa
	O. meridionalis Ng	24	AA	Australia
	O. glumaepatula Steud.	24	AA	Central & South America
Section ridleyanae	*O. brachyantha* Chev. et Roehr.	24	FF	Africa
	O. ridleyi Hook	48	HHJJ	Asia, New Guinea
	O. longiglumis Jansen	48	HHJJ	New Guinea
	O. schlechteri Pilger	48	unknown	Papua New Guinea
Section officinals	*O. officinalis* Wall ex Watt	24	CC	Asia
	O. rhizomatis D.A.Vaughan	24	CC	Sri Lanka
	O. eichingeri Peter	24	CC	Africa, Sri Lanka
	O. minuta J.S.Presl ex C.B.Presl.	48	BBCC	Philippines
	O. punctata Kotechy ex Steud.	24, 48	BB, BBCC	Africa
	O. latifolia Desv.	48	CCDD	Central & South America
	O. alta Swallen	48	CCDD	Central & South America
	O. grandiglumis (Döll.) Prod	48	CCDD	South America
	O. australiensis Domin	24	EE	Australia
Section granulata	*O. granulata* Nees et Am ex Watt	24	GG	Asia
	O. meyeriana (Zoll. et Mor. ex Steud.) Baill	24	GG	Asia

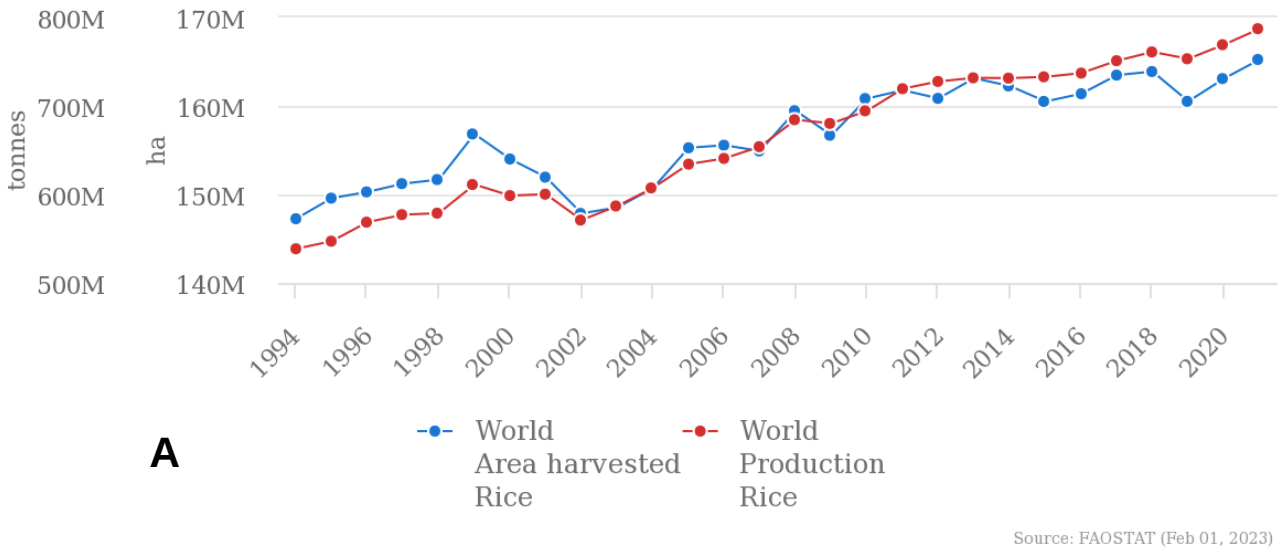
Adapted from (OECD-Organisation for Economic Co-operation and Development, 2022)

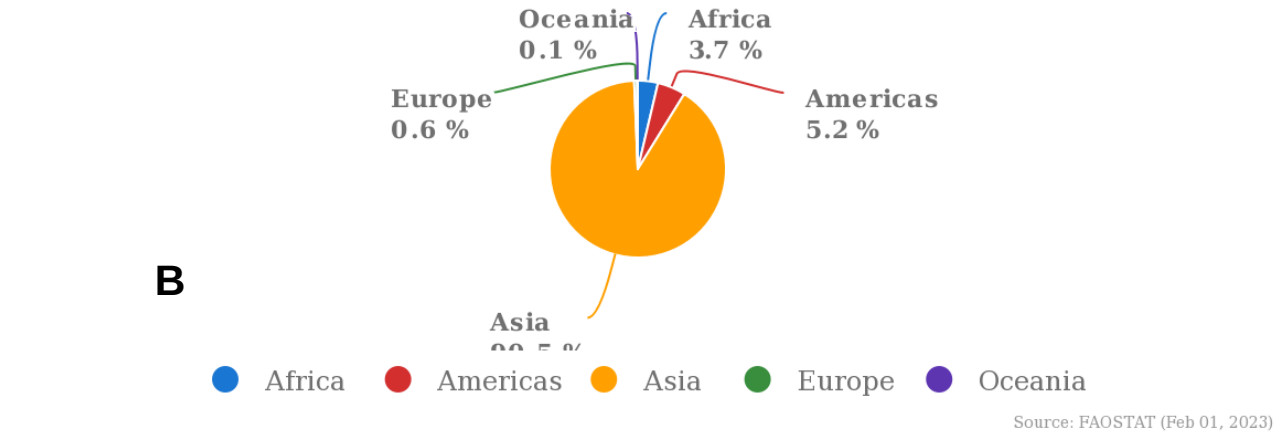
2.2 Importance of rice in Africa

Rice is one of the most important crops in the world. Worldwide, the total area under rice cultivation is around 165 million hectares with a total production of more than 787 million tons per annum accounting for more than 470 million tons of milled rice (Figure 2A) (FAOSTAT, 2023). Africa accounts for 3.7% of the total worldwide rice production, with Sub-Saharan Africa producing a total production of over 21 million tons accounting for more than 50% of African production in 2021(Figure 2B) (FAOSTAT, 2023). In Sub-Saharan Africa, rice is generally grown on small farms of 0.5 to 3 ha in size. In Africa, rice is part of the main staple foods that supply the largest quantity of calories (Sautter et al., 2006). Rice consumption is predicted to record a significant increase in Africa (Van Oort et al., 2015) and it has already overtaken other staple foods in many African countries because of the ease in preparation and digestion (Mohidem et al., 2022). Rice production has grown fast in Africa, but its consumption has grown even more rapidly (https://www.africarice.org/sustainable-productivity, accessed 2023). The rice harvested area and yield have been increasing in Sub-Saharan Africa since 2000 (Figure 2C), while the indicator for self-sufficiency (ratio between production and consumption) is below indicating that most Sub-Saharan Africa countries are still not self-sufficient in rice. Thus, if growth in yields falls to keep track with growth in consumption, then either more importation, more areas, or a combination of these two will be needed (Van Oort et al., 2015). Confronted with a growing population and increasing rice consumption per capita, African countries' policy-makers have three options to meet future demand for rice, whether they opt to increase imports, increase rice area or increase production per unit area. Often, the combination of these three options is needed to meet the growing need for the population demand for rice. But in many cases, the combination of these options is not possible (Van Oort et al., 2015).

2.3 Importance of rice in West Africa

Western Africa is the main rice-producing sub region in Africa, with Nigeria as the leading producer. In terms of the production of rice by individual countries in 2019, the three leading producers in Africa are Nigeria (8 million tonnes with approximately 5 million hectares harvested area), Egypt (6 million tonnes with approximately 779,032 hectares harvested area) and Madagascar (4 million tonnes with approximately 815,693 hectares harvested area) (FAOSTAT, 2023).





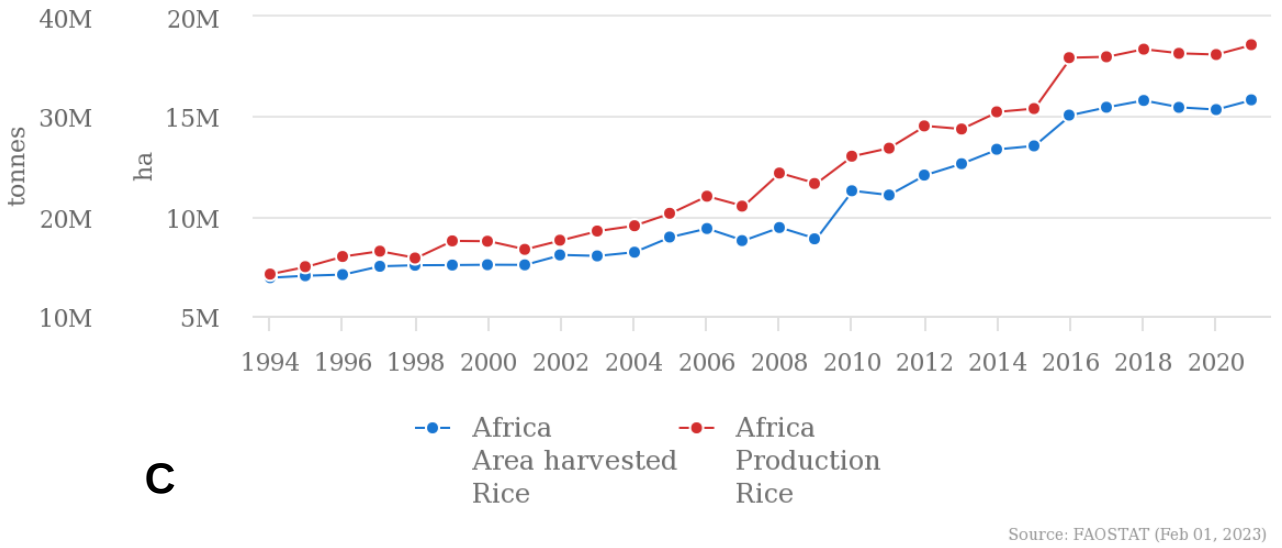


Figure 2. Total paddy rice production, harvested area and yield quantities of rice from 1994 to 2020 in the **(A)** World, **(B)** Africa; **(C)** Production share of Rice by region. *Source: Adapted from FAOSTAT, 2023*

Between 2009 and 2019 rice production in West Africa has doubled with an average of 10.1 million tons of rice per annum (Soullier et al., 2020). This as a result of an area expansion in an extensive agricultural production system rather than gains in yield production. Gains in yield contributed less to the increase in rice production, because of relatively low-quality seed as well as low adoption of improved varieties (Arouna et al., 2017), limited use of inputs and limited adoption of improved agricultural practices (Soullier et al., 2020). For the first time in history, the overall paddy production in West Africa hit more than 20 million tonnes in 2017 (Figure 3), and since then it has been wavering around that figure (FAOSTAT, 2023). This can be explained by the efforts made by the Consultative Group on International Agricultural Research (CGIAR) and National Agricultural Research and Extension Systems (NARES) to advance crop improvement programmes in Africa. Over the last decade, the annual growth rate mean in rice production is around 10.1% with Nigeria, Mali, Côte d'Ivoire, Ghana and Senegal as the most contributing countries (Soullier et al., 2020).

Since 2008, rice consumption has been increasing in Africa; especially between 2009 and 2013, the increase in rice consumption in West Africa was greater than in any other region of the continent (Soullier et al., 2020). This is largely due to increased urbanization driven by demographic growth and the rising annual per capita rice consumption (Mendez del Villar & Lançon, 2015) ranging from 10 kg in 1961 to 54 kg in 2017 (Lagos et al., 2018). Between 2009 and 2013, countries like Liberia, Guinea-Bissau, Sierra Leone and Guinea recorded the highest rice consumption rate of more than 90 kg per capita yearly; while Benin, Côte d'Ivoire, Mali, The Gambia and Senegal recorded an annual rate of 50 kg per capita rice consumption. In the meantime, the average calorie due to rice consumption increased from 367 to 384 kcal per capita on a daily basis (Soullier et al., 2020). This makes rice a strategic crop to explore in mitigating food insecurity in the region. Unfortunately, the increase in rice consumption outpaced the production gains (Lagos et al., 2018) causing the West African countries to continue importing millions of tonnes of rice to cover 40% of consumption needs (AGRA, 2018) deficit between production and consumption. Despite the vital role rice is playing in the livelihoods of the West African people, production is greatly threatened by climate-related stresses, notably drought.

2.4 Drought stress and rice production in Africa

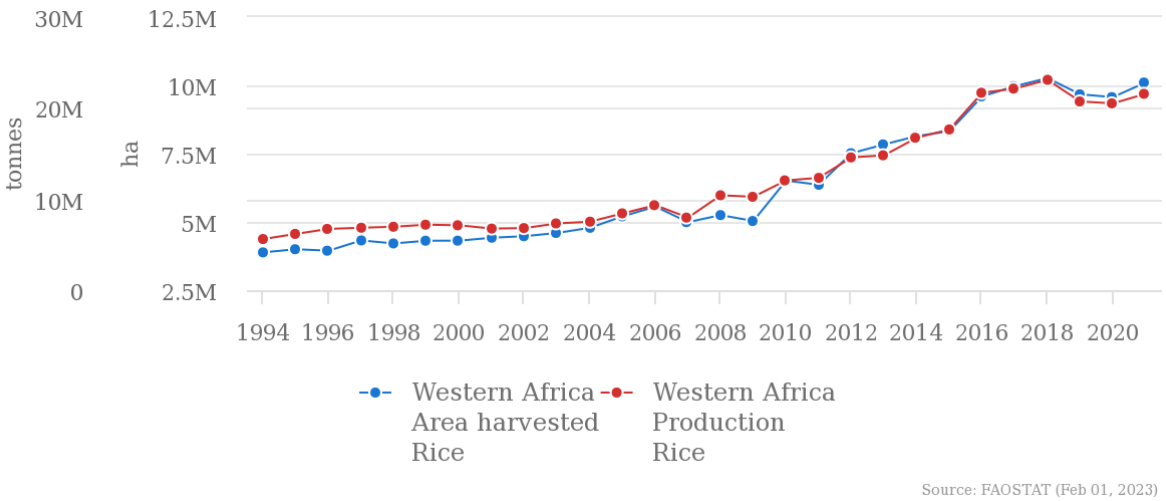


Figure 3. Total paddy rice production, harvested area and yield quantities of rice from 1994 to 2020 in West Africa. *Source: Adapted from FAOSTAT, 2023*

Drought is the most important abiotic stress that constraints rice production (Reynolds et al., 2015), and contributes to yield instability (Lanceras et al., 2004) in Sub-Saharan Africa. Based on the mapping of an abiotic stress study for rice in Africa conducted by van Oort (2018), drought affects 33% of the potential area for rice cultivation in Africa, followed by iron toxicity (12%), cold stress (7%) and salinity stress (2%). The analysis of the soil water-holding capacity conducted by Haefele et al. (2014) revealed that drought represents 19% of constraint for all rice cultivation areas in Africa, being second to low soil fertility (37.6%). Upland ecology represents about 40% of the overall area under rice cultivation in Africa, 38% for rainfed lowland, 12% for irrigated lowland while 6% for deep water and floating rice, and 4% for mangrove swamps. Thus, upland and rainfed lowland rice cultivation occupy about 80% of the overall rice production area in Africa and are most prone to drought stress (Bimpong et al., 2011). Irrigated, upland and rainfed lowland systems are the major rice production systems in West Africa. About 40% of the total area under production is occupied by rainfed lowland production, while irrigated area represents 11.6% and the upland rice system occupies 43% (RICOWAS, 2021). Rainfed lowland and irrigated production systems are the most productive (RICOWAS, 2021), but their vulnerability to the incidence and severity of drought and crop failure are expected to worsen with climate change (Bimpong et al., 2011). Drought stress is more severe in the north of 10º N and less in the south of 10º N in West Africa (van Oort, 2018). Longer dry spells and seasonal droughts are expected to increase in West Africa. Drought stress is equally more severe in the East Africa mainland, while it is less in the northern part of Madagascar. Severe drought risk is predicted in all upland soils across all climate zones in Africa, while limited drought risk is observed in lowlands in most climate zones and moderate to severe risk in a few climate zones (van Oort, 2018).

Drought has a significant adverse effect on the livelihood of rainfed lowland rice producers due to its unpredictable occurrence as a result of the current changes in climate (Serraj et al., 2009). Projections indicate that by 2080, the proportion of arid to semi-arid areas in Africa will increase from 6 to 8% (Jarvis et al., 2010). If nothing is done, significant proportions of African farmlands would become non-arable with a serious impact on agricultural productivity (Ndjiondjop et al., 2018).

2.5 Physiological implications of drought

The susceptibility of the rice crop to drought stress during various stages of its growth is well documented. The major impact of drought stress occurs at the flowering and grain-filling

stages, leading to critical grain yield and quality losses. Singh et al. (2010) observed reductions in many traits including grain yield under drought conditions. Yield decreases are attributable to the detrimental effect of drought on plant height, tiller number, panicle number, leaf area, root length, root depth and thickness, panicle exertion, spikelet fertility, leaf greenness and temperature, days to flowering and maturity, leaf rolling and leaf tip drying (Bocco et al., 2012; Ndjiondjop et al., 2012). Grain yield is reduced by drought through the shortening of the grain filling period (Shahryari et al., 2008) disrupting leaf gas exchange properties, limiting the size of the source and sink tissues, impairing phloem loading and assimilate translocation (Farooq et al., 2009). Drought during the reproductive phase, limits the photosynthetic rate leading to the carbon flux reduction in the reproductive organs, by triggering ovary abortion, and increasing pollen sterility, which results in a reduction in grain quality and yield (Boyer & Westgate, 2004; Centritto et al., 2009).

2.6 Agronomic and morphological characteristics affected by drought in rice crop

Considered as one of the drought-sensitive traits, leaf rolling was closely related to leaf water potential regardless of the time of day and was reported to be controlled directly by leaf water status (Dingkuhn et al., 1999). Several authors have used leaf rolling as a secondary trait selection criterion for assessing the sensitivity of a rice genotype to drought stress (Farooq et al., 2010; Thanh et al., 2006). The leaf rolling alongside with leaf drying and plant recovery are the easiest trait to assess during the evaluation of rice plant for sensitivity to drought stress. These three traits are scored on the scale of 0 to 9, 0 being the best, while 9 being the worst damaged (SES, 2002). For instance, the performance evaluation study conducted on eleven rice genotypes using morphological and physiological traits under drought conditions in Nigeria showed that NERICA 8 and FARO 44 were least affected and had the lowest leaf rolling score (1.33). Five out of the 11 genotypes namely FARO 64, FARO 63, FARO 55 and FARO 52 exhibited the worst leaf rolling scores ranging from 4.0 to 4.33. In general, leaf rolling scores in stressed plants were significantly higher than in non-stressed plants (Umego et al., 2020).

Number of tillers per plant and the panicles per plant are two traits considered by many breeders as yield component traits contributing to various yield increment studies (Reddyyamini et al., 2019), while other authors have reported that high tillering and panicle may not necessarily results into high yield (Venkateshwarlu et al., 2022). The later authors explained that genotypes with higher tiller/panicle number and panicle length must have had a large quantity of chaffy

grains or lower grains weight compared to other genotypes with less tillers/panicles or panicle length but with heavier grains weight. The later can be explained by low spikelet fertility (Venkateshwarlu et al., 2022). Many studies have reported the impact of drought stress on tiller and panicle number under drought stress. The evaluation of eleven rice genotypes under drought conditions resulted in an overall reduction in the number of tillers of the drought-stressed plants for all the genotypes except for NERICA 2 and NERICA 8. These two genotypes produced more tillers than the corresponding control plants and recorded individual stress response index values of 1.09 (NERICA 8) and 1.00 (NERICA 2) respectively. FARO 61 recorded the worst value (0.67) of the individual stress response index (Umego et al., 2020). The evaluation of 30 rice accessions in a greenhouse for tolerance to drought based on morphological and physiological traits under 8-days drought stress showed that panicle number had reduced (5.8-37.9%) in all the accessions except FARO-44, NERI-34, FARO-19 and IK-FS. Significant reductions were registered in 70% of the accessions with IWA-10, FARO-57, IFW-13 and IFW-07 showing the highest reductions (Afiukwa et al., 2016). Under four weeks of drought stress, the rice genotype KS-282 registered the highest panicles number per plant with a 7% reduction as compared to the non-drought conditions but also to other genotypes. The genotypes 99404 and 99417 showed low panicle numbers per plant with approximately a 29% decrease compared to well-watered conditions (Mumtaz et al., 2020).

Plant height reduction is a common feature reported in many studies under drought stress (Gobu et al., 2021; Reddyyamini et al., 2019) but up to date the opinion about whether it contributes significantly to yield increment or not under drought stress is still shared. However, many authors have reported that plant height reduction under drought stress in tolerant rice genotypes to be lesser than in the sensitive genotypes. For instance, the evaluation of eleven rice genotypes under drought conditions showed that the stressed plant exhibited an overall plant height reduction as compared to the plants under non-drought conditions except for NERICA 2, NERICA 4 and NERICA 5 with the corresponding individual stress response index values of 1.25, 1.09 and 1.18. NERICA 8 recorded the tallest height of 51.33 cm under stress conditions and this value is approximately the same for the non-drought plants (Umego et al., 2020). Moreover, the evaluation of 18 upland rice genotypes under drought stress conducted under rainout-shelter showed a reduction in plant height for most of the genotypes under drought stress compared with non-drought conditions. The landrace Ofada 2 had the highest plant height of 173.5 cm under non-drought conditions and 140.5 cm under the drought stress (Anyaoha et al., 2018), while the effect of eight days drought on 30 rice accessions screened in

a greenhouse for tolerance to drought based on morphological and physiological traits showed that only UPIA-1 and AGW-PS did not register plant height reductions whereas 65% of the remaining accessions showed significant reductions in plant height ranging from 4.5 to 23.4%, with the highest reduction registered in FARO-11 and AGW-55 (Afiukwa et al., 2016).

Spikelet fertility reduction under drought stress is considered a direct cause for yield reduction in rice under stress as reported by several authors among which Seyoum et al. (2012) and Swamy et al. (2017). Venkateshwarlu et al. (2022) reported a spikelet fertility reduction of 30 to 40% which is followed by a reduction in grain yield. Other authors also reported that an eight days drought stress effect on 30 rice accessions screened in a greenhouse for tolerance to drought based on morphological and physiological traits registered a significant reduction in the number of grains per panicle in 78% of the genotypes, whereas no effect was observed on FARO-44. The overall reductions varied from 1.9 to 40.1% with IR-119 and IJS-02 recording the lowest value while IFW-13, IHEK, IFW-07, IWA-10 had the highest reduction. Furthermore, spikelet fertility reductions of 3.7 to 20.4% were registered in 70% of the genotypes with the largest reduction in IR-119 and NERI-34 while no effects were noted in AGW-PS, FARO-19 and IWA-10 (Afiukwa et al., 2016).

Thousand-grain weight is considered as one of the most important determinants of rice grain yield and is determined by grain length, grain width and grain thickness (Zuo et al., 2022). The effect of drought stress on 30 rice genotypes evaluated in a greenhouse for tolerance to drought showed that the reduction in 1000 grain weight varied from 0.8 to 14.7% (Afiukwa et al., 2016).

The reduction in grain yield during drought stress at the flowering time is preponderantly attributed to a reduction in spikelet sterility (Liu et al., 2006). Early flowering date and short vegetative phase can play an outstanding role in crop production under terminal drought conditions by minimizing exposure to dehydration during the sensitive flowering and grain filling time (Shavrukov et al., 2017). An absence of correlation between days to flowering and grain yield under drought stress is an indication that drought tolerance shown by some genotypes during the screening is due to the drought tolerance rather than drought escape. But where there is an existing correlation between days to flowering and grain yield under drought stress, is an indication that drought tolerance shown by the genotypes is a result of drought escape than drought tolerance (Venkateshwarlu et al., 2022). Several authors reported flowering time in rice to increase under drought stress compared to non-drought conditions. Anyaoha et al. (2018), for instance, reported during the evaluation of 18 upland rice genotypes

under drought stress revealed that days to flowering increased for most of the genotypes under drought stress. The drought-tolerant checks used in this study namely IR55419-04, IRAT 109, IR84984-83-15-481-B and NERICA 4 had flowered and produced grain under both the stress and non-stress conditions. Most of the landraces and IR 64 (susceptible check) did not flower under drought stress as a result of the severity of stress. Igbemo Red flowered earliest under both water management conditions. Other authors reported that delays in 50% flowering dates were observed in almost all the accessions and ranged from 1 to 21 days during the screening of 30 rice accessions in a greenhouse under drought stress. The least delays were observed in the genotypes IK-PS, IK-FS, IHEK and FARO-44 whereas the longest delays were noted on FARO-11, FARO-19 and IFW-13 (Afiukwa et al., 2016). Drought stress during the flowering time is said to be the most detrimental to grain yield with a huge yield penalty in rice.

The screening of genotypes under drought stress permits to separate drought-tolerant cultivars from drought-sensitive ones while quantifying the yield gaps that exist under non-drought and drought stress conditions. Yield can be selected using the yield-related secondary traits provided that grain yield is having favourable association with its secondary traits. On the other hand, high-yielding genotypes are selected using direct selection of grain yield provided grain yield is highly heritable in the germplasm (Kumar et al., 2008). Under lowland drought screening conditions, a yield penalty of 30% is considered as mild drought, 31 to 65% is considerate moderate drought, while 65 to 85% is considered severe drought (Kumar et al., 2007). Grain yield reduction under drought stress is a common feature reported by several authors (Bhattarai & Subudhi, 2018; Iseki et al., 2014; Luo, 2010; Ndikuryayo et al., 2023; Ndjiondjop et al., 2010; Pantuwan et al., 2002; Sandhu & Kumar, 2017; Yue et al., 2006). Some authors reported that the evaluation of 18 upland rice genotypes under drought stress conducted under rainout-shelter revealed significant variations in the grain yield. Reduced grain yields were observed under reproductive stage drought stress compared to non-drought conditions. Two landraces, Ofada 2 and Ofada 4 recorded the highest grain yield of 508.1 g/m^2 and 470.8 g/m^2 respectively under non-drought conditions whereas ITA 117 had the highest grain yield (152.38 g/m^2) under drought stress. Among the tolerant checks, yield reduction ranged from 50% for IRAT 109 to 79% (IR84984-83-15-481-B) while a 40% reduction was for ITA 117. In summary, the drought-tolerant checks, ITA 117, and Igbemo Red yielded better than most of the landraces and the susceptible check IR 64 under the reproductive stage drought stress (Anyaoha et al., 2018). Furthermore, a four-week drought stress-induced variation in grain yield among 11 genotypes was evaluated under field conditions. The genotype KS-282 ranked

first for the grain yield with a 38% yield reduction compared to the non-drought conditions. On the other hand, 99404 recorded the lowest grain yield with a reduction of 58% under non-drought conditions (Mumtaz et al., 2020).

Grain length, grain width and grain thickness are also important indicators for assessing the appearance quality of rice (Zuo et al., 2022). The outcomes of drought stress on grain length and width of 30 rice genotypes evaluated in the greenhouse depicted that 30% of the evaluated genotypes registered significant reduction ranging from 3 to 9.4% in grain length, whereas 5.9 to 11.3% reduction was observed in grain width in 22% of the genotypes (Afiukwa et al., 2016), while a study conducted under drought stress showed that the overall mean value recorded under non-drought conditions for grain length is 9.55 mm, for grain width (2.238 mm) and grain breadth (1.607 mm), whereas under drought conditions the value recorded for grain length is 9.057 mm, for grain width (2.011 mm) and grain breadth 1.77 mm. The results showed a reduction in grain length and width under the drought stress while a slight increase was observed in grain breadth in almost all the evaluated genotypes (Haider et al., 2015).

2.7 Physiological and biochemical characteristics affected by drought stress in rice

Plant responses to droughts are complex processes involving several changes at the physiological, biochemical and molecular levels (Adnane et al., 2015; Atkinson & Urwin, 2012). Grain yield reductions is a result of leaf gas exchange parameters disruption (Farooq et al., 2009) by limiting the photosynthetic rate which leads to the carbon flux reduction in the reproductive organs, resulting in yield reduction (Centritto et al., 2009). The impairing effect of drought stress on the leaf gas exchange attributes are reported by many works. Some authors reported that four-week drought stress induced a significant reduction in transpiration rate, photosynthetic rate and stomatal conductance among 11 genotypes evaluated under field conditions. Genotype KS-282 displayed a higher transpiration rate, photosynthetic rate and stomatal conductance under drought stress than the other genotypes. KS-282 registered a reduction of 19% in photosynthetic rate, 48% in transpiration rate and 47% in stomatal conductance under drought stress compared to the non-drought conditions. On the other hand, genotypes 99404 and 99417 exhibited under the drought stress a low photosynthetic rate with a 30% reduction, a low transpiration rate with a 67% reduction and a low stomatal conductance with a 68% reduction compared to the non-drought conditions (Mumtaz et al., 2020). Other authors reported that the physiological performance conducted on two contrasting rice varieties

Heena (drought-tolerant) and Kiran (drought-sensitive) showed that the photosynthesis rate decreased by 70% in Kiran and 50% in Heena after the 7 days of drought stress with a net prominent decrease in Kiran than Heena. While comparing these two varieties to their corresponding non-drought plants, both of them exhibited decreased transpiration rate and stomatal conductance under drought and non-drought conditions. A significantly reduced transpiration was observed in Kiran (61%) and Heena (49%) and a decreased stomatal conductance in Kiran (66%) and Heena (63%) under drought conditions. Moreover, a significant decrease in Water use efficiency (WUE) was noticed under drought conditions in both varieties with a 41% higher reduction in Kiran than Heena (Tiwari et al., 2021).

Crop productivity under water deficits is largely dependent on the relative water content (RWC) and osmotic potential of the leaves. A successful growth and development of plants is subjected to elevated RWC and osmotic adjustment (Khan et al., 2017). Thus, drought stress induces the closure of stomata by decreasing transpiration rate and CO_2 uptake (de Souza et al., 2013) leading to the impairment of plant growth and development. A plethora of authors has reported the impairing effect of reduced RWC under drought stress on plant growth and development status. Some of them reported the evaluation of eleven rice genotypes under drought conditions revealed that Faro 44 recorded the lowest rate of water loss by retaining 80% - 100% of its moisture content during the first four hours and holding over 50% of its water after 6 hours. On the contrary to Faro 55 lost 45% of its moisture content only 30 min after and only 26.9% of moisture content remained after 6 hours (Umego et al., 2020). Others registered a significant reduction in leaf water potential ranging from 145 to 4000% during the appraisal of 30 rice accessions under drought stress in a greenhouse. The following landraces IJS-09, IK-FS, IJS-02, IK-PS, IJS-09, IK-FS and IJS-02, IR-119, FARO-44, IK-PS registered relatively lower reductions, whereas genotypes such as AGW-102, AGW-116 and AGW-PS displayed largest reductions (Afiukwa et al., 2016). More authors reported during the evaluation of seven rice cultivars (KDML 105, CT9993, IR58821, BT, IR62266, IR52561 and IR57514) for their tolerance to drought, a significant difference in RWC in the leaf among all the cultivars under severe drought stress conditions. But, under severe drought stress conditions, drought-tolerant genotypes CT9993 recorded 92.9% relative water content in the leaf and BT (92.3%), whereas drought-sensitive genotype IR62266 recorded 86.1% relative water content in the leaf (Bunnag et al., 2013). Furthermore, Khan et al. (2017) reported that two contrasting rice cultivars (drought-sensitive) and PR-115 (drought-tolerant) subjected to

drought stress showed a decrease in relative water content in the leaf by 25% in PR-115 and 33% in Super-7 under 10 days of drought stress conditions.

Chlorophylls are the pigments that transform light into carbohydrates, and in the meantime contribute to maintaining crop yield under stress. A diminished chlorophyll content depressed the light absorbance by meantime enhanced reflectance in the visible and infrared bands. Under various conditions, chlorophyll content has correlated with high yields (Monteoliva et al., 2021). The physiological performance conducted on drought-tolerant rice variety Heena and drought-sensitive variety Kiran after seven days of drought stress showed no effect on total chlorophyll content between the two varieties. But, the ratio of chlorophyll a/b was significantly higher in Heena than in Kiran just after resuming normal watering. Under drought stress conditions, the ratio of chlorophyll a/b registered an increase of 25% in Heena than in Kiran. While comparing the varieties performance to the non-drought plants, a decrease in carotenoid content was registered in Kiran, whereas an increase of 3% was noted in Henna under the drought stress conditions. Anthocyanin content also registered an increase of 20% in Heena than in Kiran under water deficit conditions (Tiwari et al., 2021). Furthermore, the assessment of the effect of drought stress on chlorophyll content in the rice variety BRRI Dhan-24 under drought conditions showed a decrease in chlorophyll-a content by 11.2 to 61.6% from 3 to 12 days after stress initiation, in chlorophyll-b content by 21.4% at 6 days after the starting of the drought stress and a decrease in the ratio of chlorophyll a/b by 18.2 to 58.5% from 3 to 12 days of the stress initiation. Similar decreases of 9.01 to 66.2% and 0.41 to 32.7% were also observed in total chlorophyll and carotenoids contents, respectively between 3 to 12 days of the stress treatment (Nasrin et al., 2020). Other authors reported the same tendency of reduction in chlorophyll content in two contracting rice cultivars. Two contrasting rice cultivars (drought-sensitive) and PR-115 (drought-tolerant) subjected to drought stress showed that chlorophyll content recorded a decrease in PR-115 and no significant change was noted in Super-7 under 10 days of drought stress conditions, whereas a decrease in carotenoids content was observed in both cultivars. On the other hand, anthocyanin content showed an increase of 2.3 times in PR-115 (Khan et al., 2017).

Malondialdehyde (MDA) is a secondary oxidation substance generated by membrane lipids in response to reactive oxygen species (ROS). It can be used as a drought indicator (stress indicator) to evaluate the degree of damage to plasma membranes and the ability of plants to tolerate induced stress (Zhang et al., 2021). During drought stress, there is an excess production

of ROS which increases the quantity of MDA. In rice, several authors have used it to separate the drought-tolerant lines from the sensitive lines as the sensitive lines produced more MDA under the drought stress. Some of these authors evaluated 20 genotypes based on 15% PEG6000 (dissolved in dH_2O) induced drought stress and reported a variation among the genotypes according to their level of tolerance in relation to MDA concentration. Under drought-induced conditions, the average value of MDA in drought-sensitive genotypes was 0.612 nmol/ml, whereas it was 0.511 nmol/ml in moderately tolerant genotypes and 0.39 nmol/ml in drought-tolerant genotypes. Under non-drought conditions, lower mean value of MDA was observed in drought-tolerant genotypes (0.14 nmol/ml), moderate tolerant genotypes (0.168 nmol/ml), and drought-sensitive genotypes (0.177 nmol/ml). Under both drought-induced and non-drought conditions, the average value of MDA is lower in the drought-tolerant genotypes than drought-sensitive ones (Saddique et al., 2020). Furthermore, two contrasting rice cultivars Super-7 and PR-115 subjected to drought stress showed an increase in MDA concentration in the leaf in both rice cultivars under 10 days of drought stress (Khan et al., 2017).

Proline is an amino acid which plays a significant role in plants subjected to different stress conditions. Proline acts like an excellent osmolyte, a metal chelator, a signalling molecule and an antioxidative protective molecule (Hayat et al., 2012). It is known to act as an enzyme protectant under abiotic stress (Hayat et al., 2012). Proline accumulation is commonly produced as a physiological response in several plants as response to drought stress (Mafakheri et al., 2010). In rice, several authors have reported its drought-enhancing role in drought-tolerant genotypes. For instance, during the evaluation of 20 genotypes based on 15% PEG6000 (dissolved in dH_2O) induced drought stress showed variation among the genotypes according to their level of tolerance in relation to proline accumulation. Under drought-induced conditions, the average value of proline content in drought-sensitive genotypes was 8.2 ppm, whereas it was 14.2 ppm in moderately tolerant genotypes and 17.2 ppm in drought-tolerant genotypes. Under non-drought conditions, lower mean value of proline content was observed in drought-tolerant genotypes (8.0 ppm), moderate tolerant genotypes (7.8 ppm), and drought-sensitive genotypes (8.12 ppm). Drought-tolerant genotypes recorded higher proline contents (Saddique et al., 2020). Furthermore, the assessment of the effect of drought stress on proline accumulation in the rice variety BRRI Dhan-24 under drought conditions showed that drought stress induced the increase in proline accumulation in the leaf samples by 1.3 to 10.2 times from 9 to 18 days after the stress initiation (Nasrin et al., 2020), while during the evaluation of

seven rice cultivars (KDML 105, CT9993, IR58821, BT, IR62266, IR52561 and IR57514) for their tolerance to drought, a significant difference was observed in proline accumulation among all the cultivars under non-drought and mild drought stress conditions. But, under severe drought stress conditions, moderately drought-tolerant genotypes (BT, KDML 105, IR52561 and IR62266 produced an equal high amount of proline as in the highly drought-tolerant CT9993 genotype (Bunnag et al., 2013).

2.8 Leaf reflectance characteristics affected by drought stress in rice

Leaf reflectance is generally apprehended through several vegetative indices. Among these vegetative indices, Normalized Difference Vegetation Index known as NDVI (Rouse et al., 1974), Renormalized Difference Vegetation Index known as RDVI (Roujean & Breon, 1995) and Carotenoid Reflectance Indices known as CRI1 and CRI2 (Gitelson et al., 2002) are often used to assess the leaf reflectance under drought stress. Normalized Difference Vegetation Index (NDVI) measures the greenness and health of a vegetation. It is the most used index in stress studies. It is a robust index over a large range of conditions because it combines normalized difference formulation, the use of the highest absorption and reflectance regions of chlorophyll. Nevertheless, it can get saturated under dense vegetation conditions where Leaf Area Index (LAI) becomes high. This index varies between -1 to 1. In general, the green vegetation index varies between 0.2 to 0.8 (Rouse et al., 1974). Under moderate drought conditions a significant positive correlation was observed between NDVI and grain yield, while a relatively weak correlation with grain yield was noted under severe drought conditions. Under severe drought stress conditions, genotypes with high NDVI at early growth stages finished up with lower yield at the later growth stages of the plant. This study concluded that NDVI cannot be suggested in screening genotypes for yield under severe drought conditions (Thapa et al., 2019). Another study demonstrated that under drought stress conditions, there is a trustable relationship between NDVI and grain yield across all the growing stages of the wheat plant. It was shown that under the unsaturated sensor (NDVI < 0.9), NDVI measurements can be used as a tool to select superior wheat genotypes (Naser et al., 2020). A study conducted on rice under normal growing conditions has revealed that NDVI has a significant correlation with the yield at the flowering and grain-filling stages during the wet season, whereas during the dry season it was between panicle initiation and the booting stage. It was shown that NDVI can be used in selecting high-yielding cultivars in rice breeding programs under the tropic. By using portable equipment such as PolyPen RP 410 Photon Systems Instruments, NDVI could be adopted in breeding programs (Phyu et al., 2020). Several of alike results on wheat under

drought stress and few works on rice has shown that it is possible to use NDVI in rice improvement for drought tolerance.

2.9 Nature and mechanisms of rice response to drought stress

The rice responses to drought stress depends on the type of rice genotypes, the severity of the environmental stress, and the interaction between both factors (Atlin, 2003). The combination of these three factors may result in biomass reduction under moderate effects, or complete crop failure when their effects are severe. Because the drought severity varies with rice genotypes, this factor is therefore exploited during breeding for improving varieties under drought stress. Rice response varies according to the growth stage of the plant namely the seedling stage, vegetative and reproductive stages. The reproductive stage is the most sensitive to drought and can result in 100% grain yield loss as a result of a low rate of spikelet fertility/number of filled grains (Centritto et al., 2009; Shahryari et al., 2008).

There are broadly four resistance mechanisms under drought stress: drought escape, drought avoidance, drought tolerance and drought recovery capacity. Drought escape is a mechanism adopted by plants under conditions where there will be a likelihood of water limitation during the late growth stage of the plant. Under such conditions, the plants ensure that they can complete their life-cycle quickly during the short favourable period conditions. Drought escape requires a huge metabolic rate for rapid progressive cell expansion and division. High stomata conductance associated with high gas exchange rates, effective photosynthesis, photo-respiration and low water use efficiency resulted in rapid plant development (Kooyers, 2015; Shavrukov et al., 2017).

Drought avoidance commonly known as the ‘succulent strategy’ is a mechanism by which the plant has a slow growth, associated with high stomata closure, low photosynthesis rate and low cell metabolism. The increased water use efficiency reduces water loss by preparing the plants for the coming drought and change in the environment (Fang & Xiong, 2015; Shavrukov et al., 2017).

Drought tolerance can be defined as the ability of plants to maintain a certain level of physiological activity by regulating and adjusting thousands of genes and various metabolic pathways to reduce the damage resulted from the drought stress (Mitra, 2001). This is manifested by the ability of the plant tissues to maintain a good water status under limited water conditions. This strategy is said to be the most outstanding mechanism for rice breeding.

Selection for drought tolerance can be conducted either by the using of secondary traits or direct yield selection (Atlin, 2003).

The last mechanism for drought resistance is the recovery from drought stress. It functions by maximizing the available water rather than the maximization of the water use efficiency (Lafitte et al., 2003). It functions as long as the wilting point is not reached. It can be measured by using the drought recovery score according to the standard evaluation system of the International Rice Research Institute (SES, 2002).

2.10 Breeding for drought tolerance

Targeted secondary traits have been used for effective breeding for drought tolerance in rice among which stomatal closure (Price et al., 2002; Tiwari et al., 2021), spikelet fertility and delayed flowering (Afiukwa et al., 2016; Lafitte et al., 2003; Pantuwan et al., 2002). Even though breeding for stomatal closure is important because of its association with yield reduction, however, this trait is really effective during the early drought stress stage (Price et al., 2002). Breeding for drought tolerance using seedling vigour and tillering capacity has already been done in wheat improvement (Munns & Richards, 2007) and could also be efficient and cost-effective in rice. It has been demonstrated that the contribution of plant vigour to improve tolerance to drought is possible in rice (Namuco et al., 2009).

The leaf water potential (LWP) is another trait used in breeding for drought tolerance because of its strong correlation with spikelet fertility under drought stress (Lafitte et al., 2003). However, leaf water potential is difficult to use in breeding because it is laborious to measure. Delay in flowering and panicle elongation are another two important traits but their effectiveness in breeding for drought tolerance is seen only during a short drought stress period (Afiukwa et al., 2016; Lamo, 2010). A couple of secondary putative traits used in breeding for drought tolerance have been reported by researchers. Among these traits, leaf rolling is the easiest to score oftentimes using the sharpness of the breeder's eyes, while relative water content, root depth, water use efficiency, osmotic adjustment and root pulling resistance necessitate more complex facilities before their effective use for drought tolerance improvement (Lamo, 2010). The required traits in the rice breeding program for drought tolerance are the rice genotypes showing delay in leaf rolling under drought with quick recovery abilities from stress conditions. Leaf rolling and leaf drying have been used as a criterion in a selection for drought tolerance varieties during the vegetative growth drought stage (Farooq et al., 2009; Thanh et al., 2006; Umego et al., 2020). The number of filled grains

under drought at the reproductive stage drought stress is the most important determinant of yield under drought stress (Yue et al., 2006) and its gives clear information on the genotypic response to stress (Lafitte et al., 2003) and can, therefore, be used for genetic studies on drought tolerance.

Asides the use of secondary traits as breeding criteria for drought tolerance in rice, it has been long believed that grain yield is not suitable as a direct selection criterion in breeding for drought tolerance rice. In the past two decades, researchers at the International Rice Research Institute (IRRI) have demonstrated that grain yield is fit to be used as a direct selection for drought-tolerant rice variety. Hence, grain yield has been used as the main criteria for successful development and release of 17 high-yielding drought-tolerant rice varieties in Asia and Africa (Dixit et al., 2014; Kumar et al., 2014). Some of the drought-tolerant varieties released in West Africa/Africa are FARO44, FARO62, FARO64, FARO65, NERICA1, NERICA4 and NERICA8.

2.11 Application of QTL for the development of rice genotype tolerant to drought stress

Simple sequence repeats (SSR) markers with their advantage of being multi-allelic are still widely used in rice for various purposes including *de novo* QTLs discovery and Genomic-Assisted breeding for QTL introgression. Unlike SSR markers, single nucleotide polymorphism (SNP) markers are essentially bi-allelic and deliver many more markers at low cost per marker with Next Generation Sequencing (NGS) technologies (Rasheed et al., 2017; Yadav et al., 2019). Advantages and disadvantages of Single Nucleotide Polymorphism (SNP) and Single Sequence Repeat (SSR) markers are presented in figure 4.

The use of QTL mapping to unravel the genetic control of traits has significantly increased during the past three decades. On the other hand, the use of this tool (QTL) to uncover the genetic control of drought tolerance traits in rice has tremendously increased during the past 20 years, based on the scientific works that have been published on drought tolerance during this period. See the resumé of published drought-tolerant QTL mapping works since the year 2000 in Selamat & Nadarajah (2021) and Khahani et al. (2021). The motivation behind the identification of QTL is to spot out useful genomic regions to be used to identify the genes responsible for the agronomic and ecological performance of major QTL and their use in Genomic-Assisted breeding (GAB) such as Marker-Assisted Selection (MAS) (Khowaja et al.,

2009). Several advanced statistical methods and models have been developed to improve QTL localization (Veyrieras et al., 2007), but all these approaches have led to QTL locations with a relatively large confidence interval (CI) of about 10 cM (Kearsey, 1998) due to the limited number of individuals and generations used in the experiments. Also, most of the QTL studies are done using bi-parental mapping population which is strongly influenced by the environments, marker sets, choice of parents, population type and size (Van & McHale, 2017; Izquierdo et al., 2018; Lei et al., 2018; Zhao et al., 2018). Moreover, most of the QTL have been identified using mortal generations (F_2, BC_1 or BC_2) with a single genetic background and in a limited number of environments (Table 2). Such QTL cannot be effective in Genomic-Assisted Breeding (GAB) programs since the successful implementation of GAB depends on the effect and consistency of the QTL across several genetic backgrounds and environments (Swamy et al., 2011). One way to confirm the effect of QTL across different genetic backgrounds is to conduct QTL validation experiments which can be time and resources consuming. The advances made in the areas of bioinformatics, biostatistics and genomics (whole genome (WGS) sequencing, SNP discovery, transcriptomics) has led to improve QTL localizations and gene discovery through various novels and improved approaches. QTL mapping through Association mapping of GWAS analysis is one of these novel and improved approaches.

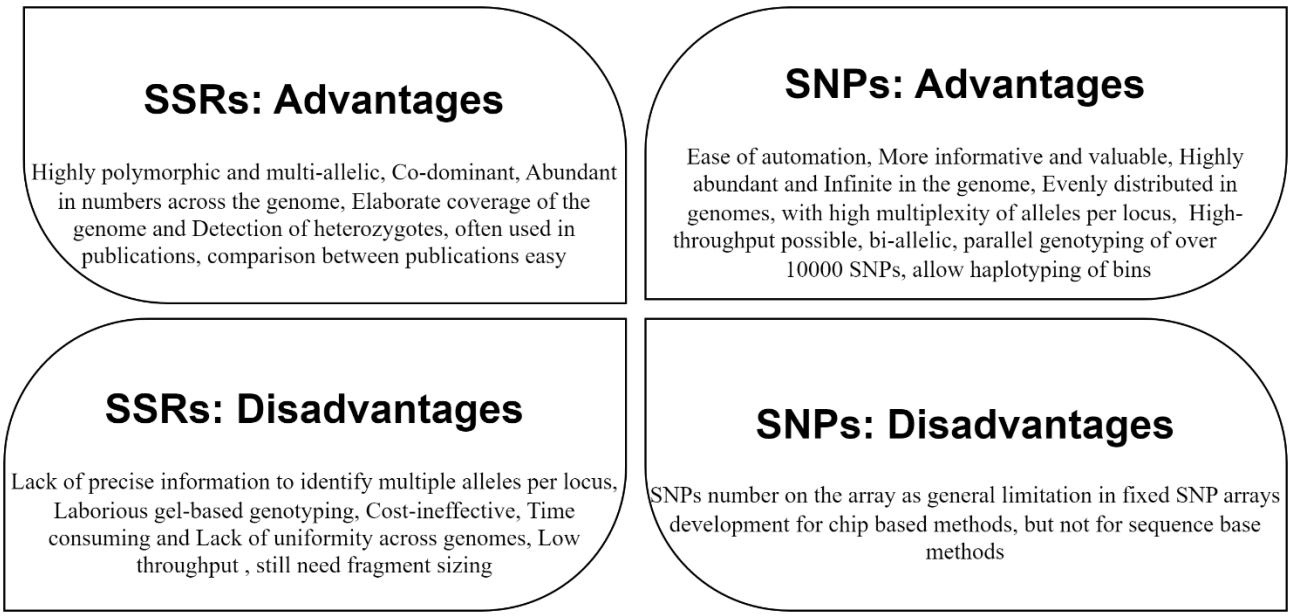


Figure 4. Advantages and disadvantages of Single Nucleotide Polymorphism (SNP) and Single Sequence Repeat (SSR) markers

Table 2. Summary of QTL studies for GY, GW, CHLa, PH, GN, CC, PN, LRS, PL, TWU, HI, TOL, STI, SPP, DRS, CT, RL traits in rice under water deficit conditions

Parents Involved	Mapping Cross type	Number of Markers	Type of Marker	Population Size	Number of QTLs	References
IR20 x Nootripathu	RIL	108	SSR	220	60	Rajurkar et al. (2019)
Cocodrie × Nagina 22 (N22)	F_2	152	SNP, SSR, InDel	190	8	Baisakh et al. (2020)
OM1490 x WAB880-1-38-18-20-P1-HB	BC	20	SSR	229	6	Lang & Buu (2008)
Super Basmati x IR55419-04	F_2	73	SSR	418	21	Sabar et al. (2019)
Bala × Azucena	RIL	163	RFLP, AFLP, BAC, SSR	177	24	Chandra et al. (2006)
Krishnahamsa x CR 143-2-2	RIL	77	SSR	190	19	Barik et al. (2019)
WAB638- 1/BRS-PRIMAVERA	RIL	581	SNP, SilicoDArT	94	28	Adeboye et al. (2021)
Cocodrie x Vandana	F_2	213	SSR, SNP, InDel	187	6	Solis et al. (2018)
Sepidroud x Gharib	RIL	143	ISSR, SSR, IRAP, REMAP	150	30	Gilevaei (2020)
IR 58821 x IR 52561	RIL	399	RFLP, AFLP	148	38	Manickavelu et al. (2006)
Kali Aus x 2*IR64, Kali Aus x 2*MTU1010	BC	134	SSR	300	9	Palanog et al. (2014)
Banglami x Ranjit	F_2	110	SSR	120	11	Verma et al. (2017)
Krishnahamsa x CR 143-2-2	RIL	77	SSR	190	3	Barik et al. (2020)
Swarna x WAB 450-I-B-P-157-2-1	BIL	162	SSR	202	61	Saikumar et al. (2014)
Moroberekan x Apo	BIL	108	SSR, STS	289	45	Sellamuthu et al. (2015)
IR64 x INRC10192	RIL	113	SSR	140	36	Srividhya et al. (2011)
IR62266 x Norungan	RIL	108	SSR	232	79	Suji et al. (2011)
IR64 x Cabacu	RIL	201	SNP	154	12	Trijatmiko et al. (2014)
Danteshwari x Dagad deshi	RIL	162	SSR, HvSSR	122	20	Kumar Verma et al. (2014)
Xiaobaijingzi × Kongyu131	RIL	104	SSR	220	34	Xing et al. (2014)

GY-Grain Yield, GW-Grain Weight, CHLa-Chlorophyll a, PH-Plant Height, GN-Grain Number, CC-Chlorophyll Content, PN-Panicle Number, LRS-Leaf Rolling Score, PL-Panicle Length, TWU-Total Water Uptake, HI-Harvest Index, TOL-Tolerance Index, STI-Stress Tolerance Index, SPP-Spikelet per panicle, DRS-Drought Resistance score, CT-Canopy Temperature and RL-Root Length, BC-backcross, BIL-Backcross Inbred Lines DH-Double Haploids, RIL-Recombinant Inbred Lines

2.11.1 Bi-parental QTL mapping

Bi-parental mapping is the most used QTL mapping approach of important agronomic and quality traits such as grain yield under water deficit. It is useful for mapping large effects and stable QTL and often fails to identify small effects QTL. Bi-parental mapping has been used to identify large effects of drought-tolerant QTL for grain yield, yield-related traits and physiological traits in rice in several works among which Adeboye et al. (2021) and Sangodele et al. (2014) in West Africa. The large effects of drought tolerance QTL are therefore used in MAS to improve the rice yield of susceptible varieties. However, this kind of analysis involving only two parents limits the possibility of verifying QTLs in other germplasms before being applied for marker-assisted selection (MAS). In order to increase genetic gain, there is a need to use Genome-wide Association mapping (GWAS) to identify small effects and more reliable QTLs.

2.11.2 Genome-wide Association mapping of QTL

Moreover, GWAS take advantage of low linkage disequilibrium to achieve better physical resolution. It generates high-resolution mapping because it is based on historical recombination events and the distribution of SNPs across the genome of natural populations (Liu et al., 2016). The GWAS have been used to identify several drought tolerance QTLs for grain yield and yield-related traits in rice (Bhandari et al., 2020; Huang et al., 2010; Pantalião et al., 2016). While GWAS is undoubtedly an efficient tool for plant breeding (Rebolledo et al., 2015) and the identification of small effects QTL, bi-parental mapping of QTL remains a valid option for the identification of large effects QTL. The SNPs identified through GWAS analysis can be used as cofactors to increase the accuracy of the prediction of genomic selection (Pantalião et al., 2016).

2.11.3 Genomic selection

The incorporation of new tools such as Genomic Selection (GS) into crop improvement programs will contribute to increasing genetic gain as it has the ability to select for small effects QTLs. Genomic Selection is an improved version of marker-assisted selection (MAS) which allows an easy selection of promising genotypes. It allows the breeders to select for the promising single plants for field phenotypic selection based on the Genomic Estimated Breeding Value (GEBV). Genomic Estimated Breeding Value (GEBV) is calculated on a training population using a statistical model to estimate all marker effects. The calculated GEBV can just be used to make selection from the validation population without phenotypic

data (Larkin et al., 2019; Sandhu & Kumar, 2017). This makes the selection easier; the breeding cycles become shorter, multiple breeding programs can be conducted simultaneously and the breeding becomes cost-effective (Sandhu & Kumar, 2017). Despite the breakthrough the Genomic Selection is bringing about in crop breeding, MAS is still useful for the introgression of large effects and stable QTL.

The development of rice varieties tolerant to drought with high yield potential and good grain quality is the current challenge that tropical agriculture is facing in the era of fast-changing climate. The effective discovery and mapping of QTL/genes for yield and yield-related traits under drought conditions and assessing the performance of these traits using high-throughput genotyping and high-throughput phenotyping platforms is the first step in developing drought-tolerant varieties. The next step is to incorporate the most promising genes into popular and widely adopted rice cultivars through Genomic-assisted breeding (GAB). In rice, different kinds of fixed SNP chips have been developed to find an association between phenotype and genotype in the process of QTLs mapping (Thomson et al., 2017). These includes 1M SNP chips (McCouch et al., 2010), 6K SNP chips (Yadav et al., 2019; Yu et al., 2014), 44K SNP chips (Tung et al., 2010), 50K SNP chips (Chen et al., 2014; Singh et al., 2015) and 700K SNP arrays (Zhao et al., 2011).

2.12 Gene expression in response to drought stress

Stress signals primarily induced drought defense mechanisms in plants. Abscisic acid (ABA) and reactive oxygen species (ROS) are two endogenous phytohormones known to function as signalling and defense mechanism in drought. Gene expression or induce in transcript abundance regulates ABA biosynthesis pathway and ROS production (Cruz De Carvalho, 2008; Tuteja, 2007). Changes in genes or proteins expression are results of several changes in transcripts or proteins abundance. This highlights the crucial role of transcriptional and post-transcriptional regulation in cellular functions adaptation to the changes in the environment (Ciarmiello et al., 2011). An understanding of the changes in gene regulatory patterns and the underlying mechanisms in different drought-tolerant genotypes, will help develop drought-tolerant rice cultivars under drought stress (Ciarmiello et al., 2011). Recent studies have identified many genes conferring tolerance to rice plant under drought stress.

ABA responsive AP2-like gene 1 (ARAG1) and locus linked to abscisic acid (ABA) are well-known to play an important role in regulation of plant's responses to water deprivation and water use optimization (Selamat & Nadarajah, 2021). *ARAG1, APETALA2/ethylene-responsive*

element binding protein 148 and *AP2/EREBP-type transcription factor OsAP211* are family of genes that expressed in inflorescences, roots, immature plant embryos and seed germination phase (Zhao et al., 2010) through the regulation of abscisic acid sensitivity and transcription factor activity. *ABA responsive AP2-like gene 1* involved in the response to abscisic acid stimulus and mediated signalling as well as cold and drought stresses responsive pathways (Zhao et al., 2010).

CALCINEURIN B-LIKE PROTEIN-INTERACTING PROTEIN KINASE 12 (OsCIPK12) intervenes in regulating protein serine/threonine kinase activity (Benjamins et al., 2001), in phosphorylation of proteins' amino acids, ATP and manganese ion binding as well as signal transduction among cells. The overexpressing of *OsCIPK12* under drought stress in transgenic plants has resulted in higher accumulated of proline and soluble sugars contents than the wild type, and has significantly improved tolerance to drought in japonica rice (Xiang et al., 2007).

OsGRETCHENHAGEN3-2 (OsGH3-2) influences plant responses to certain stimulus such as light stimulus and auxin stimulus. This gene plays an important role in tillering, dwarfism, leaf size, crown and hair roots development as well as cold and drought tolerance by regulating indoleacetic acid metabolic process, auxin homeostasis, acid-amino acid ligase activity, indole-3-acetic acid amido synthetase activity and negative regulation of auxin mediated signalling pathway. *OsGH3-2* gene is expressed in the anther, inflorescence, seed viability, seed longevity and roots, abscisic acid content and internode length. It was reported that *OsGH3-2* of GH3 gene family modulates endogenous abscisic acid (ABA) and free indole-3-acetic acid (IAA) homeostasis and improves drought tolerance in rice (Du et al., 2012).

The Rice WRKY gene13 (*OsWRKY13*) gene regulates an opposite cross talk between bacterial infection and drought stress through sequence-specific cis-elements binding on the promoters of the drought-resistance-related gene such as *SNAC1 (for STRESS RESPONSIVE NO APICAL MERISTEM, ARABIDOPSIS TRANSCRIPTION ACTIVATION FACTOR1/2, CUP-SHAPED COTYLEDON)* and *WRKY45-1* (defense-responsive gene) (Qiu et al., 2008; Xiao et al., 2013). *OsWRKY13* gene intervenes in the regulation of salicylic acid mediated signalling pathway and negatively regulates transcription factor activity.

APETALA 2 domain 39 (OsAP2-39) negatively regulates ethylene biosynthetic process and induces response to water deprivation and cold stresses. The overexpression of *OsAP2-39* has led to reduction in number of seeds and biomass in the transgenic rice genotypes. The *OsAP2-39* directly controlled Elongation of Upper most Internode (EUI) and OsNCED-1 through both in vivo and in vitro analysis (Yaish et al., 2010).

Calcium dependent protein kinase (OsCDPK7) is a protein kinase which regulates the response to abiotic stresses by inducing response to abiotic stimulus, response to auxin stimulus, response to cytokinin stimulus, response to gibberellin stimulus, regulating abscisic acid mediated signalling as well as calcium-mediated signalling. *OsCDPK7* is a positive regulator involved in salt and drought stresses tolerance in rice (Saijo et al., 2000).

The *basic leucine zipper (b-ZIP) transcription factor 72* are regulatory proteins involved in regulating abscisic acid mediated signalling, abscisic acid stimulus, leaf senescence, seed germination and gene expression in tolerance to drought. The *b-ZIP* plays a vital role during plant developmental stages and provides resistance to plants towards abiotic stresses (Yang et al., 2019). The overexpression of *OsbZIP72* transgenic rice plants revealed ABA hypersensitivity and enhanced expression of ABA response genes as well as drought-tolerant genes. The *OsbZIP72* genes induces expression of drought tolerance in rice through ABA signalling (Lu et al., 2009).

2.13 Type of gene actions controlling drought tolerance

Gathering necessary information about the genetic effects of the agronomic and morphological traits is important to formulate effective breeding strategies for drought-tolerant rice varieties development (Gaoh et al., 2020). The knowledge of nature and different types of gene action is crucial for achieving genetic improvement in rice for drought tolerance. Despite several years of studies on the type of gene action controlling rice agro-morphological traits, there is still not a consensus on the type of gene action that controls these characteristics because the results of the reported studies depend largely on the trial environments and the source of the genetic materials used in the trials. A genetic study has been conducted to determine the inheritance and gene action that control drought tolerance in five segregating generations using interspecific crosses involving two parents, F_1, F_2 and F_3 through the generation mean analysis. The results revealed that additive effects were more predominant than non-additive effects for pollen viability and seed set in the crosses. The results also showed that additive effects for filled grains were predominant under both drought stress and non-drought conditions than the non-additive effects. On the other hand, high heritability estimates were recorded for leaf rolling under drought stress, implying that additive effects were more important (Lamo, 2010). During the study of the genetic effects of morphological and physiological traits that control drought stress tolerance, it was discovered that both additive and non-additive genetic effects were predominant in controlling these traits (Efisue et al., 2009).

CHAPTER 3 RESEARCH METHODOLOGY

3.1 Presentation of the study areas

The field screening and the screenhouse experiments were carried out at the Crops Research Institute of the Council for Scientific and Industrial Research (CSIR-CRI) in Fumesua-Kumasi, Ghana. Fumesua is located between 6.7º 09′ N, and 1.5º 72′ W at 15 kilometres from the centre of Kumasi (Figure 5). The area is part of the Ashanti region, a deciduous forest agro-ecological zone characterized by a bi-modal rainfall pattern. The major season is between April to July, while the minor season spans from September to October. The average annual rainfall is 1300 mm while the average temperature is 26.3°C throughout most of the year with the highest being 28.0°C between March and April. Lower temperatures of 26.1°C are experienced during the major season in June and July. The experiments were conducted in the field of the Rice section and the biotechnology laboratory of the CSIR-CRI.

The greenhouse screening experiment was conducted at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen (JLU), Germany. Transcriptome (gene expression) analysis was conducted in growth chambers at the School of Biological, Earth and Environmental Sciences of University College Cork (UCC), Ireland.

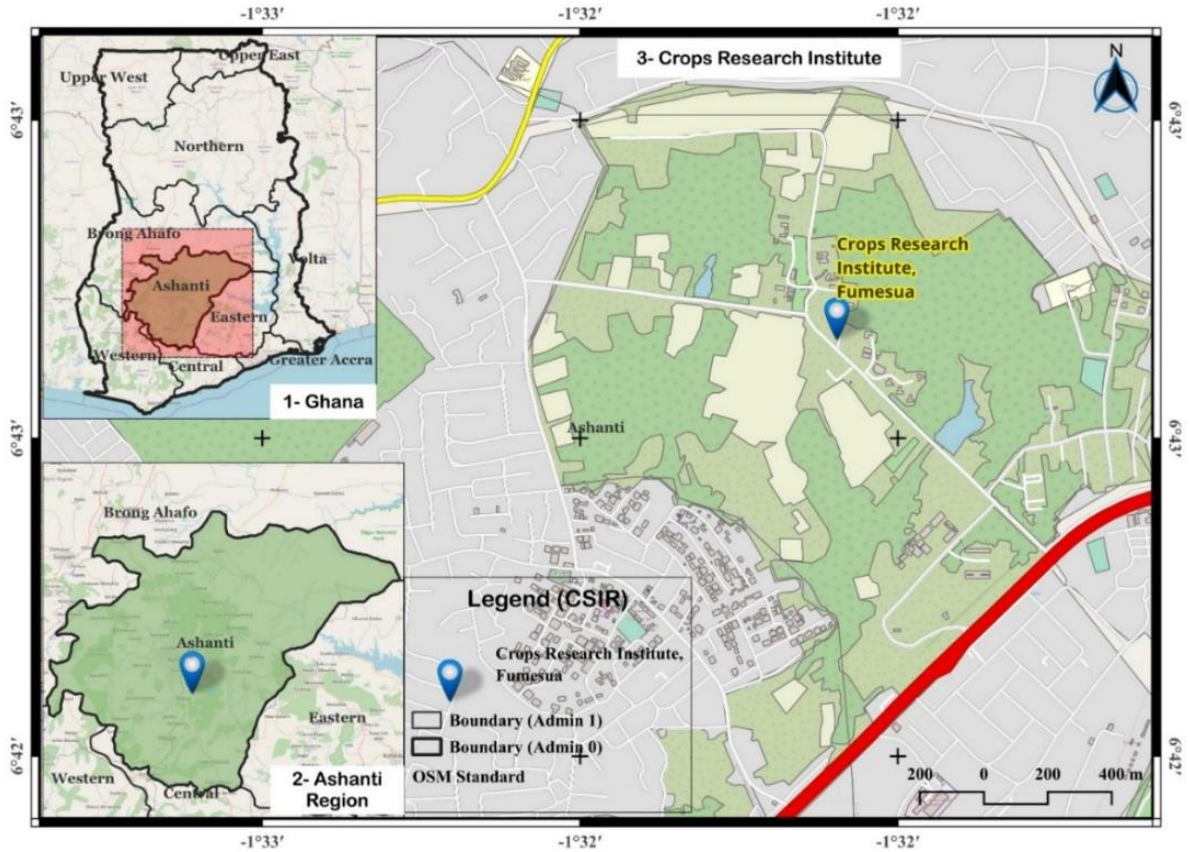


Figure 5. Crops Research Institute of the Council for Scientific and Industrial Research (CSIR-CRI) in Fumesua-Kumasi, Ghana.

3.2 Climate data

The climate data such as rainfall data, temperature and relative humidity during crop growing seasons of the field experiment were collected from the meteorological centre of Crops Research Institute of the Council for Scientific and Industrial Research (CSIR-CRI) in Fumesua-Kumasi, Ghana.

3.3 Equipment

The field screening was done under the rainout shelter facilities, while the greenhouse screening was done in a greenhouse facility. The screening of the crosses progenies was done in the screenhouse. The soil volumetric water content (%, v/v) was measured by the soil moisture TRIME-PICO TDR (IMKO, Ettlingen, Germany). The leaf gas exchange attributes were measured using the LI-600 portable photosynthesis meter (LI-COR Inc., Lincoln, NE, USA). Chlorophyll content was measured using CCM-200plus Chlorophyll Content Meter (Opti-Sciences, Inc., 8 Winn Avenue, Hudson NH 03051). Satake moisture meter (model MOISTEX SS7, United States of America) was used to measure the moisture content of the rice grain. Leaf reflectance parameters were measured using the PolyPen RP 410 Photon Systems Instruments, Průmyslová 470, 664 24 Drásov, Czech Republic. All the biochemical and molecular analysis was done using the laboratory facilities.

3.4 Methodology

3.4.1 Combination of phenotyping and SNP markers-based drought-tolerant QTLs for the selection of drought-tolerant genotypes under field conditions

3.4.1.1 Field Evaluation of hundred rice germplasm for yield and yield related traits

This experiment took place in the long dry season (November - March) of 2021/2022 season using 100 genotypes of rice collected from CSIR-CRI rice genebank. The 100 genotypes used are presented in Annex 3. The genotypes were cultivated under the upland irrigated system. Among these 100 genotypes, APO (APO is used worldwide as a drought-tolerant check). APO displays a reduced water use alongside with limited biomass loss under drought stress conditions. Results showed that the strong antioxidant power of APO gives it the ability to maintain a stable grain yield under drought stress (Melandri et al., 2021) and UPLR17 (which is a local drought-tolerant variety) were used as tolerant checks. Direct seeding was done on 25/09/2021 and following a 10 x 10 alpha-lattice design with three replicates in a block within the replicate design. The plot size was 1m x 1m with row and hill spacing of 20 cm. All lines

were tested following two water managements in this experiment: normal irrigation (non-drought) and simulated water deficit conditions by stopping irrigation (drought stress) from active vegetative stage to reproductive stages. The drought stress was done during the vegetative stage before maximum tillering to the booting stage (reproductive stage). The stress started 50 days after sowing and was maintained by stopping irrigation for 24 days starting from 13/11/2021 to 06/12/2021. After the drought stress period, the stressed plants were subjected to 5 days of drought stress throughout the late stages of rice. During the stress period where the rainout shelter was placed, it was ensured that the plants have water through sprinkler irrigation. This is in accordance with the total water required including irrigation and precipitation needed for upland rice cultivation (750 mm to 1400 mm) according to Kato & Katsura (2014). We completed this recommended rainfall with sprinkled irrigation every two days when the rain doesn't fall in order to keep the soil moisture. The data on drought sensitivity trait and chlorophyll content were collected when at least 70% of the genotypes showed severe leaf rolling (SES, 2002) and the average soil moisture content is below 5%. The soil moisture TRIME-PICO TDR (IMKO, Ettlingen, Germany) was used to measure the soil volumetric water content (%, v/v) at the depth of 10 cm of the soil surface on 30/11/2021. The fields were fertilized with N90, P60 and K60 kg/ha applied by hand broadcasting. N was applied at 3 increments. The first third of N and the full amounts of P and K were applied during final land preparation using the NPK fertilizer. The second and third amounts of N were applied at the tillering stage and at panicle initiation, respectively, using the urea. Weeds were controlled using a selective herbicide Mega super (bispyribac-sodium 400g/L) at the rate of three litres per hectare at the initial stage and prior to flowering. Insects were controlled using Sunpyrifos 48% ec (chlorpyrifos-ethyl) at the rate of two litres per hectare at the flowering stage. Experiments were harvested when 80-85% of the grains per panicle became straw (yellow) coloured (IRRI-International Rice Research Institute, 2009).

3.4.1.2 QTL profiling

The DNA extraction, quality and quantity analyses, the genotyping and QTL profiling were done using the service of INTERTEK (ScanBi Diagnostics AB, Alnarp-Sweden), Sweden. Leaf samples collection and preparation were done in the Lab at CSIR-CRI, Ghana. Leaves were collected at 28 days after planting on three biological replicates using blotter (tissue) papers protocol. Three leaf discs (6 mm in diameter) of samples were collected in 96-well plates and oven-dried for 24 hours at 50 °C. The samples were then packaged and shipped to INTERTEK, Sweden, for genotyping and analysis. The QTL profile data were then sent back to the Lab at

CSIR-CRI, Ghana, where this information was used to assist in the selection of the genotypes with tolerance to drought. The information on QTLs (*qDTY1.1, qDTY2.2, qDTY12.1*) and SNPs used are summarized in Table 3.

Table 3. The information on QTLs and SNPs used for the genotyping of 100 genotypes screened under drought stress in 2021 at CSIR-Crops Research Institute, Kumasi, Ghana.

Target QTL	Intertek SNP ID	Chromosome number	Position (bp)	Favorable allele	Unfavorable allele
DTY1.1	snpOS00400	1	38081544	G	C
DTY1.1	snpOS00402	1	39014751	A	G
DTY1.1	snpOS00408	1	39610271	G	T
DTY2.2	snpOS00412	2	1050171	C	A
DTY2.2	snpOS00413	2	2542883	T	A
DTY2.2	snpOS00414	2	4871846	A	G
DTY2.2	snpOS00415	2	6267235	C	T
DTY12.1	snpOS00483	12	17393569	G	C
DTY12.1	snpOS00484	12	17396363	A	G

3.4.1.3 Phenotyping

The panicles were hand-harvested and manually threshed to obtain the paddy. Grains were sun-dried to approximately 14% moisture content before collecting the data. Satake moisture meter (model MOISTEX SS7, United States of America) was used to measure the moisture content of the various samples of the rice grain.

- **Grain yield**

The paddy yield per plant was recorded at 14% standard moisture content on five randomly selected plants per plot per replicate after threshing. Each plot final grain weight was then adjusted to 14% moisture content (adjusted grain weight). The average weight of the three replicated plots was retained as each germplasm grain yield in grams.

$$Adjusted\ grain\ weight\ = \frac{Harvested\ yield\ \times\ Standard\ moisture\ content}{Harvested\ moisture\ content}$$

- **Grain yield-related traits**

Days to 50% flowering (DTF) were recorded when 50% of the plants on each plot have shown flowering. The average of the three replicates was recorded as DTF per germplasm. Other grain yield-related traits such as plant height (PH) in cm, number of effective tillers (TN), panicle length (PL) in cm and hundred grains weight (GW) in grams were recorded on five randomly selected plants per plot per replicate at physiological maturity of the rice crop. The grain length (mm) and grain width (mm) were recorded on five randomly selected grains per plot per replicate after threshing at 14% or less moisture content.

- **Drought Sensitivity (DRS)**

Drought Sensitivity (DRS) was measured by leaf rolling and leaf drying during drought stress period and spikelet fertility at the physiological maturity stage using 0 to 9 points scale.

Leaf rolling was scored as follows: 0 (Leaves healthy), 1 (Leaves start to fold (shallow)), 3 (Leaves folding (deep V-shape)), 5 (Leaves fully cupped (U-shape)), 7 (Leaves margins touching (0-shape)), and 9 (Leaves tightly rolled (V-shape)).

Leaf drying was scored as follows: 0 (No symptoms), 1 (Slight tip drying), 3 (Tip drying extended up to ¼), 5 (One-fourth to ½ of all leaves dried), 7 (More than 2/3 of all leaves fully dried), and 9 (All plants apparently dead, length in most leaves fully dried).

The scoring of spikelet fertility was as follows: 1 (More than 80%), 3 (61-80%), 5 (41-60%), 7 (11-40%), and 9 (Less than 11%), fertile. The percentage of spikelet fertility was recorded on five randomly selected plants per plot per replicate at the physiological maturity of the rice crop

by counting the well-filled and unfilled grains to calculate the percentage of the well-filled grains.

- **Plants Recovery from Drought (DRR)**

Scores are taken after 10 days following irrigation soaking as 1 (90-100% of plants recovered), 3 (70-89%), 5 (40-69%), 7 (20-39%), and 9 (0-19%). Ten days after resuming watering, the number of plants that recovered out of the total number of rice plants per plot per replicate was counted and the percentage of recovered plants was calculated per plot per replicate and a score was assigned.

- **Chlorophyll Content**

The chlorophyll content was estimated using Chlorophyll Content Index (CCI) on three randomly selected plants per plot per replicate using CCM-200plus Chlorophyll Content Meter (Opti-Sciences, Inc., 8 Winn Avenue, Hudson NH 03051) during drought stress period at the booting stage of the rice plants. The data were collected one time on 2nd fully expanded leaves.

3.4.2 Physiological and biochemical characterization of selected West Africa rice genotypes in response to drought stress under greenhouse conditions

3.4.2.1 Plant materials

A subset of 14 diverse West Africa rice genotypes sourced from Crops Research Institute (CSIR-CRI), Kumasi, Ghana rice genebank was used for this experiment. These 14 genotypes were selected out of 100 genotypes screened against drought stress under rain-out shelter at CSIR-CRI from September 2021 to March 2022. These genotypes were selected based on relative values of grain yield-related traits using relative grain yield as primary selection criteria for a genotype tolerance to drought. The genotypes consisted of seven putative drought-tolerant genotypes (Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65) and CRI-Enapa (G11)) and seven putative drought-sensitive genotypes (ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78)). This experiment was conducted at the Institute for Agronomy and Plant Breeding of Justus-Liebig-Universität Giessen, Germany.

3.4.2.2 Drought stress treatment at vegetative stage and reproductive phases

Twelve-day-old seedlings were transplanted into pots filled with ready topsoil for potting on 24/08/2022. The top soil is prepared following the mixture of 30 litters of organic soil plus 10

litters of ceramic soil plus 160 grams of slow-release fertilizer (15-9-11+2MgO+TE) following Wu et al. (2021). The humidity of the soil in the pots was measured every two days during the drought stress phases and once a week during the whole experiment using the soil moisture meter (TRIME-PICO TDR, IMKO, Ettlingen, Germany). Thirty-four days after transplanting (the vegetative stage before maximum tillering), drought stress was applied on 26/09/2022 by withholding the water until the plants showed clear symptoms of drought stress on 22/10/2022 (27 days since watering was withheld). At the reproductive stage (when the plants were flowering), drought stress was applied on 01/12/2022 by withholding the water until the plants showed clear symptoms of drought stress on 16/12/2022 (16 days since watering was withheld). Non-drought plants were kept under well-watered conditions at 100% field capacity (FC). The 100% FC of our soil was 57.75 vol/vol, while the wilting point was 10.66 vol/vol. All the rice genotypes were grown in the greenhouse with an average temperature between 25 to 30^{o}C with 70% relative humidity with the light on from 8 a.m. to 4 p.m. A completely randomized block design (RCBD) with 6 replications was used. Each replication contained both the non-drought (including 14 genotypes) and the drought stress (including 14 genotypes) plates. Each plate contained four of five litter pots. The replications 4, 5, and 6 were used for destructive samplings at vegetative and reproductive stages, therefore each pot contained two plants. The replications 1, 2 and 3 were used for biomass estimation and therefore contained one plant per pot and were left untouched till full maturity. Pots were watered every three days with the same amount of water per pot throughout the rice growing cycle except the drought stress pots during the stress periods at vegetative and reproductive stages.

3.4.2.3 Data collection

- **Number of tillers**

The number of tillers was counted on all the 14 genotypes at the end of the vegetative stressed phase on each plant per treatment (non-drought and drought stress) per genotype and per replicate.

- **Days to flowering**

Days to flowering (DTF) were recorded when the first panicle on each plant per pot has shown flowering.

- **Leaf drying score**

Leaf drying score was recorded on all 14 genotypes at the end of the reproductive stressed phase on each plant per treatment (non-drought and drought stress) per genotype and per replicate.

Leaf drying is scored as follows: 0 (no symptoms), 1 (slight tip drying), 3 (tip drying extended up to ¼), 5 (one-fourth to ½ of all leaves dried), 7 (more than 2/3 of all leaves fully dried), and 9 (all plants apparently dead, length in most leaves fully dried) (SES, 2002).

- **Biomass yield**

The aboveground biomass (grains + stover) was harvested and weighed to record the biomass weight on all the 14 genotypes at the maturity stage on each plant per treatment (non-drought and drought stress) per genotype per replicate. The average of the six replications was recorded as aboveground biomass yield (Bio).

- **Grain yield**

The panicle was harvested at full maturity stage, manually threshed and weighed to record the grain weight on all the 14 genotypes at the maturity stage on each plant per treatment (non-drought and drought per genotype per replicate. The average of the six replications was recorded as grain yield per plant (GYP).

- **Leaf gas exchange parameters**

Throughout the drought stress period, leaf gas exchange attributes were measured using the LI-600 portable photosynthesis meter (LI-COR Inc., Lincoln, NE, USA). The medium portion of the 2nd fully expanded leaf of each genotype per treatment (non-drought and drought) per replicate was used to measure the following physiological parameters between 9 AM and 1 PM: stomatal conductance (gsw) in mol m^{-2} s^{-1}, transpiration rate (E) in mol m^{-2} s^{-1}, electron transport rate (ETR) in µmol m^{-2} s^{-1} and the quantum yield of fluorescence (PhiPS II). The leaf gas exchange parameters were measured 4 times respectively on 5, 11, 18 and 27 days on the same rice plant per genotype during the vegetative drought stress period noted as 5D, 11D, 18D and 27D, respectively. While, during the reproductive drought stress period, the leaf gas exchange parameters were measured on 14 days after the stress initiation on the same plant used at vegetative stages measurements.

- **Leaf reflectance parameters**

Throughout the drought stress period, leaf reflectance parameters were measured using the PolyPen RP 410 Photon Systems Instruments (Czech Republic). The medium portion of the 2nd fully expanded leaf of each genotype per treatment per replicate under both under non-drought and drought stress conditions were used to measure the following parameters between 1 PM and 4 PM: normalized difference vegetation index (NDVI) (Rouse et al., 1974), renormalized difference vegetation index (RDVI) (Roujean & Breon, 1995) and carotenoid reflectance

indices (CRI1 and CRI2) (Gitelson et al., 2002). The CRI 1 and 2 were calculated to estimate carotenoid concentration in relation to chlorophyll concentration. The leaf reflectance parameters were measured 4 times respectively on 5, 11, 18 and 27 days on the same rice plant for each genotype during the vegetative drought stress period noted as 5D, 11D, 18D and 27D, respectively. While, during reproductive drought stress period, the leaf reflectance parameters were measured two times on 14 days after the stress initiation on the same plant used for measurements at vegetative stage.

The leaf reflectance parameters were estimated using the following parameters:

$$NDVI = \frac{RNIR - RRED}{RNIR + RRED}$$

$$RDVI = \frac{R780 - R670}{\sqrt{R780 + R670}}$$

$$CRI1 = \frac{1}{R510} - \frac{1}{R550}$$

$$CRI2 = \frac{1}{R510} - \frac{1}{R700}$$

Where, R stands for a given wavelength reflectance; NDVI stands for normalized difference vegetation index; RDVI stands for renormalized difference vegetation index; CRI1 and CRI2 stand for carotenoid reflectance indices 1 and 2; RNIR stands for a wavelength reflectance in near infrared; RRED stands for wavelength reflectance in red.

- **Leaf relative water content**

Top-most fully expanded leaves were sampled after 27 days of drought stress on each plant per genotype per treatment both under non-drought and drought stress conditions on replicates 4, 5 and 6. The sampling proceeded quickly. The leaf samples consisting of mid-leaf sections of about 1×7 cm were cut with scissors from each leaf. Each sample was placed in a pre-weighed airtight 15 ml conic tubes (Falcon®). Tubes were immediately placed on ice. The tubes were weighed to obtain leaf sample weight (W), after which the sample was immediately hydrated to full turgidity for 4 h under normal room light and temperature. Leaf samples received water into the tube to a level of 1-2 cm after which the tube is capped. After hydration, the samples were taken out of the water and were well dried of any surface moisture quickly and lightly with tissue paper and immediately weighed to obtain the fully turgid weight (TW). Samples were then oven dried at 80^{o}C for 24h and weighed (after being cooled down in a desiccator) to

determine the dry weight (DW). All weighing was done to the nearest mg. The leaf relative water content (RWC) was calculated for each genotype following this formula:

$$RWC\ (\%) = \left[\frac{(W - DW)}{(TW - DW)}\right] \times 100$$

Where,

W - Sample fresh weight

TW - Sample turgid weight

DW - Sample dry weight.

- **Determination of Malondialdehyde concentration**

The Malondialdehyde (MDA) concentration was estimated in seven out of the 14 genotypes namely G100, G99, G2, G11, G22, G53 and G78. These genotypes were selected based on the data obtained from the leaf gas exchanges and leaf reflectance parameters as well as relative water content and tillers number.

The samples (leaves + shoots) were harvested and put in liquid nitrogen and stored thereafter at -80 °C. The MDA concentration was estimated following the modified protocol of (Hodges et al., 1999). Plant materials were homogenized in liquid nitrogen using a chilled mortar and pestle and 100 mg samples were weighed and put into 2 ml tubes. One and half (1.5) ml of 0.1 % Trichloroacetic acid (TCA) was added to the powder and vortexed vigorously. The extraction tubes were then put into the ultrasonic cleaner filled with icy water and the ultrasonication was run for 5 minutes and the extraction tubes were thereafter centrifuged at 14000 × g for 15 minutes at 4°C. The ultrasonication step is meant to improve the extraction of MDA from the samples. The supernatants were transferred into new tubes and centrifuged for 2 minutes at 14000 × g at 4°C to make the solution clear. Two aliquots of 500 µl extracts were pipetted into 14 ml Falcon-Tubes. Five hundred (500) µl RS I (0.01 % (v/v) BHT in 20 % TCA (v/v)) was added to one aliquot and 500 µl RS II (0.65 % TBA (2-Thiobarbituric acid) solved in RS I (w/v)) to the other one and both vortexed vigorously. Five hundred (500) µl of 0.1% TCA was used as a blank. The samples were heated at 95°C for 30 minutes in the water bath and the reaction ended up on ice for 5 minutes. The samples were transferred to 1.5 ml tubes and centrifuged at 8000 × g for 10 minutes at 4°C. Two analytical replicates of a 100 µl per sample were added to the 96-well microplate, respectively. A blank of 100 µl of 0.1 % TCA was added to the microplate in two analytical replicates. This blank is different from the 0.1% TCA added at the beginning. Absorbance was measured at 440, 532 and 600 nm.

The calculation of MDA concentration is as follows:

$$MDA\ equivalent\ \left(\frac{nmol}{ml}\right) = \left[\frac{(A-B)}{44.857}\right] \times 10^3$$

$$A\ =\ [(Abs\ 532RSII\ -\ Abs\ 600RSII) -\ (Abs\ 532RSI\ -\ Abs\ 600RSI)]$$

$$B\ =\ [(Abs\ 440RSII\ -\ Abs\ 600RSII) \times\ 0{,}0571]$$

Where, RSI and RSII stand for reagent solution 1 and 2, respectively; Abs stands for absorbance; A and B stand for two data values calculated based on the absorbance at different wavelength in RSI and RSII.

- **Determination of Proline concentration**

The proline concentration was estimated in seven out of the 14 genotypes namely G100, G99, G2, G11, G22, G53 and G78. These genotypes were selected based on the data obtained from the leaf gas exchanges and leaf reflectance parameters as well as relative water content and tiller number. The determination of the proline concentration was done according to Bates et al. (1973) as modified by Frimpong et al. (2021). Each rice germplasm shoots and leaves samples were crushed to powder in liquid nitrogen and stored thereafter at -80 °C. Fifty to 100 mg of plant samples were weighed in chilled 2 ml tubes. Quickly 1.5 ml of sulfosalicylic acid dihydrate 3% was added to the tube. The samples were vortexed vigorously and centrifuged at 12000 × g for 10 minutes at 4°C, and the supernatants were transferred into the new 1.5 ml tubes. Glass test tubes were prepared and 500 µl of the samples' extracts were added in the test tubes. Subsequently, 500 µl of acetic acid and 500 µl ninhydrin reagent (2.5%) (2.5 g ninhydrin was dissolved in 60 ml of Glacial Acetic acid and 40 ml of 6M phosphoric acid) were added. Next, the samples were incubated at 100^{o}C for 60 minutes and the reaction was terminated in ice. Then, 1.5ml of toluene was added to the test tubes containing the reaction mix (1:1 ratio to reaction mix) and vortexed vigorously. The solution is left at room temperature for 30 minutes until the separation of the two phases. Three analytical replicates of a 200 µl per sample of chromophore containing toluene (upper phase) were added to the 96-well microplate, respectively. A blank of 200 µl of toluene was added to the microplate in three analytical replicates. Absorbance was measured at 520 nm. All the solutions preparation was done under the hood. The proline concentration of each sample was determined using the standard curve. A proline standard solution of 50 mg/L was prepared in 3% sulfosalicylic acid dihydrate using L-proline and was diluted from 0 to 50 ppm to generate the standard curve (Table 4). All the proline standard solutions followed the same procedure as plant samples.

Table 4. Proline standard solutions from 50 mg/L stock solution

Concentration and volume	Standard solution stock							
Required concentration (mg/l)	0	5	10	20	25	30	40	50
Volume of 50 mg/l stock solution (ml)	0	0.1	0.2	0.4	0.5	0.6	0.8	1
Volume of sulphosalicylic acid 3% (ml)	1	0.9	0.8	0.6	0.5	0.4	0.2	0
Total Volume (1 ml)	1	1	1	1	1	1	1	1

3.4.3 Transcriptome analysis of a set of contrasting selected West Africa rice genotypes in response to drought stress

3.4.3.1 Plant materials

A subset of 4 genotypes were selected out of 100 genotypes screened against drought stress under rain-out shelter at CSIR-CRI from September 2021 to March 2022. The genotypes consisted of two drought-tolerant genotypes, APO (G99) and CRI-Enapa (G11), and two drought-sensitive genotypes, ART132-35-1-1-B-B (G36) and CRI-AMANKWATIA (G1). This experiment was conducted at the School of Biological, Earth and Environmental Sciences (BEES), University College Cork (UCC), Cork, Ireland from June to December 2023.

3.4.3.2 Evaluation of the rice genotypes in pots under drought stress

Seven-day old rice seedlings were transplanted into 500 ml transparent pots. The pots were filled with ready to use compost soil of about 400 g. At the beginning of the experience, 100 ml of water was added to each pot. Three seedlings were planted per plot. The plots were placed in the growth chamber under 12 h light and 12 h night. The drought stress started when the seedlings were 10 days old after transplantation and lasted 30 days. Water was withheld from the drought stress plots. Each irrigated pot was topped up to its original weight every three days throughout the experiment which lasted for 40 days. Depending on the quantity of water loss by each irrigated pot, the top up water varied between 40 to 80 ml every three days. Basically, the drought stress was stopped when the water content in the water deficit plots reached 50%. Pots were weighted every two days to track the water loss. Data were collected on shoot fresh weight and root fresh weight.

3.4.3.3 RNA extraction, quantification and integrity/degradation

Non-drought and drought stress plants were sampled at the same time between 4 to 5 hours after light on. Samples were collected in liquid nitrogen on three biological replicates of the shoots from each treatment, and stored at -80^{o}C until RNA extraction. Each biological replicate was from a pool of 6 individual plants. Total RNA was isolated from the tissues using the RNeasy® (QIAGEN GmbH, QIAGEN Strasse 1; 40724 Hilden, Germany). The RNA was treated with DNase I to eliminate any contaminating DNA. The RNA concentration was measured using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA; ND-2000), and then the quality and concentration of RNA samples were determined using Qubit. Only a high-quality total RNA (1 µg) sample ($OD^{260/280}$ = ~2.0, $OD^{260/230} \geq 2.0$, RIN $\geq$ 6.0, 28S:18S $\geq$ 1.0) was used as input material to construct the RNA-seq library.

Integrity/degradation of RNAs was checked on 1.5% agarose gel, and using Agilent 4200 TapeStation Systems (© Agilent Technologies, Inc. 2020, USA) according to the manufacturer's protocol.

3.4.3.4 Quantitative real-time reverse transcription-PCR (qRT-PCR) analysis

All analyses were performed on two biological replicates (biological replicates are data collected on biologically different samples) and three technical replicates (technical replicates are repeated measurements taken on the same sample) per sample, collected as described for the RNA extraction. The cDNA synthesis was performed using NZY First-Strand cDNA Synthesis Kit, separate oligos (nzytech, Lisbon, Portugal) according to the manufacturer's protocol. The qRT-PCR was used to verify a subset of selected known drought genes involved in drought response mechanisms, using Takara SYBR Green Taq Polymerase according to the manufacturer's protocol. The primers of the genes used were retrieved from Huang et al. (2014), Kaur et al. (2023), Park & Jeong (2023), Zhang et al. (2016), (Table 5). Three rice drought responsive genes with various function categories were selected and tested in 20 µL reactions using the SYBR® Green PCR Master Mix kit (Applied Biosystems, CA, USA), following the manufacturer's protocol, via an ABI Prism 7900 Sequence Detection System (Applied Biosystems). The relative expression of each gene was calculated according to the method of $2^{-\triangle Ct}$ (Udvardi et al., 2008). The *Actin 1* gene (*LOC_Os03g50885*) was used as endogenous references for the qRT-PCR analysis.

Table 5. Primers used for the qRT-PCR among the rice genotypes evaluated under drought stress in pots at University College Cork (UCC), Cork, Ireland in 2023

S/N	Gene Name	Gene ID	Forward Primer (5′→ 3′)	Reverse Primer (5′→ 3′)
1	*Transcription factor BHLH6*	*LOC_Os04g23550*	TGCGAGGCAACGATTTAGT	GCTGGACCACCTTATTATTCAT
2	*Cytokinin-O-glucosyltransferas-1*	*LOC_Os05g08480*	CATCAGTGGCATCAGAAGTCG	GCAGCATTATTATTGCCATTGT
3	*DUF26 kinases*	*LOC_Os07g43560*	AACCATACCCTGTAACCGA	CCTGAAAATACAATAAATACACAA
4	*Actin1*	*LOC_Os03g50885*	TTGCTGACAGGATGAGCAAG	TGGAATGTGCTGAGAGATGC

S/N-Serial number; Gene ID-Gene Identity to retrieve the gene across databases.

3.4.4 Genetic basis behind the expression of tolerance to drought stress among the rice breeding lines using generation mean analysis

3.4.4.1 Plant Materials

The plant materials used in this study consisted of F_1 and F_2 hybrid plants obtained from two crosses, their respective three parents involved in the crosses and the Backcross 1 and 2 (BC_1 and BC_2). The selected parental lines contrast with respect to tolerance to drought stress. The parent APO is drought-tolerant while the two other parents CRI-Agrarice and Jasmine85 are drought-sensitive varieties. These genotypes also contrasted in terms of performance for some agronomic traits such as flowering date, tiller number, hundred-grain weight and presence of aroma.

3.4.4.2 Development of F_2, and backcross (BC_1, and BC_2) generations

Two F_1 hybrid generations were developed using selected parents with contrasting drought tolerance characteristics. The crossing was done from January 2021 to March 2022 to develop segregating generations namely F_2 and backcross generations. The F_2 generations for each cross were developed through the selfing of F_1 individuals. To develop BC_1 and BC_2 generations for each cross combination, F_1 individuals were crossed with their respective parent P_1 (female parent) and parent P_2 (male parent). To develop the backcross generations, only true F_1 plants with the base of the rice plants coloured in pink were used.

3.4.4.3 Crossing scheme

During the development of BC_1 and BC_2 generations, both parents (P_1 and P_2) plants were used as donors (pollen sources) and F_1 plants as receivers (female plants/recurrent parents). Which means to develop the progenies of BC_1 generation pollens were collected from P_1 plants to pollinate F_1 plants. Similarly, to develop the progenies of BC_2 generation pollens from P_2 plants were collected to pollinate F_1 plants (Figure 6). The emasculation was generally done early in the morning between 5:30 A.M. to 6:30 A.M. daily. Soon after the emasculation, the emasculated panicles were covered with paper envelopes to avoid foreign pollen contamination. The pollination was usually done between 09:00 A.M. and 12:30 A.M. Soon after the pollination, the crossed panicles were covered with paper envelopes to avoid foreign pollen contamination and appropriately labelled. The crossed panicles were harvested at maturity, sun-dried for 2 weeks, and threshed to collect crossed seeds. The crossed seeds at the mid-centre of the crossed panicles were only collected to ensure the high quality of crossed seeds and to reduce the probability of collecting selfed seeds (Pujar et al., 2022).

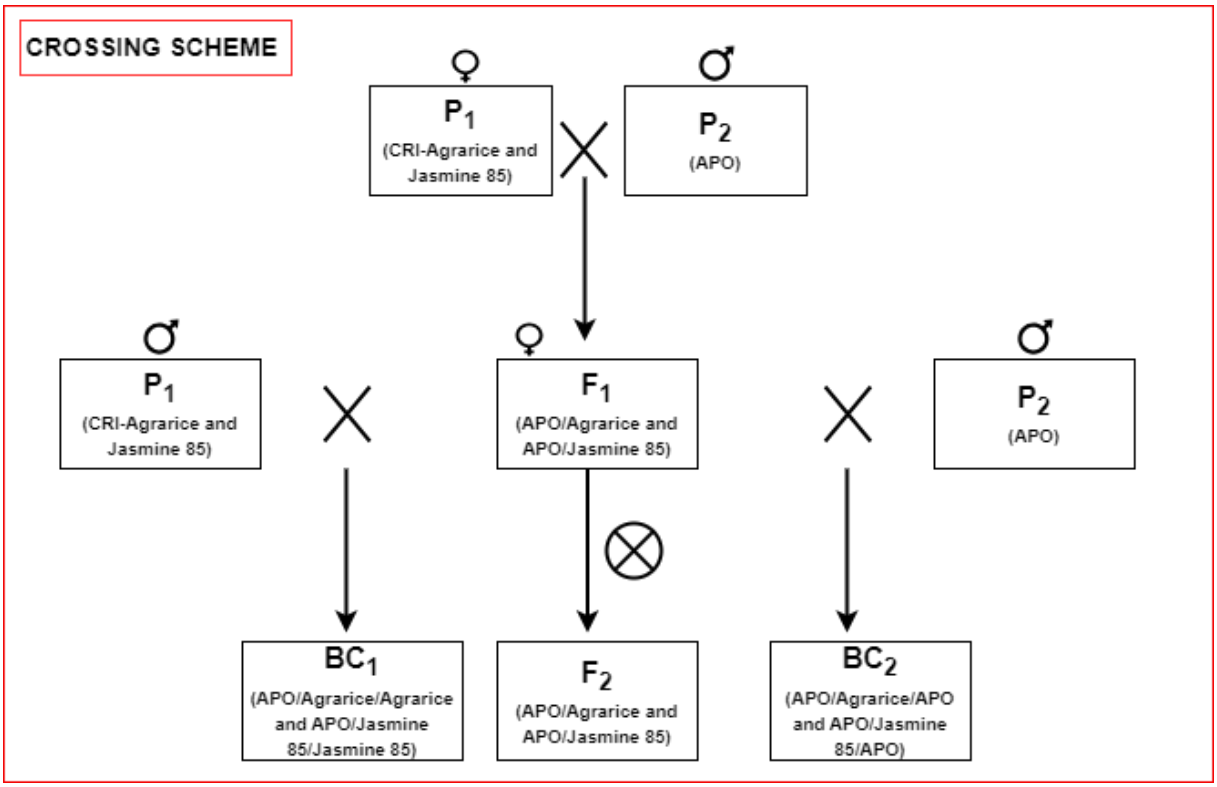


Figure 6. The Crossing scheme between the drought-tolerant APO (P_2) and the drought-sensitive genotypes CRI-Agrarice ($P_{1\text{-}1}$) and Jasmine 85 ($P_{1\text{-}2}$). APO is the male donor and CRI-Agrarice and Jasmine 85 are the female receivers in the development of the F_1 generation. To develop the backcross generations 1 and 2 (BC_1 and BC_2), F_1 generation was used as female, while P_1 and P_2 as donors. F_1 generation was selfed to develop F_2 seeds.

3.4.4.4 Evaluation of the six populations under drought stress

The six populations (P_1, P_2, F_1, BC_1, BC_2, and F_2) for each cross were evaluated in a completely randomized block design (RCBD) with three replications at CSIR-CRI, Fumesua-Kumasi, Ghana in the screenhouse between June to December 2022. The rainout shelter was used to keep the plants off rainfall. A block of RCBD consisted of three rows with 10 P_1 and 10 P_2 plants per row, and one F_1 plant per row; two rows with 20 BC_1 and BC_2 plants per row; and six rows with 20 F_2 plants per row, thereby using all the F_1 and backcross progenies. A direct sowing was done for the F_2 and Parents generations while F_1 and backcross generations were pre-germinated before transplanting. The direct sowing was done on 11/06/2022 while the transplanting of the F_1 and BC_1 and BC_2 progenies was done on 16/06/2022. The plants were grown using 1.5 litters of pots filled with top soil with one plant per pot. All recommended agronomic practices were followed for good crop growth. Observation was done on all three replications and respective plants. The drought stress started on 09/08/2022 by withholding the water from the experimental pots for 5 days during which close to 80% of the rice plants showed severe leaf rolling. The stressed plants were scored on 13/08/2022 and just before the pots were flooded with water. Twenty-four (24) hours after, the water was drained out of the pots and the stress resumed for another 5 days. The stress circle continued following this process throughout the late stages of the rice plant growth. At each stress phase, the leaf rolling score and leaf drying score were recorded. The well-watered plants were used as control.

3.4.4.5 Morphological and physiological traits performance

Data were collected on 30 P_1 plants, 30 P_2 plants, 3 F_1 plants, 120 F_2 plants, 40 BC_1 plants and 40 BC_2 plants on all 3 repetitions.

- **Grain yield**

All the harvested grains per individuals' plants were sun-dried till the moisture content reached 14%, thereafter the grain yield was recorded on individual plant in grams.

- **Grain yield-related traits**

Days to flowering (DTF) were recorded when the first panicle of each plant showed flowering. The yield-related traits such as plant height (PH) in cm, number of effective tillers (TN), panicle length (PL) in cm and spikelet fertility score (SPFS), leaf rolling score, leaf drying score and recovery from drought were recorded on each plant per replicate at physiological maturity of the rice crop.

3.4.4.6 Transgressive segregation analysis

For the F_2 populations, descriptive statistics such as the coefficient of variation (C.V.%), the range, the maximum and minimum values, variance and standard error for each variable were determined as a measure of the variability.

The transgressive segregants in the F_2 populations were identified by counting the number of plants whose values were below that of the inferior parent or above that of the superior parent (extreme values of progenies compared to their parental lines) by a difference of 5% (Cazzola et al., 2020). For the traits like plant height and days to flowering, the segregants with values lower than those of the parents were recorded as transgressive. The limit was 70 cm for plant height and 75 days for the flowering date for all the crossing populations. The transgression index (TI) was calculated to assess the presence of transgressive segregants in the crossing generations according to Koide et al. (2019).

$$Transgression\ Index\ (TI) = \frac{R}{D}$$

Where, R is the range of variation between F_2 for any trait; D is the difference between the average values of the parents for the same trait. For the sake of conformity, we took the absolute value of $D = |P1 - P2|$.

3.4.4.7 Generation mean analysis

The Analysis of variance was done following a completely randomized block design.

- **Test for Epistasis**

The four scaling tests (A, B, C, and D) according to the method of Mather (1949) were used for the testing of epistasis and are computed below:

$$A = 2\underline{BP_1} - \underline{P_1} - \underline{F_1}$$

$$B = 2\underline{BP_2} - \underline{P_2} - \underline{F_1}$$

$$C = 4\underline{F_2} - 2\underline{F_1} - \underline{P_1} - \underline{P_2}$$

$$D = 2\underline{F_2} - \underline{BC_1} - \underline{BC_2}$$

Where, $\underline{P_1}$, $\underline{P_2}$, $\underline{F_1}$, $\underline{F_2}$, $\underline{BC_1}$, and $\underline{BC_2}$ are means of different generations.

The variances of the quantities A, B, C, and D were estimated from the variances of different generations as below:

$$VA = 4V\left(\underline{BC_1}\right) + V\left(\underline{P_1}\right) + V(\underline{F_1})$$

$$VB = 4V\left(\underline{BC_2}\right) + V\left(\underline{P_2}\right) + V\left(\underline{F_1}\right)$$

$$VC = 16V\left(\underline{F_2}\right) + 4V\left(\underline{F_1}\right) + V\left(\underline{P_1}\right) + V\left(\underline{P_2}\right)$$

$$VD = 4V\left(\underline{F_2}\right) + V\left(\underline{BC_1}\right) + V\left(\underline{BC_2}\right)$$

Where,

VA, VB, VC, and VD are the variances of A, B, C, and D scales, respectively;

V($\underline{P_1}$), V($\underline{P_2}$), V($\underline{F_1}$), V($\underline{F_2}$), V($\underline{BC_1}$) and V($\underline{BC_2}$) are the variances of P_1, P_2, F_1, F_2, BC_1, and BC_2 generations, respectively.

Standard errors of the scales A, B, C, and D were estimated by taking the square root of the four variances. The t-test was used to test for the presence of epistasis at the significance level of 0.05 and 0.01 with their corresponding degrees of freedom. For a given test, the degrees of freedom were calculated as the sum of the degrees of freedom of various generations involved in that scaling test, whereas, the degrees of freedom for any generation was calculated as the total number of observations minus the number of replications (Pujar et al., 2022). The t values were calculated as follow:

$$t\ value\ of\ scale\ A\ = \frac{A}{\sqrt{VA}}$$

$$t\ value\ of\ scale\ B\ = \frac{B}{\sqrt{VB}}$$

$$t\ value\ of\ scale\ C\ = \frac{C}{\sqrt{VC}}$$

$$t\ value\ of\ scale\ D\ = \frac{D}{\sqrt{VD}}$$

- **Six parameters model**

If any of the scaling tests was significant then the genetic effects were estimated by fitting the data into six-parameter models of the generation mean analysis according to Hayman (1958, 1960). The genetic parameters estimated are mean effect (m), additive gene effects (d), dominance gene effects (h), and three types of non-allelic gene interactions namely additive × additive (i), additive × dominance (j), and dominance × dominance (l). These genetic parameters were calculated according to the following parameters:

$$Mean\ effect\ (m) = \underline{F_2}$$

$$Additive\ effects\ (d) = \underline{BC_1} - \underline{BC_2}$$

$$Dominance\ effects\ (h) = \underline{F_1} - 4\underline{F_2} - 0.5\underline{P_1} - 0.5\underline{P_2} + 2\underline{BC_1} + 2\underline{BC_2}$$

$$Additive \times Additive\ gene\ interaction\ (i) = 2\underline{BC_1} - 2\underline{BC_2} - 4\underline{F_2}$$

$$Additive \times Dominance\ gene\ interaction\ (j) = \underline{BC_1} - \underline{BC_2} - 0.5\underline{P_1} + 0.5\underline{P_2}$$

$$Dominance \times Dominance\ gene\ interaction\ (l) = \underline{P_1} + \underline{P_2} + 2\underline{F_1} + 4\underline{F_2} - 4\underline{BC_1} - 4\underline{BC_2}$$

Where, $\underline{P_1}$, $\underline{P_2}$, $\underline{F_1}$, $\underline{F_2}$, $\underline{BC_1}$, and $\underline{BC_2}$ are means of different generations.

The variances of the above gene interaction are estimated below:

$$Vm = V\left(\underline{F_2}\right)$$

$$Vd = V\left(\underline{BC_1}\right) + V\left(\underline{BC_2}\right)$$

$$Vh = V\left(\underline{F_1}\right) + 16V\left(\underline{F_2}\right) + 0.25V\left(\underline{P_1}\right) + 0.25V\left(\underline{P_2}\right) + 4V\left(\underline{BC_1}\right) + 4V\left(\underline{BC_2}\right)$$

$$Vi = 4V\left(\underline{BC_1}\right) + 0.25V\left(\underline{BC_2}\right) + 16V\left(\underline{F_2}\right)$$

$$Vj = V\left(\underline{BC_1}\right) + V\left(\underline{BC_2}\right) + 0.25V\left(\underline{P_1}\right) + 0.25V\left(\underline{P_2}\right)$$

$$Vl = V\left(\underline{P_1}\right) + V\left(\underline{P_2}\right) + 4V\left(\underline{F_1}\right) + 16V\left(\underline{F_2}\right) + 16V\left(\underline{BC_1}\right) + 16V\left(\underline{BC_2}\right)$$

Where,

$V(\underline{P_1})$, $V(\underline{P_2})$, $V(\underline{F_1})$, $V(\underline{F_2})$, $V(\underline{BC_1})$ and $V(\underline{BC_2})$ are the variances of P_1, P_2, F_1, F_2, BC_1, and BC_2 generations, respectively.

The significance of the gene effects m, d, h, i, j, and l were tested using the t-test. Standard errors were calculated by taking the square root of the variance of each component. The significance of the gene effects was done using the t-test as in the case of the scaling test above. Statistical analyses were done using the R scripts according to the formula of Nadarajan et al. (2016). The R code used is in the annex 1 and 2.

- **Heterosis**

Heterosis over mid-parent (HMP) was estimated as the increase or reduction in percentage observed in the F_1 generation over that of the mid-parent according to Fonseca & Patterson (1968). The mid-parent residual heterosis (MRH) was also estimated in the F_2 progeny following the formula of Rao (1980).

$$HMP\ (\%) = \left(\frac{\left(\underline{F_1} - \underline{MP}\right)}{\underline{MP}}\right) \times 100$$

$$MRH\ (\%) = \left(\frac{\left(\underline{F_2} - \underline{MP}\right)}{\underline{MP}}\right) \times 100$$

- **Heritability and genetic advance**

Broad-sense heritability (h^2_{bs}), narrow-sense heritability (h^2_{ns}), and genetic advance (GA) were estimated according to Warner (1952). The genetic advance as a percentage of the mean (GAM) was calculated as follows by Johnson et al. (1955). Calculations were done using the following formulas:

$$h^2_{bs}(\%) = \left(\frac{V\left(\underline{F_2}\right) - \frac{V\left(\underline{P_1}\right) + V\left(\underline{P_2}\right) + V\left(\underline{F_1}\right)}{3}}{V\left(\underline{F_2}\right)} \right) \times 100$$

$$h^2_{ns}(\%) = \left(\frac{2V\left(\underline{F_2}\right) - \left(V\left(\underline{BC_1}\right) + V\left(\underline{BC_2}\right)\right)}{V\left(\underline{F_2}\right)} \right) \times 100$$

$$GA = \frac{V\left(\underline{F_2}\right) - V\left(\underline{F_1}\right)}{\sqrt{V\left(\underline{F_2}\right)}} \times K$$

$$GAM\ (\%) = \frac{GA}{\underline{F_2}} \times 100$$

V($\underline{P_1}$), V($\underline{P_2}$), V($\underline{F_1}$), V($\underline{F_2}$), V($\underline{BC_1}$) and V($\underline{BC_2}$) are the variances of P_1, P_2, F_1, F_2, BC_1, and BC_2 generations, respectively. K is the selection differential, and K is 2.06 at a 5% selection intensity.

Broad-sense heritability (h^2_{bs}) and narrow-sense heritability (h^2_{ns}) estimates were classified as: Low (0-30%), moderate (30-60%) and High (above 60 %), while the genetic advance as percent of mean (GAM) was classified as: Low (less than 10%), moderate (10-20%), high (more than 20%) according to Johnson et al. (1955).

- **Degree of Dominance**

The degree of dominance (DD), which is calculated as the square root of the ratio of dominance variance (Vh) to additive variance (Vd), was estimated following (Robinson et al., 1949). The calculation was done using the following formula:

$$Degree\ of\ dominance\ (DD) = \sqrt{\frac{Vh}{Vd}}$$

3.5 Statistical analysis

Analysis of variance

Analysis of variance (ANOVA) for each trait was done by using the GLM procedure of the Statistical Analysis System (SAS) version 9.4 for Windows. To ensure normal distribution of

the traits, before the analysis of variance, all the traits collected under field and greenhouse screening were transformed using z-score standardisation in Microsoft Excel. A trait with a skewness between -2 to +2 and kurtosis between -7 to +7 is considered to be normally distributed. Duncan's multiple rank test was used to separate the means among the genotypes screened in the drought stress experiments after the significance of the ANOVA.

- The z-score computation formula is below:

$$z - score = \frac{(X - \mu)}{\sigma}$$

Where, X is a single raw data value; μ stands for the mean of the dataset; and σ stands for the standard deviation of the dataset.

- The model for measurements on a plot for alpha-lattice design (Y_{ijk}) is:

$$Y_{ijk} = \mu + R_i + B_{ij} + T_k + e_{ijk}$$

Where, μ stands for general mean; R_i stands for fixed effect of replicate i; B_{ij} stands for random effect of block j within replicate i; T_k stands for random effect of treatment k; e_{ijk} stands for residuals effect.

- The model for measurements on a plot for randomized complete-block design (RCBD) (Y_{ij}) is:

$$Y_{ij} = \mu + R_i + T_j + e_{ij}$$

Where, μ stands for general mean; R_i stands for fixed effect of replicate i; T_j stands for random effect of treatment k; e_{ij} stands for residuals effect.

To test the presence of significant variability in the distribution of the traits under the field screening across both non-drought and drought stress conditions, Levene's statistic test of homogeneity of variance was carried first and it turned out that there was not homogeny in variance for all the traits under study. Since there was not homogeny in the variance, the nonparametric Mann-Whitney U test was conducted.

Descriptive statistics and paired samples t-test between traits performance under drought and non-drought conditions were performed with the software SPSS version 25. Graphics were made using R and Microsoft Excel. R software packages were used to run the generation mean analyses.

- The coefficient of variation (C.V.%) is calculated as follow:

$$Coefficient\ of\ variation = \frac{Standard\ deviation}{Mean}$$

Association analysis

Principal component analysis (PCA), Pearson correlation and multiple linear regression analysis (SAS software) were done to understand variations and relationships among various traits and treatments. The PCs with an eigenvalue greater than one were retained for interpretation (Kaiser, 1958). The visualization of the Pearson correlation using graphics was generated using Visplore data analysis tools (https://visplore.com/), while the visualization of the PCA biplot was generated with R software.

- Pearson's correlation coefficient was calculated following this formula:

$$r_{xy} = \frac{n\sum xy - (\sum x)(\sum y)}{\sqrt{[n\sum x^2 - (\sum x)^2][n\sum y^2 - (\sum y)^2]}}$$

Where, r_{xy} stands for Pearson's correlation coefficient; *x* is the variable 1; *y* is the variable 2; *n* is the sample size; and Σ represents a summation of all values.

- Multiple linear regression was computed following this formula:

$$Y_i = \alpha_0 + \alpha_1 X_{i1} + \alpha_2 X_{i2} + \cdots + \alpha_p X_{ip} + \varepsilon_i$$

Where, for each observation *i= 1, 2, ..., n*, in the above formula n observations is for one dependent variable and p independent variables; Y_i is the i^{th} observation of the dependent variable, X_{ij} is i^{th} observation of the j^{th} independent variable, *j = 1, 2, ..., p*. The values α_j represent parameters to be estimated, and ε_i is the i^{th} independent identically distributed normal error.

Classification of the genotypes into their tolerance classes

The classification of the genotypes into their tolerance classes was done based on the relative value for each trait per genotype between non-drought and drought stress management following this formula:

$$Relative\ Trait\ Value\ (Drought\ risk\ index) = \frac{Trait\ Value\ under\ drought\ stress}{Trait\ Value\ under\ non-drought}$$

If the trait relative value is equal to 1, there is no drought stress, and if it is equal to 0, complete crop failure due to drought stress. The relative grain yield (Tolerance index) was considered first followed by other yield-related and physiological traits. Correlation analysis and PCA were

conducted among the different traits using trait relative values to determine the relationship and select priority traits to involve in selecting the drought-tolerant genotypes.

The multi-trait genotype-ideotype distance index (MGIDI) implemented in R, was also used to select the genotypes showing tolerance to drought (Olivoto & Nardino, 2021). To compute the MGIDI, the trait relative value (drought risk index) was used as input data following the formula:

$$MGIDI_i = \sqrt{\sum_{j=1}^{f} (\gamma_{ij} - \gamma_j)^2}$$

Where, $MGIDI_i$ is the multi-trait genotype-ideotype distance index for the i^{th} row/genotype/treatment; γ_{ij} is the score of the i^{th} row/ genotype/treatment in the j^{th} factor *(i = 1, 2, ..., g; j = 1, 2, ..., f)*, being g and f the number of rows/genotypes/treatments and factors, respectively; and γ_j is the j^{th} score of the ideotype. The row/genotype/treatment with the lowest MGIDI is then closer to the ideotype and therefore presents desired values for all the p traits; *g, f and p* represent the number of rows/genotypes/treatments, respectively.

The genotypes selected as drought-tolerant based on phenotypic data are compared with the genotyping based on the known drought QTL profile to confirm the tolerant status of the given genotypes.

- Heritability in the broad-sense (h^2_{bs}) was computed following Allard (1960):

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_e}{nreps}}$$

Where, σ^2_g and σ^2_e are the genotypic and error variances respectively; and nreps is the number of replications.

Broad-sense Heritability (h^2_{ns}) estimates were categorized as: Low (0-30%), moderate (30-60%) and High (above 60 %) according to Johnson et al. (1955).

CHAPTER 4 RESULTS AND DISCUSSION

4.1 Results

4.1.1 Combination of phenotyping and SNP markers-based drought-tolerant QTLs for the selection of drought-tolerant genotypes under field conditions

4.1.1.1 Meteorological conditions and drought Stress

The weather data including the rainfall and temperature data during the trial season (November 2021- March 2022) are represented in Figure 7. The total precipitation in the experiment area during the rice-growing season was 1133.53 mm during 63 rainy days. The mean minimum to maximum temperatures during the growing season of the rice crop season ranged from 22.77°C in August 2021 to 24.23°C in February 2022 and from 25.24°C to 27.77°C, respectively (Figure 7B), while the relative humidity ranged from 76.37% in January 2022 to 95.9% in August 2021 (Figure 7A). The average soil temperature around the root zone of rice plant at 10 cm depth was 32.15°C under drought stress and 30.54°C under non-drought conditions. Soil temperature was generally higher than the maximum air temperature during the rice growing-season. The measurement of the electrical conductivity indicated "too dry" under drought stress, while 55.22 $m.S.m^{-1}$ was recorded under non-drought conditions. During this study, clear symptoms of drought stress were seen in the field at 18 days after the stress with volumetric soil moisture content less than 5% vol (2.05% vol) of approximately 10 cm of soil depths.

4.1.1.2 Variation of agronomical and physiological traits under non-drought and drought stress water regimes

Descriptive statistics showing the variation among the genotypes for all the traits under non-drought and drought stress conditions are presented in Table 6, respectively.

All the agronomical and physiological traits studied in this experiment showed normal distributions based on the skewness and kurtosis data which ranged between -2 to +2 and -7 to +7, respectively under both non-drought and drought stress conditions except the leaf drying score that recorded a skewness of 3.51 and a kurtosis of 12.81.

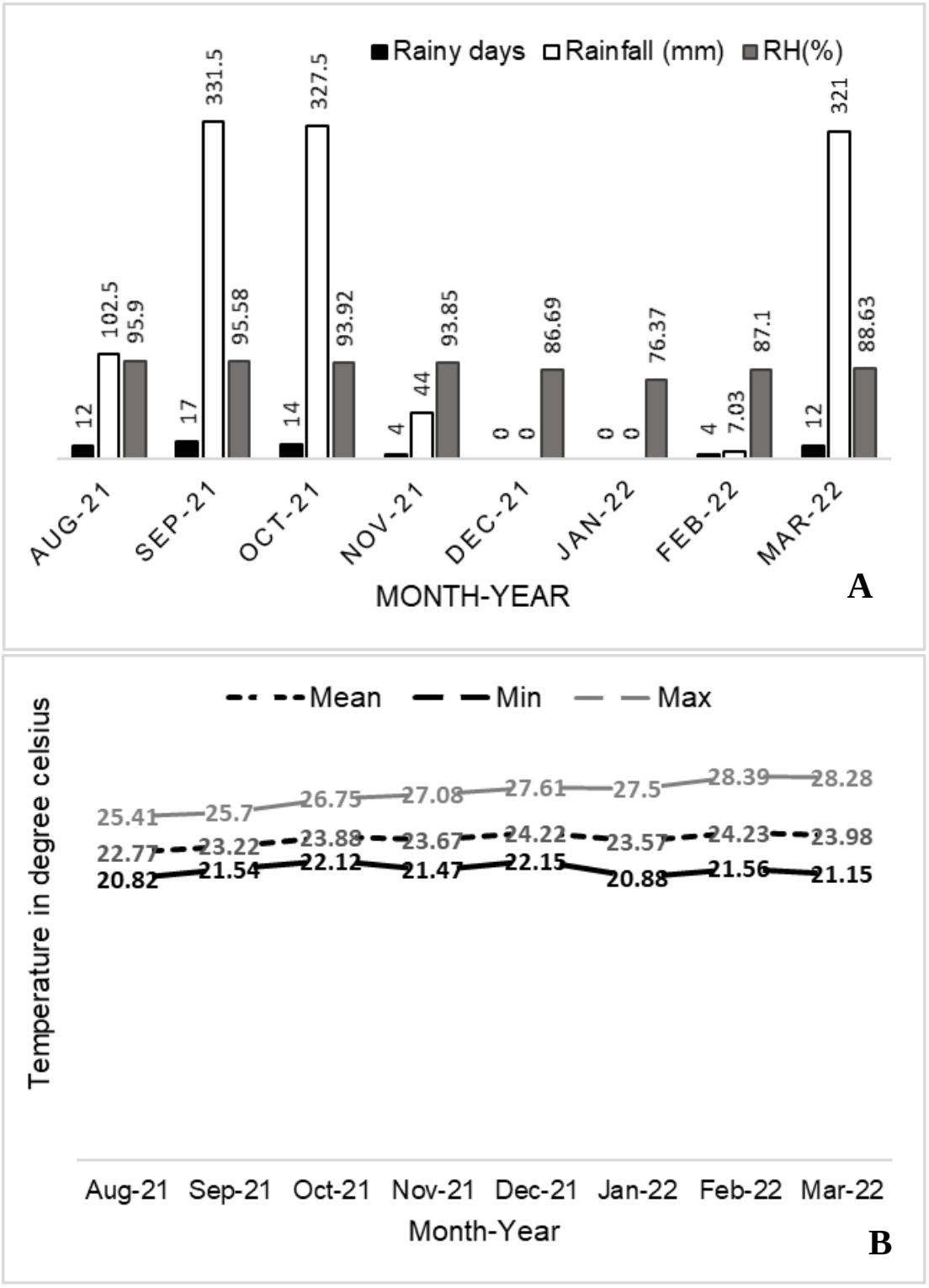


Figure 7. Meteorological conditions at CSIR-Crops Research Institute, Kumasi, Ghana from August 2021 to March 2022: **(A)** Number of rainy days in the month, the quantity of rainfall in the month (mm) and relative humidity (%); **(B)** air minimum and maximum temperatures (°C), and the temperature mean value (°C); *Source: weather data were collected from the meteorological center at CSIR-Crops Research Institute, Kumasi, Ghana*

Table 6. Descriptive statistics showing the variation among the genotypes for all the traits evaluated under non-drought and drought stress conditions in Fumesua-Kumasi, Ghana in 2021-2022

Trait	Mini		Maxi		Mean		SD		σ^2		Skewness		Kurtosis	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
Chlorophyll Content Index	12.37	5.99	27.6	21.6	19.27	14.47	3.05	3.65	9.31	13.33	0.16	-0.15	0.29	-0.66
Spikelet Fertility Score	1	1	3	9	1.5	4.8	0.87	2.58	0.76	6.65	1.17	0.16	-0.64	-1.07
Grain Yield per Plant(g)	5.44	0	39.09	15.00.	18.77	3.08	8.09	2.76	65.44	7.63	0.55	1.53	-0.54	3.34
Days to Flowering	62	71	95	101	83.12	91.67	4.12	5.63	16.98	31.66	-1.26	-1.28	7.2	2.55
Tiller Number per Plant	6	4	19	9	11.14	5.27	2.38	1.07	5.68	1.15	0.64	0.8	0.73	0.65
Panicle Number per Plant	5	0	17	7	10.2	4.41	2.24	1.09	5.01	1.19	0.47	-0.07	0.33	2.09
Plant Height(cm)	66.63	56	148.4	105.93	100.21	76.53	14.94	9.45	223.12	89.23	0.33	0.45	0.5	0.24
Panicle Length(cm)	16.47	10.7	38.6	31.88	23.87	20.12	3.95	3.45	15.62	11.91	1.28	0.93	2.87	2.96
Grain Length(mm)	6.01	4.58	10.13	12.06	8.46	8.19	0.74	1.21	0.55	1.46	-0.44	-0.33	0.26	1.61
Grain width(mm)	1.17	1.12	2.65	4.11	2.22	2.16	0.28	0.45	0.08	0.2	-1.16	0.76	1.8	3.85
Hundred Grains Weight(g)	2.05	1.16	3.55	4.02	2.97	2.55	0.34	0.5	0.12	0.25	-0.43	0.29	-0.36	0.82
Leaf Rolling Score	-	1	-	9	-	5.6	-	1.61	-	2.61	-	-0.27	-	1
Leaf Drying Score	-	1	-	5	-	1.2	-	0.67	-	0.44	-	3.51	-	12.81
Drought Recovery	-	1	-	5	-	1.66	-	1.03	-	1.06	-	1.18	-	0.34

ND-Under non-drought; UD-Under drought stress; Mini-Minimum; Maxi-Maximum; SD-Standard deviation; σ^2- Variance

In this experiment drought stress has occasioned wide variation under drought stress for some traits while larger variations were obtained for others under the non-drought conditions. Chlorophyll content index (CCI) registered a slightly wider variation under drought stress ranging from 5.99 CCI to 21.60 CCI with a standard deviation (SD) of 3.65 as compared to the non-drought conditions where the range was 12.37-27.60 CCI with a SD=3.05 (Table 6). Spikelet fertility score recorded a wide variation under drought stress with a range from 1 to 9 (SD=2.58) as compared to the non-drought conditions where the range was 1-3 with a SD=0.87 (Table 6). Grain yield per plant in grams (g) registered a large variation under non-drought conditions ranging from 5.44 to 39.09 g/plant with a SD of 8.09, while under drought stress the range varied from 0.00 to 15.00 g/plant with a SD=2.76 (Table 6). Days to flowering registered a slightly wider variation under drought stress (range: 71 to 101 days and SD= 5.63 as compared to the non-drought conditions where the range is 62-95 days with a SD= 4.12 (Table 6). Tiller number recorded a wider variation under non-drought conditions (range= 6.00 to 19.00; SD=2.38) than under drought stress where the range was 4-9 with a SD=1.07 (Table 6). Panicle number registered a wider variation under non-drought conditions (range= 5.00 to 17.00; SD=2.24) compare to the drought stress where the range was 0-7 with a SD=1.09 (Table 6). Plant height (cm) showed a wider variation under non-drought conditions ranging from 66.63 to 148.40 cm with a standard deviation (SD) of 14.94 as compared to the drought stress where the range was 56.00-105.93 cm with a SD=9.45 (Table 6). Panicle length (cm) registered a slightly wider variation under non-drought conditions ranging from 16.47 to 38.60 cm with a standard deviation (SD) of 3.95 compared to the drought stress where the range was 10.70-31.88 cm with a SD= 3.45 (Table 6). Grain length (mm) and grain width (mm) registered a slightly wider variation under drought stress ranging from 4.58 to 12.06 mm (grain length) and 1.12 to 4.11 mm (grain width) with a standard deviation (SD) of 1.21 (grain length) and 0.45 (grain width) compared to non-drought conditions where the range was 6.01-10.13 mm with a SD= 0.74 for grain length and 1.17-2.65 mm with a SD of 0.28 for grain width (Table 6). Hundred grains weight in grams (g) displayed a slightly large variation under drought conditions ranging from 1.16 to 4.02 g with a SD of 0.50, while under non-drought conditions, the range varied from 2.05 to 3.55 g with a SD= 0.34 (Table 6).

4.1.1.3 Agronomic and physiological performance of the rice genotypes under both water regimes

4.1.1.3.1 Analysis of variance and mean performance

The analysis of variance (ANOVA) revealed the presence of significant differences among the rice genotypes for spikelet fertility percentage, days to flowering and plant height under non-drought conditions, while under drought stress, significant differences were observed on grain yield per plant, plant height, hundred grains weight, leaf rolling score and leaf drying score (Table 7).

To test the presence of significant variability in the distribution of the traits across both non-drought and drought stress conditions, a Mann-Whitney U test across both water regimes was conducted. The Mann-Whitney U test revealed the presence of significant differences in the distribution of all the traits across both non-drought and drought stress conditions except for grain length and grain width indicating a major role that the environment will be playing in the expression of these traits in this germplasm (Table 8). Defined as a measure of the dispersion of the variable around the mean, the coefficient of variation permits quantifying the extent of variability in relation to the mean of the germplasm. Under non-drought conditions, C.V. ranged from 4.79% for days to flowering to 130.79% for CCI (Table 7). The coefficient of variation was generally high in this study. Heritability in broad-sense ranged from 1.50% for CCI to 69.86% for the days to flowering. Heritability in broad-sense was high for days to flowering (69.86%), plant height (65.39%) and moderate for spikelet fertility (44.30%). Under drought stress, a wide range of variation among the 100 rice genotypes was noted for all the traits except days to flowering who recorded a C.V. of 7.38% (Table 7). The largest C.V. was observed on recovery from drought stress (74.68%), followed by grain yield per plant (71.72%). The highest heritability in broad-sense was recorded by hundred grains weight (96.14%), followed by grain yield per plant (59.85%), leaf rolling score (42.29%) and spikelet fertility (40.63%). Panicle length depicted the least broad-sense heritability (1.40%).

The mean performance under both non-drought and drought stress conditions are presented in Annexes 3 and 4. For all the investigated traits in this study, a general reduction was observed among the genotypes under drought stress as compared to the non-drought conditions.

Table 7. Mean square from the analysis of variance of 100 rice genotypes evaluated for 11 morpho-physiological traits under non-drought and drought stress conditions at Fumesua-Kumasi, Ghana in 2021-2022

Traits	Rep (D.F=2)		Block (Rep) (D.F=27)		Genotype (D.F=99)		Residual (D.F=171)		C.V. (%)		h^2_{bs}	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
Chlorophyll Content Index	1.59	2.47	0.93	1.69**	0.99	0.99	0.98	0.82	130.79	37.5	1.50	19.68
Spikelet Fertility Score	3.86**	0.47	0.94	0.67	1.11*	1.03	0.74	0.73	10.27	46.59	44.30	40.63
Grain Yield per Plant(g)	4.65**	1.72	0.74	0.44	1.11	1.20**	0.91	0.61	66.14	71.72	19.20	59.85
Days to Flowering	14.81**	8.46*	0.67	3.17	1.59**	2.05	0.51	2.65	4.79	7.38	69.86	-43.55
Tiller Number per Plant	10.81**	3.80*	1.74**	1.49*	0.75	0.97	0.74	0.89	29.88	31.89	1.19	8.52
Panicle Number per Plant	16.56**	9.53**	1.62**	1.03	0.71	0.81	0.71	0.93	29.76	32.2	0.84	-25.08
Plant Height(cm)	17.77**	3.32*	0.81	1.33	1.38**	1.34**	0.55	0.87	15.71	17.22	65.39	37.59
Panicle Length(cm)	17.47**	2.58	0.99	1.00	0.94	1.07	0.83	1.06	25.07	26.08	14.29	1.40
Grain Length(mm)	4.31*	3.85*	0.87	0.77	0.98	1.03	0.92	0.83	11.73	14.79	9.17	37.11
Grain width(mm)	6.48**	0.29	0.86	1.08	0.94	0.98	0.99	1.50	17.99	24.5	-8.75	-
Hundred Grains Weight(g)	2.67	0.02	1.03	0.41*	1.27	1.27**	1.38	0.12	18.18	11.97	-12.63	96.14
Leaf Rolling Score	-	30.38**	-	0.65	-	1.07**	-	0.64	-	36.21	-	42.29
Leaf Drying Score	-	5.15**	-	1.14	-	1.16*	-	0.80	-	66.61	-	33.13
Drought Recovery	-	11.71**	-	1.90**	-	0.83	-	0.75	-	74.68	-	10.95

*. Significant difference for the trait at the 0.05 level; **. Significant difference for the trait at the 0.01 level; Rep-Replication; D.F-Degree of freedom; C.V.-Coefficient of variation in %; h^2_{bs} - Heritability in broad-sense; ND-Under non-drought; UD-Under drought stress

Table 8. Distribution of 11 morpho-physiological traits across non-drought and drought stress conditions among the 100 rice genotypes evaluated at Fumesua-Kumasi, Ghana in 2021-2022

Null hypothesis	*p-value* (Mann-Whitney U test)	Decision
The distribution of chlorophyll content Index is the same across non-drought and drought stress conditions	<0.0001	Reject the null hypothesis: there was significance differences in the distribution of these traits across non-drought and drought stress conditions
The distribution of spikelet fertility score is the same across non-drought and drought stress conditions		
The distribution of grain yield per plant (g) is the same across non-drought and drought stress conditions		
The distribution of days to flowering is the same across non-drought and drought stress conditions		
The distribution of tiller number is the same across non-drought and drought stress conditions		
The distribution of panicle number is the same across non-drought and drought stress conditions		
The distribution of plant height (cm) is the same across non-drought and drought stress conditions		
The distribution of panicle length (cm) is the same across non-drought and drought stress conditions		
The distribution of hundred grains weight (g) is the same across non-drought and drought stress conditions		
The distribution of grain length (mm) is the same across non-drought and drought stress conditions	0.092	Retain the null hypothesis: there was not significance differences in the distribution of these traits across non-drought and drought stress conditions
The distribution of grain width (mm) is the same across non-drought and drought stress conditions	0.115	

Asymptotic significances are displayed; Significant difference for the trait is at the 0.05 level

Genotype G6 performed best for the grain yield per plant (15 g), followed by hundred grains weight (4.02 g) under drought stress. Genotype G6 also recorded the best relative grain yield, best relative spikelet fertility scores and 12 days delay in flowering. Genotype G6 is followed by G16, G59, G62, G79 which recorded a grain yield of 10 g per plant each. Genotype G6 also recorded the highest relative hundred grains weight, highest leaf rolling score with the lowest leaf drying score and the lowest recovery from drought score. The highest relative grain yield (0.88) obtained by G6 implied that the performance under both drought conditions (15 g) and non-drought conditions (17.14 g) are similar with no statistically significant difference.

The same performance applied to leaf greenness (CCI) under which G6 recorded high relative CCI (0.99) implying that the performance under both drought conditions (14.22 CCI) and non-drought conditions (14.41 CCI) are statistically similar. But in general, CCI decreased under drought stress as compared to non-drought conditions in this study. Genotype G28 recorded the highest plant high under drought stress (105.93 cm), with a relative plant height of 0.89, while G16 recorded the lowest plant height of 56 cm with a relative value of 0.56 implying that this genotype recorded a reduction of a half in height as compared to the non-drought conditions. The following genotypes, G6, G10, G34, G7, G93, G3, G50, G23, G94, G88, G37, G51 recorded hundred grains weight greater than 3.00 g under the stress with a relative hundred grains weight greater than 1.00 for all the above-cited genotypes. Relative hundred grains weight (seed index) ≥ 1 implied that these genotypes performed better under drought stress compared to the non-drought conditions for this trait. It is also important to note that all these genotypes recorded a leaf rolling score higher than 5.00 except G10 which recorded a leaf rolling score of 1.00. In this study, only three genotypes namely G10, G64 and the check G99 recorded the lowest leaf rolling score (LRS) and recovery from drought score (DRR) of the value of 1.00 (the lower the LRS and DRR, the better the performance of the genotypes under the stress).

The genotype G100 recorded a DDR=1 and LRS=5 implying its ability to recover quickly from drought stress. The genotypes G44 and G21 recorded the lowest relative spikelet fertility score of 0.33 while G99, G3, G21, G90, G96, G24, G31, G70, G11, G79, G60, G71, G33, G72, G38, G28 and G6 scored 1.00 as a relative spikelet fertility score. Even though G11 recorded a low grain yield relative value of 0.07, it recorded the best relative spikelet fertility score of 1.00, fewer days of delay to flowering of 3 days, a relatively high relative CCI (0.70) and relative hundred grains weight (0.75) coupled with lowest leaf drying and recovery from drought score of 1.00. The genotypes G77 and G41 flowered at the same time under both non-drought and

drought stress conditions at 83 and 81 days after sowing, respectively. Delay in 50% flowering dates were observed in almost all the accessions and ranged from 1 to 34 days. The following genotypes, G94, G59, G50, G68, G20, G58, G97, G79, G63, G11, G9, G62, G57 on the other hand, recorded delay in days to flowering between 1 to 3 days. Making them to have similar performance under both water regimes, synonym of probable tolerance or escape to drought stress. On the contrary to the other genotypes in this present study, these following genotypes namely G67, G5, G87, G31 flowered 17 days, 12 days, 4 days, 3 days and 1 respectively, earlier under drought stress than under non-drought conditions.

Overall, the results showed that grain yield and yield components, and physiological traits in this study recorded significant reduction under manifested drought stress through the delay in the growth and development of the plants especially for the drought-sensitive genotypes.

4.1.1.3.2 Association analyses of agronomical and physiological traits under non-drought and drought stress water regimes

- **Pearson correlation analysis**

The Pearson correlation coefficients among the different traits under non-drought and drought stress conditions are presented in Figures 8 and 9, respectively. The Pearson correlation table under both drought stress and non-drought conditions is presented in the annexes 5 and 6.

Under non-drought conditions, the following relationships were obtained: tiller number per plant (TN) and panicle number per plant (PN) recorded a highly significant positive correlation between themselves (r=0.972) whereas both of them recorded a highly significant positive relationship with grain width (GW) and a significant negative correlation with chlorophyll content index (CCI). Grain length (GL) recorded positive and significant relationships with spikelet fertility score and grain yield. Grain yield and hundred grains weight recorded significant positive relationships between themselves. Panicle length showed a highly significant positive correlation with plant height, while it was significantly and negatively correlated with grain width and hundred grains weight.

Under drought stress, the following relationships were obtained: spikelet fertility score showed a significant negative relationship with chlorophyll content index, grain yield, hundred grains weight, while a highly significant positive relationship was established with leaf rolling score. The chlorophyll content index showed a significant positive correlation with hundred grains weight, while a highly significant negative association was observed with leaf rolling score

(LRS) and recovery from drought (DRR). Days to flowering registered a significant and a positive correlation with grain length.

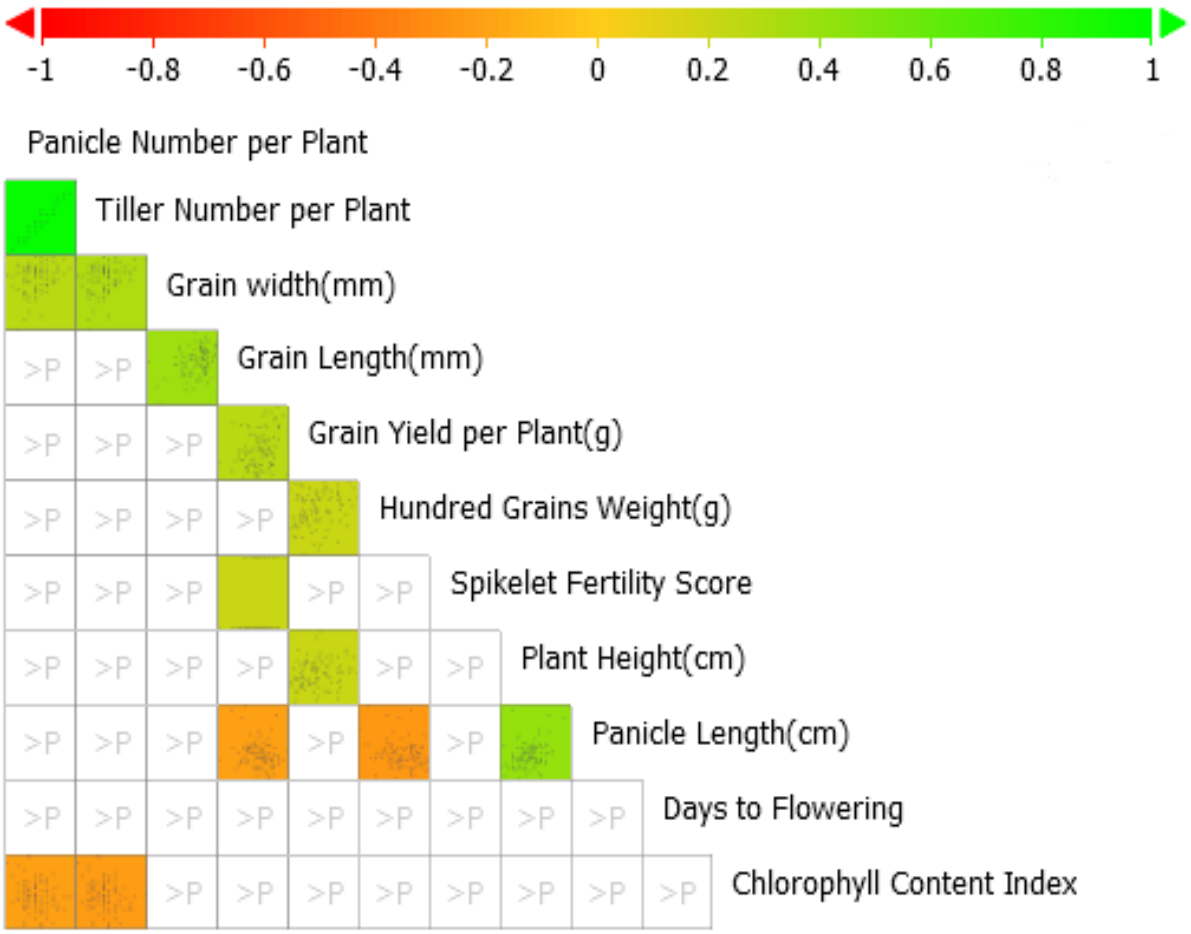


Figure 8. Estimate of Pearson correlations of 100 rice genotypes evaluated under non-drought at Fumesua-Kumasi, Ghana in 2021-2022. >P – non-significant correlation. The light green and green colours indicate positive significant correlation. The orange colour indicates negative significant correlation. The numbers between the ranges -1 to +1 represent the correlation value following the colour gradient.

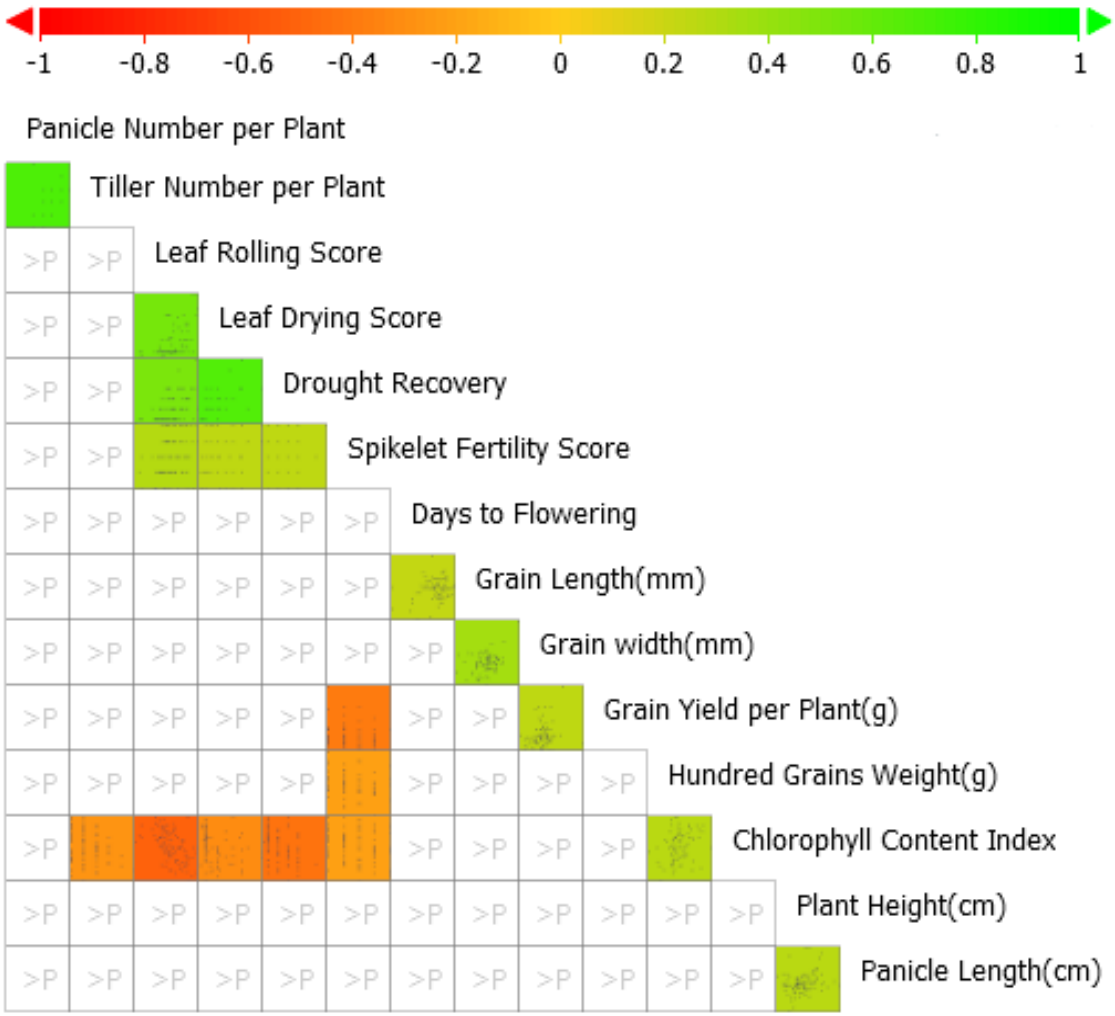


Figure 9. Estimate of Pearson correlations of 100 rice genotypes evaluated under drought stress at Fumesua-Kumasi, Ghana in 2021-2022. >P – non-significant correlation. The light green and green colours indicate positive significant correlation. The orange colour indicates negative significant correlation. The numbers between the ranges -1 to +1 represent the correlation value following the colour gradient.

Tiller number and panicle number per plant recorded a highly significant positive correlations among themselves as well as plant height and panicle length, and the same trend applied for grain width and grain length. A highly positive and significant correlation was observed between leaf rolling score and recovery from drought. The increase in hundred grains weight and grain yield is a result of an increase in chlorophyll content index under drought stress with the ability to maintain a low leaf rolling and high recovery from drought stress.

- **Principal component analysis**

To decipher the relatedness among the various traits studied in this experiment, principal component analysis (PCA) was performed for rice genotypes, and conditions to establish any clustering based on 11 morphological and physiological traits under non-drought conditions, and 14 morphological and physiological traits under drought stress conditions. principal component analysis (PCA) generated principal components (PCs). Under non-drought conditions, the PCA registered five principal components with eigenvalues > 1 cumulating 71.38% of the total variation (Table 9). The contribution of each variable and attribute to the variability on each principal component is presented in Table 9. The first PC1 explained about 21.62% of the total variation. The PC2 and PC3 explained about 15.35% and 13.81% of the total variation. The PC4 and PC5 explained each 11.18% and 9.41% of the total variation, respectively. The parameters in each principal component were left out based on significant factor loading values less than or equal to 0.1. The PC1 was more positively contributed to by grain yield, tiller number and panicle number per plant, grain width and grain length, confirming the positive correlations observed among these traits. The PC2 was more positively contributed to by chlorophyll content index, spikelet fertility score, grain yield per plant, grain width and grain length, and hundred grains weight. The PC3 was more positively contributed to by spikelet fertility score, grain yield per plant, plant height and panicle length, grain width and grain length. The PC4 was more positively contributed to by chlorophyll content index, panicle length, grain width and grain length. The PC5 was more positively contributed to by chlorophyll content index, grain yield per plant, days to flowering, panicle length, and hundred grains weight. Chlorophyll content index, tiller and panicle number per plant, plant height, grain yield, hundred grains weight and grain width contributed more to variability among the genotypes under non-drought conditions. This can be explained by the trends of correlation that exist among these traits. Under drought stress, the PCA registered five principal components with eigenvalues > 1 cumulating 64.18% of the total variation (Table 10).

Table 9. Principal components analysis of morpho-physiological traits of 100 rice genotypes evaluated under non-drought conditions at Fumesua-Kumasi, Ghana in 2021-2022

Designation	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Chlorophyll Content Index	-0.18	0.18	-0.02	0.55	0.40	0.23	0.56	0.01	0.16	0.29	0.02
Spikelet Fertility Score	0.09	0.18	0.44	-0.12	-0.53	0.12	0.55	0.31	0.05	-0.24	-0.03
Grain Yield per Plant(g)	0.14	0.27	0.47	-0.21	0.41	-0.17	0.09	-0.58	0.13	-0.29	0.00
Days to Flowering	-0.02	0.03	-0.11	-0.61	0.45	0.54	0.09	0.29	-0.13	-0.04	0.03
Tiller Number per Plant	0.58	-0.25	-0.08	-0.02	0.07	-0.14	0.20	0.05	0.04	0.09	0.71
Panicle Number per Plant	0.57	-0.28	-0.08	-0.04	0.14	-0.15	0.20	0.07	0.04	0.14	-0.70
Plant Height(cm)	-0.16	-0.26	0.61	-0.10	0.06	-0.10	-0.05	0.05	-0.39	0.60	0.03
Panicle Length(cm)	-0.15	-0.46	0.33	0.19	0.29	-0.07	-0.19	0.43	0.40	-0.38	0.01
Grain Length(mm)	0.32	0.39	0.21	0.03	-0.08	0.28	-0.44	0.13	0.51	0.38	0.00
Grain width(mm)	0.35	0.12	0.17	0.46	0.09	0.33	-0.25	0.08	-0.58	-0.31	-0.02
Hundred Grains Weight(g)	0.00	0.52	-0.06	-0.04	0.25	-0.60	-0.03	0.52	-0.16	0.02	0.01
Eigenvalue	2.38	1.69	1.52	1.23	1.04	0.83	0.77	0.56	0.54	0.43	0.02
Proportion (%)	21.62	15.35	13.81	11.18	9.41	7.5	6.99	5.09	4.93	3.9	0.22
Cumulative (%)	21.62	36.97	50.78	61.96	71.38	78.88	85.86	90.95	95.88	99.78	100

PC-Principal component

Table 10. Principal components analysis of morpho-physiological traits of 100 rice genotypes evaluated under drought stress at Fumesua-Kumasi, Ghana in 2021-2022

Designation	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Chlorophyll Content Index	-0.41	-0.21	0.01	0.01	-0.14	0.03	0.39	0.30	0.30	0.25	0.49	0.22	-0.08	0.27
Spikelet Fertility Score	0.32	-0.14	-0.06	-0.13	0.31	-0.11	0.53	0.46	-0.10	0.16	-0.44	-0.08	0.11	0.13
Grain Yield per Plant(g)	-0.16	0.16	0.18	0.41	-0.33	-0.51	-0.06	0.11	-0.25	0.45	-0.08	-0.27	0.09	-0.04
Days to Flowering	0.08	-0.10	0.37	-0.37	0.26	-0.08	-0.53	0.35	0.30	0.26	0.14	-0.16	0.15	-0.08
Tiller Number per Plant	0.11	0.60	-0.12	-0.11	-0.17	0.29	-0.08	0.06	0.08	0.08	0.00	-0.20	0.20	0.62
Panicle Number per Plant	0.09	0.61	-0.09	-0.18	0.04	0.06	0.22	0.07	0.03	0.29	0.15	0.26	-0.09	-0.58
Plant Height(cm)	0.08	0.06	0.12	0.37	0.63	0.08	0.17	-0.44	0.14	0.28	0.22	-0.26	-0.03	0.09
Panicle Length(cm)	-0.02	0.07	-0.17	0.61	0.25	0.20	-0.34	0.41	0.03	-0.02	-0.12	0.42	0.08	0.01
Grain Length(mm)	-0.05	0.18	0.57	-0.03	0.19	0.05	0.09	0.17	-0.60	-0.30	0.28	0.13	-0.02	0.13
Grain width(mm)	-0.09	0.22	0.52	0.19	-0.11	-0.05	0.24	0.01	0.56	-0.37	-0.31	-0.01	0.09	-0.09
Hundred Grains Weight(g)	-0.22	-0.17	0.32	-0.04	-0.16	0.65	0.00	-0.11	-0.15	0.42	-0.38	0.03	-0.09	-0.07
Leaf Rolling Score	0.46	-0.02	0.24	-0.03	-0.12	-0.26	-0.09	-0.25	0.08	0.24	-0.08	0.58	-0.28	0.32
Leaf Drying Score	0.44	-0.21	0.09	0.16	-0.28	0.20	0.13	-0.07	-0.03	0.04	0.29	0.07	0.68	-0.17
Drought Recovery	0.45	-0.07	0.05	0.24	-0.24	0.22	0.00	0.29	0.07	-0.08	0.21	-0.37	-0.58	-0.10
Eigenvalue	2.73	1.95	1.65	1.40	1.26	0.99	0.90	0.70	0.62	0.54	0.47	0.36	0.25	0.17
Proportion (%)	19.50	13.93	11.77	9.99	9.00	7.07	6.44	5.00	4.44	3.87	3.39	2.58	1.82	1.21
Cumulative (%)	19.50	33.43	45.19	55.18	64.18	71.26	77.70	82.70	87.14	91.01	9.44	96.97	98.79	100

PC-Principal component

The contribution of each variable and attribute to the variability on each principal component is presented in Table 10. The first PC1 explained about 19.50% of the total variation. The PC2 and PC3 explained about 13.93% and 11.77% of the total variation, respectively. The PC4 and PC5 explained about 9.99% and 9.00% of the total variation, respectively. The PC1 was more positively contributed to by spikelet fertility score, leaf rolling score and recovery from drought score which depicted the positive correlations observed among these traits and chlorophyll content index contributed more negatively confirming the negative correlation recorded with the spikelet fertility score, leaf rolling score and recovery from drought score during the correlation analysis. The PC2 was more positively contributed to by the number of tillers and panicles per plant, grain width and grain length. The PC3 was more positively contributed to by days to flowering, grain width and grain length, hundred grains weight and leaf rolling score. The PC4 was more positively contributed to by chlorophyll grain yield, plant height, panicle length, and recovery from drought. The PC5 was more positively contributed to by spikelet fertility score, days to flowering, plant height, panicle length. Chlorophyll content index, spikelet fertility score, tiller and panicle number per plant, plant height, grain yield, hundred grains weight and leaf rolling score contributed more to variability among the genotypes under the drought stress. This explained the trends of correlation that exist among these traits under the stress conditions.

4.1.1.4 Predictors of drought tolerance genotype using relative trait value

In order to determine the secondary traits to use in addition to the grain yield for the selection of the potential drought-tolerant genotypes, correlation coefficients using the relative value of each trait commonly called drought risk index (Bouman et al., 2001) were calculated. The Pearson correlation based on the drought risk index is presented in Figure 10, while the correlation table is presented in the annex 7. Based on drought risk index, relative grain yield recorded a high significant positive correlation with relative grain length, relative grain width and relative hundred grains weight, but significantly and negatively correlated with relative spikelet fertility score. Relative spikelet fertility score recorded significant and negative correlation with relative hundred grains weight. Based on the correlation analysis under drought stress and the correlation using the drought risk index, it was derived that chlorophyll content, spikelet fertility, the low leaf rolling capacity, the high recovery capacity of the plant from drought, grain length, grain width and hundred grains weight are the best predictors for the grain yield among these genotypes under drought stress.

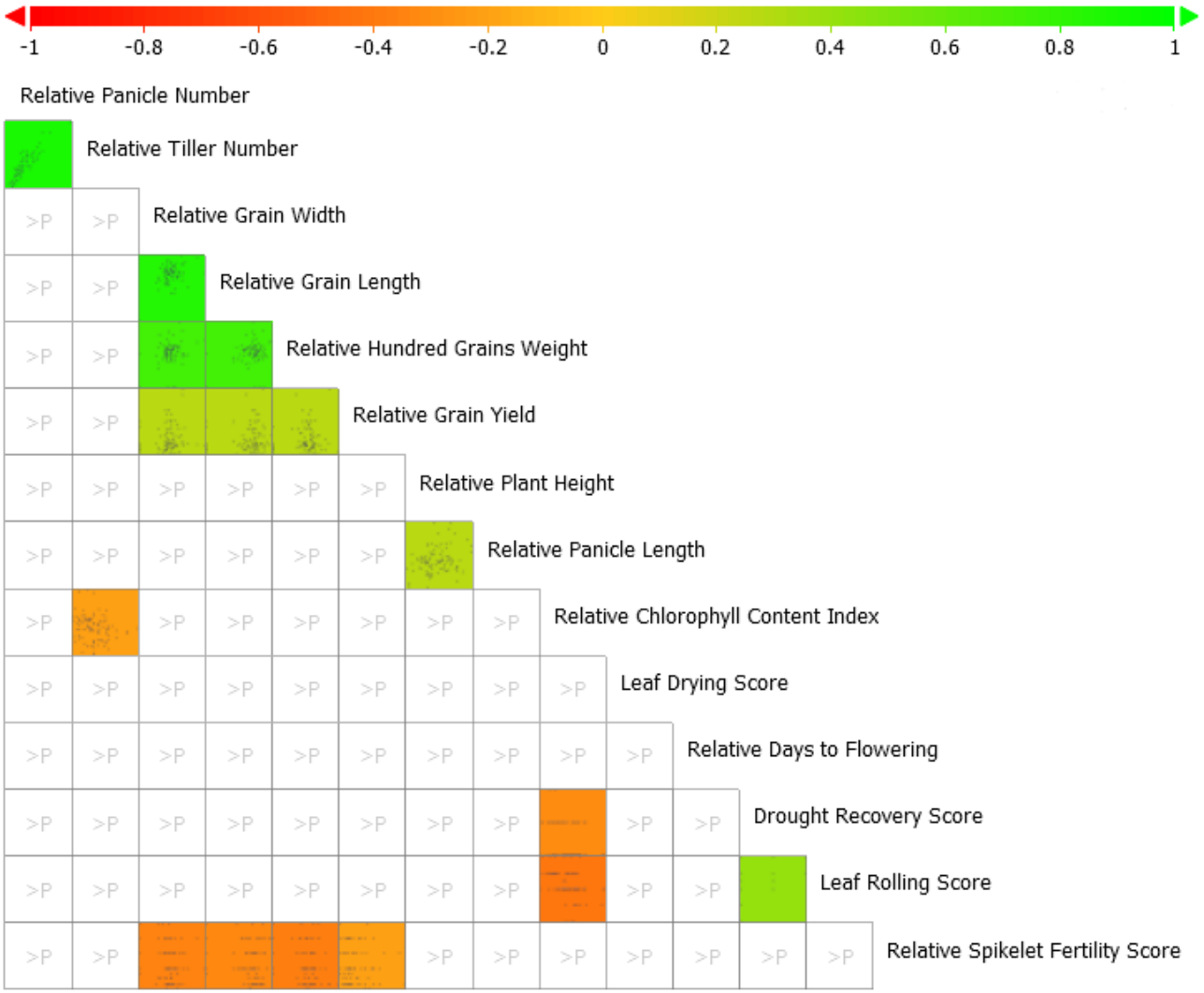


Figure 10. Estimate of Pearson correlations of 100 rice genotypes evaluated under drought stress using the drought risk index or relative value of each trait at Fumesua-Kumasi, Ghana, in 2021-2022. >P – non-significant correlation. The light green and green colours indicate positive significant correlation. The orange colour indicates negative significant correlation. The numbers between the ranges -1 to +1 represent the correlation value following the colour gradient.

The correlation analysis is confirmed by the principal component analysis where the contribution of the traits was highlighted and ranked using a colour gradient with the highest contributing trait represented in red and the lowest contributing traits in blue. The PCA revealed that tiller number, panicle number, grain length, grain width, hundred grains weight were the most contributing traits in descending order (Figure 11). These traits were followed by spikelet fertility score, CCI. In this current study, it can be derived that the selection of a given genotype as drought-tolerant must combine the relative value of the following traits to be close to 1 (drought risk index of each trait is ≤ or ≥ 1): relative grain yield, relative CCI, relative spikelet fertility scores, leaf rolling score, recovery from drought, relative grain length, relative grain width and relative hundred grains weight. The selection for drought tolerance must first target the above-mentioned traits, before expanding it to other secondary traits.

4.1.1.5 Selection of the potential drought-tolerant genotypes based on the morpho-physiological traits

In this current study, relative grain yield has been used as a main selection criterion followed by other secondary traits relative values (Annex 8). Using relative grain yield as main selection criterion, eight genotypes (G6, G62, G73, G79, G100, G99, G65 and G11) were selected as potential drought-tolerant genotypes and presented in Table 11.

In the current study, MGIDI index was also used to select the tolerant genotypes. The outputs of the MGIDI index computation under field conditions is presented in Annex 9. Out of the 14 traits inputted in the MGIDI computation model, only 10 were used to compute the index. The traits used to compute the MGIDI index were relative spikelet fertility score, relative grain yield, relative plant height, relative grain length, relative leaf rolling, relative leaf drying, relative recovery from drought, relative chlorophyll content index, relative days to flowering and relative tiller number. The following genotypes were selected in the chronological order: Viwonor short (G60), UPLR-17 (G100), SR35250-2-4-2-3 (G77), APO (G99), SA69-SARI (G79), UPL 32 (G66), Togo Marshall (G6), SR35266-2-12-4-1-SARI (G74), GR18-SARI (G65), ART75-33-1-1-B-B (G44), SR34590-HB3433-6-2-1 (G81), SR35266-2-12-4-1 (G21), SR35311-HB3497-87 (G89), AGRA-CRI-LOL-1-11 (G14), CRI-Mpuntuo (G10). The full name of the genotypes with their corresponding ID are presented in the Annex 3. The genotype ranking based on the MGIDI index is presented in Figure 12.

In this current study, the following genotypes Viwonor short (G60), UPLR-17 (G100), APO (G99), SA69-SARI (G79), Togo Marshall (G6) and GR18-SARI (G65) were consisted across

both selection methods used, namely relative grain yield as a main selection criterion followed by other secondary traits relative values, and MGIDI index.

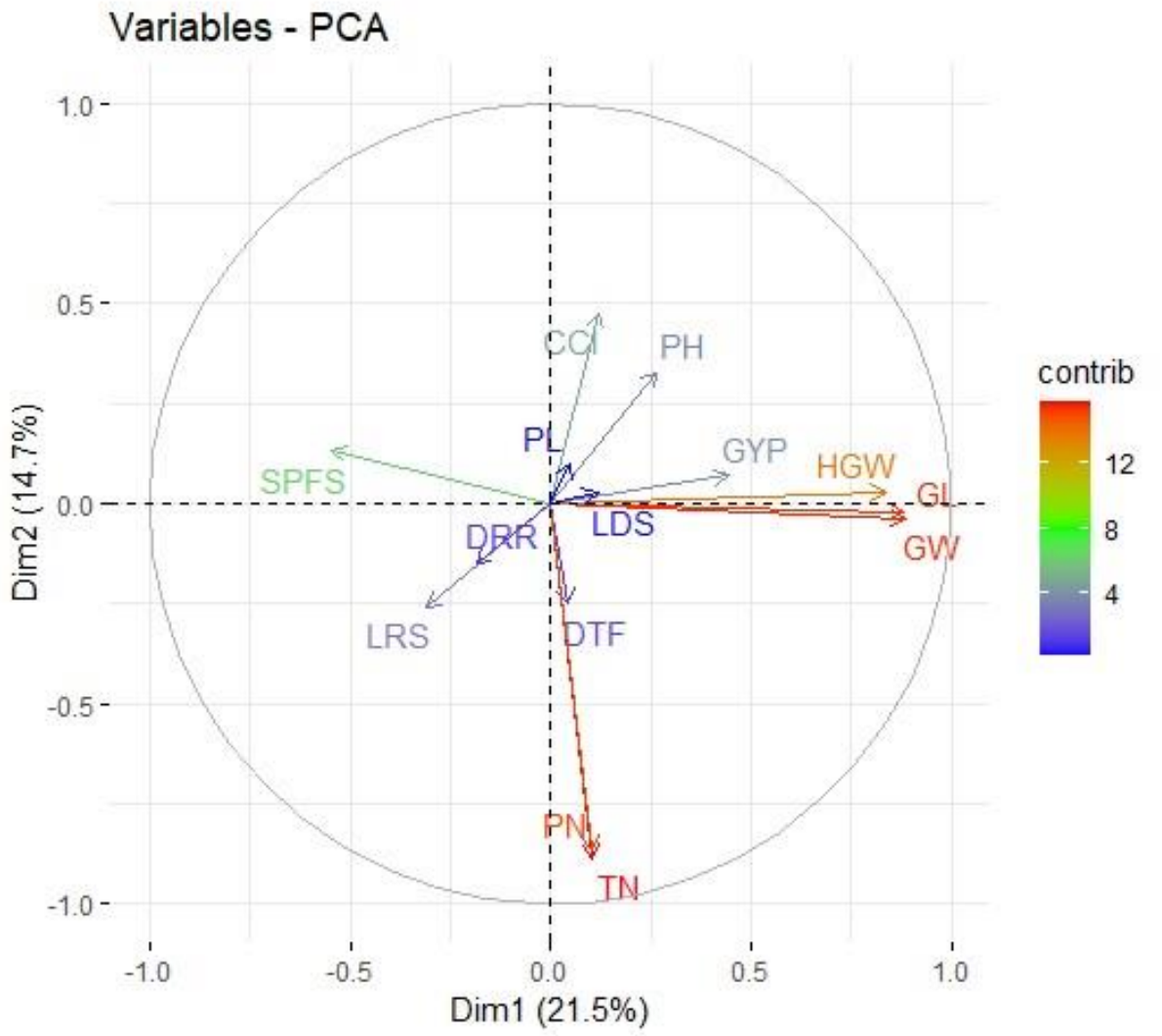


Figure 11. Principal component analysis (PCA) showing the contribution of each trait in the variation among 100 rice genotypes evaluated under drought stress using the drought risk index or relative value of each trait at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana, in 2021-2022. The highest contributing trait is represented in red and the lowest contributing traits in blue. The genotypes were represented by the black dots. CCI-Chlorophyll Content Index, SPFS-Spikelet Fertility Score, GYP-Grain Yield per Plant in g, DTF-Days to Flowering, TN-Tiller Number per Plant, PN-Panicle Number per Plant, PH-Plant Height in cm, PL-Panicle Length in cm, GL-Grain Length in mm, GW-Grain width in mm, HGW-Hundred Grains Weight in g, LRS-Leaf Rolling Score, LDS-Leaf Drying Score, DRR-Drought Recovery

Table 11. Selected potential drought-tolerant genotypes using relative grain yield as main selection criterion, following by other secondary traits relative value among 100 rice genotypes evaluated under drought stress at Fumesua-Kumasi, Ghana, in 2021-2022.

ID	Selected Genotype	Reasons for selection
G6	Togo Marshall	Leaf greenness (high relative CCI), High relative grain yield, Efficient recovery from drought, High relative hundred grains weight, High relative grain length, High relative grain width, Best relative spikelet fertility score (the lower the score, the higher the spikelet fertility according to rice standard evaluation score).
G62	KE40	High relative grain yield, Low delay in days to flowering (when the relative days to flowering are close to one, the better the tolerance to drought), High relative grain width.
G73	SR35266-2-12-1-1	High relative grain yield, High relative plant height, Efficient recovery from drought.
G79	SA69-SARI	Leaf greenness, High relative yield, Low delay in days to flowering, High relative panicle length, Efficient recovery from drought, Best relative spikelet fertility score.
G100	UPLR-17	High relative grain yield, Low delay in days to flowering, Efficient recovery from drought, Breeder's choice based on field performance.
G99	APO	High relative grain yield, Low delay in days to flowering, Low leaf rolling, Efficient recovery from drought, Best relative spikelet fertility score.
G65	GR18-SARI	High relative grain yield, Leaf greenness, High relative panicle length.
G11	CRI-Enapa	Tolerant to short-term drought and is confirmed during this experiment based on best relative spikelet fertility score, low delay in days to flowering, and efficient recovery from drought.

ID-Genotype identity

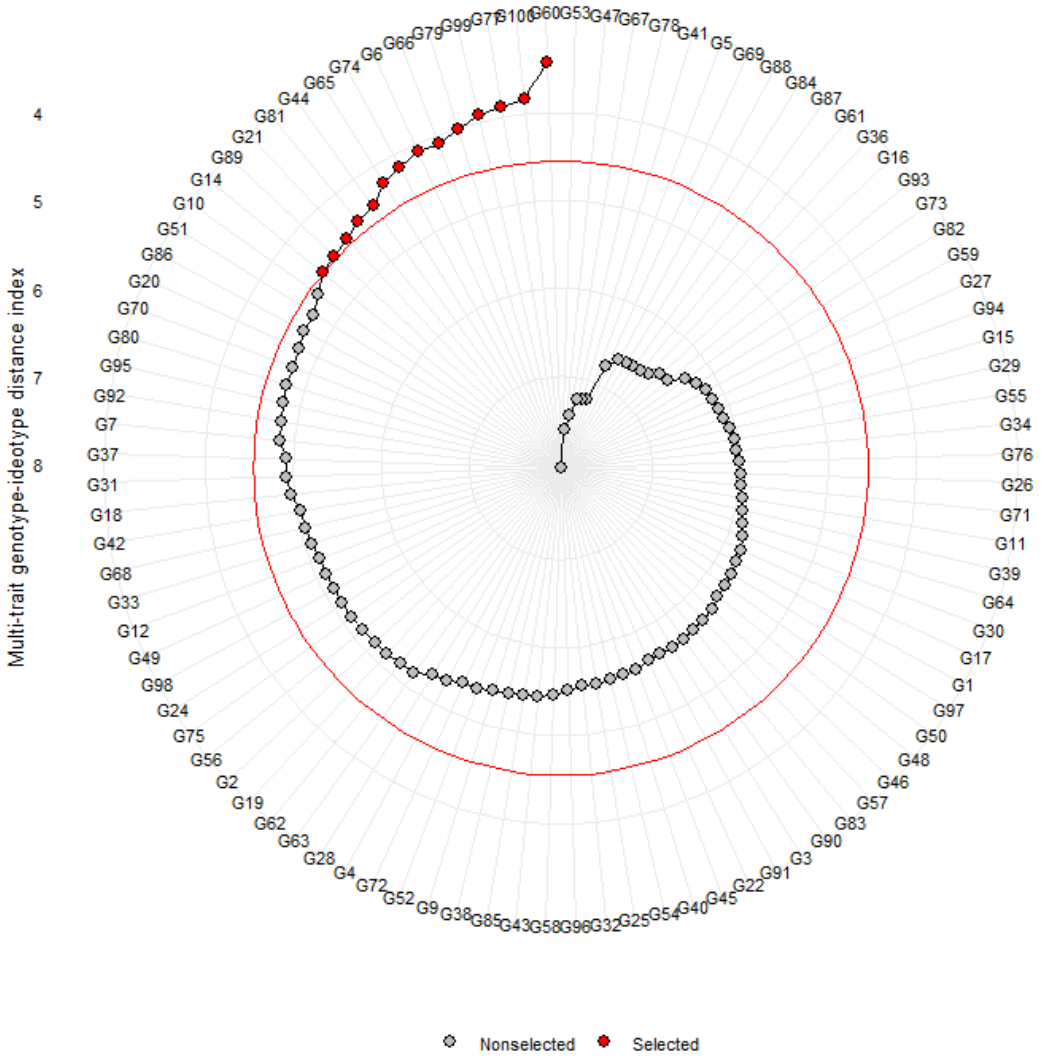


Figure 12. Ranking of the 100 genotypes in ascending order for the MGIDI index under field conditions. The selected genotypes are shown in red. The circle represents the cut-point according to the selection pressure, and the selection intensity is 15. The full name of the genotypes with their corresponding ID are presented in the annex 3. The following genotypes were selected as drought-tolerant genotypes in chronological order: Viwonor short (G60), UPLR-17 (G100), SR35250-2-4-2-3 (G77), APO (G99), SA69-SARI (G79), UPL 32 (G66), Togo Marshall (G6), SR35266-2-12-4-1-SARI (G74), GR18-SARI (G65), ART75-33-1-1-B-B (G44), SR34590-HB3433-6-2-1 (G81), SR35266-2-12-4-1 (G21), SR35311-HB3497-87 (G89), AGRA-CRI-LOL-1-11 (G14), CRI-Mpuntuo (G10).

4.1.1.6 Selection of the potential drought-tolerant genotypes based on known drought QTL profile

The genotyping results revealed that at least one of the nine known drought tolerance QTL used in this study is present in each genotype. The QTL profiles obtained, are presented in the annex 10. All the genotypes selected as potential drought-tolerant genotypes contained at least three known drought tolerance QTL used in this study (Table 12). The genotyping results provided well-defined favourable and unfavourable alleles of each QTL presented in each genotype. Among the genotypes selected as drought-tolerant based on MGIDI index, 50% (G14, G44, G60, G66, G79, G99 and G100) contained the favourable allele of QTL *DTY1.1*, 50% (G14, G44, G60, G65, G74, G77 and G79) contained the favourable allele of DTY2.2 and 21.43% (G6, G14, G99 and G100) contained the favourable allele of *DTY12.1*, while 21.43% of the selected genotypes (G10, G21 and G81) contained none of the favourable alleles of QTLs used in this study. The QTL profile couldn't be established for G89.

Table 12. QTL results of the selected potential drought-tolerant genotypes among the 100 genotypes evaluated under drought stress based on grain yield in Fumesua-Kumasi, 2021-2022

ID	QTL ID	DTY1.1	DTY1.1	DTY1.1	DTY12.1	DTY12.1	DTY2.2	DTY2.2	DTY2.2	DTY2.2
	SNP ID	snpOS00400	snpOS00402	snpOS00408	snpOS00483	snpOS00484	snpOS00412	snpOS00413	snpOS00414	snpOS00415
	FAVORABLE ALLELE	G	A	G	C	T	A	C	G	A
Selected Genotypes										
G6	Togo Marshall	C:C	G:G	T:T	C:C	G:A	C:C	A:A	A:A	T:T
G62	KE40	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G73	SR35266-2-12-1-1	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G81	SR34590-HB3433-6-2-1	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G79	SA69-SARI	G:G	A:A	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G99	APO	G:G	A:A	G:G	C:C	G:G	-	-	-	-
G100	UPL R17	G:G	A:A	G:G	C:C	G:G	-	-	-	-
G65	GR18-SARI	C:C	G:G	T:T	G:G	A:A	A:A	A:A	G:G	T:T
G11	CRI-Enapa	G:G	G:G	T:T	G:G	G:G	A:A	A:A	A:A	T:T

Selected genotypes with tolerance to drought using relative grain yield as selection main selection criterion followed by the secondary traits' relative values; ID-Genotype identity; QTL ID-Quantitative Trait Locus Identity; SNP ID-Single Nucleotide Polymorphism Marker Identity; DTY-Drought-tolerant QTL for grain yield

4.1.2 Physiological and biochemical characterization of selected West Africa rice genotypes in response to drought stress under greenhouse conditions

4.1.2.1 Changes in moisture content of the soil under drought stress at vegetative and reproductive stages

Throughout the experiment the soil moisture content was kept equal or above the field capacity (FC) of the soil (57.75 vol/vol) except during the drought stress phases in the stress pots. In all the stress pots, it was ensured that the soil moisture content was not below the wilting point (10.66 vol/vol) before re-watering and topping-up to FC. Under the vegetative stage drought stress, there was a progressive decrease in the soil moisture with an average soil water loss of 6.09 vol/vol every four days, while under the reproductive stage drought stress, a rapid soil moisture loss was observed with an average soil water loss of 9.99 vol/vol every four days. The summary of the variation in soil moisture content is presented in Figure 13 under vegetative (A) and reproductive (B) stages of drought. The rice plants started to show severe drought stress symptoms when the soil moisture reached 18.14 vol/vol at the vegetative stage and 18.33 vol/vol at the reproductive stage on average.

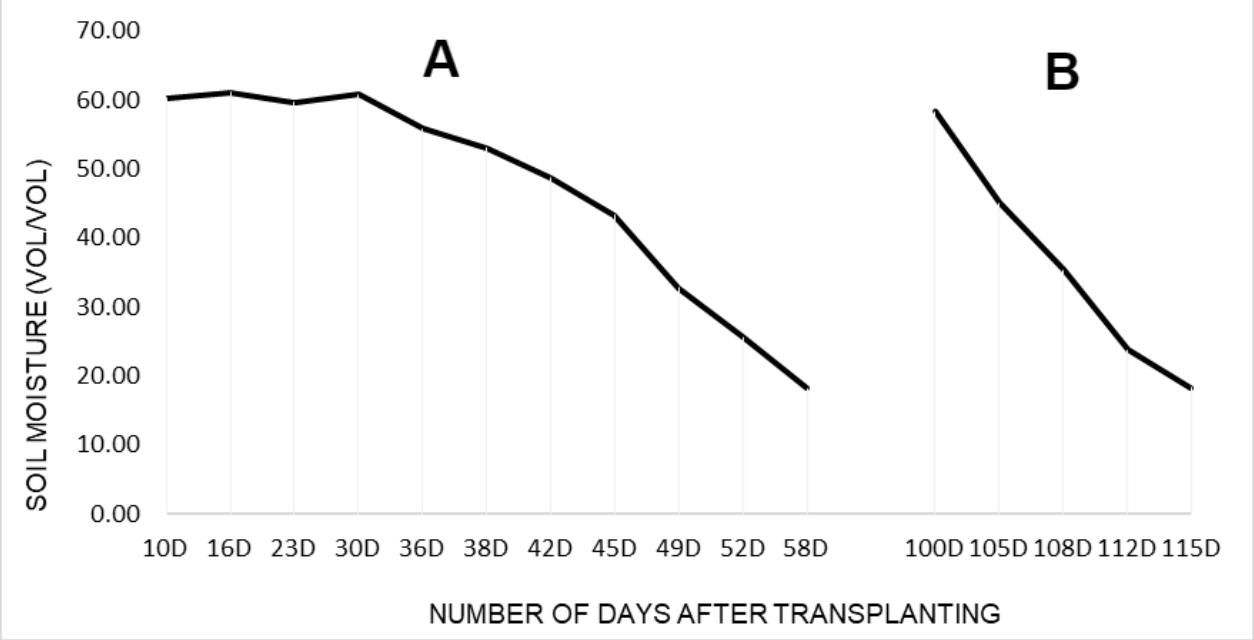


Figure 13. Average variation in soil moisture content among 14 rice genotypes evaluated in the greenhouse for their tolerance to drought at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022, **(A)** vegetative stage drought, **(B)** reproductive stage drought. 10D…115D (days after the transplanting); 30D-initiation of the vegetative stage drought stress; 100D-initiation of the reproductive stage drought stress

4.1.2.2 Weekly changes in physiological and leaf reflectance parameters of the genotypes during the vegetative drought stage

The data were collected on the different genotypes at a time interval of 5, 11, 18 and 27 days after the stress initiation (5D, 11D, 18D and 27D, respectively) on drought-stressed rice plants to determine the changes in the physiological and leaf reflectance parameters. For the physiological parameters, stomatal conductance (gsw) in mol m^{-2} s^{-1} recorded a progressive decrease from 5D to 27D on all the genotypes except on the previously identified two drought-tolerant genotypes G100 and G99. Genotype (G100) recorded an increase of 29.28% from the 18D (0.158 mol m^{-2} s^{-1}) to 27D (0.205 mol m^{-2} s^{-1}) while G99 recorded the lowest reduction of 17.89% from the 18D (0.251 mol m^{-2} s^{-1}) to 27D (0.206 mol m^{-2} s^{-1}) in Figure 14A. For the quantum yield of fluorescence (PhiPS II), a progressive reduction was equally observed from 5D to 27D on all the genotypes except two previously identified drought-tolerant genotypes G100 and G99, and G63 which recorded a slight increase over the time interval of 5D to 27D (Figure 14B). Transpiration rate (E) in mol m^{-2} s^{-1} recorded the similar pattern as stomatal conductance. A progressive and rapid decrease was recorded from 5D to 27D on all the genotypes except on the two drought-tolerant genotypes G100 and G99. G100 recorded an increase of 89.97% of transpiration rate from the 18D (1.726 mol m^{-2} s^{-1}) to 27D (3.279 mol m^{-2} s^{-1}) while G99 recorded an increase of 20.33% from the 18D (2.447 mol m^{-2} s^{-1}) to 27D (2.944 mol m^{-2} s^{-1}, Figure 14C). Electron transport rate (ETR) in μmol m^{-2} s^{-1} recorded high ETR values at 5D and 27D for all the genotypes except G100 which recorded a progressive decrease in ETR from 5D to 27D (Figure 14D). For leaf reflectance parameters, NDVI recorded high values at 5D followed by a progressive decrease from 11D to 27D in all the rice genotypes expect G99 and G78 which recorded a slight and progressive increase at 11D to 27D (Figure 15A). The RDVI recorded higher values on 5D and 27D while the lowest values were obtained on 11D (Figure 15B). Carotenoid reflectance index 1 and 2 (CRI1 and CRI2) displayed similar pattern. Both indexes (CRI1 and CRI2) scored highest at 5 days after drought stress initiation (5D) followed by a rapid decrease at 11D, 18D and 27D. The previously selected two drought-tolerant genotypes namely G99 and G100, and G78 maintained the highest CRI1 and CRI2 values at 27 days after the drought stress initiation (Figure 15C and D). In this study, CRI1 and CRI2, physiological parameters such as stomatal conductance, transpiration rate, Electron transport rate and PhiPS II exhibited enough variation and pattern for tolerance to drought among

the genotypes and therefore can be used as a selection criterion at the vegetative stage drought stress.

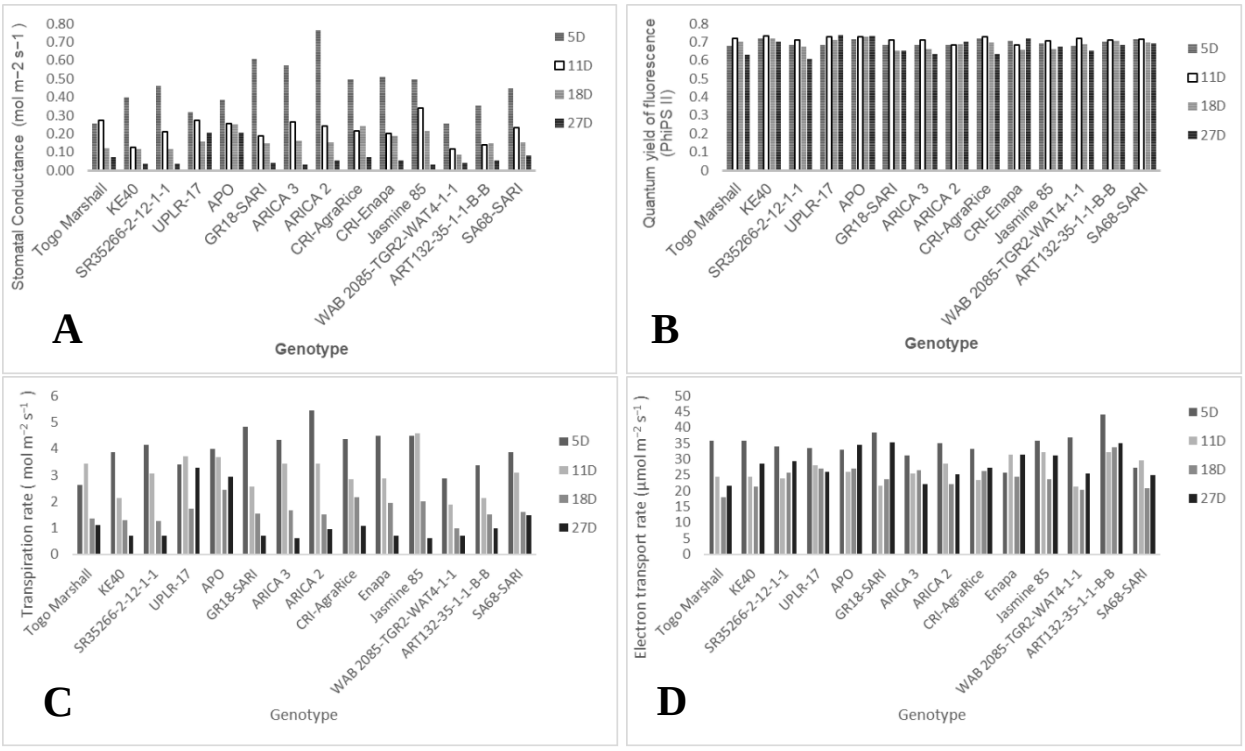


Figure 14. Variation in **(A)** stomatal conductance, **(B)** quantum yield of fluorescence (PhiPS II), **(C)** transpiration rate and **(D)** electron transport rate (ETR) among 14 rice genotypes evaluated in the greenhouse under vegetative stage drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022. 5D: 5-day after the drought stress initiation; 11D: 11-day after the drought stress initiation; 18D: 18-day after the drought stress initiation; 27D: 27-day after the drought stress initiation. Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

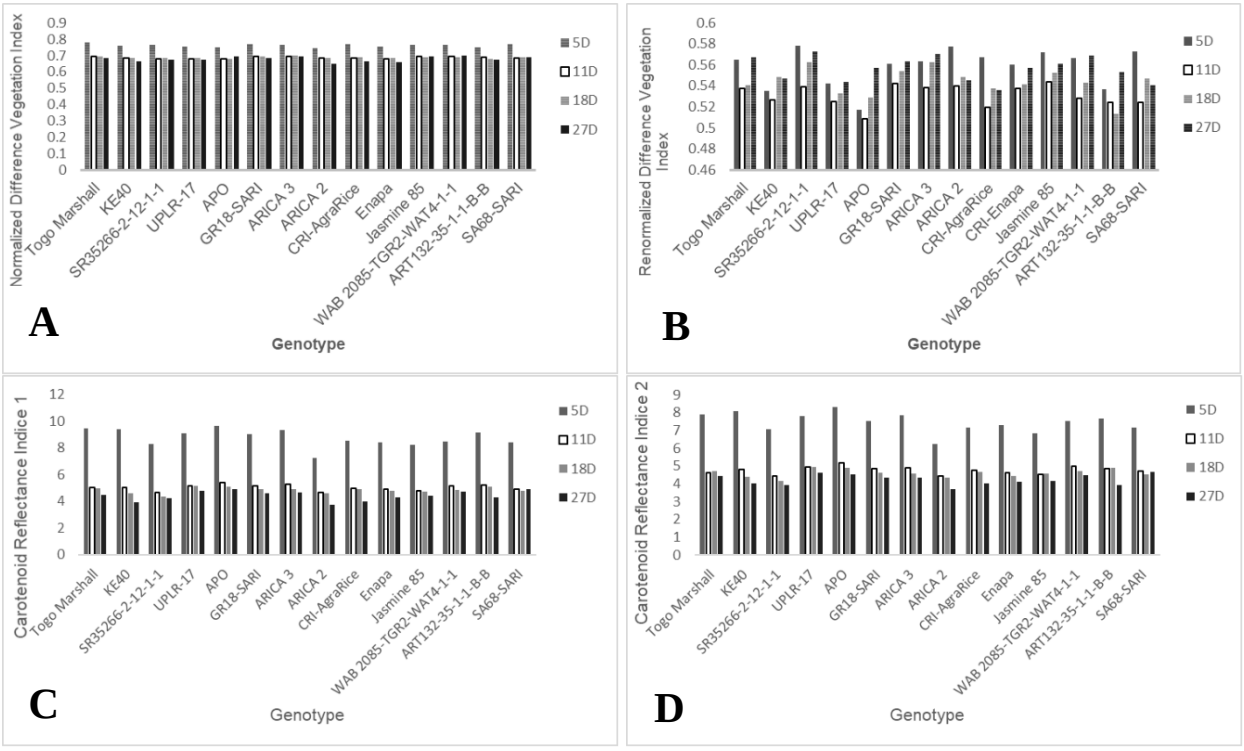


Figure 15. Variation in **(A)** Normalized Difference Vegetative Index (NDVI) and **(B)** Renormalized Difference Vegetative Index (RDVI), **(C)** Carotenoid Reflectance Index 1 (CR1) and **(D)** Carotenoid Reflectance Index 2 (CR2) among 14 rice genotypes evaluated in the greenhouse under vegetative stage drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022. 5D: 5-day after the drought stress initiation; 11D: 11-day after the drought stress initiation; 18D: 18-day after the drought stress initiation; 27D: 27-day after the drought stress initiation. Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

4.1.2.3 Mean performances of the rice genotypes under both vegetative stage drought stress and non-drought conditions based on the physiological and leaf reflectance parameters

Overall genotypes mean for each trait, coefficient of variations (C.V.%) and broad-sense heritability (h^2_{bs}) from the analyses of variances of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought stress conditions at 5, 11, 18 and 27 days after the drought stress initiation is presented in Table 13.

- **At five days (5D) after the drought stress initiation**

The analysis of variance (ANOVA) revealed the presence of significant differences among the rice genotypes for Normalized difference vegetative index (NDVI), Carotenoid reflectance index 1 (CRI1) and Carotenoid reflectance index 2 (CRI2) under non-drought conditions (Table 14), while under drought stress conditions, significant differences were observed on stomatal conductance, NDVI and Renormalized difference vegetative index (RDVI) (Table 14) during 5 days after the drought stress initiation (5D). Under both non-drought and drought stress conditions NDVI and RDVI recorded low C.V. and moderate to high broad-sense heritability. Low to moderate C.V. were obtained under non-drought conditions (NDVI= 1.87 and RDVI= 3.95) and drought stress (NDVI= 2.01 and RDVI= 4.48). Moderate to high C.V. were obtained under the non-drought conditions (CRI1= 13.43 and CRI2= 13.63) and drought stress (CRI1= 13.09 and CRI2= 12.97) combined with moderate heritability values (Table 15 and 16). High C.V. and moderate heritability were also recorded for stomatal conductance under both drought stress and non-drought conditions. The means performance with the ranking of the genotypes using the Duncan multiple rank test is presented in Table 15. Genotypes G63 recorded the highest stomatal conductance value of 0.763 mol m^{-2} s^{-1} under drought stress and 0.749 mol m^{-2} s^{-1} under non-drought conditions. Genotype G63 is followed by G65 under both water regimes and both genotypes are not statistically different in their mean performance at 5 days after the drought stress initiation. The lowest value of 0.254 mol m^{-2} s^{-1} of stomatal conductance under 5 days drought stress was occupied by G53, while Togo Marshall recorded the lowest value (0.287 mol m^{-2} s^{-1}) under non-drought conditions. Statistically, G53 showed a difference in the mean performance with G63 and G65. Genotype G6 recorded the highest NDVI of 0.780 under both drought stress and non-drought conditions.

Table 13. Overall genotypes mean for each trait, coefficient of variations (C.V.%) and broad-sense heritability (h^2_{bs}) among 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought stress conditions at University of Giessen, Germany in 2022, at 5, 11, 18 and 27 days after the start of the drought treatment.

Water regimes																							
	5 days after drought stress initiation						11 days after drought stress initiation						18 days after drought stress initiation						27 days after drought stress initiation					
	Non-drought			Drought stress			Non-drought			Drought stress			Non-drought			Drought stress			Non-drought			Drought stress		
TRAITS	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}	GM	C.V.	h^2_{bs}
TN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	11.92	30.72	76.48	8.30	30.59	62.93
gsw	0.47	56.52	43.62	0.45	46.08	53.69	0.35	61.55	35.79	0.22	60.32	35.5	0.53	49.43	63.61	0.16	55.08	48.65	0.51	43.22	42.9	0.07	84.10	70.98
E	3.98	41.63	25.51	4.01	34.99	24.59	4.14	42.38	39.02	3.06	44.91	44.27	3.46	25.10	70.16	1.65	39.50	57.19	3.98	32.59	-	1.18	73.23	71.51
PhiPS II	0.69	4.70	-	0.69	5.77	0.33	0.70	5.74	47.94	0.71	3.65	36.9	0.69	6.65	58.29	0.69	6.60	35.67	0.68	6.57	-	0.68	8.80	34.26
ETR	35.22	22.16	13.08	34.23	29.43	-	33.39	88.59	17.2	26.60	30.45	-	23.84	26.44	-	24.32	34.14	-	28.35	22.73	29.44	28.41	30.98	-
NDVI	0.76	1.87	80.36	0.76	2.01	58.69	0.68	1.62	74.55	0.69	1.51	45.94	0.69	1.49	45.33	0.69	1.63	2.83	0.69	1.83	24.43	0.68	4.07	23.63
CRI1	8.49	13.43	54.21	8.76	13.09	48.07	5.02	7.37	42.24	5.02	5.96	68.77	4.85	7.65	51.63	4.84	6.67	61.74	4.85	6.47	78	4.42	16.11	20.30
CRI2	7.22	13.63	58.67	7.46	12.97	48.41	4.76	7.62	44.66	4.77	6.63	64.34	4.63	8.34	49.18	4.61	7.24	60.54	4.64	6.76	79.28	4.24	12.02	35.86
RDVI	0.57	3.95	41.84	0.56	4.48	69.18	0.53	3.94	-	0.53	3.94	34.2	0.54	4.11	29.87	0.54	3.45	53.46	0.55	3.72	67.93	0.56	3.45	39.89

GM-Overall mean of the genotypes for each trait; TN-Tillers number; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; C.V.- Experimental coefficient of variation in %, h^2_{bs}-Broad-sense heritability

Table 14. Mean square from the analysis of variance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought conditions at University of Giessen, Germany in 2022, 5 days after the start of the drought treatment

TRAITS	REPETITION (D.F.=5)		GENOTYPE (D.F.=13)		RESIDUAL (D.F.=60)		*p-value* (REPETITION)		*p-value* (GENOTYPE)	
	ND	UN	ND	UN	ND	UN	ND	UN	ND	UN
gsw	4.00**	2.71**	1.21	1.54*	0.71	0.74	0.0002	0.0060	0.0812	0.0296
E	4.86**	2.46*	0.91	1.08	0.70	0.86	<.0001	0.0218	0.2404	0.2608
PhiPS II	3.92**	4.53**	0.78	0.71	0.78	0.77	0.0006	0.0002	0.4569	0.5280
ETR	9.67**	7.76**	0.51	0.45	0.41	0.55	<.0001	<.0001	0.2760	0.6431
NDVI	0.86	1.05	2.92**	1.90*	0.63	0.82	0.2433	0.2799	<.0001	0.0139
CRI1	0.47	1.33	1.85*	1.55	0.87	0.85	0.7510	0.1818	0.0257	0.0582
CRI2	0.56	1.45	1.97*	1.55	0.85	0.84	0.6530	0.1445	0.014	0.0569
RDVI	1.58	1.45	1.41	2.21**	0.86	0.71	0.1210	0.0856	0.1002	0.0014

** Significance at 1% level; * Significance at 5% level; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; ND-Under non-drought; UD-Under drought stress; D.F.-Degree of freedom,

Table 15. Mean performance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 5 days drought conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Management	ID	Genotype	gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
Non-drought	G6	Togo Marshall	0.287a	3.001a	0.680a	33.16abc	0.780b	8.757abc	7.312abc	0.577a
Non-drought	G62	KE40	0.524a	4.037a	0.713a	34.50	0.744d	8.317abc	7.171abc	0.549a
Non-drought	G78	SR35266-2-12-1-1	0.454a	3.858a	0.711a	36.48	0.759ac	7.710ac	6.570ac	0.571a
Non-drought	G100	UPLR-17	0.290a	3.159a	0.700a	39.26	0.760ac	9.787b	8.420b	0.535a
Non-drought	G99	APO	0.522a	4.339a	0.715a	39.05	0.758ac	8.771abc	7.458abc	0.566a
Non-drought	G65	GR18-SARI	0.655a	4.749a	0.709a	30.17	0.766ab	8.966abc	7.673ab	0.571a
Non-drought	G5	ARICA 3	0.549a	4.344a	0.682a	37.84	0.767ab	8.758abc	7.415abc	0.571a
Non-drought	G63	ARICA 2	0.749a	5.230a	0.678a	33.73	0.753acd	7.418c	6.149c	0.567a
Non-drought	G2	CRI-Agrarice	0.367a	3.362a	0.692a	36.51	0.773ab	8.814abc	7.404abc	0.567a
Non-drought	G11	CRI-Enapa	0.398a	3.577a	0.715a	32.57	0.736d	7.366c	6.273c	0.571a
Non-drought	G22	Jasmine 85	0.395a	3.700a	0.694a	33.35	0.757ac	7.734ac	6.610ac	0.555a
Non-drought	G53	WAB 2085-TGR2-WAT4-1-1	0.387a	3.659a	0.685a	40.18	0.772ab	9.104ab	7.860ab	0.567a
Non-drought	G36	ART132-35-1-1-B-B	0.494a	4.150a	0.669a	30.08	0.758ac	8.549abc	7.175abc	0.570a
Non-drought	G78	SA68-SARI	0.566a	4.607a	0.698a	36.21	0.783b	8.799abc	7.542abc	0.579a
Drought	G6	Togo Marshall	0.255c	2.625a	0.680a	35.83	0.780b	9.459a	7.904	0.565acd
Drought	G62	KE40	0.400abc	3.870a	0.721a	35.71	0.759abc	9.379a	8.064a	0.535bd
Drought	G73	SR35266-2-12-1-1	0.463abc	4.151a	0.684a	34.01	0.767abc	8.285a	7.092a	0.578c
Drought	G100	UPLR-17	0.318ac	3.393a	0.684a	33.41	0.754ac	9.077a	7.789a	0.542abcd
Drought	G99	APO	0.385abc	3.976a	0.717a	32.89	0.750ac	9.667a	8.328a	0.517bd
Drought	G65	GR18-SARI	0.608ab	4.834a	0.684a	38.44	0.769ab	9.003a	7.531a	0.561acd
Drought	G5	ARICA 3	0.571ab	4.334a	0.682a	31.07	0.765abc	9.354a	7.861a	0.563acd
Drought	G63	ARICA 2	0.763b	5.435a	0.684a	34.99	0.747c	7.266a	6.248a	0.577c
Drought	G2	CRI-Agrarice	0.495abc	4.363a	0.717a	33.17	0.771ab	8.549a	7.175a	0.567acd
Drought	G11	CRI-Enapa	0.512abc	4.502a	0.707a	25.64	0.754ac	8.380a	7.321a	0.560acd
Drought	G22	Jasmine 85	0.497abc	4.471a	0.695a	35.73	0.765abc	8.214a	6.823a	0.572ac
Drought	G53	WAB 2085-TGR2-WAT4-1-1	0.254c	2.871a	0.678a	36.80	0.763abc	8.490a	7.517a	0.566acd
Drought	G36	ART132-35-1-1-B-B	0.354abc	3.369a	0.702a	44.15	0.752ac	9.148a	7.661a	0.537abd
Drought	78	SA68-SARI	0.446abc	3.872a	0.716a	27.38	0.771ab	8.405a	7.173a	0.573c

gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; abcd- letter used to rank the genotypes based on the Duncan multiple rank test, the mean value with the same letter for a particular trait under the drought or non-drought means these genotypes are not statistically different in their mean performance for that trait under weather the drought or non-drought conditions; ID-Genotype Identity

Genotype G6 is followed by G2 and G78 under drought stress. Under non-drought conditions, SA68-SARI topped first (0.783) followed by G6 and G2. Under both water regimes the three genotypes are not statistically different in their mean performance at 5 days after the drought stress initiation. The lowest value of 0.747 of NDVI under 5 days drought stress was occupied by G63, while G11 recorded the lowest value (0.736) under non-drought conditions. Statistically, G63 showed a difference in the mean performance with G6 but not with G2 and G78 under 5 days drought stress. On the other hand, under the non-drought conditions G11 showed a statistical difference in the mean performance with G6, G2 and G78.

- **At 11 days (11D) after the drought stress initiation**

At 11 days after the drought stress initiation (11D), ANOVA revealed the presence of significant differences among the rice genotypes for NDVI under non-drought conditions (Table 16). Under drought stress conditions, ANOVA showed significant differences for CRI1 and CRI2 (Table 16). Under both non-drought and drought stress conditions all the leaf reflectance parameters namely NDVI, RDVI, CRI1 and CRI2 recorded low to moderate C.V. and moderate to high heritability. Low to moderate C.V. obtained under non-drought conditions (NDVI= 1.62, RDVI= 3.94, CRI1= 7.37 and CRI2= 7.62) and drought stress (NDVI= 1.51, RDVI= 3.94, CRI1= 5.96 and CRI2= 6.63) were obtained at 11D. Moderate heritability under non-drought conditions (CRI1= 42.24 and CRI2= 44.66) and high heritability under drought stress (CRI1= 68.77 and CRI2= 64.34) were recorded at 11D in this study (Table 16). High C.V. and moderate heritability were also recorded for stomatal conductance and transpiration rate under both drought stress and non-drought conditions. The means performance with the ranking of the genotypes using the Duncan multiple rank test is presented in Table 17.

In general, the mean performance of all the genotypes has been decreased notably under drought stress compared to the non-drought conditions for stomatal conductance and transpiration rate for all the genotypes except G100 and G6. These genotypes have been previously identified as having the ability to tolerant drought stress in our previous field experiment. Genotype G22 recorded the highest stomatal conductance (0.340 mol m^{-2} s^{-1}) and transpiration rate (4.593 mol m^{-2} s^{-1}) under drought stress and 0.557 mol m^{-2} s^{-1} and 6.504 mol m^{-2} s^{-1} respectively for stomatal conductance and transpiration rate under non-drought conditions. Genotype G22 was followed by G100 and G6 under drought stress for stomatal conductance while G100 and G99 for transpiration rate. Under

non-drought conditions, G22 was followed by G63 and G65 for stomatal conductance and G63 and G99 for transpiration rate.

Table 16. Mean square from the analysis of variance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought stress conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022, 11 days after the start of the drought treatment

TRAITS	REPETITION (D.F.=5)		GENOTYPE (D.F.=13)		RESIDUAL (D.F.=60)		*p-value* (REPETITION)		*p-value* (GENOTYPE)	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
gsw	3.88**	4.44**	1.11	1.13	0.73	0.72	0.0004	0.0001	0.1360	0.1201
E	5.15**	3.74**	1.03	1.28	0.65	0.73	<.0001	0.0005	0.1155	0.0718
PhiPS II	6.61**	4.00**	1.02	1.10	0.55	0.71	<.0001	0.0002	0.0529	0.1254
ETR	5.80**	11.28**	0.77	0.25	0.66	0.29	<.0001	<.0001	0.3274	0.6023
NDVI	0.20	0.47	2.59**	1.60	0.72	0.91	0.9218	0.7660	0.0003	0.0706
CRI1	2.06*	0.65	1.39	2.31**	0.81	0.75	0.0383	0.5101	0.0822	0.0015
CRI2	2.52**	0.39	1.37	2.16**	0.77	0.80	0.0112	0.7816	0.0672	0.0048
RDVI	1.61	2.61*	0.87	1.22	0.97	0.83	0.1573	0.0140	0.5645	0.1549

** Significance at 1% level; * Significance at 5% level; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; ND-Under non-drought; UD-Under drought; D.F.-Degree of freedom

Table 17. Mean performance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 11 days drought conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Management	ID	Genotype	gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
Non-Drought	G6	Togo Marshall	0.184a	2.659a	0.700a	29.44a	0.692ace	5.185a	4.828a	0.525a
Non-Drought	G62	KE40	0.242a	3.073a	0.727a	23.65a	0.674bd	5.015a	4.803a	0.519a
Non-Drought	G73	SR35266-2-12-1-1	0.365a	3.936a	0.705a	24.72a	0.687abce	4.937a	4.723a	0.541a
Non-Drought	G100	UPLR-17	0.249	3.550a	0.699a	63.08a	0.678be	5.099a	4.917a	0.523a
Non-Drought	G99	APO	0.427a	5.025a	0.730a	30.87a	0.685abce	5.421a	5.185a	0.519a
Non-Drought	G65	GR18-SARI	0.475a	4.891a	0.688a	31.01a	0.691ace	5.182a	4.860a	0.534a
Non-Drought	G5	ARICA 3	0.321a	3.815a	0.686a	24.73a	0.688abce	5.173a	4.858a	0.534a
Non-Drought	G63	ARICA 2	0.533a	5.284a	0.684a	29.61a	0.688abce	4.682a	4.404a	0.546a
Non-Drought	G2	CRI-Agrarice	0.291a	3.621a	0.698a	34.16a	0.693ace	5.052a	4.783a	0.538a
Non-Drought	G11	CRI-Enapa	0.274a	3.494a	0.723a	23.98a	0.662d	4.789a	4.504a	0.525a
Non-Drought	G22	Jasmine 85	0.557a	6.504a	0.714a	26.39a	0.684abce	4.982a	4.711a	0.523a
Non-Drought	G53	WAB 2085-TGR2-WAT4-1-1	0.200a	2.990a	0.651a	61.02a	0.695ac	5.245a	5.029a	0.532a
Non-Drought	G36	ART132-35-1-1-B-B	0.444a	4.228a	0.686a	32.59a	0.680abe	4.769a	4.499a	0.528a
Non-Drought	G78	SA68-SARI	0.405a	4.873a	0.674a	32.29a	0.698c	4.778a	4.548a	0.539a
Drought	G6	Togo Marshall	0.273a	3.429a	0.719a	24.44a	0.694a	4.995abcd	4.642abd	0.537a
Drought	G62	KE40	0.125a	2.140a	0.731a	24.47a	0.686a	5.009abcd	4.821abcd	0.527a
Drought	G73	SR35266-2-12-1-1	0.211a	3.070a	0.709a	24.03a	0.682a	4.643b	4.440b	0.539a
Drought	G100	UPLR-17	0.275a	3.703a	0.728a	27.95a	0.682a	5.139acd	4.941acd	0.525a
Drought	G99	APO	0.256a	3.672a	0.727a	26.00a	0.678a	5.382c	5.173c	0.508a
Drought	G65	GR18-SARI	0.190a	2.554a	0.710a	21.66a	0.694a	5.159acd	4.860abcd	0.542a
Drought	G5	ARICA 3	0.264a	3.422a	0.710a	25.49a	0.694a	5.259ac	4.910acd	0.538a
Drought	G63	ARICA 2	0.241a	3.428a	0.684a	28.48a	0.683a	4.681b	4.443b	0.540a
Drought	G2	CRI-Agrarice	0.214a	2.844a	0.727a	23.29a	0.685a	4.965abcd	4.763abcd	0.520a
Drought	G11	CRI-Enapa	0.200a	2.883a	0.683a	31.36a	0.681a	4.926abd	4.618abd	0.538a
Drought	G22	Jasmine 85	0.340a	4.593a	0.707a	32.08a	0.692a	4.773bd	4.548bd	0.544a
Drought	G53	WAB 2085-TGR2-WAT4-1-1	0.116a	1.875a	0.719a	21.35a	0.695a	5.173acd	5.016ac	0.528a
Drought	G36	ART132-35-1-1-B-B	0.138a	2.125a	0.711a	32.19a	0.689a	5.185acd	4.837abcd	0.524a
Drought	G79	SA68-SARI	0.234a	3.083a	0.714a	29.60a	0.683a	4.921abd	4.711abd	0.524a

gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; abcde- letter used to rank the genotypes based on the Duncan multiple rank test, the mean value with the same letter for a particular trait under the drought or non-drought means these genotypes are not statistically different in their mean performance for that trait under weather the drought or non-drought conditions; ID-Genotype identity

The lowest stomatal conductance (0.116 mol m^{-2} s^{-1}) and transpiration (1.875 mol m^{-2} s^{-1}) under 11 days drought stress was occupied by G53, while G6 recorded lowest value for stomatal conductance (0.184 mol m^{-2} s^{-1}) and transpiration rate (2.659 mol m−2 s−1) under non-drought conditions. Statistically, there was no difference in the mean performance among all the genotypes at 11 days after the drought stress initiation under each water regime for the stomatal conductance and transpiration rate. Genotype G53 recorded the highest NDVI of 0.695 under drought stress. Genotype G53 was followed by G6, G5 and G65 recording NDVI of 0.694 each under drought stress. Under non-drought conditions, G78 topped first (0.698) followed by G53, G2 and G6. Under non-drought conditions, these four genotypes showed statistical differences in their mean performance at 11 days after the drought stress initiation, while no statistical difference was seen under drought stress conditions. The lowest value of 0.678 of NDVI under 11 days drought stress was occupied by G99, while G11 recorded the lowest value (0.662) under non-drought conditions. Statistically, G99 showed no significant difference in the mean performance with other genotypes under 11 days drought stress. On the other hand, under non-drought conditions G11 showed a statistical difference in the mean performance with G53, G6, G2 and G78. Genotype G99 recorded the highest CRI1 (5.382) and CRI2 (5.173) under drought stress. G99 is followed by G5 recording CRI1 of 5.259 and by G53 recording CRI2 of 5.016 under drought stress. Under non-drought conditions, G99 topped first for both CRI1 (5.421) and CRI2 (5.185) followed by G53. Under both water regimes, these genotypes showed no statistical differences among themselves in their mean performance at 11-day after the drought stress initiation. The lowest value of CRI1(4.682) and CRI2 (4.404) under non-drought conditions was occupied by G63, while G73 recorded the lowest value of CRI1 (4.643) and CRI2 (4.440) under non-drought conditions. Statistically, G73 showed a significant difference in the mean performance with other genotypes under 11 days drought stress. On the other hand, under non-drought conditions, G73 showed no statistically difference in the mean performance with other genotypes.

- **At 18 days (18D) after the drought stress initiation**

At 18 days after the drought stress initiation (18D), ANOVA revealed the presence of significant differences among the rice genotypes for transpiration rate, CRI1, CRI2 and RDVI under non-drought conditions (Table 18). Under drought stress, ANOVA revealed significant differences for PhiPS II, NDVI, RDVI, CRI1 and CRI2 (Table 18).

Table 18. Mean square from the analysis of variance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought stress conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany 2022, at 18 days after the start of the drought treatment

TRAITS	REPETITION (D.F.=5)		GENOTYPE (D.F.=13)		RESIDUAL (D.F.=60)		*p-value* (REPETITION)		*p-value* (GENOTYPE)	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
gsw	5.29**	0.81	1.17	1.17	0.62	0.99	<.0001	0.5407	0.0521	0.3049
E	4.48**	2.82*	1.43*	1.02	0.64	0.97	<.0001	0.0130	0.0180	0.3728
PhiPS II	1.60	1.47	1.31	2.36**	0.88	0.86	0.1225	0.1329	0.1461	0.0016
ETR	4.20**	4.26**	0.99	0.90	0.78	0.90	0.0004	0.0005	0.2502	0.4620
NDVI	1.17	2.16*	0.99	2.12*	0.98	0.84	0.3244	0.0301	0.4598	0.0040
CRI1	3.01**	5.18**	1.70**	2.71**	0.68	0.70	0.0017	<.0001	0.0081	<.0001
CRI2	2.67**	4.53**	1.72**	2.55**	0.70	0.74	0.0047	<.0001	0.0101	0.0001
RDVI	2.94**	7.00**	1.49*	1.75**	0.70	0.71	0.0025	<.0001	0.0252	0.0048

** Significance at 1% level; * Significance at 5% level; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; ND-Under non-drought; UD-Under drought stress; D.F.-Degree of freedom;

Under both non-drought and drought stress conditions all the leaf reflectance parameters namely NDVI, RDVI, CRI1 and CRI2 recorded moderate C.V. and moderate to high heritability. Moderate C.V. was obtained under non-drought conditions (CRI1= 7.65 and CRI2= 8.34) and drought stress (CRI1= 6.67 and CRI2= 7.24), and moderate heritability under non-drought conditions (CRI1= 51.63 and CRI2= 49.18) and high heritability under drought stress (CRI1= 61.74 and CRI2= 60.54) was obtained at 18 days drought stress in this study (Table 18). High C.V. and moderate to high heritability were also recorded for stomatal conductance and transpiration rate under both drought stress and non-drought conditions. The means performance with the ranking of the genotypes using the Duncan multiple rank test is presented in Table 19 at 18 days drought stress.

In general, the mean performance of all the genotypes has been reduced notably under drought stress compared to the non-drought conditions for stomatal conductance and transpiration rate for all the genotypes. Genotype G99 recorded the highest stomatal conductance (0.251 mol m^{-2} s^{-1}) and transpiration rate (2.447 mol m^{-2} s^{-1}) and PhiPS2 (0.726) under drought stress. Genotype G99 was followed by G2 under drought stress for stomatal conductance, transpiration rate while G62 and G100 for PhiPS2. Under non-drought conditions, the genotypes G63 recorded the highest stomatal conductance (1.003 mol m^{-2} s^{-1}) and transpiration rate (4.929 mol m^{-2} s^{-1}) and G99 for PhiPS2 (0.732). Genotype G63 is followed by G78 for stomatal conductance and G5 for transpiration rate and G99 is followed by G62 and G100 for PhiPS2. The lowest stomatal conductance (0.086 mol m^{-2} s^{-1}) and transpiration rate (0.981 mol m^{-2} s^{-1}) under 18 days drought stress was occupied by G53 and G65 (0.652) for PhiPS2, while G53 recorded lowest value for stomatal conductance (0.295 mol m^{-2} s^{-1}) and transpiration rate (2.459 mol m^{-2} s^{-1}) and G63 (0.626) for PhiPS2 under non-drought conditions. Statistically, there was different in the mean performance at 18 days after the drought stress initiation between G99 and G53 for transpiration rate under non-drought conditions and PhiPS2 under drought stress. The genotype G5 recorded the highest NDVI of 0.697 under drought stress. Genotype G5 was followed by G65 and G6 recording NDVI of 0.694 and 0.693, respectively under drought stress. Under non-drought conditions, G6 topped first (0.697) for NDVI followed by G78. Under drought conditions these, genotypes showed statistical differences in their means performance at 18 days after the drought stress initiation, while no statistical difference was seen under non-drought conditions. The lowest value of 0.675 and 0.680 of NDVI was occupied by G99, under non-drought conditions and 18 days drought stress, respectively.

Table 19. Mean performance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 18 days drought conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Management	ID	Genotype	gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
Non-drought	G6	Togo Marshall	0.379a	2.845ac	0.646a	21.60a	0.697a	4.831ab	4.594bcde	0.553ab
Non-drought	G62	KE40	0.509a	3.281ac	0.722a	25.95a	0.683a	4.907abc	4.733ace	0.528ab
Non-drought	G73	SR35266-2-12-1-1	0.525a	3.500ac	0.678a	25.39a	0.684a	4.571ac	4.454a	0.547b
Non-drought	G100	UPLR-17	0.363a	2.799abc	0.718a	26.19a	0.686a	5.091b	4.894d	0.527ac
Non-drought	G99	APO	0.499a	3.575b	0.732a	25.36a	0.675a	5.069ab	4.834bde	0.517ac
Non-drought	G65	GR18-SARI	0.487a	3.255abc	0.693a	21.83a	0.689a	5.079ab	4.821abcde	0.536ab
Non-drought	G5	ARICA 3	0.677a	4.232abc	0.671a	26.20a	0.691a	5.196ab	4.909abcde	0.537b
Non-drought	G63	ARICA 2	1.003a	4.929ac	0.626a	21.61a	0.683a	4.594ac	4.301ac	0.538ab
Non-drought	G2	CRI-Agrarice	0.611a	3.953ab	0.702a	21.07a	0.691a	4.941ab	4.723bcde	0.530abc
Non-drought	G11	CRI-Enapa	0.468a	3.474ab	0.662a	25.98a	0.682a	4.442abc	4.129abce	0.551ab
Non-drought	G22	Jasmine 85	0.520a	3.517ab	0.695a	24.82a	0.692a	4.686abc	4.465abcde	0.549ab
Non-drought	G53	WAB 2085-TGR2-WAT4-1-1	0.295a	2.459c	0.700a	23.34a	0.688a	4.795ab	4.662bcde	0.547ab
Non-drought	G36	ART132-35-1-1-B-B	0.357a	2.665ac	0.703a	21.00a	0.683a	4.800ab	4.535bd	0.528c
Non-drought	G78	SA68-SARI	0.723a	3.942abc	0.691a	23.49a	0.695a	4.871abc	4.709abcde	0.534ab
Drought	G6	Togo Marshall	0.120a	1.350a	0.701bd	18.09a	0.693c	4.967abce	4.697acd	0.541b
Drought	G62	KE40	0.115a	1.310a	0.717ab	21.27a	0.686abcd	4.601abde	4.408abcd	0.548abc
Drought	G73	SR35266-2-12-1-1	0.117a	1.249a	0.675abd	25.84a	0.684abcd	4.377d	4.165bd	0.563ab
Drought	G100	UPLR-17	0.158a	1.726a	0.709abd	27.00a	0.687abcd	5.149c	4.944c	0.533ac
Drought	G99	APO	0.251a	2.447a	0.726b	27.05a	0.680b	5.108ac	4.880ac	0.529c
Drought	G65	GR18-SARI	0.150a	1.559a	0.652bd	23.65a	0.694acd	4.927ace	4.622ac	0.554ab
Drought	G5	ARICA 3	0.164a	1.679a	0.659b	26.43a	0.697ac	4.893ace	4.567ac	0.563ab
Drought	G63	ARICA 2	0.151a	1.504a	0.688b	22.03a	0.686abcd	4.612bd	4.350bd	0.548ab
Drought	G2	CRI-Agrarice	0.242a	2.176a	0.699abcd	26.14a	0.691acd	4.882abce	4.692ac	0.537ac
Drought	G11	CRI-Enapa	0.190a	1.958a	0.658b	24.44a	0.685bd	4.754bd	4.444b	0.541ab
Drought	G22	Jasmine 85	0.217a	2.010a	0.662abd	23.75a	0.688acd	4.743bde	4.568abd	0.552ab
Drought	G53	WAB 2085-TGR2-WAT4-1-1	0.086a	0.981a	0.689abcd	20.32a	0.691acd	4.863abce	4.717ac	0.543ab
Drought	G36	ART132-35-1-1-B-B	0.147a	1.497a	0.706abcd	33.69a	0.681bd	5.112abce	4.911ac	0.514c
Drought	G78	SA68-SARI	0.151a	1.618a	0.696abcd	20.81a	0.689acd	4.778abce	4.531abcd	0.547abc

gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; abcde- letter used to rank the genotypes based on the Duncan multiple rank test, the mean value with the same letter for a particular trait under the drought or non-drought means these genotypes are not statistically different in their mean performance for that trait under weather the drought or non-drought conditions; ID-Genotype identity

Statistically, G99 showed a significant difference in the mean performance with other genotypes under 18 days drought stress. On the other hand, under non-drought conditions, no statistical difference was observed among the genotypes. Genotype G100 recorded the highest value of CRI1 (5.149) and CRI2 (4.944), while G73 and G5 recorded the highest value for RDVI (0.563) under drought stress. Genotype G100 was followed by G36 (CRI1= 5.112 and CRI2= 4.911). Under non-drought conditions, G5 topped first for both CRI1(5.196) and CRI2(4.909) followed by G100, while G6 topped first for RDVI (0.553) followed by G11. Under both water regimes, these genotypes showed no statistical differences among themselves in their means performance at 18 days after the drought stress initiation. The lowest value of CRI1(4.442) and CRI2(4.129) under non-drought conditions was occupied by G11, while G99 showed the lowest value for RDVI (0.517). Genotype G73 recorded lowest value of CRI1(4.377) and CRI2(4.165) under drought stress, while G36 showed the lowest value for RDVI (0.514).

- **At 27 days (27D) after the drought stress initiation**

At 27 days after the drought stress initiation (27D), ANOVA revealed the presence of significant differences among the rice genotypes for TN, CRI1, CRI2 and RDVI under non-drought conditions (Table 20). Under drought stress, ANOVA showed significant differences among the rice genotypes for TN, stomatal conductance, and transpiration rate (Table 20). Under both non-drought and drought stress, all the leaf reflectance parameters namely NDVI, RDVI, CRI1 and CRI2 recorded low to moderate C.V. and moderate to high heritability. Moderate C.V. was obtained under non-drought conditions (CRI1= 6.47 and CRI2= 6.76) and drought stress (CRI1= 16.11 and CRI2= 12.02), while high heritability under non-drought conditions (CRI1= 78 and CRI2= 79.28) and moderate heritability under drought stress (CRI2= 35.86) were obtained (Table 24 and 25). High C.V. and moderate to high heritability were also recorded for tiller number, stomatal conductance and transpiration rate under both drought stress and non-drought conditions. The means performance with the ranking of the genotypes using the Duncan multiple rank test is presented in Table 21 under 27 days drought stress. In general, the mean performance of all the genotypes has been reduced notably by more than 60% under drought stress compared to the non-drought conditions for stomatal conductance and transpiration rate for all the genotypes except G99 and G100 which were previously identified as drought-tolerant based on the field experiment.

Table 20. Mean square from the analysis of variance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022, at 27 days after starting of the drought treatment

TRAITS	REPETITION (D.F.=5)		GENOTYPE (D.F.=13)		RESIDUAL (D.F.=60)		*p-value* (REPETITION)		*p-value* (GENOTYPE)	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
TN	2.33**	1.72	2.36**	1.92**	0.59	0.74	0.0036	0.0542	0.0001	0.0065
gsw	4.03*	0.33	1.06	1.72*	0.72	0.65	0.0107	0.6121	0.2058	0.0200
E	5.00**	0.96	0.70	1.67*	0.76	0.62	0.0058	0.2328	0.5563	0.0183
PhiPS II	1.70	0.95	0.76	1.19	1.02	0.91	0.2114	0.3681	0.7025	0.2750
ETR	0.09	4.00*	1.14	0.73	0.99	0.95	0.9128	0.0277	0.3705	0.6845
NDVI	0.30	5.64**	1.27	0.88	0.93	0.67	0.8053	0.0003	0.2265	0.2567
CRI1	1.68**	5.83**	2.19**	0.82	0.52	0.68	0.0345	0.0002	0.0004	0.3183
CRI2	2.07**	4.81**	2.18**	1.06	0.49	0.69	0.0121	0.0009	0.0002	0.1579
RDVI	1.69	0.36	1.82**	1.37	0.62	0.92	0.0602	0.7606	0.0060	0.1703

** Significance at 1% level; * Significance at 5% level; TN-Tiller number; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; ND-Under non-drought; UD-Under drought stress; D.F.-Degree of freedom;

Table 21. Mean performance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 27 days drought conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Management	ID	Genotype	gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI	TN
Non-drought	G6	Togo Marshall	0.581a	4.711a	0.709a	24.80a	0.695a	4.684ac	4.395ac	0.562a	19.00c
Non-drought	G62	KE40	0.380a	3.496a	0.706a	30.12a	0.683a	4.687ac	4.464ac	0.546a	10.17abde
Non-drought	G73	SR35266-2-12-1-1	0.314a	2.739a	0.686a	28.01a	0.690a	4.602ac	4.440ac	0.555a	11.83abde
Non-drought	G100	UPLR-17	0.510a	4.525a	0.710a	32.79a	0.690a	5.083c	4.910c	0.542a	6.80bd
Non-drought	G99	APO	0.468a	4.214a	0.689a	35.91a	0.690a	5.652b	5.492b	0.492b	8.17bde
Non-drought	G65	GR18-SARI	0.580a	4.174a	0.662a	35.77a	0.695a	5.097c	4.831c	0.546a	12.00ade
Non-drought	G5	ARICA 3	0.443a	3.745a	0.690a	31.14a	0.692a	5.028c	4.732c	0.543a	13.17ade
Non-drought	G63	ARICA 2	0.690a	4.085a	0.683a	27.47a	0.679a	4.389a	4.128a	0.555a	10.60abde
Non-drought	G2	CRI-Agrarice	0.407a	3.499a	0.687a	22.72a	0.699a	4.688ac	4.503ac	0.560a	8.83bde
Non-drought	G11	CRI-Enapa	0.453a	2.112a	0.556a	25.06a	0.678a	4.849ac	4.620ac	0.543a	12.00ade
Non-drought	G22	Jasmine 85	0.869a	5.705a	0.686a	25.43a	0.698a	4.890ac	4.687ac	0.550a	13.40ad
Non-drought	G53	WAB 2085-TGR2-WAT4-1-1	0.389a	3.922a	0.676a	25.62a	0.704a	5.096c	4.903c	0.543a	13.83ad
Non-drought	G36	ART132-35-1-1-B-B	0.390a	3.653a	0.711a	27.14a	0.684a	4.584ac	4.423ac	0.538a	11.50abde
Non-drought	G78	SA68-SARI	0.681a	5.109a	0.687a	24.90a	0.704a	4.541ac	4.370ac	0.566a	14.67ac
Drought	G6	Togo Marshall	0.074b	1.120c	0.631a	21.62a	0.684a	4.483a	4.424a	0.567a	11.50b
Drought	G62	KE40	0.038b	0.707c	0.703a	28.50a	0.663a	3.949a	4.027a	0.547a	9.50ab
Drought	G73	SR35266-2-12-1-1	0.035b	0.691c	0.609a	29.34a	0.676a	4.195a	3.938a	0.573a	10.17ab
Drought	G100	UPLR-17	0.205a	3.279b	0.738a	26.03a	0.674a	4.764a	4.641a	0.544a	5.50c
Drought	G99	APO	0.206a	2.944ab	0.732a	34.58a	0.694a	4.902a	4.543a	0.557a	5.67c
Drought	G65	GR18-SARI	0.040b	0.701c	0.654a	35.29a	0.684a	4.588a	4.370a	0.564a	8.83abc
Drought	G5	ARICA 3	0.031b	0.613c	0.633a	22.16a	0.697a	4.683a	4.368a	0.571a	8.83abc
Drought	G63	ARICA 2	0.057b	0.955c	0.701a	25.08a	0.649a	3.705a	3.706a	0.546a	7.50ac
Drought	G2	CRI-Agrarice	0.074b	1.065c	0.634a	27.26a	0.665a	3.990a	4.010a	0.536a	7.17ac
Drought	G11	CRI-Enapa	0.056b	0.692c	0.721a	31.36a	0.657a	4.281a	4.128a	0.557a	9.50ab
Drought	G22	Jasmine 85	0.031b	0.599c	0.676a	31.10a	0.693a	4.429a	4.159a	0.561a	7.50ac
Drought	G53	WAB 2085-TGR2-WAT4-1-1	0.040b	0.714c	0.652a	25.54a	0.701a	4.703a	4.482a	0.569a	9.33ab
Drought	G36	ART132-35-1-1-B-B	0.055b	0.988c	0.682a	35.06a	0.676a	4.267a	3.938a	0.553a	8.67abc
Drought	G78	SA68-SARI	0.080b	1.471ac	0.691a	24.86a	0.689a	4.892a	4.689a	0.541a	7.17ac

TN-tiller number; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; abcde- letter used to rank the genotypes based on the Duncan multiple rank test, the mean value with the same letter for a particular trait under the drought or non-drought means these genotypes are not statistically different in their mean performance for that trait under weather the drought or non-drought conditions; ID-Genotype Identity

Genotype G99 recorded the highest stomatal conductance (0.206 mol m^{-2} s^{-1}) followed by G100 (0.205 mol m^{-2} s^{-1}) and G78 (0.080 mol m^{-2} s^{-1}), while G22 recorded the lowest value of 0.031mol m^{-2} s^{-1} under the 27-days drought stress. Genotype G100 recorded the highest transpiration rate (3.279 mol m^{-2} s^{-1}) followed by G99, G78 and G6 under drought stress, while G22 recorded the lowest value of 0.599 mol m^{-2} s^{-1}. Genotype G100 recorded the highest PhiPS2 (0.738) followed by G99, G11 and G62 under drought stress, while G73 recorded the lowest value of 0.609.

Under non-drought conditions, the genotype G22 recorded the highest stomatal conductance (0.869 mol m^{-2} s^{-1}) followed by G63 and G78, while G73 recorded the lowest value of 0.314 mol m^{-2} s^{-1}. G22 recorded the highest transpiration rate (5.705 mol m^{-2} s^{-1}) followed by G78, G6 and G100 under non-drought conditions, while G11 recorded the lowest value of 2.112 mol m^{-2} s^{-1}. G36 recorded the highest PhiPS2 (0.711) followed by G100, G6 and G62 under non-drought conditions, while G11 recorded the lowest value of 0.556. Statistically, there was a significative difference in the mean performance at 27 days after the drought stress initiation between G99 and G22, and between G100 and G22 for stomatal conductance and transpiration rate under drought stress conditions, respectively. Genotype G53 recorded the highest NDVI of 0.701 under drought stress. Genotype G53 was followed by G5 and G99 recording NDVI of 0.697 and 0.694, respectively under drought stress conditions. Under non-drought conditions, SA68-SARI topped first (0.704) followed by G53 for NDVI. The lowest value of 0.678 and 0.649 of NDVI was occupied by G11 and G63, under non-drought conditions and 27 days drought stress, respectively.

Under both water regimes no statistical difference was observed between G11 and G63 with other genotypes. Genotype G99 recorded the highest value of CRI1 (4.902) followed by G78 and G100, while G63 recorded the lowest value of CRI1 (3.705) under 27 days drought stress. Genotype G78 recorded the highest value of CRI2 (4.689) followed by G100 and G99 while G63 recorded the lowest value CRI2 (3.706) under 27 days drought stress. Genotype G73 recorded the highest value of RDVI (0.573) followed by G5 and G53, while G2 recorded the lowest value of RDVI (0.536) under 27 days drought stress. Under non-drought conditions, G99 recorded the highest value of CRI1 (5.652) followed by G65 and G53, while G63 recorded the lowest value of CRI1 (4.389) under non-drought conditions. Genotype G99 recorded the highest value of CRI2 (5.492) followed by G100 and G53, while G63 recorded the lowest value of CRI2 (4.128) under non-drought

conditions. Genotype G78 recorded the highest value of RDVI (0.566) followed by Togo Marshall and G2, while G99 recorded the lowest value of RDVI (0.492) under non-drought conditions.

4.1.2.4 Correlation among the physiological and leaf reflectance parameters of the rice genotypes under both vegetative stage drought and non-drought conditions

The Pearson correlation analysis conducted 5 days after the drought stress initiation revealed that under both water regimes, stomatal conductance and transpiration rate had a strong positive significant correlation with each other, and both of them were positively associated with RDVI, while negatively related to PhiPS2, NDVI, CRI1 and CRI2 (Annex 11 and 12). Both indexes (CRI1 and CRI2) had a strong positive significant correlation with each other, and both were negatively correlated with RDVI and NDVI which recorded a positive association with each other under both water regimes.

Under 11 days drought stress, Pearson correlation analysis revealed under both water regimes, strong positive significant correlation between stomatal conductance and transpiration rate, and both of them were positively associated with RDVI, while negatively related to PhiPS2, CRI1 and CRI2 (Annex 13 and 14). These explained the fact that, under 11 days drought conditions, the previously identified drought-tolerant genotypes, G100, G6 and G99 managed to maintain high stomatal conductance and transpiration rate as compared to the non-drought conditions, while all others genotypes have registered a drastic decrease. Both indexes (CRI1 and CRI2) had a strong positive significant correlation with each other, and both were negatively significantly correlated with RDVI and NDVI which recorded a positive association with each other under both water regimes. In the difference to the 5 days after the stress initiation, stomatal conductance and transpiration rate recorded a positive correlation with NDVI under non-drought conditions, while under drought stress, stomatal conductance recorded a positive association with NDVI, and transpiration rate had a negative relationship under 11 days drought stress.

Under 18 days drought stress, Pearson correlation analysis revealed under both water regimes, a strong positive significant correlation between stomatal conductance and transpiration rate, and both of them were positively associated with RDVI under non-drought, while negatively related to PhiPS2, CRI1, CRI2 and RDVI under drought stress (Annex 15 and 16). Both indexes (CRI1 and CRI2) had a strong positive significant correlation with each other, and both were negatively

significantly correlated with RDVI and NDVI which recorded a positive association with each other under both water regimes. In the difference to the 5 days after the stress initiation, stomatal conductance and transpiration rate recorded a positive correlation with NDVI under non-drought conditions, while under drought stress, stomatal conductance recorded a positive association with NDVI, and transpiration rate had a negative relationship under 18 days drought stress.

Under 27 days drought stress, Pearson correlation analysis revealed under drought stress, a strong positive significant correlation between stomatal conductance and transpiration rate, and both of them were positively associated to NDVI, PhiPS2, CRI1, CRI2 and RDVI (Annex 17 and 18). These explained the fact that, under 27 days drought conditions, the previously identified drought-tolerant genotypes, G100 and G99 managed to maintain high stomatal conductance and transpiration rate as compared to the non-drought conditions, while all other genotypes have decreased notably. Both indexes (CRI1 and CRI2) had a strong positive significant correlation with each other, and both were positively and significantly correlated with RDVI and NDVI which recorded a positive significant association with each other under drought stress. Stomatal conductance recorded a positive correlation with CRI1 and CRI2 under non-drought conditions, while transpiration rate recorded a negative association with CRI1 and CRI2, and a positive relationship with stomatal conductance, NDVI, RDVI and PhiPS2.

4.1.2.5 Selection of genotypes tolerant to drought stress based on the physiological and leaf reflectance parameters at vegetative stage

In order to conduct the biochemical characterisation, seven out of the 14 genotypes were selected using the relative value (drought risk index) of the leaf gas exchanges attributes and leaf reflectance parameters used in this screening. The relative value of the leaf gas exchange attributes and leaf reflectance parameters are presented in Annex 19. At 5 days drought stress, G11 and G73 were selected as tolerant to 5 days drought stress based on high relative NDVI, relative CRI, relative CRI2, relative stomatal conductance and relative transpiration rate. Genotypes G6 and G100 were selected as tolerant to 11 days drought stress based on high relative RDVI, relative stomatal conductance and relative transpiration rate. Genotypes G99 and G100 were selected as tolerant to 18 days drought stress based on high relative NDVI, relative CRI, relative CRI2, relative stomatal conductance and relative transpiration rate. Genotypes G99 and G100 were selected as tolerant to 27 days drought stress based on high relative NDVI, relative CRI, relative CRI2, relative stomatal

conductance and relative transpiration rate. Genotypes G11 and G78 were selected as tolerant to 27 days drought stress based on high relative PhiPS2, relative CRI, relative CRI2, relative stomatal conductance and relative transpiration rate.

4.1.2.6 Mean performance of the rice genotypes under both vegetative stage drought stress and non-drought conditions based on biochemical traits

At 27 days after the drought stress initiation (27D), ANOVA revealed the presence of significant differences among the rice genotypes for malondialdehyde (MDA) concentration and proline content under drought stress (Tables 22 and 23). Under non-drought conditions, ANOVA showed no significant differences for MDA, relative water content (RWC) and proline content (Table 24). Under both non-drought and drought stress conditions, MDA, proline content, and RWC (%) recorded high C.V. except RWC which recorded moderately low C.V. under non-drought condition. High heritability was obtained for MDA (79.60) and proline content (86.75), whereas RWC (43.48) recorded moderate heritability under drought stress indicating the presence of large variability among the genotypes for these traits (Tables 22, 23 and 24).

In general, the means performance of all the genotypes has been reduced notably by more than 14% under drought stress compared to the non-drought conditions for RWC (%) for all the genotypes except G11 (1.58%), G99 (8.43%) and G100 (5.43%) which were previously identified as drought-tolerant based on the field experiment. The means performance of all the genotypes has been increased notably by more than 45% under drought stress compared to the non-drought conditions for MDA concentration for all the genotypes except G11 (25.15%), G99 (39.37%) and G100 (43.65%). The proline content analysis also revealed that the means performance of G78 (94.69%) and G100 (93.24%) has notably increased under drought stress than that of G22 (81.73%) which is considered as drought-sensitive variety based on the field experiment. The means performance with the ranking of the genotypes using the Duncan multiple rank test is presented in Figures 16, 17 and 18 after 27 days of drought stress. Genotype G22 recorded the highest MDA (15.08 nmol ml^{-1}) followed by G53 (12.90 nmol ml^{-1}), while G11 recorded the lowest value of 6.56 nmol ml^{-1} under 27 days drought stress. Genotype G78 recorded the highest proline content (39.87 mg l^{-1}) followed by G100 (12.69 mg l^{-1}), while G22 recorded the lowest value of 11.18 mg l^{-1}. Genotype G11 recorded the highest RWC (86.55%) followed by G100 (83.78%) and G99 (81.79%) under drought stress, while G6 recorded the lowest value of 54.76%. These three

genotypes namely G11, G100 and G99 topped first for relative RWC values of 0.98, 0.95 and 0.92, respectively. Based on the above results from MDA, proline content and RWC (%) analysis, the following genotypes namely G78, G11, G100 and G99 were selected as showing tolerance to drought stress.

Table 22. Analysis of variance and broad-sense heritability (h^2_{bs}) of seven rice genotypes evaluated for malondialdehyde (MDA) concentration under 27 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Source	Degree of freedom	Mean square (non-drought)	Mean square (drought stress)	*p-value* (non-drought)	*p-value* (drought stress)
Model	8	0.447	1.836*	0.9397	0.0137
Replicate	2	0.630	0.829	0.6417	0.1962
Genotype	6	0.386	2.171**	0.9345	0.0094
Residual	12	1.369	0.443	-	-
C.V. (%)	-	52.20	23.87	-	-
h^2_{bs}	-	-	79.60	-	-

** Significance at 1% level; * Significance at 5% level; MDA- malondialdehyde; C.V.- Experimental coefficient of variation; h^2_{bs}-Broad-sense heritability; Model is a GLM procedure for randomised complete block design (RCBD) implemented in SAS software.

Table 23. Analysis of variance and broad-sense heritability (h^2_{bs}) of seven rice genotypes evaluated for proline content concentration under 27 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Source	Degree of freedom	Mean square (non-drought)	Mean square (drought stress)	*p-value* (non-drought)	*p-value* (drought stress)
Model	8	0.791	1.713	0.7024	0.0705
Replicate	2	0.246	0.810	0.6961	0.1753
Genotype	6	0.973	2.014*	0.5346	0.0439
Residual	12	1.223	0.608	-	-
C.V. (%)	-	66.63	67.27	-	-
h^2_{bs}	-	-	69.81	-	-

** Significance at 1% level; * Significance at 5% level; MDA- malondialdehyde; C.V.- Experimental coefficient of variation; h^2_{bs}-Broad-sense heritability; Model is a GLM procedure for randomised complete block design (RCBD) implemented in SAS software.

Table 24. Analysis of variance and broad-sense heritability (h^2_{bs}) of 14 rice genotypes evaluated for relative water content concentration under 27 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Source	Degree of freedom	Mean square (non-drought)	Mean square (drought stress)	*p-value* (non-drought)	*p-value* (drought stress)
Model	15	0.739	2.197	0.8151	0.1878
Replicate	2	0.026	0.904	0.9775	0.5531
Genotype	13	0.850	2.395	0.7143	0.1474
Residual	25	1.156	1.492	-	-
C.V. (%)	-	3.90	20.77	-	-
h^2_{bs}	-	-	43.48	-	-

** Significance at 1% level; * Significance at 5% level; MDA- malondialdehyde; C.V.- Experimental coefficient of variation; h^2_{bs}-Broad-sense heritability; Model is a GLM procedure for randomised complete block design (RCBD) implemented in SAS software.

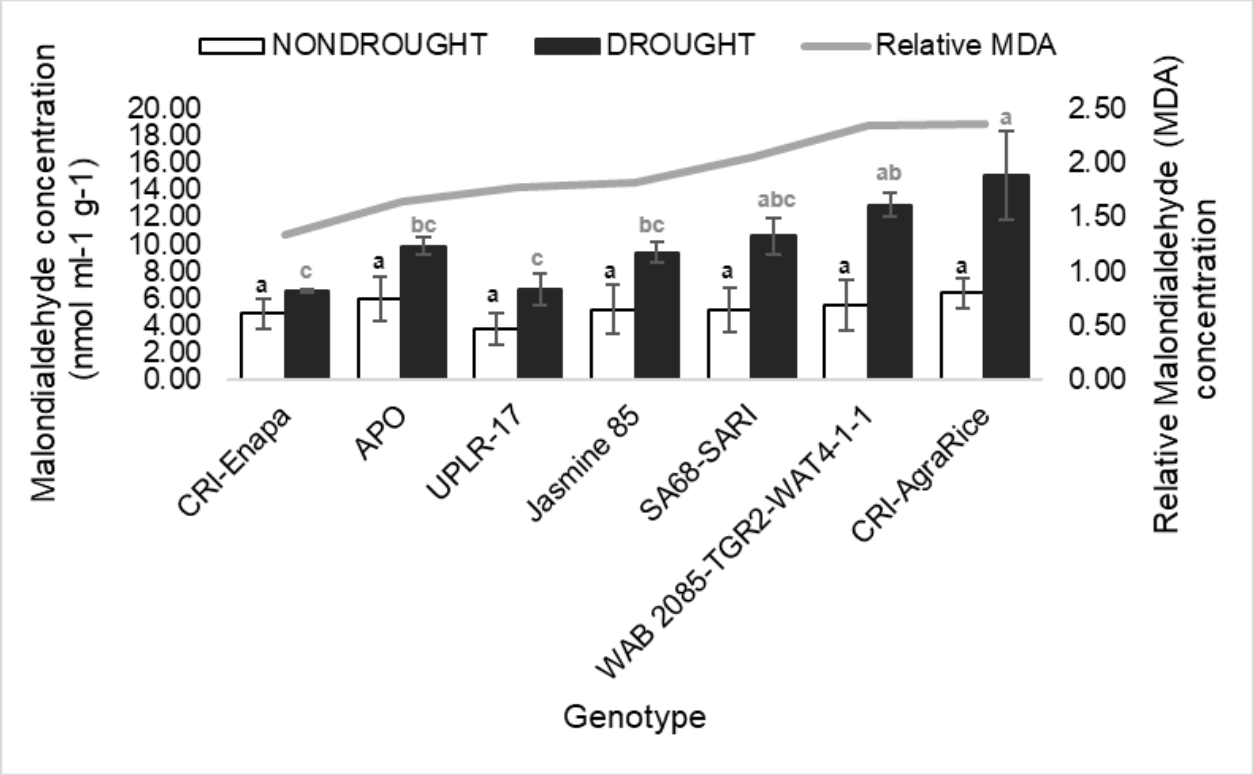


Figure 16. Shoot malondialdehyde (MDA) concentration in 7 rice genotypes evaluated under 27 days drought conditions at the University of Giessen, Germany, in 2022. Data presented are means ±SE (n=3). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on relative values of MDA (nmol ml^{-1} g^{-1}) for each genotype. Relative values were calculated as value under drought stress/value under non-drought conditions per genotype. The genotypes with their corresponding ID: UPLR-17 (G100), APO (G99), CRI-Enapa (G11), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53) and SA68-SARI (G78).

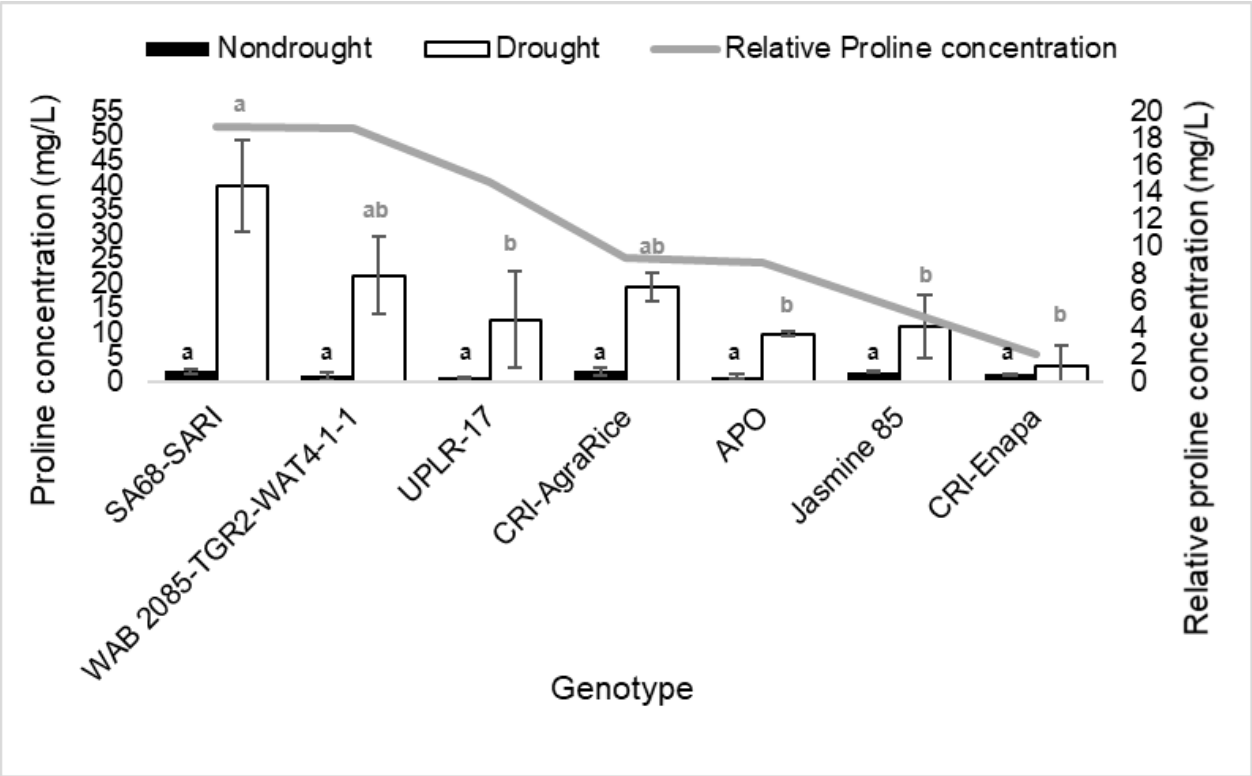


Figure 17. Shoot proline concentration in 7 rice genotypes evaluated under 27 days drought conditions at the University of Giessen, Germany, in 2022. Data presented are means ±SE (n=3). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on relative values of proline concentration (mg/l) for each genotype. Relative values were calculated as value under drought stress/value under non-drought conditions per genotype. The genotypes with their corresponding ID: UPLR-17 (G100), APO (G99), CRI-Enapa (G11), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53) and SA68-SARI (G78).

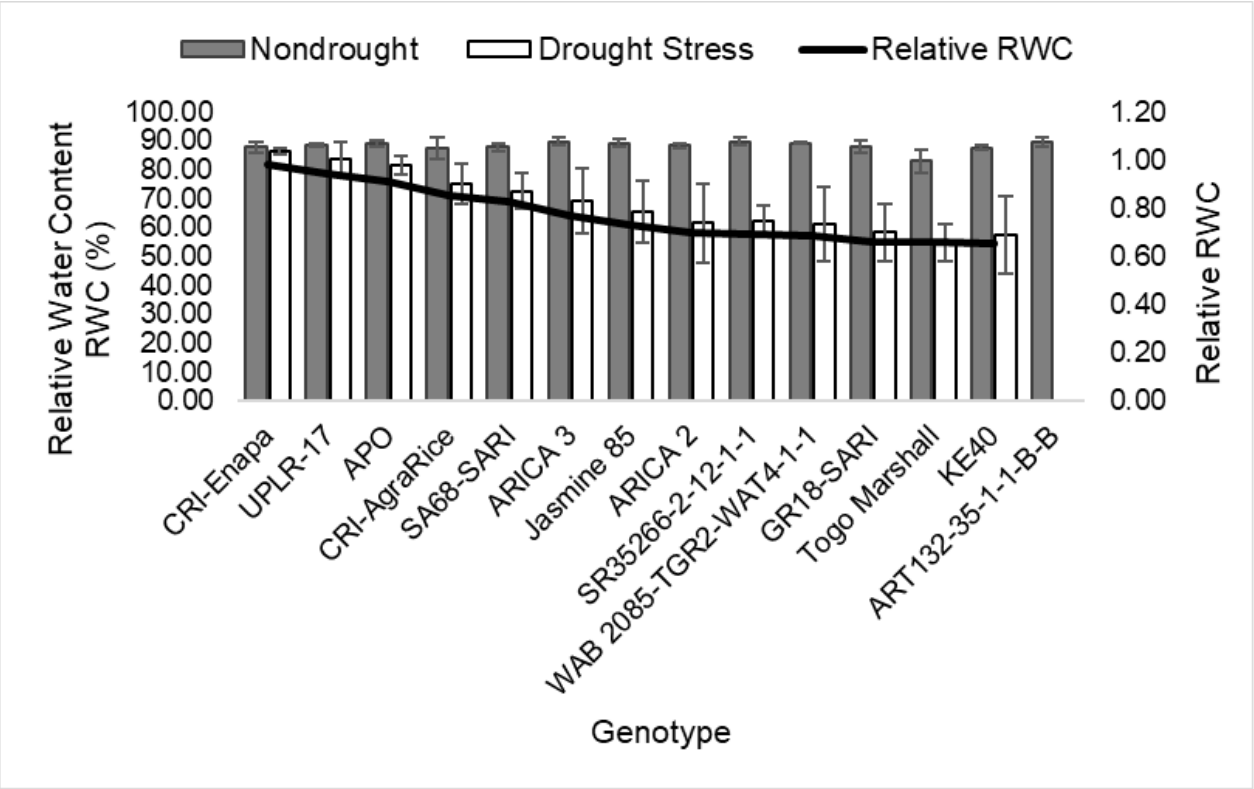


Figure 18. Relative water content in 14 rice genotypes evaluated under 27 days drought conditions at the University of Giessen, Germany, in 2022. Data presented are means ±SE (n=3). There was no significant different among the genotypes in their mean performance under either non-drought or drought conditions, based on ANOVA (P>5%). From left to right, genotypes are classified from best to worst performance, respectively, based on relative values of RWC (%) for each genotype. Relative values were calculated as value under drought stress/value under non-drought conditions per genotype. The genotypes with their corresponding ID: Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

4.1.2.7 Mean performance of the rice genotypes under both reproductive stage drought stress and non-drought conditions based on the physiological and leaf reflectance parameters

During the reproductive stage of drought stress, ANOVA revealed the presence of significant differences among the rice genotypes for ETR and RDVI under non-drought conditions (Table 25). Under drought stress conditions, ANOVA revealed no significant differences for all the traits among the genotypes (Table 25). Under both non-drought and drought stress conditions, all the physiological and leaf reflectance parameters recorded moderate to high C.V. and low to moderate heritability (Table 25). The means performance with the ranking of the genotypes using the Duncan multiple rank test is presented in Table 26 under reproductive drought stress stage. In general, the mean performance of all the genotypes has been reduced notably under drought stress compared to the non-drought conditions for stomatal conductance, transpiration rate and PhiPS2 for all the genotypes except G11 for stomatal conductance and PhiPS2, and G100 for transpiration rate. Genotype G100 recorded the highest stomatal conductance (0.353 mol m^{-2} s^{-1}), while G53 recorded the lowest value of 0.090 mol m^{-2} s^{-1} under reproductive drought stress. Genotype G100 recorded the highest transpiration rate (2.948 mol m^{-2} s^{-1}), while G5 recorded the lowest value of 0.919 mol m^{-2} s^{-1} under reproductive drought stress. Genotype G11 recorded the highest PhiPS2 (0.689) followed by G100 (0.645) under reproductive drought stress, while G36 recorded the lowest value of 0.379. Genotype G100 recorded the highest NDVI of 0.693 under drought stress followed by G78, G99 and G11 with the lowest value of 0.628 for G36. Under drought stress conditions, G11 topped first for RDVI (0.571) followed by G62 and G99 with the lowest value of 0.513 for G2. Genotype G11 recorded the highest drought risk index for stomatal conductance or relative stomatal conductance (1.135), relative PhiPS2 (1.172), relative CRI1 (1.104), relative CRI2 (1.063) and topped second for relative transpiration rate (0.980), third for relative RDVI (1.035). Genotype G100 recorded the highest transpiration rate (1.020), relative ETR (1.553), relative NDVI (1.035), and topped second for relative stomatal conductance (0.754), relative PhiPS2 (0.950), relative CRI1 (1.051), relative CRI1 (1.039) with a high value of relative RDVI (1.001). Based on the above results from the physiological and leaf reflectance parameters analysis using the relative value of the traits, the following genotypes namely, CRI-Enapa (G11), UPLR-17 (G100), APO (G99) and SA68-SARI (78) were selected as showing tolerance to reproductive stage drought stress.

Table 25. Mean square from the analysis of variance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under non-drought and drought stress conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022, at reproductive stage

TRAITS	REPETITION (D.F.=5)		GENOTYPE (D.F.=13)		RESIDUAL (D.F.=56)		*p-value* (REPETITION)		*p-value* (GENOTYPE)		C.V. (%)		h^2_{bs}	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
gsw	0.59	0.56	1.25	0.98	0.98	1.06	0.7008	0.7585	0.2595	0.5401	50.08	101.89	23.27	-
E	3.75**	1.41	1.02	1.10	0.76	0.97	0.0008	0.2181	0.2160	0.3488	35.25	81.52	28.05	14.41
PhiPS II	1.94	2.82*	0.91	0.99	0.96	0.85	0.0887	0.0111	0.5128	0.3255	13.88	30.76	-	17.11
ETR	4.69**	3.094*	1.27*	1.21	0.60	0.73	<.0001	0.0026	0.0260	0.0980	34.00	34.25	56.14	44.30
NDVI	3.74**	1.68	0.64	0.62	0.87	1.06	0.0021	0.1791	0.7157	0.8522	4.86	6.83	-	-
CRI1	2.87*	1.65	0.69	0.66	0.91	1.02	0.0139	0.1730	0.6961	0.8023	15.32	24.41	-	-
CRI2	2.30*	1.80	1.04	0.61	0.88	1.03	0.0341	0.1387	0.3177	0.8519	12.74	20.81	16.66	-
RDVI	0.63	2.46*	1.70*	0.71	0.88	0.95	0.6137	0.0363	0.0445	0.7145	4.94	6.66	51.10	-

** Significance at 1% level, * Significance at 5% level, gsw-Stomatal conductance, E-transpiration rate, PhiPS II-Quantum yield of fluorescence, ETR-Electron transport rate, NDVI-Normalized difference vegetative index, CRI1-Carotenoid reflectance index 1, CRI2-Carotenoid reflectance index 2, RDVI-Renormalized difference vegetative index, ND-Under non-drought; UD-Under drought stress; D.F.-Degree of freedom, C.V.- Experimental coefficient of variation, h^2_{bs}-Broad-sense heritability

Table 26. Mean performance of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under reproductive drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Management	ID	Genotype	gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
Non-drought	G6	Togo Marshall	0.638a	3.367a	0.652a	12.57c	0.676a	4.160a	3.962a	0.543acd
Non-drought	G62	KE40	0.568a	3.204a	0.683a	20.83abc	0.660a	4.243a	4.068a	0.513abd
Non-drought	G73	SR35266-2-12-1-1	0.608a	3.074a	0.617a	17.19ac	0.681a	4.255a	4.083a	0.552ac
Non-drought	G100	UPLR-17	0.468a	2.889a	0.679a	18.94ac	0.669a	4.242a	4.073a	0.541acd
Non-drought	G99	APO	0.390a	2.426a	0.652a	19.33ac	0.687a	4.269a	3.981a	0.548acd
Non-drought	G65	GR18-SARI	0.591a	3.041a	0.683a	19.36ac	0.680a	4.460a	4.297a	0.527abcd
Non-drought	G5	ARICA 3	0.895a	4.111a	0.644a	22.01abc	0.685a	4.571a	4.371a	0.532abcd
Non-drought	G65	ARICA 2	0.743a	3.945a	0.648a	27.54ab	0.651a	3.854a	3.682a	0.510bd
Non-drought	G2	CRI-Agrarice	0.532a	3.705a	0.676a	31.27b	0.679a	4.060a	3.881a	0.539acd
Non-drought	G11	CRI-Enapa	0.276a	1.835a	0.588a	20.95abc	0.666a	3.875a	3.686a	0.552ac
Non-drought	G22	Jasmine 85	0.521a	3.345a	0.587a	21.76abc	0.682a	4.011a	3.795a	0.556c
Non-drought	G53	WAB 2085-TGR2-WAT4-1-1	0.662a	3.806a	0.677a	21.99abc	0.685a	4.599a	4.403a	0.526abcd
Non-drought	G36	ART132-35-1-1-B-B	0.620a	3.473a	0.754a	20.55ac	0.663a	4.788a	4.513a	0.496b
Non-drought	G78	SA68-SARI	0.688a	3.886a	0.697a	19.49ac	0.688a	4.399a	4.211a	0.542acd
Drought	G6	Togo Marshall	0.260a	1.865a	0.539a	19.28a	0.660a	3.827a	3.712a	0.536a
Drought	G62	KE40	0.278a	2.289a	0.615a	27.26a	0.638a	3.232a	3.227a	0.556a
Drought	G73	SR35266-2-12-1-1	0.116a	1.230a	0.460a	19.27a	0.664a	3.744a	3.662a	0.542a
Drought	G100	UPLR-17	0.353a	2.948a	0.645a	29.40a	0.693a	4.460a	4.234a	0.542a
Drought	G99	APO	0.160a	1.162a	0.582a	23.60a	0.674a	3.897a	3.664a	0.551a
Drought	G65	GR18-SARI	0.225a	1.901a	0.601a	22.79a	0.655a	3.854a	3.643a	0.532a
Drought	G5	ARICA 3	0.100a	0.919a	0.589a	22.36a	0.670a	4.204a	4.052a	0.516a
Drought	G63	ARICA 2	0.227a	1.673a	0.390a	16.96a	0.659a	3.673a	3.555a	0.544a
Drought	G2	CRI-Agrarice	0.159a	1.235a	0.618a	26.96a	0.652a	3.948a	3.868a	0.513a
Drought	G11	CRI-Enapa	0.314a	1.797a	0.689a	23.47a	0.673a	4.277a	3.919a	0.571a
Drought	G22	Jasmine 85	0.242a	1.836a	0.554a	30.55a	0.659a	4.018a	3.902a	0.541a
Drought	G53	WAB 2085-TGR2-WAT4-1-1	0.090a	0.927a	0.486a	24.52a	0.664a	3.921a	3.828a	0.536a
Drought	G36	ART132-35-1-1-B-B	0.350a	2.347a	0.379a	7.77a	0.628a	3.059a	3.355a	0.526a
Drought	G78	SA68-SARI	0.113a	1.216a	0.497a	25.66a	0.677a	4.386a	4.116a	0.526a

gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; abcde- letter used to rank the genotypes based on the Duncan multiple rank test, the mean value with the same letter for a particular trait under the drought or non-drought means these genotypes are not statistically different in their mean performance for that trait under weather the drought or non-drought conditions; ID-Genotype Identity

4.1.2.8 Mean performance of the rice genotypes under drought stress based on grain yield and yield-related traits

ANOVA revealed the presence of significant differences among the rice genotypes for all the grain yield and yield-related traits namely days to flowering (DTF), leaf drying score (LDS), aboveground biomass (grain + stover) and grain yield per plant under both drought stress and non-drought conditions except DTF under non-drought conditions (Table 27 and 28). Under both non-drought and drought stress conditions for all the grain yield and yield-related traits namely LDS, aboveground biomass and grain yield per plant recorded high C.V. except DTF which had moderate C.V. High heritability was obtained for all the grain yield and yield related traits namely DTF, LDS, aboveground biomass and grain yield per plant under both non-drought and drought stress except DTF which recorded moderate heritability under non-drought conditions indicating that selection will be effective for these traits.

In general, the flowering date of all the genotypes has been delayed at least by more than 5 days under drought stress compared to the non-drought conditions except G99, G100 and G11 which flowered earlier under drought stress compared to the non-drought conditions with 1.17 days, 3.37 days and 6.00 days, respectively. Genotype G5 recorded the highest delay in DFT (14.67 days) followed by G36 (13.50 days), while G2 recorded the lowest value of 5.67 days under drought stress. On the other hand, the highest LDS were obtained on G36 (7.00) and G53 (5.67), while G78, G100 and G11 ranked lowest with LDS of 1.17, zero and zero, respectively. Genotype G99 recorded an LDS of 2.50, while G6 scored 3.00. The mean performance of all the genotypes has been reduced notably under drought stress compared to non-drought conditions for the aboveground biomass except G100 which recorded a similar aboveground biomass under non-drought (109.16 g) and drought stress (108.71 g) conditions with a relative biomass of 1.00. Second to G100, G11 recorded a relative biomass of 0.87 with aboveground biomass of 239.52 g under drought stress and 275.53 g under non-drought conditions. Genotype G53 ranked lowest for a relative biomass value of 0.43 with aboveground biomass of 279.65 g under drought stress and 643.32 g under non-drought conditions, implying its high sensitivity to drought stress. The mean performance of all the genotypes has been reduced notably under drought stress compared to the non-drought conditions for grain yield. Genotype G100 recorded the highest relative grain yield value of 0.62 with the grain yield of 8.18 g per plant under drought stress and 13.26 g per plant under non-drought conditions, confirming its tolerance to drought stress.

Table 27. Mean square from the analysis of variance of 14 rice genotypes evaluated for days to flowering and leaf drying score under non-drought and drought stress conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Source	Degree of freedom	Mean square DTF (non-drought)	Mean square DTF (drought stress)	Mean square LDS (drought stress)	*p-value* DTF (non-drought)	*p-value* DTF (drought stress)	*p-value* LDS (drought stress)
Model	18	2.176**	2.958**	2.531**	0.0002	<.0001	<.0001
Replicate	5	5.415**	1.091*	5.431**	<.0001	0.0172	<.0001
Genotype	13	0.844	3.540**	1.536**	0.2169	<.0001	0.0018
Residual	57	0.629	0.359	0.499	-	-	-
C.V. (%)	-	5.25	4.18	84.72	-	-	-
h^2_{bs}	-	29.81	91.07	70.76	-	-	-

** Significance at 1% level; * Significance at 5% level; DTF- Days to flowering; LDS- Leaf drying score; C.V.- Experimental coefficient of variation; h^2_{bs}-Broad-sense heritability; Model is a GLM procedure for randomised complete block design (RCBD) implemented in SAS software.

Table 28. Mean square from the analysis of variance of 14 rice genotypes evaluated for aboveground biomass and grain yield per plant under non-drought and drought stress conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Source	Degree of freedom	Mean square Biomass (non-drought)	Mean square Biomass (drought stress)	Mean square Grain yield (non-drought)	Mean square Grain yield (drought stress)	*p-value* biomass (non-drought)	*p-value* biomass (drought stress)	*p-value* grain yield (non-drought)	*p-value* grain yield (drought stress)
Model	18	2.636**	2.219*	2.516**	2.337**	<.0001	0.0204	<.0001	<.0001
Replicate	5	1.287*	0.937	1.662*	1.321	0.0337	0.5080	0.0178	0.0670
Genotype	13	3.144**	2.696**	2.768**	2.587**	<.0001	0.0089	<.0001	<.0001
Residual	58	0.492	1.079	0.553	0.601	-	-	-	-
C.V. (%)	-	36.07	29.79	42.51	68.91	-	-	-	-
h^2_{bs}	-	85.54	74.72	83.15	81.29	-	-	-	-

** Significance at 1% level; * Significance at 5% level; C.V.- Experimental coefficient of variation; h^2_{bs}-Broad-sense heritability; biomass- aboveground biomass (grain + stover); Model is a GLM procedure for randomised complete block design (RCBD) implemented in SAS software.

Genotype G73 ranked second to G100 with a relative grain yield of 0.34, a grain yield per plant of 11.83 g under drought stress and 34.53 g under non-drought conditions. Next to G73, was G99 which scored 0.32 of relative grain yield with the grain yield per plant of 9.33 g under drought stress and 29.52 g under non-drought conditions. The lowest relative grain yield of 0.03 was recorded by G5 with a grain yield per plant of 0.29 g under drought stress and 9.60 g under non-drought conditions. The genotypes performances in the greenhouse under drought and non-drought conditions after two weeks of drought stress at the reproductive stage are presented in Figure 19. The means performance with the ranking of the genotypes under drought stress using the Duncan multiple rank test is presented in Figures 20, 21, 22 and 23.

Based on the above results from grain yield and relative yield-related traits analysis and using relative grain yield (drought risk index for grain yield) as a main selection criterion: UPLR-17 (G100) was selected because it showed high relative grain yield, no LDS, high relative biomass with earliness in flowering. APO (G99) was selected because it showed moderate relative grain yield, low LDS, high relative biomass with early flowering. SR35266-2-12-1-1 (G73) was selected because it showed moderate relative grain yield, low LDS, high relative biomass. CRI-Enapa (G11) was selected because it showed no leaf drying, high relative biomass and earliness in flowering.

4.1.2.9 Relatedness and regression analysis of grain yield with yield attributes, biochemical, physiological and leaf reflectance parameters of the rice genotypes under reproductive stage drought conditions

The Pearson correlation analysis conducted at reproductive stage drought revealed that under drought stress, grain yield has a negative significant correlation with delay in flowering and DTF, and positively significantly associated with RDVI, while negatively with no significance related to LDS. This implies that the genotypes with early flowering under drought stress and low leaf drying score tended to have a high relative grain yield and high aboveground relative biomass values, therefore showing more tolerance to drought. This is confirming the consistent tolerance shown by G100, G11 and G99 (the three genotypes which flowered earlier under drought stress compared to the non-drought conditions in this study) throughout the analysis of the various traits and parameters under various numbers of days after the drought stress initiation (5D, 11D, 18D & 27D) at vegetative stage and reproductive stage drought. The LDS, DTF and delay in flowering recorded a positive significant correlation among themselves, whereas these three traits recorded a significant positive association with RWC.

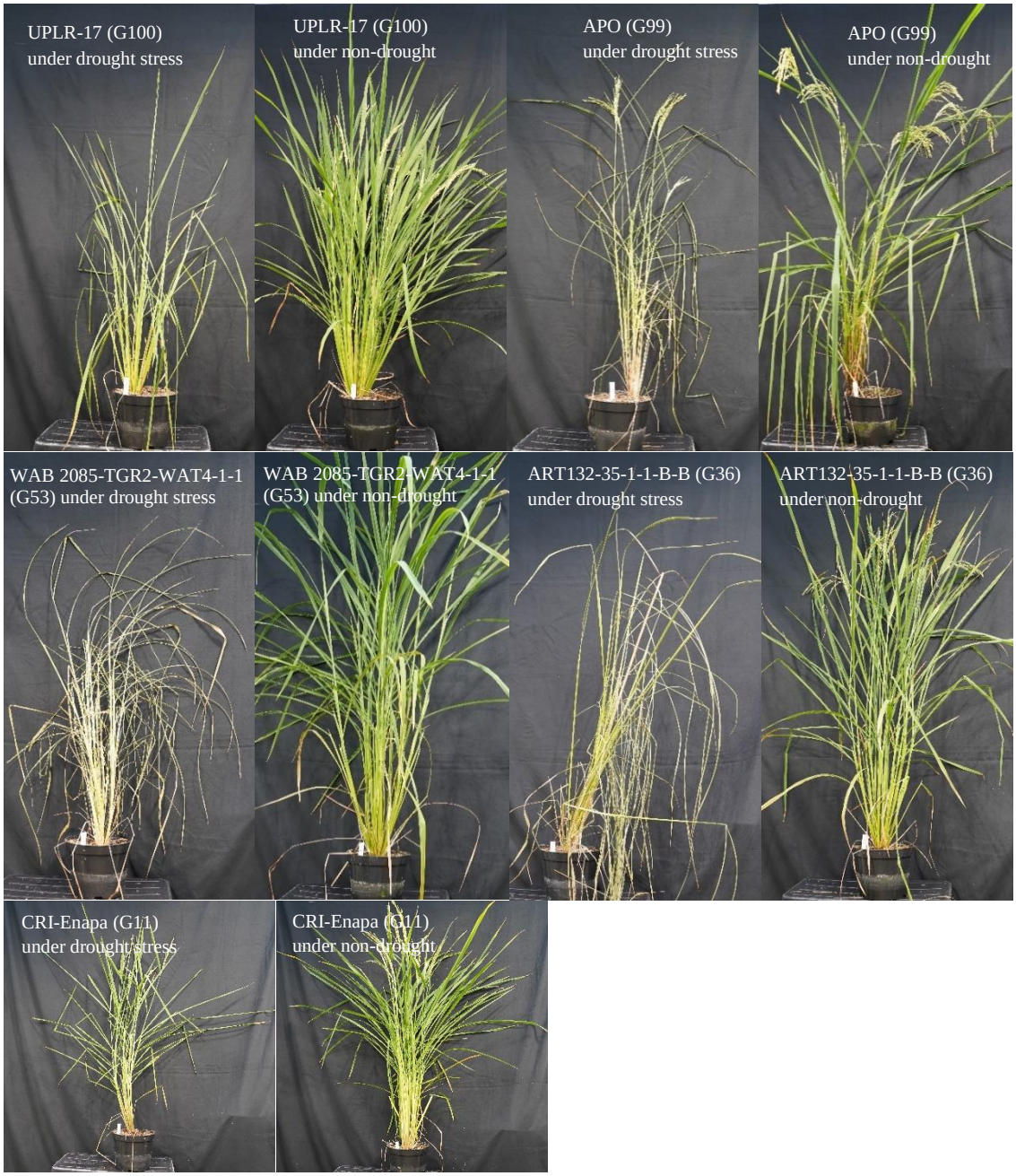


Figure 19. Performance of some genotypes under drought and non-drought conditions evaluated for physiological parameters at the reproductive stage after 14 days of drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

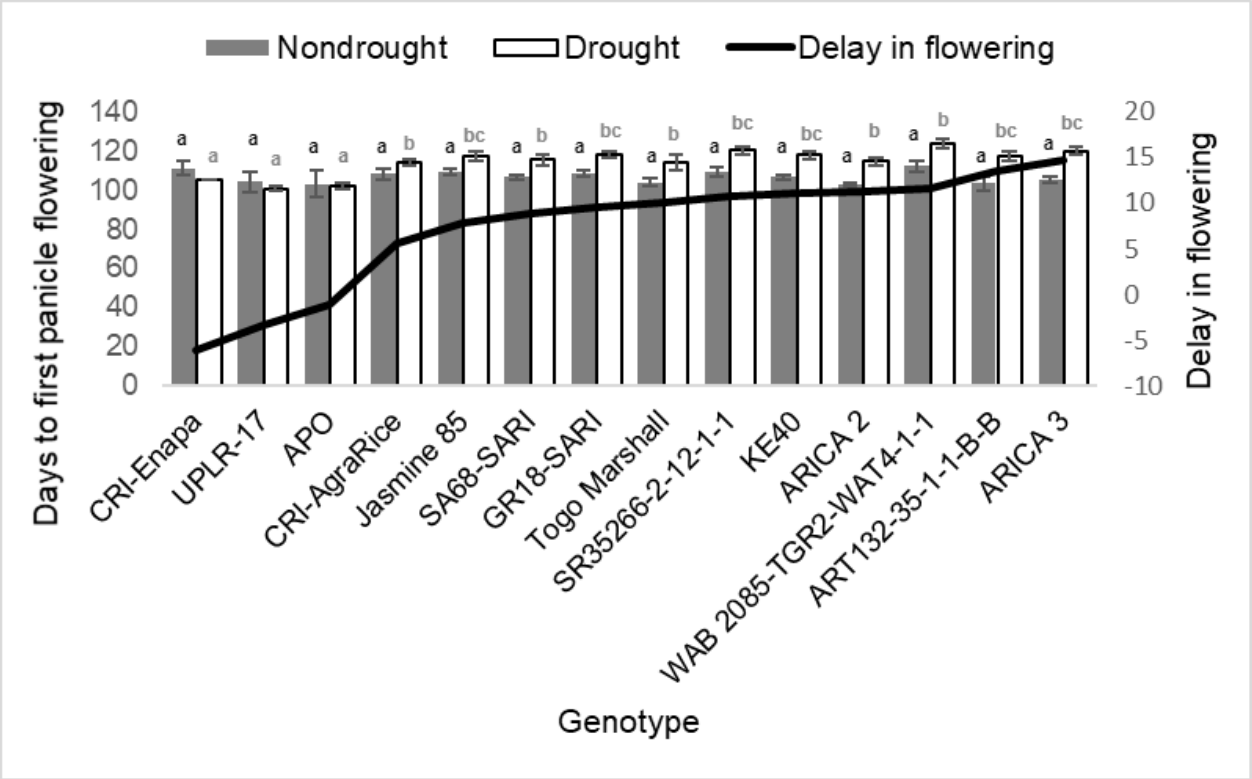


Figure 20. Mean performance of 14 rice genotypes evaluated for days to flowering at the reproductive stage under drought at the University of Giessen, Germany, in 2022. Data presented are means ±SE (n=6). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on delay in flowering for each genotype. Delay in flowering is calculated as number days to flowering under drought stress - number days to flowering under non-drought conditions per genotype. Wherever, the delay in flowering is negative, indicating that the genotype flowered early under drought stress than under non-drought conditions. The genotypes with their corresponding ID: Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

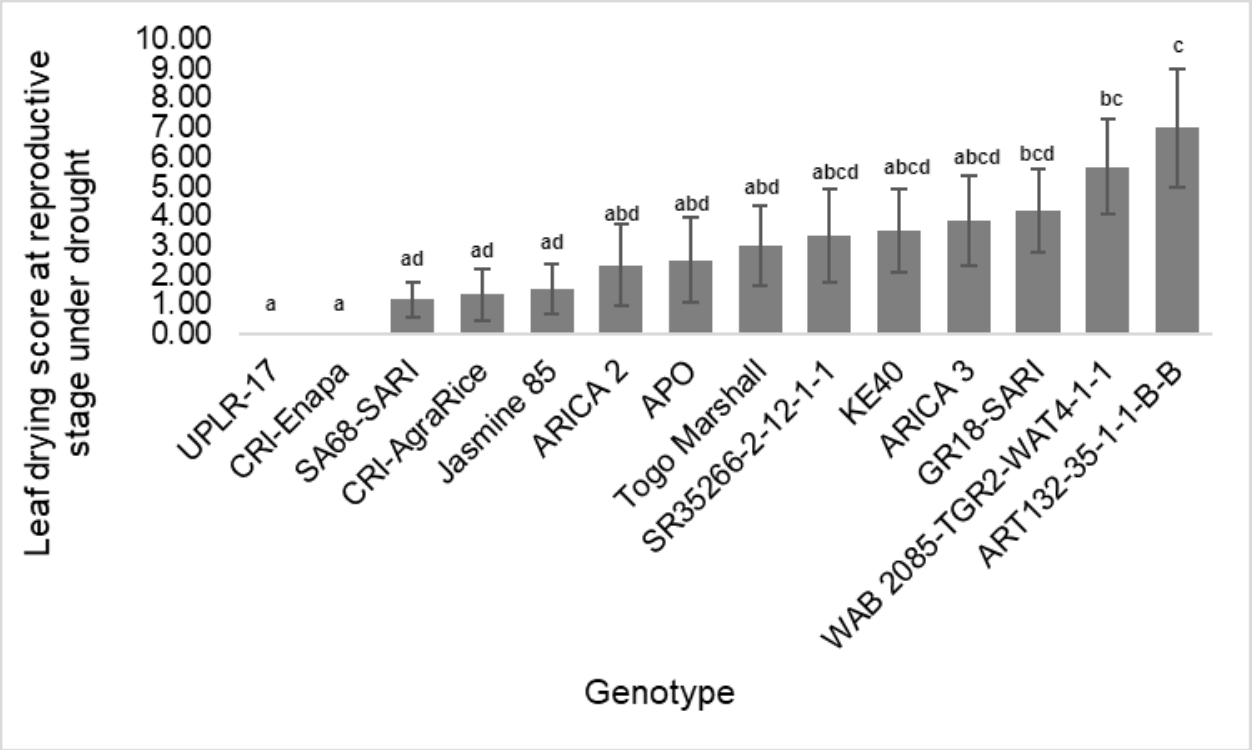


Figure 21. Mean performance of 14 rice genotypes evaluated for leaf drying score at the reproductive stage under drought at the University of Giessen, Germany in 2022. Data presented are means ±SE (n=6). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on leaf drying score at the reproductive stage under drought for each genotype. The lower the score, the better the performance of the genotype under drought stress. The genotypes with their corresponding ID: Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

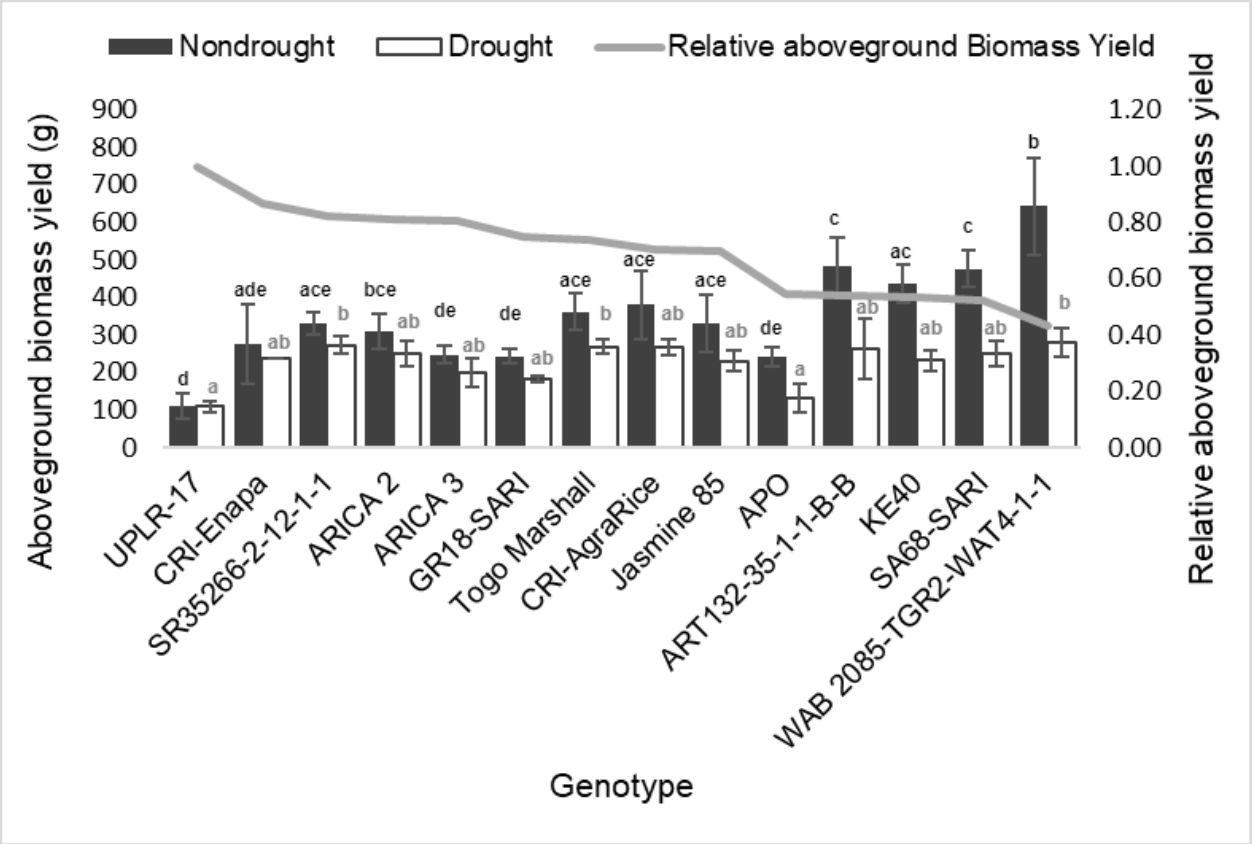


Figure 22. Mean performance of 14 rice genotypes evaluated for aboveground biomass at the reproductive stage under drought at the University of Giessen, Germany, in 2022. Data presented are means ±SE (n=6). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on relative values of aboveground biomass (g) for each genotype. Relative values were calculated as value under drought stress/value under non-drought conditions per genotype. The genotypes with their corresponding ID: Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

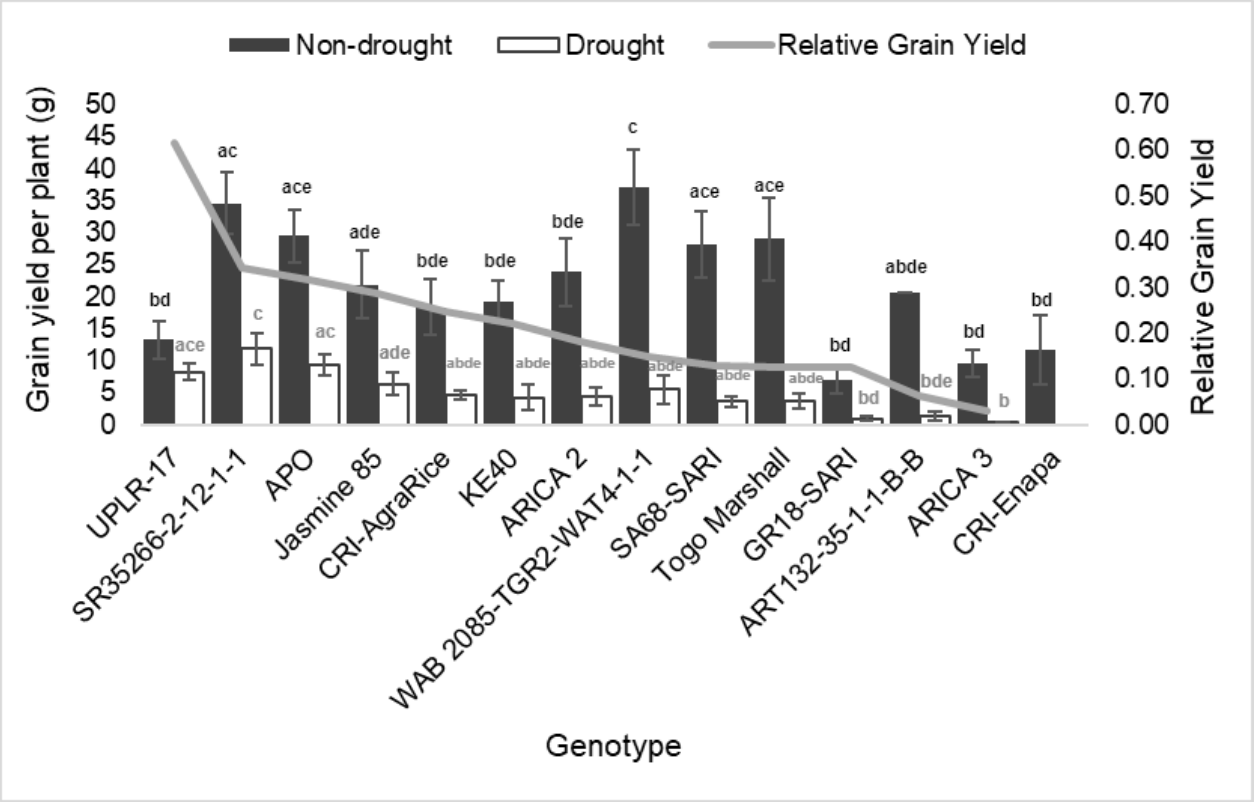


Figure 23. Mean performance of 14 rice genotypes evaluated for grain yield at the reproductive stage under drought at the University of Giessen, Germany, in 2022. Data presented are means ±SE (n=6). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on relative values of grain yield (g) for each genotype. Relative values were calculated as value under drought stress/value under non-drought conditions per genotype. The genotypes with their corresponding ID: Togo Marshall (G6), KE40 (62), SR35266-2-12-1-1 (G73), UPLR-17 (G100), APO (G99), GR18-SARI (G65), CRI-Enapa (G11), ARICA 3 (G5), ARICA 2 (G63), CRI-AgraRice (G2), Jasmine 85 (G22), WAB 2085-TGR2-WAT4-1-1 (G53), ART132-35-1-1-B-B (G36) and SA68-SARI (G78).

Pearson correlation analysis revealed under both water regimes, a strong positive significant correlation between stomatal conductance and transpiration rate, and both of them were positively associated with RWC (Table 29). Both indexes (CRI1 and CRI2) had a strong positive significant correlation with each other, and both were negatively correlated with RDVI and positively correlated with NDVI, whereas NDVI and RDVI recorded a positive association with each other and with grain yield under both water regimes. Aboveground biomass recorded a negative non-significant association with grain yield under drought stress, while a positive significant association under non-drought conditions. Stomatal conductance and transpiration rate recorded a negative non-significant association with grain yield and aboveground biomass under drought stress, while positive non-significant association under non-drought conditions.

The regression analysis using grain yield as dependent variable and RDVI as explanatory variable recorded R^2 =0.3366 with the model significance (Table 30), implying that close to 34% of the variability of the dependent variable grain yield was explained by the explanatory variable RDVI (Figure 24.). This confirmed the positive significant correlation (r=0.555) recorded between grain yield and RDVI under drought stress (Table 29). Given the R^2= 0.3140, 31% of the variability of the dependent variable grain yield was explained by the explanatory variable delay in flowering, but the model underlying this relationship between them was not significant. However, this confirmed the negative significant correlation of r= -0.559 recorded between grain yield and delay in flowering under drought stress. Taken together, delay in flowering and RDVI explained 43% of the variability of the dependent variable grain yield confirming the correlation pattern depicted between grain yield, delay in flowering and RDVI under drought stress. On the other hand, 44% of the variability of the dependent variable grain yield was explained by the two explanatory variables aboveground biomass and delay in flowering, while the leaf drying score explained close to 15% of the variability of the dependent variable grain yield under drought stress (Table 30), implying that the ability of the genotype to maintain its water status and prevent leaf drying under drought stress contributed up to 15% to the final yield performance of the genotype.

4.1.2.10 Rational between the selected genotypes under the field experiment and the greenhouse experiment

Tables 29 shows Pearson correlation among traits under non-drought and drought stress conditions, while Table 30 indicates regression analysis between grain yield and its related traits and Table 31 summarizes rational analysis between field and greenhouse experiments of

selected genotypes. Figure 24 shows regression analysis between grain yield and renormalized difference vegetative index (RDVI).

It is important to note that the genotypes G78 was not selected under the field conditions because of its bad performance in grain yield and spikelet fertility score, however, it exhibited high relative panicle length combined with high recovering ability from drought. The genotypes G11, G100 and G99 showed more consistency in tolerance to drought under the field screening as well as the greenhouse screening. These genotypes flowered earlier under drought stress as compared to the non-drought conditions and recorded low leaf drying under both field screening and greenhouse screening. One important trait all the genotypes manifested in commons was their ability to recover quickly from the drought stress and to regain their normal physiological and physical status. Based on both the field and greenhouse screening, it can be concluded that G11, G100 and G99 exhibited enhanced tolerance to drought compared to the remaining genotypes evaluated in this study.

Table 29. Pearson correlations among 14 rice genotypes evaluated for 17 grain yield and its related traits, physiological and leaf reflectance parameters and biochemical traits under non-drought and drought stress conditions at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Traits	Water stress	Biomass	GYP	LDS	DTF	Delay	gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI	MDA	Proline	RWC
TN	UD	0.650*	-0.242	0.420	0.568*	0.458	-0.038	-0.113	-0.137	-0.360	-0.416	-0.357	-0.378	0.086	0.120	0.315	-0.634*
	ND	0.424	0.262		0.172		0.397	0.299	-0.137	-0.477	0.263	0.125	0.139	0.113	0.093	0.995	-0.533*
Biomass	UD	1	-0.174	0.333	0.676**	0.545*	-0.247	-0.350	-0.498	-0.361	-0.533*	-0.373	-0.307	-0.172	0.594	0.570	-0.506
	ND	1	0.559*		0.355		0.278	0.440	0.373	0.100	0.091	0.384	0.381	-0.378	0.457	0.937	-0.021
GYP	UD		1	-0.395	-0.385	-0.559*	-0.129	-0.049	0.040	0.285	0.432	0.176	0.115	0.555*	-0.605	-0.890	0.348
	ND		1	-	0.083		0.072	0.159	-0.035	-0.196	0.204	0.041	0.006	0.099	0.474	0.996	-0.043
LDS	UD			1	0.657*	0.727**	-0.141	-0.138	-0.580*	-0.641*	-0.667**	-0.710**	-0.599*	-0.327	0.576	0.261	-0.727**
	ND			1	-	-	-	-	-	-	-	-	-	-	-	-	-
DTF	UD				1	0.899**	-0.479	-0.399	-0.480	-0.218	-0.541*	-0.394	-0.304	-0.448	0.664	0.374	-0.788**
	ND				1	-	-0.224	-0.156	-0.391	0.128	0.323	-0.070	-0.017	0.341	0.153	0.817	0.175
Delay	UD					1	-0.372	-0.275	-0.644*	-0.416	-0.598*	-0.529	-0.410	-0.559	0.724	0.523	-0.851**
	ND					1	-	-	-	-	-	-	-	-	-	-	-
gsw	UD						1	0.929**	0.165	-0.170	-0.207	-0.251	-0.234	0.408	-0.802*	-0.864	0.200
	ND						1	0.900**	0.289	0.082	0.088	0.433	0.478	-0.431	0.137	0.722	0.054
E	UD							1	0.154	-0.027	-0.130	-0.210	-0.175	0.304	-0.725	-0.743	0.072
	ND							1	0.375	0.334	0.099	0.338	0.376	-0.421	0.260	0.867	0.038
PhiPS2	UD								1	0.704**	0.400	0.508	0.387	0.273	-0.506	-0.763	0.534
	ND								1	0.042	-0.136	0.690**	0.687**	-0.725**	0.069	-0.318	-0.005
ETR	UD									1	0.510	0.607*	0.525	0.145	-0.096	-0.984	0.366
	ND									1	-0.222	-0.264	-0.255	-0.257	0.641	0.611	0.348
NDVI	UD										1	0.908**	0.833**	0.168	-0.747	0.088	0.701**
	ND										1	0.347	0.337	0.586*	0.572	0.972	0.138
CRI1	UD											1	0.955**	-0.029	-0.652	0.403	0.688**
	ND											1	0.991**	-0.447	0.025	-0.058	0.303
CRI2	UD												1	-0.229	-0.406	0.211	0.595*
	ND												1	-0.449	-0.046	-0.139	0.282
RDVI	UD													1	-0.795*	-0.998*	0.213
	ND													1	-0.124	0.488	-0.107
MDA	UD														1	0.704	-0.595
	ND														1	0.998*	-0.052
Proline	UD														1	-	-0.072
	ND															1	0.056

** Significance at 1% level; * Significance at 5% level; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI2-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index; GYP- Grain yield per plant in gram; DTF- Days to flowering; Biomass- Aboveground biomass yield in gram; MDA- malondialdehyde concentration; Proline- Proline accumulation; RWC- Relative water content in %; Delay-Delay in flowering; TN-Tiller number; LDS-Leaf drying score; ND-Under non-drought; UD-Under drought; Only seven genotypes were involved in the computation of the correlation of MDA and Proline with other traits.

Table 30. Regression analysis between grain yield and its related traits, physiological and leaf reflectance parameters among 14 rice genotypes evaluated under drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

Number of variables	Variables	Model significance (Pr > F)	MSE	R^2	Adjusted R^2	Mallows' Cp	Akaike's AIC	Schwarz's SBC	Amemiya's PC	Equation of the model (GYP)
1	Delay	0.058	9.167	0.3140	0.245	2	28.400	29.370	0.800	GYP = 8.014-0.352×Delay
1	LDS	0.207	11.411	0.1541	0.069	2	31.027	31.996	0.987	GYP = 7.055-0.692×LDS
1	RDVI	0.048*	8.955	0.3366	0.270	2	28.119	29.089	0.774	GYP = -77.938+155.082×RDVI
2	Biomass / Delay	0.075	8.442	0.4372	0.312	3	28.146	29.601	0.767	GYP = 2.765+3.209E-02×Biomass-0.601×Delay
2	Delay / RDVI	0.080	7.651	0.4302	0.304	3	26.966	28.421	0.777	GYP = -49.939-0.254×Delay+106.724×RDVI

* Significance at 5% level; RDVI-Renormalized difference vegetative index; GYP- Grain yield per plant in gram; DTF- Days to flowering; LDS- Leaf drying score; Delay- Delay in days to flowering Biomass- Aboveground biomass yield in gram

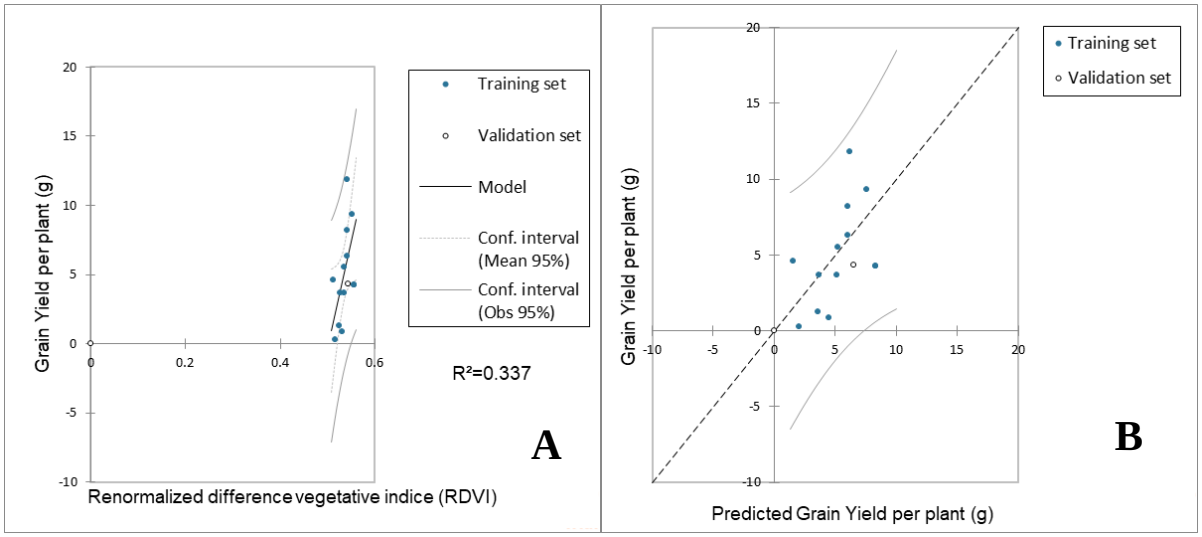


Figure 24. Regression analysis between grain yield and Renormalized difference vegetative index (RDVI) among 14 rice genotypes evaluated under drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022: (**A**) Regression of grain yield by RDVI; (**B**) Predicted grain yield with the regression model

Table 31. Rational analysis between the common selected genotypes under the field experiment at CSIR-Crops Research Institute, Ghana in 2021 and the greenhouse experiment at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022 under drought stress

Experiment sites/Genotypes	CRI-Enapa (G11)	UPLR-17 (G100)	APO (G99)	SA68-SARI (G78)	SR35266-2-12-1-1 (G73)
Greenhouse experiment	Consistent tolerance based physiological and leaf reflectance parameters at vegetative and reproductive drought stress	Consistent tolerance based physiological and leaf reflectance parameters at vegetative and reproductive drought stress	Consistent tolerance based physiological and leaf reflectance parameters at vegetative and reproductive drought stress	Consistent tolerance based physiological and leaf reflectance parameters at vegetative and reproductive drought stress	-
	-	High proline accumulation under drought		High proline accumulation under drought	
	Low relative MDA	Low relative MDA	Low relative MDA		-
	High relative RWC	High relative RWC	High relative RWC	High relative RWC	-
	-	High relative grain yield			-
	Zero LDS	Zero LDS	Low LDS	-	Low LDS
	High relative biomass	High relative biomass	High relative biomass		High relative biomass
	Early flowering under drought	Early flowering under drought	Early flowering under drought		-
	High relative tiller number	High relative tiller number	High relative tiller number		High relative tiller number
Field experiment		High relative grain yield	High relative grain yield		High relative grain yield
		-	-		High relative plant height
	Efficient recovery from drought	Efficient recovery from drought	Efficient recovery from drought	Not selected under the field conditions due to poor yield performance	Efficient recovery from drought
	Early flowering under drought	Early flowering under drought	Early flowering under drought		-
	-	-	Low leaf rolling		-
	Low relative spikelet fertility score		Low relative spikelet fertility scores		-

LDS- Leaf drying score; MDA- malondialdehyde concentration; RWC- Relative water content in %

4.1.3 Transcriptome analysis of four contrasting genotypes selected out of 100 West Africa rice germplasms in response to drought stress

4.1.3.1 Evaluation of the rice genotypes in pots under drought stress

After 30 days of drought stress when the drought pots reached 50% of water content, G99 (622.04±146.93 mg) recorded the highest shoot fresh weight under non-drought conditions, while G11 (359.21±171.62 mg) recorded the lowest. Under drought conditions, G11 (315.43±30.58 mg) recorded the highest shoot fresh weight, while G1 (174.55±58.33 mg) recorded the lowest. Genotypes G11 and G36 topped highest for relative shoot fresh weight (Figure 25).

At 50% soil water content, G99 (131.26±11.22 mg) recorded the highest root fresh weight under non-drought conditions, while G36 (46.49±23.05 mg) recorded the lowest. Under drought conditions, G36 (35.27±14.26 mg) recorded the highest root fresh weight, while G99 (26.43±3.90 mg) recorded the lowest. Genotype G36 topped highest for relative root fresh weight (Figure 25). At 50% soil water content, the plant under drought stress have showed clear symptoms of drought as presented in Figure 26.

4.1.3.2 RNA extraction

Under non-drought conditions, the average RNA concentration across all the genotypes was 1186.34 ng/µL. Under drought conditions, the average RNA concentration across all the genotypes was 1218.61 ng/µL. The RNA concentration of all the genotypes per replicate is presented in Table 32. The RNA Integrity/degradation checked on 1.5% agarose gel showed that RNA for none of the genotypes was degrading (Figure 27).

Figure 25 shows the shoot fresh weight and root fresh weight among the rice genotypes evaluated in growth chambers under non-drought and drought stress conditions, while Figure 26 shows phenotypic performance of the four rice genotypes evaluated under drought stress in growth chambers. Table 32 shows the RNA concentration observed among the rice genotypes evaluated under drought stress in growth chambers and Figure 27 shows the RNA Integrity/degradation checked on 1.5% agarose gel.

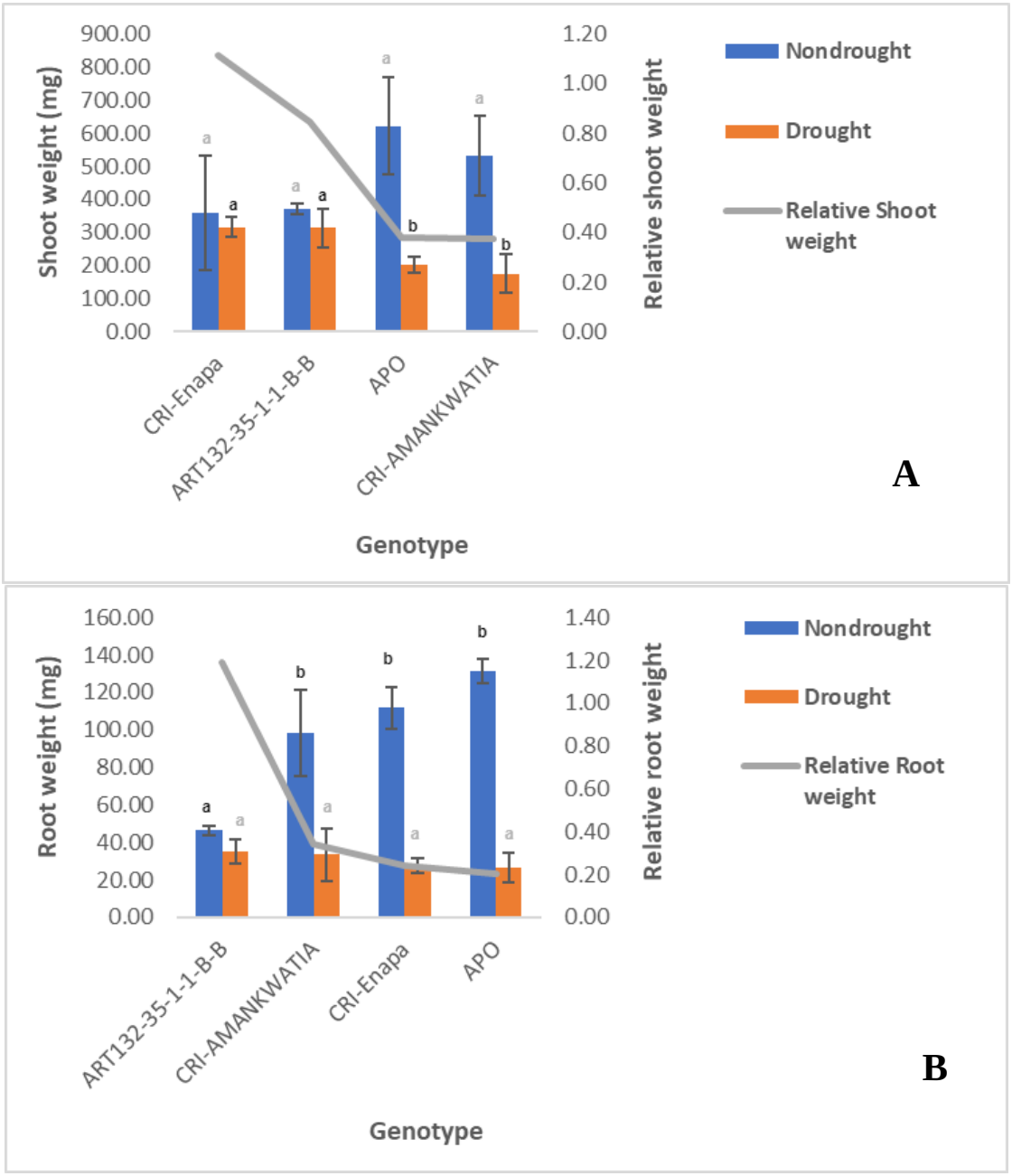


Figure 25. **(A)** shoot fresh weight and **(B)** root fresh weight among the rice genotypes evaluated in growth chambers under drought stress at University College Cork (UCC), Cork, Ireland in 2023. Data presented are means ±SE (n=6). Genotypes CRI-Amankwatia (G1), ART132-35-1-1-B-B (G36), CRI-Enapa (G11), APO (G99) with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%). From left to right, genotypes are classified from best to worst performance, respectively, based on relative values of shoot fresh weight (mg) and root fresh weight (mg) for each genotype. Relative shoot fresh weight (mg) and root fresh weight (mg) were calculated as value under drought stress/value under non-drought conditions per genotype.

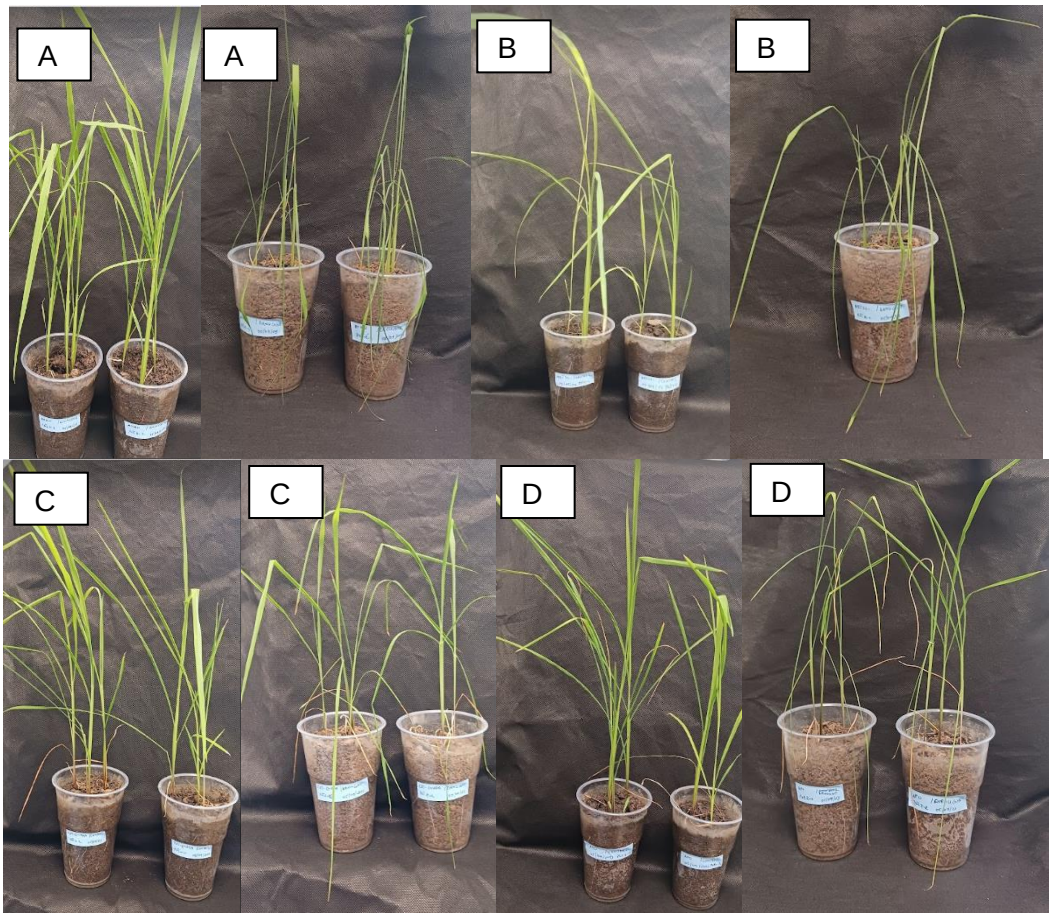


Figure 26. Performance of the four rice genotypes evaluated under drought stress in growth chambers at University College Cork (UCC), Cork, Ireland in 2023. (**A1)** CRI-Amankwatia (G1) under non-drought conditions, (**A2)** CRI-Amankwatia (G1) under drought conditions; (**B1)** ART132-35-1-1-B-B (G36) under non-drought conditions, **(B2)** ART132-35-1-1-B-B (G36) under drought conditions; **(C1)** CRI-Enapa (G11) under non-drought conditions, **(C2)** CRI-Enapa (G11) under drought conditions **(D1)** APO (G99) under non-drought conditions, **(D2)** APO (G99) under drought conditions

Table 32. RNA concentration observed among the rice genotypes evaluated under non-drought and drought conditions in growth chambers at University College Cork (UCC), Cork, Ireland in 2023

RNA quantification technique			NANODROP		QUBIT	
Rep	ID	Genotype	RNA-non-drought (ng/µL)	RNA-Drought (ng/µL)	RNA-non-drought (ng/µL)	RNA-Drought (ng/µL)
1	G99	APO	834.80	1025.70	1176	1624
2	G99	APO	883.30	1700.50	776	884
3	G99	APO	997.9	699.40	1225	856
1	G36	ART132-35-1-1-B-B	1430.20	1523.00	1364	1312
2	G36	ART132-35-1-1-B-B	2141.20	960.00	1364	412
3	G36	ART132-35-1-1-B-B	1756.00	1487.20	896	1484
1	G1	CRI-Amankwatia	1017.30	1222.50	-	-
2	G1	CRI-Amankwatia	856.30	1432.00	-	-
3	G1	CRI-Amankwatia	846.00	298.50	-	-
1	G11	CRI-Enapa	1533.60	1011.70	700	1104
2	G11	CRI-Enapa	1232.50	1329.50	1392	776
3	G11	CRI-Enapa	1361.80	2125.80	1056	1532

Rep-Replication; ID-Genotype identity

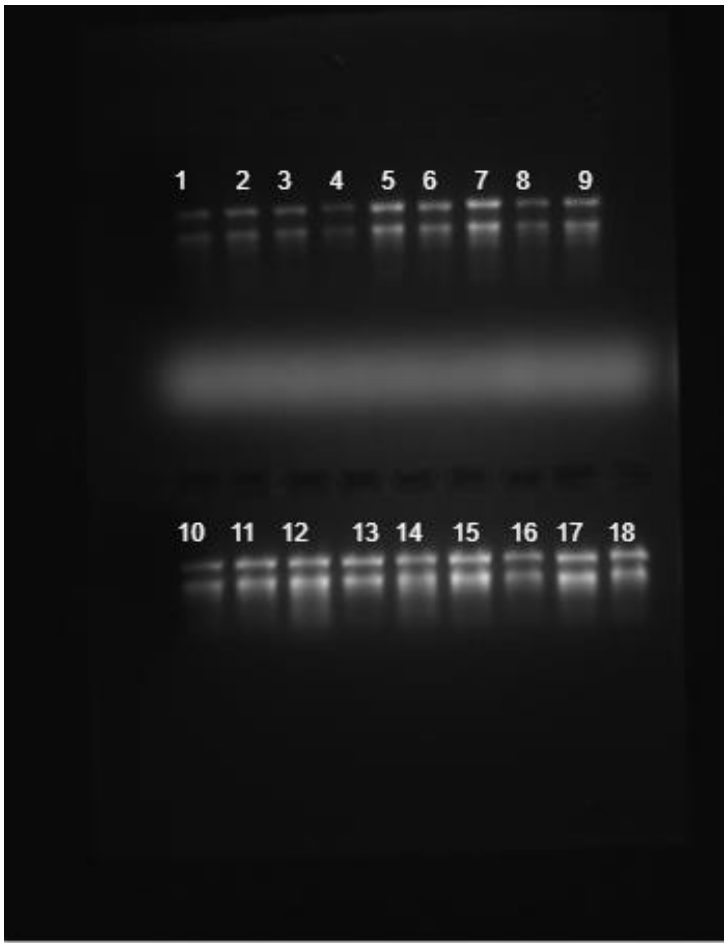


Figure 27. Assessment of RNA quality by denaturing gel electrophoresis from the rice genotypes evaluated under drought stress in growth chambers at University College Cork (UCC), Cork, Ireland in 2023. Integrity/degradation of RNA checked on 1.5% agarose gel showed no degrading RNA among the genotypes:

(1) APO(G99)/non-drought/R1; **(2)** APO(G99)/Drought/R1;

(3) APO(G99)/non-drought/R2; **(4)** APO(G99)/Drought/R2;

(5) APO(G99)/non-drought/R3; **(6)** APO(G99)/Drought/R3;

(7) CRI-Enapa(G11)/non-drought/R1; **(8)** CRI-Enapa(G11)/Drought/R1;

(9) CRI-Enapa(G11)/non-drought/R2; **(10)** CRI-Enapa(G11)/Drought/R2;

(11) CRI-Enapa(G11)/non-drought/R3; **(12)** CRI-Enapa(G11)/Drought/R3;

(13) ART132-35-1-1-B-B(G36)/non-drought/R1;

(14) ART132-35-1-1-B-B(G36)/Drought/R1;

(15) ART132-35-1-1-B-B(G36)/non-drought/R2;

(16) ART132-35-1-1-B-B(G36)/Drought/R2;

(17) ART132-35-1-1-B-B(36)/non-drought/R3;

(18) ART132-35-1-1-B-B(G36)/Drought/R3; R=Replicate

4.1.3.3 Quantitative real-time reverse transcription-PCR (qRT-PCR) analysis

The analysis of variance (Figure 28) showed that there was no significant difference among the expression level of the genotypes used in this study under non-drought conditions for all the drought responses genes used namely *LOC_Os04g23550 (Basic-helix-loop helix family protein, transcription factor, BHLH6), LOC_Os05g08480 (Cytokinin-O-glucosyltransferase-1, Cyt-o-Gluc), LOC_Os07g43560 (DUF26 kinases, DUF26K)*. On the other hand, the expression levels of genes *BHLH6* and *Cyt-o-Gluc* in the genotype G99 ($P \leq 0.05$) was significantly different from the expression levels in the remaining three genotypes (G36, G99 and G1) under drought stress. No significant difference ($P \geq 0.05$) was observed among the genotypes for the expression of *DUF26K* under drought stress.

LOC_Os04g23550 (Basic-helix-loop helix family protein, transcription factor, BHLH6) was upregulated in all the genotypes. The *BHLH6* is 2.5x induced in G99 under drought stress compared to non-drought conditions. In G11 (0.9x), G36 (1.7x) and G1 (1.6x) there was no significant difference in relative expression between both drought and non-drought conditions. *LOC_Os05g08480 (Cytokinin-O-glucosyltransferase-1, Cyt-o-Gluc)* is upregulated in all the genotypes. The *Cyt-o-Gluc* was 32.5x induced in G99, 6.5x in G36 and 5.5x in G1 under drought stress compared to non-drought conditions, while G11 registered only 1.4x increase in relative expression under drought stress compared to the non-drought conditions. In G11, there was no significant difference in relative expression between both drought and non-drought conditions. *LOC_Os07g43560 (DUF26 kinases have homology to DUF26 containing loci, DUF26K)* was upregulated in G99 and G36. The *DUF26K* was 7.0x induced in G99 and 3.0x in G36 under drought stress compared to non-drought conditions, while G11 (0.4x) and G1 (0.3x) were downregulated under drought stress compared to the non-drought conditions. There was significant difference in relative expression for all the genotypes between drought and non-drought conditions. The consistent upregulation of the three drought responsive genes *(LOC_Os04g23550, LOC_Os05g08480, LOC_Os07g43560)* in G99, confirmed it enhance tolerance to drought as discovered during the field screening. The even expression levels of the two genes *(LOC_Os04g23550, LOC_Os05g08480)* under both drought and non-drought conditions in G11 can be explained by the fact that, G11 is known to be tolerant to short-term drought stress, based on this, these drought response genes might be always expressing independent of the growing conditions (stress or not). All the expression levels for the three genes are represented in Figure 28.

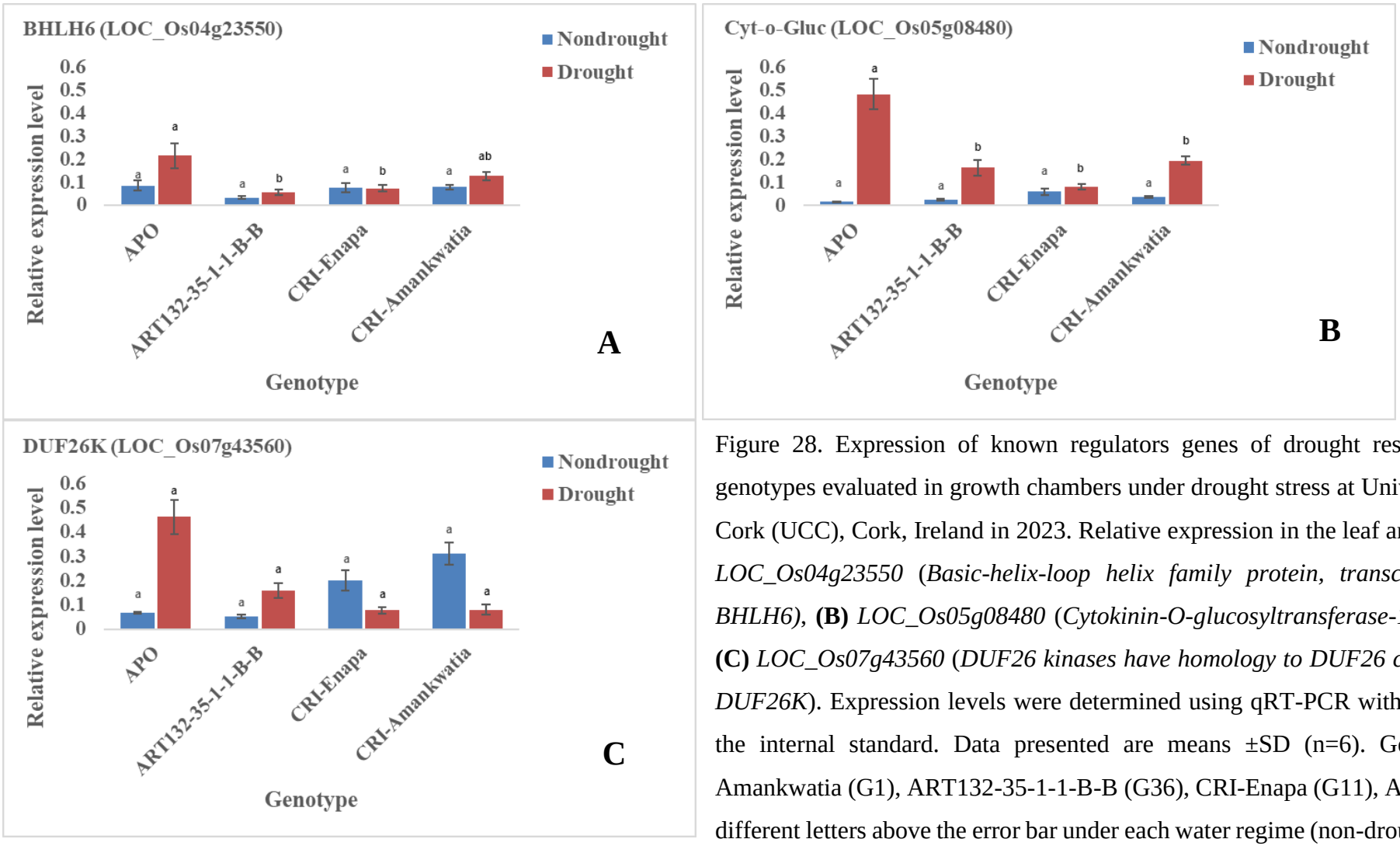


Figure 28. Expression of known regulators genes of drought responses in rice genotypes evaluated in growth chambers under drought stress at University College Cork (UCC), Cork, Ireland in 2023. Relative expression in the leaf and shoot of **(A)** *LOC_Os04g23550* (*Basic-helix-loop helix family protein, transcription factor, BHLH6)*, **(B)** *LOC_Os05g08480* (*Cytokinin-O-glucosyltransferase-1, Cyt-o-Gluc*), **(C)** *LOC_Os07g43560* (*DUF26 kinases have homology to DUF26 containing loci, DUF26K*). Expression levels were determined using qRT-PCR with rice Actin1 as the internal standard. Data presented are means ±SD (n=6). Genotypes CRI-Amankwatia (G1), ART132-35-1-1-B-B (G36), CRI-Enapa (G11), APO (G99) with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

4.1.4 Genetic basis behind the expression of tolerance to drought stress among the rice breeding lines using generation mean analysis

4.1.4.1 Mean comparison of the rice parents involved in the development of the six generations under both non-drought and drought stress conditions

Under non-drought conditions, there was no significant difference in the two parental varieties namely CRI-Agrarice (Agra) and Apo for tiller number, panicle number, panicle length (cm), DTF and grain yield per plant (g) based on t-test$_{0.05}$, whereas plant height (cm) showed a significant difference in the mean performance of Agra and Apo (Table 33). There was also no significant difference in the two parental varieties namely Jasmine 85 (J.85) and Apo for tiller number, panicle length (cm) and grain yield per plant (g) based on t-test$_{0.05}$, whereas panicle number, plant height (cm) and DTF, showed a significant difference in the mean performance of J.85 and Apo under non-drought conditions (Table 33).

Under drought stress, there was no significant difference in the two parental varieties namely Agra and Apo for tiller number, panicle number, panicle length (cm), SPFS, LRS, LDS and grain yield per plant (g) based on t-test$_{0.05}$, whereas DRR, plant height (cm) and DTF showed a significant difference in the mean performance of Agra and Apo (Table 33). There was no significant difference in the two parental varieties namely J.85 and Apo for tiller number, panicle number, plant height (cm), panicle length (cm), LDS and grain yield per plant (g) based on t-test$_{0.05}$, whereas SPFS, LRS, DRR, and DTF showed significant difference in the mean performance of Agra and Apo under drought stress (Table 33).

4.1.4.2 Mean performance of the parents (P_1 and P_2) and their progenies (F_1, F_2, BC_1 and BC_2) of Agra/APO and J.85/Apo crosses under drought stress

Under non-drought conditions, ANOVA across the six populations (recipient parent (P_1), donor parent (P_2) and their respective progenies (F_1, F_2, BC_1 and BC_2)) has revealed significant differences for tiller number, panicle number, plant height and DTF at 1% in Agra/Apo cross, whereas in J.85/Apo cross in addition to these traits, grain yield per plant showed significance at 5%. Only panicle length did not show significant differences among the six populations of both crosses under non-drought conditions (Annex 20 and 21). Under drought stress, ANOVA showed significant differences in all the traits (LRS, LDS, DRR, SPFS, tiller number, plant height, DTF and grain yield per plant) except panicle number and panicle length in Agra/Apo cross, whereas in J.85/Apo cross, ANOVA showed significant differences in all the traits (LRS, LDS, DRR, SPFS, tiller number, plant height and DTF) except panicle number, panicle length and grain yield per plant (Annex 22 and 23).

Table 33. Differences in the mean performance of the parents involved in Agra/Apo and J.85/Apo crosses evaluated under non-drought and drought stress conditions at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Experimental Conditions	Drought stress conditions						Non-drought conditions					
Cross	AGRA/APO			J.85/APO			AGRA/APO			J.85/APO		
Parents	CRI-Agrarice	APO	*p-value*	Jasmine 85	APO	*p-value*	CRI-Agrarice	APO	*p-value*	Jasmine 85	APO	*p-value*
TN	4.17	4.70	0.19	4.43	4.70	0.52	8.21	8.93	0.25	7.73	8.93	0.08
PN	2.69	3.17	0.31	2.93	3.17	0.62	6.93	8.07	0.07	6.40	8.07	0.01*
PH	75.48	85.67	0.00**	86.10	85.67	0.88	92.21	100.64	0.00**	95.13	100.64	0.01**
PL	18.21	20.10	0.14	20.30	20.10	0.88	22.31	23.18	0.75	23.60	23.18	0.43
DTF	94.77	90.43	0.00**	93.93	90.43	0.00**	92.60	91.46	0.07	93.13	91.46	0.01**
GYP	9.00	8.44	0.70	9.32	8.44	0.44	14.29	15.71	0.30	14.66	15.71	0.48
LRS	4.73	4.86	0.89	0.83	4.86	0.00**	-	-	-	-	-	-
LDS	2.90	2.97	0.77	3.47	2.97	0.09	-	-	-	-	-	-
DRR	4.00	4.93	0.01*	3.37	4.93	0.00**	-	-	-	-	-	-
SFPS	7.07	6.00	0.06	2.87	6.00	0.00**	-	-	-	-	-	-

**-Significant at 1% based on two-tails t-test; *-Significant at 5% based on two-tails t-test; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant

Overall, the mean performance of the six populations has decreased significantly under drought stress compared to the non-drought conditions for both crosses Agra/Apo and J.85/Apo for all the studied traits. The paired t-test conducted in Agra/Apo cross revealed significant differences in the mean performance among the lines of the six populations between non-drought and drought stress conditions for the following traits tiller number (p-value=0.004), panicle number (p-value=0.012), plant height (p-value=0.001), panicle length (p-value=0.043) and grain yield (p-value=0.035), whereas days to flowering (p-value=0.954) showed no significance. In J.85/Apo cross, the paired t-test revealed significant differences in tiller number (p-value=0.013), plant height (p-value=0.035), whereas panicle number (p-value=0.098), panicle length (p-value=0.297), days to flowering (p-value=0.798) and grain yield (p-value=0.159) showed no significance.

The highest reduction in tiller number of 57.14% was observed on the F_1 of the cross Agra/Apo (F1-Agra/Apo), and 53.13% in the BC_1 of the cross J.85/Apo (BC1-J.85/Apo/J.85), while the lowest reduction of 30.76% for Agra/Apo cross was observed in the BC_2 cross (BC2-Agra/Apo/Apo) and 27.27% in the F_1 of the cross J.85/Apo (F1-J.85/Apo) (Figure 29).

The highest reduction in panicle number of 61.19% was observed on the P_1 of the cross Agra/Apo (P1-Agra), and 60.77% in the P_2 of the cross J.85/Apo (P2-Apo), while the lowest reduction of 11.43% for Agra/Apo cross was observed in the BC_1 cross (BC1-Agra/Apo/Agra) and 0.00% in the F_1 of the cross J.85/Apo (F1-J.85/Apo). The backcross 1, BC1-J.85/Apo/J.85 recorded an increase of 52.00% (Figure 30) for panicle number.

The highest reduction in plant height of 25.97% was observed on the F_2 of the cross Agra/Apo (F2-Agra/Apo), and 26.42% in the BC_2 of the cross J.85/Apo (BC2-J.85/Apo/Apo), while the lowest reduction of 10.45% for Agra/Apo cross was observed in the F_1 cross (F1-Agra) and 2.71% in the BC_1 of the cross J.85/Apo (BC1-J.85/Apo/J.85) (Figure 31).

The highest reduction in panicle length of 24.71% was observed on the BC_2 of the cross Agra/Apo (BC2-Agra/Apo/Apo), and 20.36% in the BC_2 of the cross J.85/Apo (BC2-J.85/Apo/Apo), while the lowest reduction of 11.32% for Agra/Apo cross was observed in the P_2 (P2-Apo) and 2.82% in the F_1 of the cross J.85/Apo (F1-J.85/Apo). The F_1 progenies, F1-Agra/Apo recorded an increase of 14.67%, whereas the backcross 1, BC1-J.85/Apo/J.85 recorded an increase of 17.54% for panicle length (Figure 32).

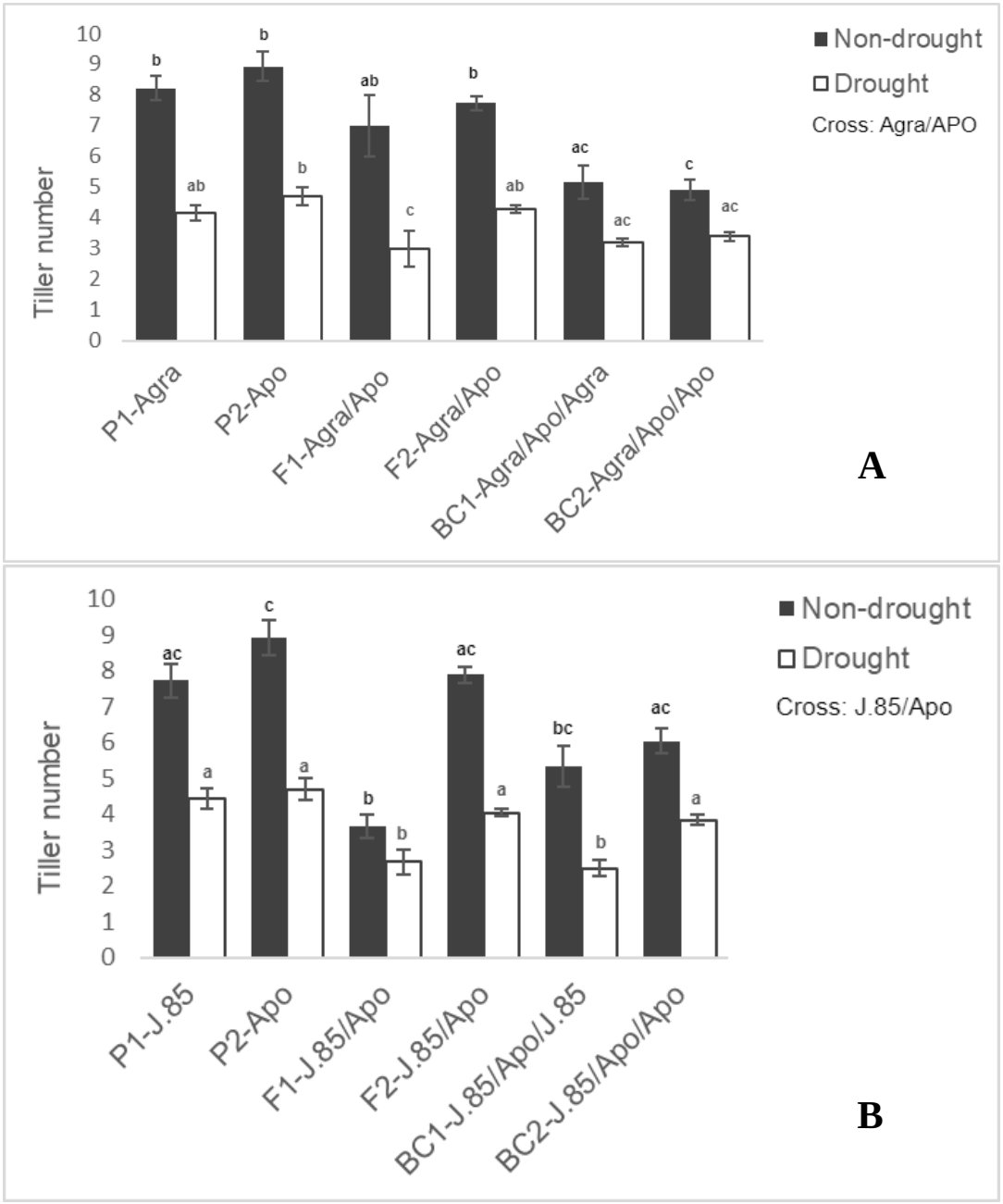


Figure 29. Mean performance of the lines of the six populations of **(A)** Agra/Apo and **(B)** J.85/Apo crosses evaluated under drought stress for tiller number at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022. Data presented are means ±SE (n=30 (P_1 and P_2); n=3 (F_1); n=120 (F_2); n=40 (BC_1 and BC_2)). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

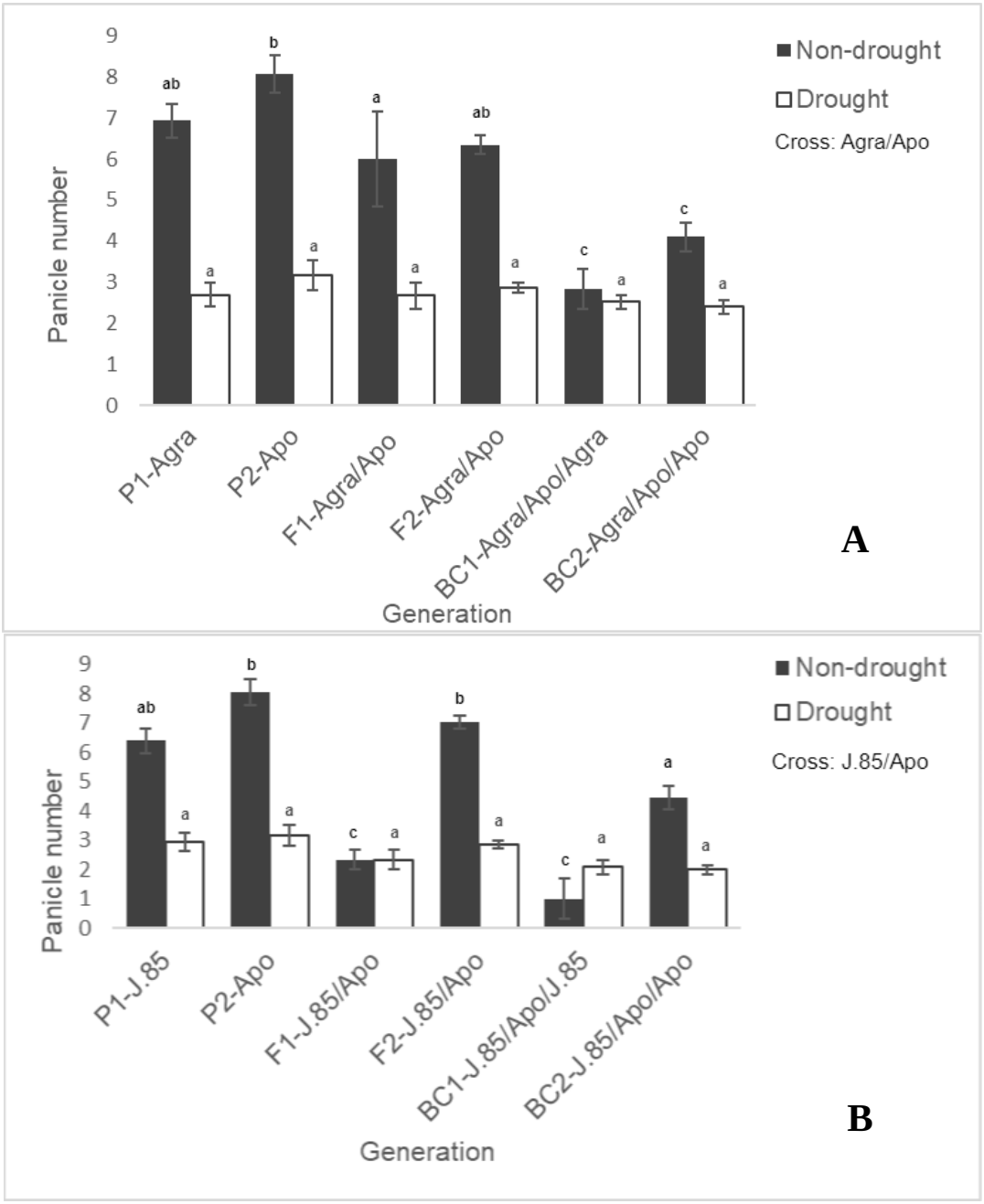


Figure 30. Mean performance of the lines of the six populations of **(A)** Agra/Apo and **(B)** J.85/Apo crosses evaluated under drought stress for panicle number at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022. Data presented are means ±SE (n=30 (P_1 and P_2); n=3 (F_1); n=120 (F_2); n=40 (BC_1 and BC_2)). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

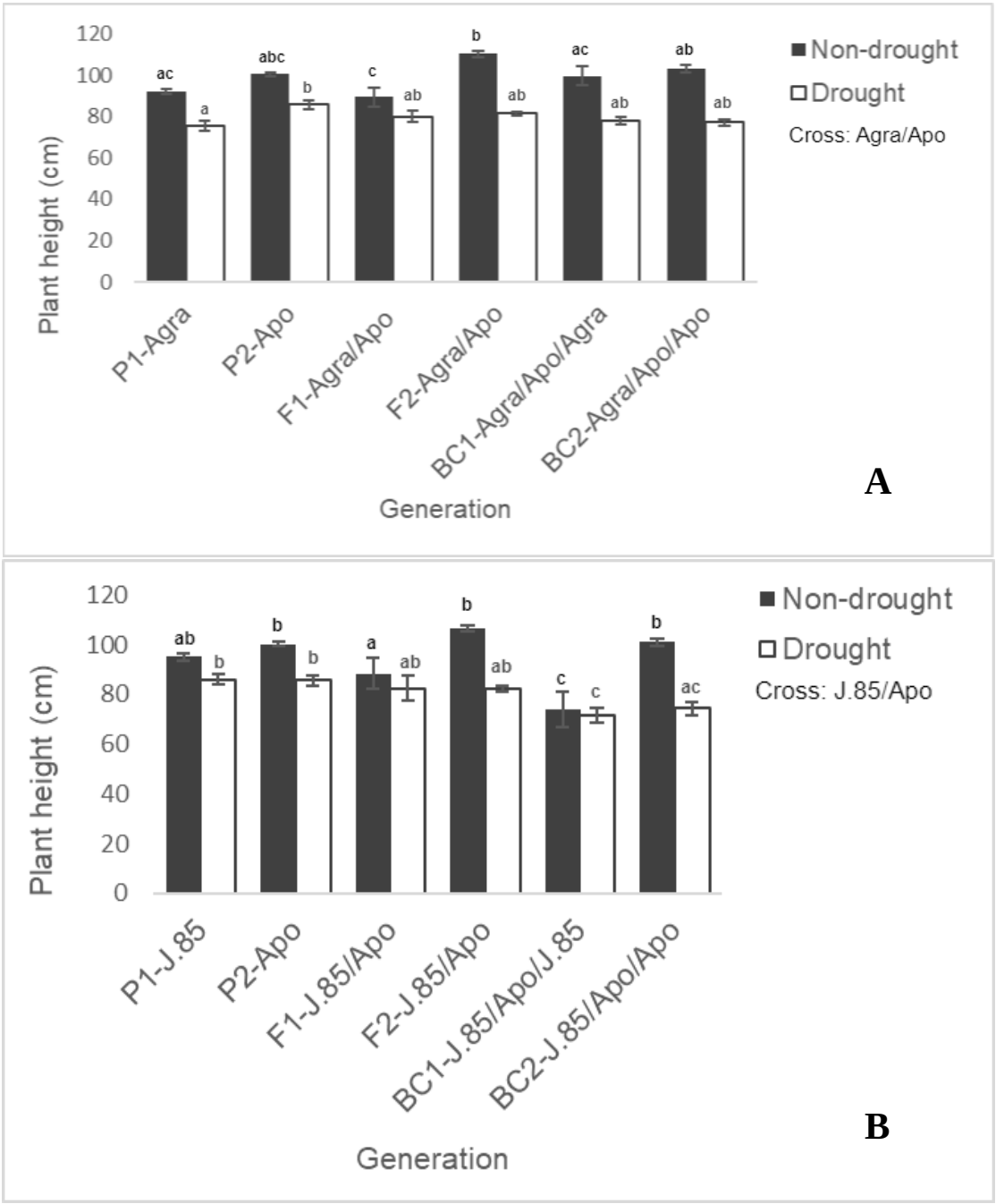


Figure 31. Mean performance of the lines of the six populations of **(A)** Agra/Apo and **(B)** J.85/Apo crosses evaluated under drought stress for plant height at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022. Data presented are means ±SE (n=30 (P_1 and P_2); n=3 (F_1); n=120 (F_2); n=40 (BC_1 and BC_2)). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

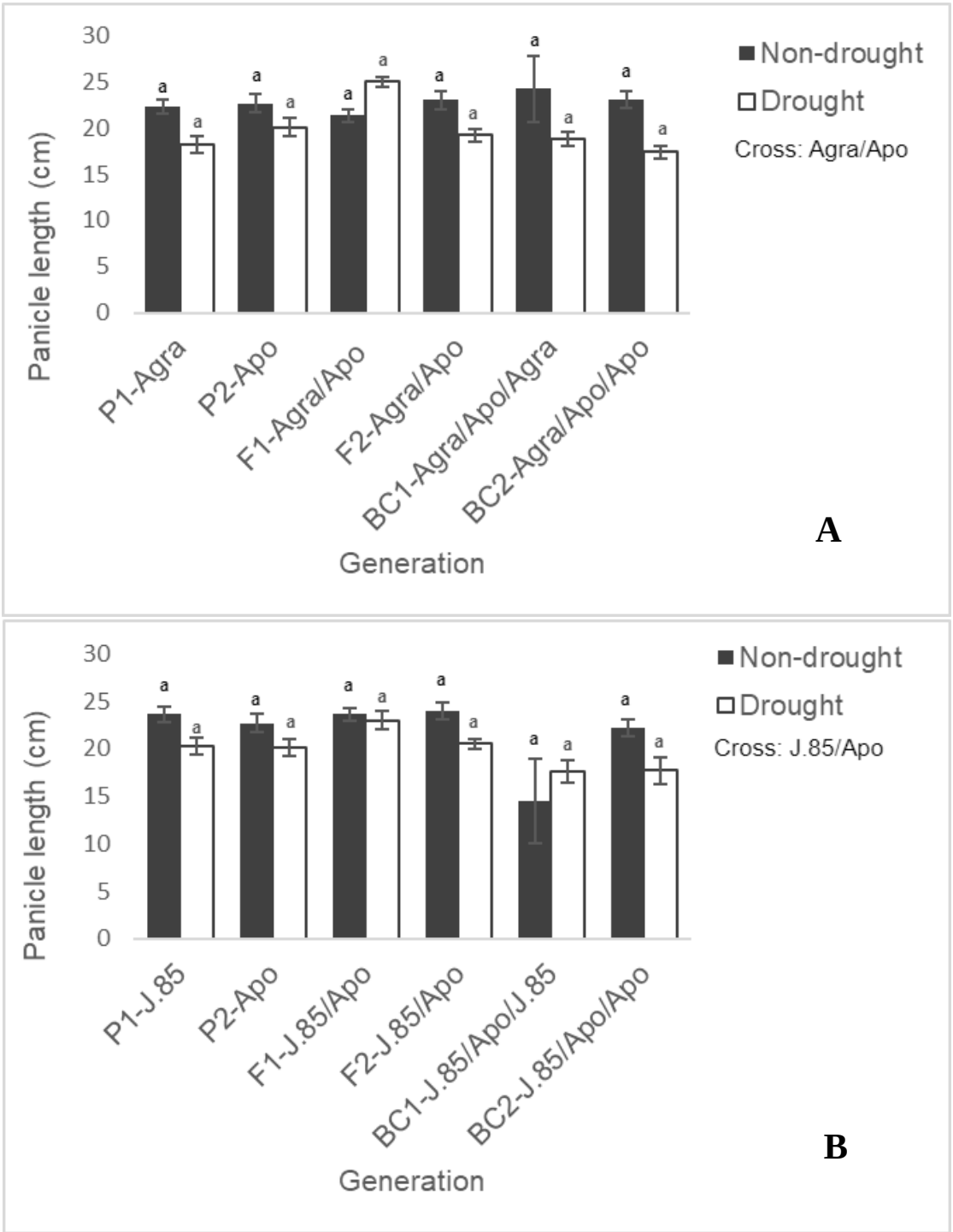


Figure 32. Mean performance of the lines of the six populations of **(A)** Agra/Apo and **(B)** J.85/Apo crosses evaluated under drought stress for panicle length at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022. Data presented are means ±SE (n=30 (P_1 and P_2); n=3 (F_1); n=120 (F_2); n=40 (BC_1 and BC_2)). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

The reductions of 1.13% and 4.64% were observed on the donor parent Apo (P2-Apo) and BC_1 of the cross Agra/Apo (BC1-Agra/Apo/Agra), respectively for days to flowering (DTF), while the increase of 2.29%, 1.77%, 2.09% and 0.69% for Agra/Apo cross were observed in the P_1 (P1-Agra), F1-Agra/Apo, F2-Agra/Apo and BC2-Agra/Apo/Apo, respectively. A reduction of 6.94% was observed on the BC_1 of the cross Agra/Apo (BC1-Agra/Apo/Agra) for DTF, while the increase of 0.85%, 3.47%, 0.54% and 0.57% for Agra/Apo cross were observed in the P_1 (P1-Agra), F1-Agra/Apo, F2-Agra/Apo and BC2-Agra/Apo/Apo, respectively (Figure 33).

The highest reduction in grain yield per plant (g) of 46.29% was observed on the P_2 of the crosses Agra/Apo and J.85/Apo (P2-Apo), while the lowest reduction of 10.74% for Agra/Apo cross was observed in the F_2 (F2-Agra/Apo) and 29.07% in the F_2 of the cross J.85/Apo (F2-J.85/Apo). The BC_1 progenies, BC1-Agra/Apo/Agra recorded an increase of 5.74%, whereas the backcross 1, BC1-J.85/Apo/J.85 recorded an increase of 42.71% for grain yield per plant in grams (Figure 34).

4.1.4.3 Transgressive segregation analysis

All the agro-morphological traits studied in all the F_2 populations generated from the crosses Agra/Apo and J.85/Apo showed normal distributions based on the skewness and kurtosis data which stayed in the ranges of -2 to +2 and -7 to +7 respectively under both non-drought and drought stress conditions. Descriptive statistics showing the variation among the F_2 lines derived from the crosses Agra/Apo and J.85/Apo for all the traits under non-drought and drought stress conditions are presented in Tables 34 and 35, respectively. Under non-drought conditions, the F_2 plants from the cross Agra/Apo ranged from 2 to 14 for tiller number, 1 to 12 for panicle number, 69 to 145 cm for plant height, 0 to 51 cm for panicle length, 87 to 96 days for DTF and 1 to 30 g for grain yield per plant. The transgressive index (TI) of the Agra/Apo population was high for tiller number (11.28), panicle number (9.86), plant height (67.91), panicle length (50.64) and grain yield per plant (20.30), while moderate for DTF (7.86) indicating that tiller number, panicle number, plant height, panicle length and grain yield per plant of many lines of the Agra/Apo F_2 progenies exceeded those of a range between their parents showing the presence of transgressive phenotypes. Days to flowering (DTF) recorded zero extreme phenotypes, while the lowest plant height was equivalent to that of an extremely short line (Figure 35). Under non-drought conditions, the F_2 lines from the cross J.85/Apo ranged from 2 to 14 for tiller number, 1 to 14 for panicle number, 73 to 134 cm for plant height, 11 to 40 cm for panicle length, 87 to 94 days for DTF and 5 to 30 g for grain yield per plant.

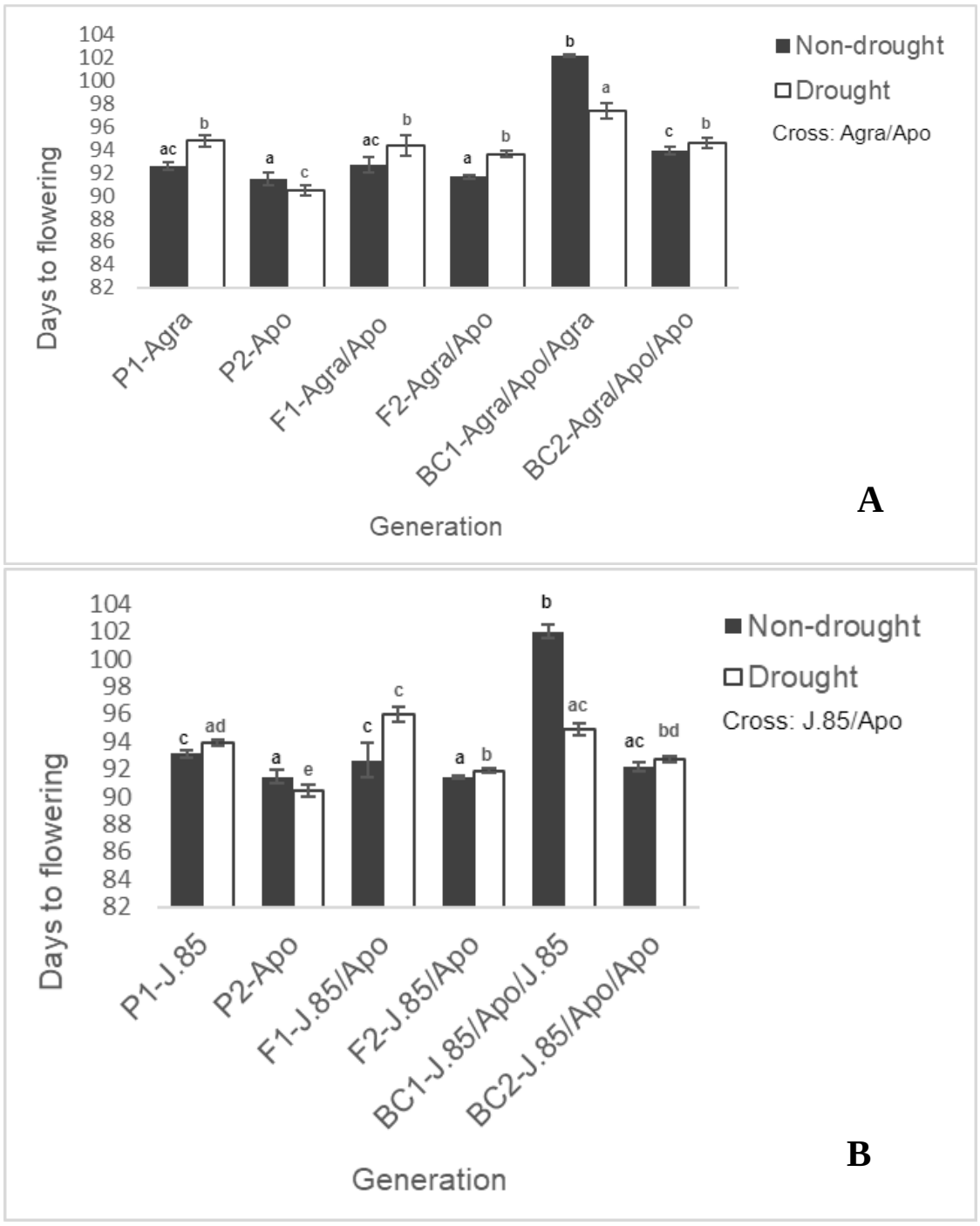


Figure 33. Mean performance of the lines of the six populations of **(A)** Agra/Apo and **(B)** J.85/Apo crosses evaluated under drought stress for days to flowering at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022. Data presented are means ±SE (n=30 (P_1 and P_2); n=3 (F_1); n=120 (F_2); n=40 (BC_1 and BC_2)). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

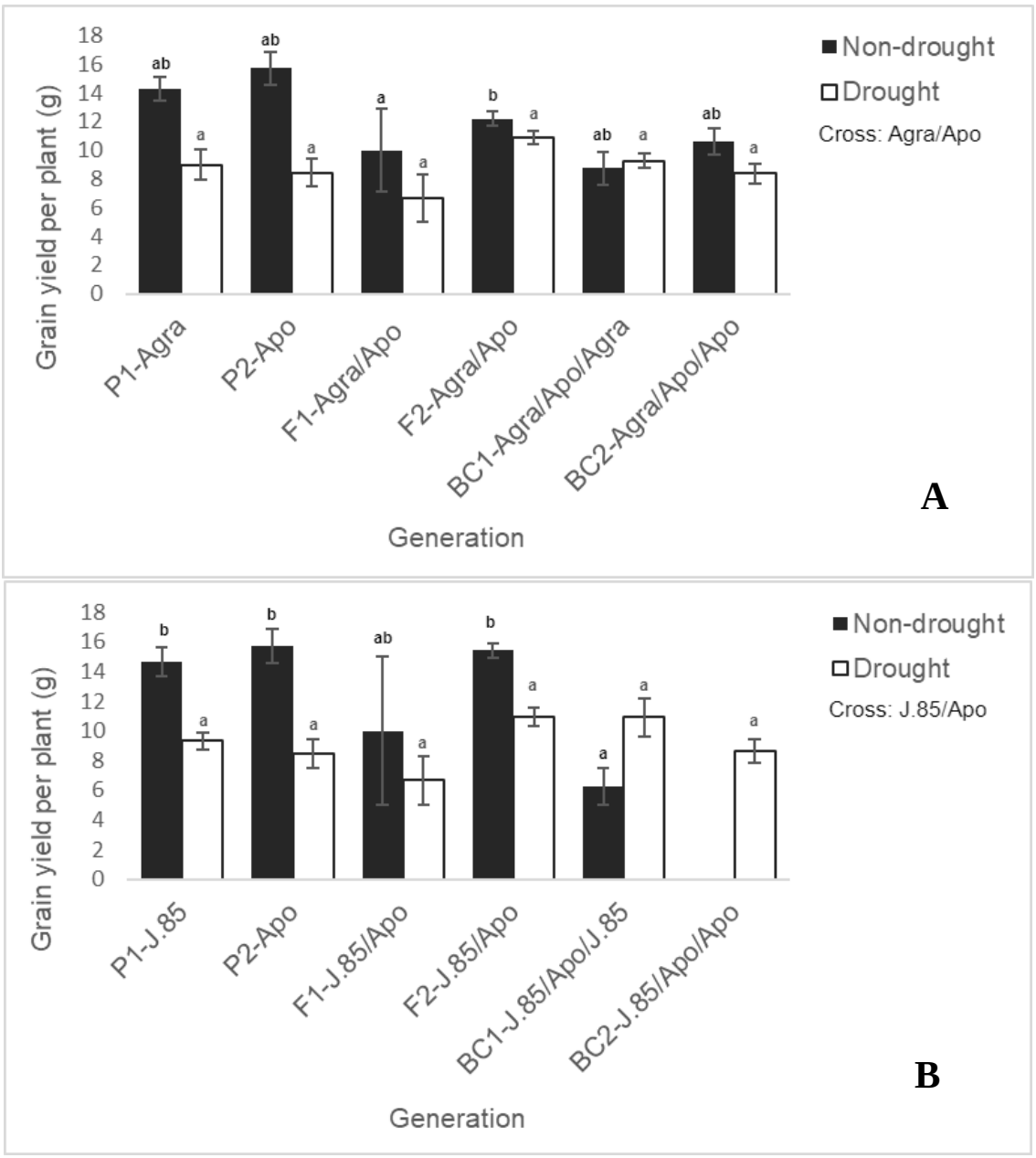


Figure 34. Mean performance of the lines of the six populations of **(A)** Agra/Apo and **(B)** J.85/Apo crosses evaluated under drought stress for grain yield per plant (g) at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022. Data presented are means ±SE (n=30 (P_1 and P_2); n=3 (F_1); n=120 (F_2); n=40 (BC_1 and BC_2)). Genotypes with different letters above the error bar under each water regime (non-drought or drought conditions) are significantly different in their mean performance, based on Duncan multiple rank test (P<5%).

Table 34. Descriptive statistics showing the variation among the F_2 lines derived from the crosses Agra/Apo for all the traits under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

TRAITS	Minimum		Maximum		Mean		Variance		Skewness		Kurtosis	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
TN	2	2	14	8	7.73±0.22	4.28±0.12	5.75	1.69	0.14	0.65	-0.26	0.08
PN	1	0	12	7	6.35±0.23	2.86±0.12	6.40	1.52	0.26	0.21	-0.75	0.43
PH (cm)	69	54	145	110	110.08±1.21	81.41±1.01	174.74	118.46	-0.15	0.06	0.14	0.15
PL (cm)	0	4	51	34	23.01±0.54	19.22±0.43	34.35	21.11	0.30	0.21	5.48	1.96
DTF	87	86	96	101	91.68±0.17	93.64±0.26	3.37	8.05	-0.19	0.35	0.52	0.62
GYP (g)	1	1	30	25	12.20±0.51	10.89±0.46	29.91	23.64	0.56	0.44	0.30	0.21
LRS	-	0	-	9	-	6.82±0.31	-	11.54	-	-1.26	-	-0.12
LDS	-	0	-	7	-	3.31±0.13	-	2.03	-	-0.26	-	0.47
DRR	-	1	-	7	-	3.44±0.12	-	1.64	-	0.36	-	0.37
SFPS	-	1	-	9	-	5.65±0.23	-	6.03	-	-0.33	-	-0.78

LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; ND-Under non-drought; UD-Under drought

Table 35. Descriptive statistics showing the variation among the F_2 lines derived from the crosses J.85/Apo for all the traits under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

TRAITS	Minimum		Maximum		Mean		Variance		Skewness		Kurtosis	
	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
TN	2	2	14	7	7.89±0.21	4.04±0.10	5.39	1.05	0.47	0.75	-0.06	0.06
PN	1	0	14	7	7.03±0.22	2.87±0.13	5.51	1.72	0.32	0.41	0.04	0.22
PH (cm)	73	50	134	104	106.73±1.00	82.22±1.06	117.93	123.10	-0.46	-0.47	0.27	0.35
PL (cm)	11	8	40	33	23.94±0.39	20.56±0.42	17.61	19.11	0.17	0.28	1.45	1.07
DTF	87	84	94	97	91.39±0.11	91.88±0.17	1.42	3.28	-0.67	0.01	1.15	3.93
GYP (g)	5	1	30	50	15.44±0.48	10.95±0.59	26.14	37.47	0.12	2.52	-0.34	13.71
LRS	-	0	-	9	-	5.42±0.37	-	16.40	-	-0.42	-	-1.69
LDS	-	0	-	9	-	3.75±0.16	-	3.11	-	0.24	-	0.59
DRR	-	0	-	7	-	4.08±0.14	-	2.40	-	0.08	-	-0.10
SFPS	-	1	-	9	-	5.55±0.21	-	5.22	-	-0.41	-	-0.79

LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; ND-Under non-drought; UD-Under drought

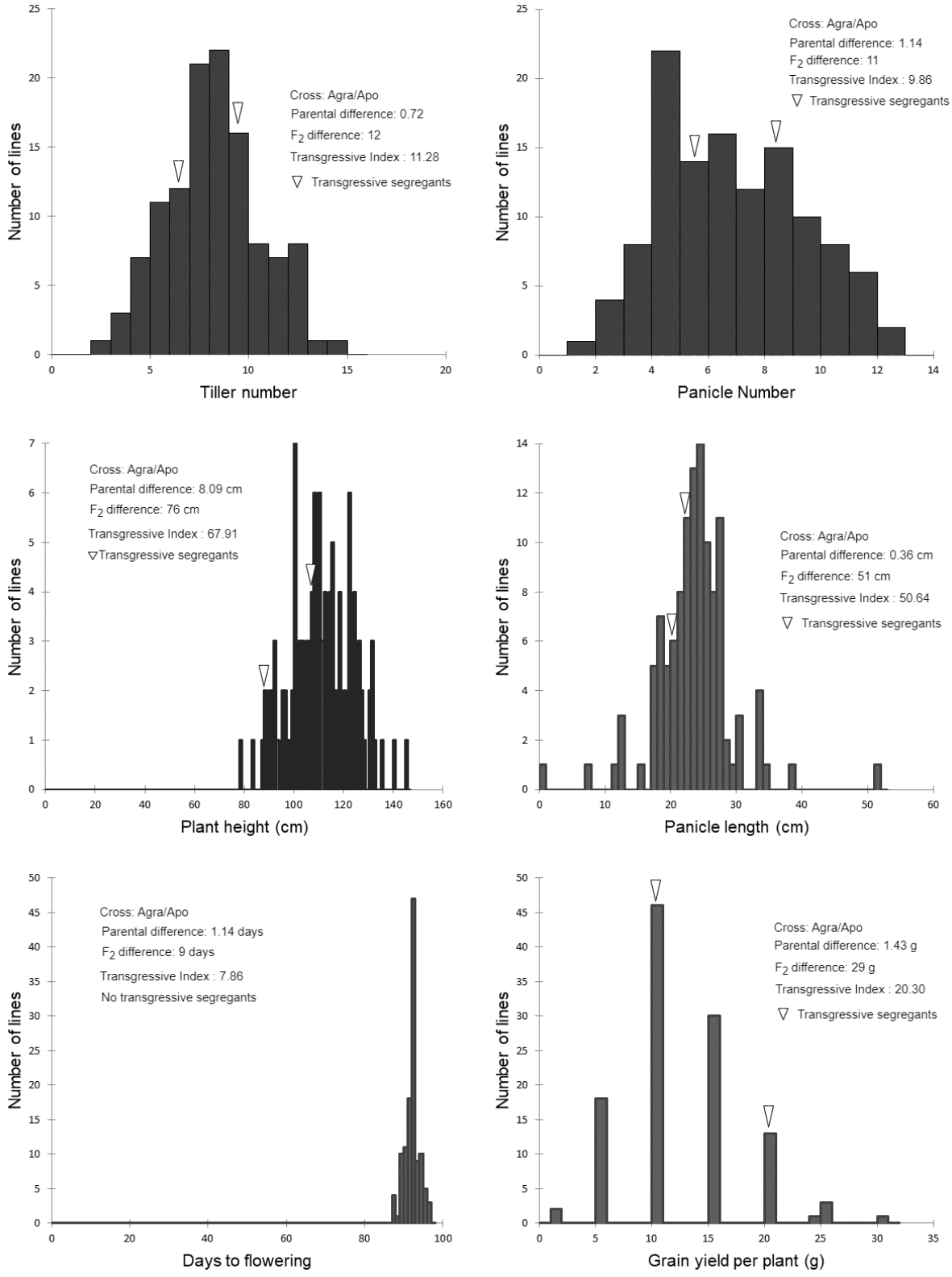


Figure 35. Histogram showing the transgressive analysis in the F_2 population of Agra/Apo cross evaluated under non-drought conditions for tiller number, panicle number, plant height, panicle length, days to flowering and grain yield per plant at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

The transgressive index (TI) of the J.85/Apo population was high for tiller number (10.04), plant height (11.81), panicle length (31.07) and grain yield per plant (23.60), while moderate for panicle number (7.78) and DTF (4.19) indicating that tiller number, panicle number, plant height, panicle length and grain yield per plant of several lines of the J.85/Apo F_2 population exceeded those of a range between their parents showing then, the presence of transgressive phenotypes. Days to flowering (DTF) recorded zero transgressive phenotypes, while the lowest plant height was equivalent to that of an extremely short line (Figure 36).

Descriptive statistics showing the variation among the F_2 lines derived from the crosses Agra/Apo and J.85/Apo for all the traits under drought stress is presented in Tables 34 and 35, respectively. Under drought stress, the F_2 plants from the cross Agra/Apo ranged from 0 to 9 for LRS, 0 to 7 for LDS, 1 to 7 for DRR, 1 to 9 for SPFS, 2 to 8 for tiller number, 0 to 7 for panicle number, 54 to 110 cm for plant height, 4 to 34 cm for panicle length, 86 to 101 days for DTF and 1 to 25 g for grain yield per plant. The transgressive index (TI) of the Agra/Apo progenies was high for LRS (69.91), LDS (105.00), tiller number (11.37), panicle number (14.67), panicle length (15.85) and grain yield per plant (42.86), while moderate for DRR (6.43), SFPS (7.50), plant height (5.50) and DTF (3.46) indicating that LRS, LDS, DRR, SPFS, tiller number, panicle number, plant height, panicle length and grain yield per plant of many lines of the Agra/Apo F_2 progenies exceeded those of a range between their parents showing the presence of transgressive phenotypes. Days to flowering (DTF) recorded zero favorable extreme phenotypes while 5 unfavorable, while the lowest plant height was equivalent to that of an extremely short line (Figures 37A and 37B). Under drought stress, the F_2 lines from the cross J.85/Apo ranged from 0 to 9 for LRS, 0 to 9 for LDS, 0 to 7 for DRR, 1 to 9 for SPFS, 2 to 7 for tiller number, 0 to 7 for panicle number, 54 to 104 cm for plant height, 8 to 33 cm for panicle length, 84 to 97 days for DTF and 1 to 50 g for grain yield per plant. The transgressive index (TI) of the Agra/Apo progenies was high for LDS (18.00), tiller number (18.75), panicle number (30.00), plant height (124.62), panicle length (125.00) and grain yield per plant (55.59), while low to moderate for LRS (2.23), DRR (4.47), SFPS (2.55) and DTF (3.71) indicating that LRS, LDS, DRR, SPFS, tiller number, panicle number, plant height, panicle length and grain yield per plant of several lines of the J.85/Apo F_2 progenies exceeded those of a range between their parents by exhibiting the presence of transgressive phenotypes. Days to flowering (DTF) recorded one favorable extreme phenotype which was equivalent to that of an extreme early-flowering line in F_2 population of J.85/Apo, while five transgressive late-flowering phenotypes were observed in F_2 progenies of Agra/Apo (Figures 38A and 38B).

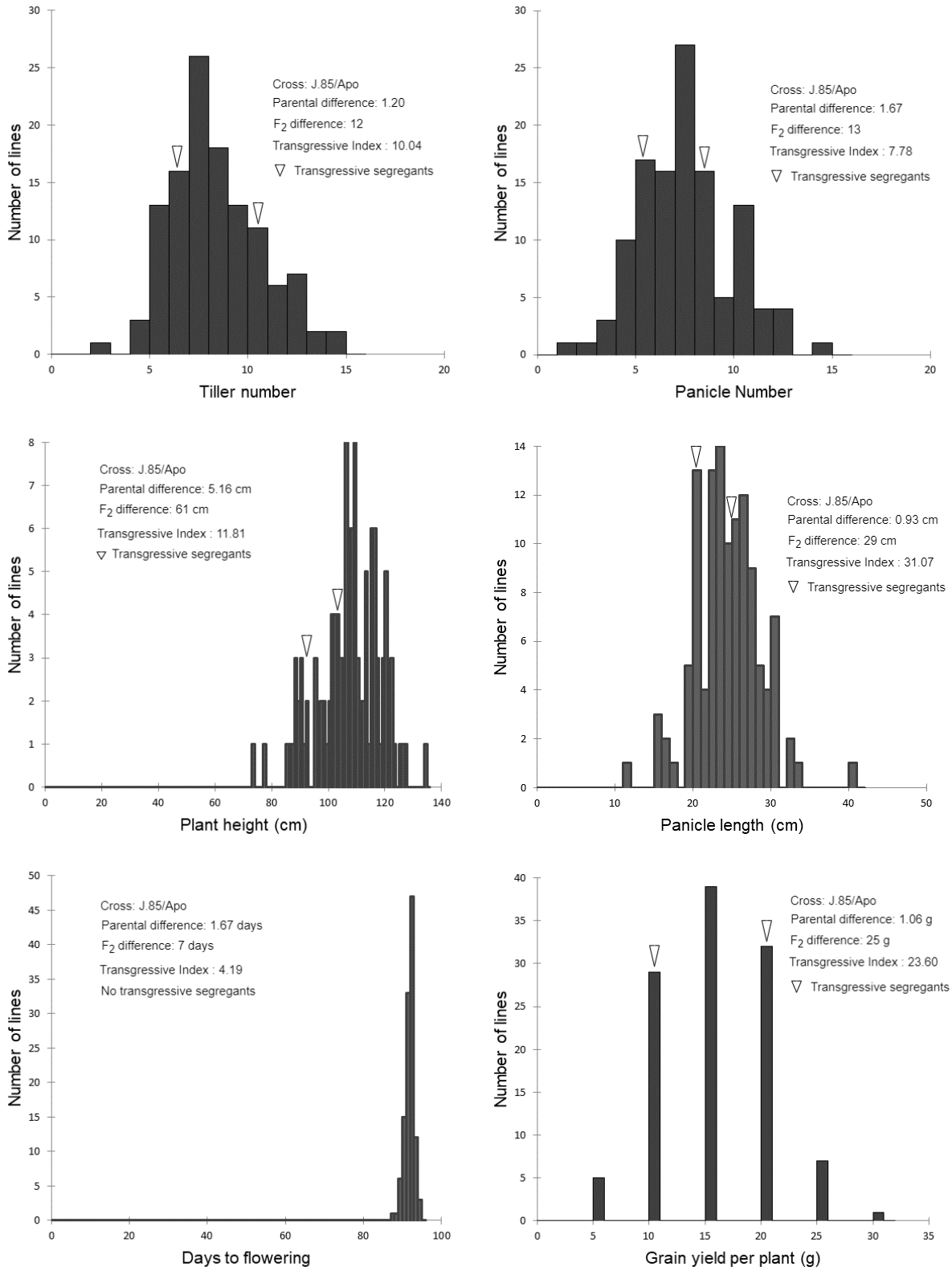


Figure 36. Histogram showing the transgressive analysis in the F_2 population of J.85/Apo cross evaluated under non-drought conditions for tiller number, panicle number, plant height, panicle length, days to flowering and grain yield per plant at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

A

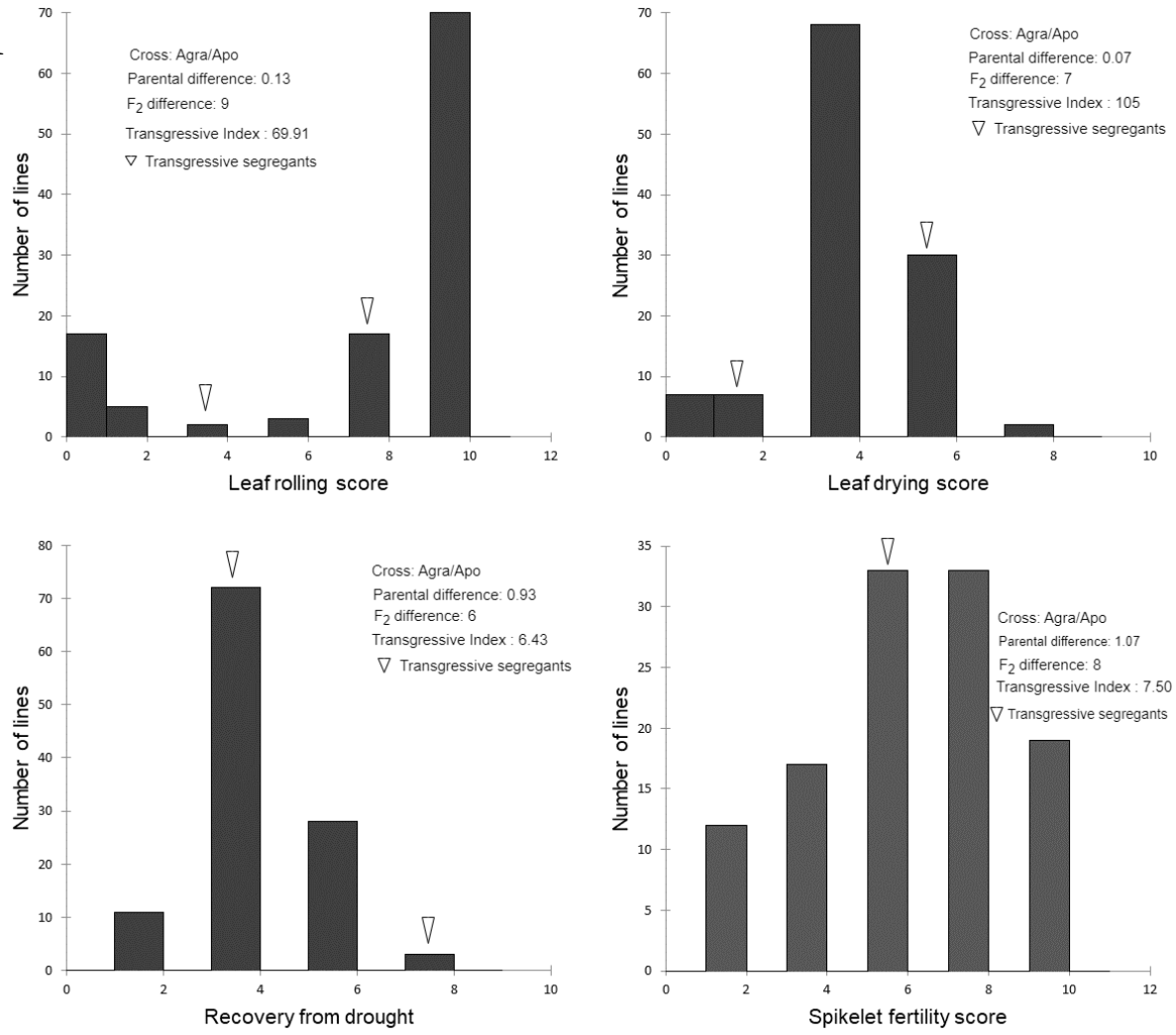


Figure 37A. Histogram showing the transgressive analysis in the F_2 population of Agra/Apo cross evaluated under drought stress for leaf rolling score, leaf drying score, recovery from drought and spikelet fertility score at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

B

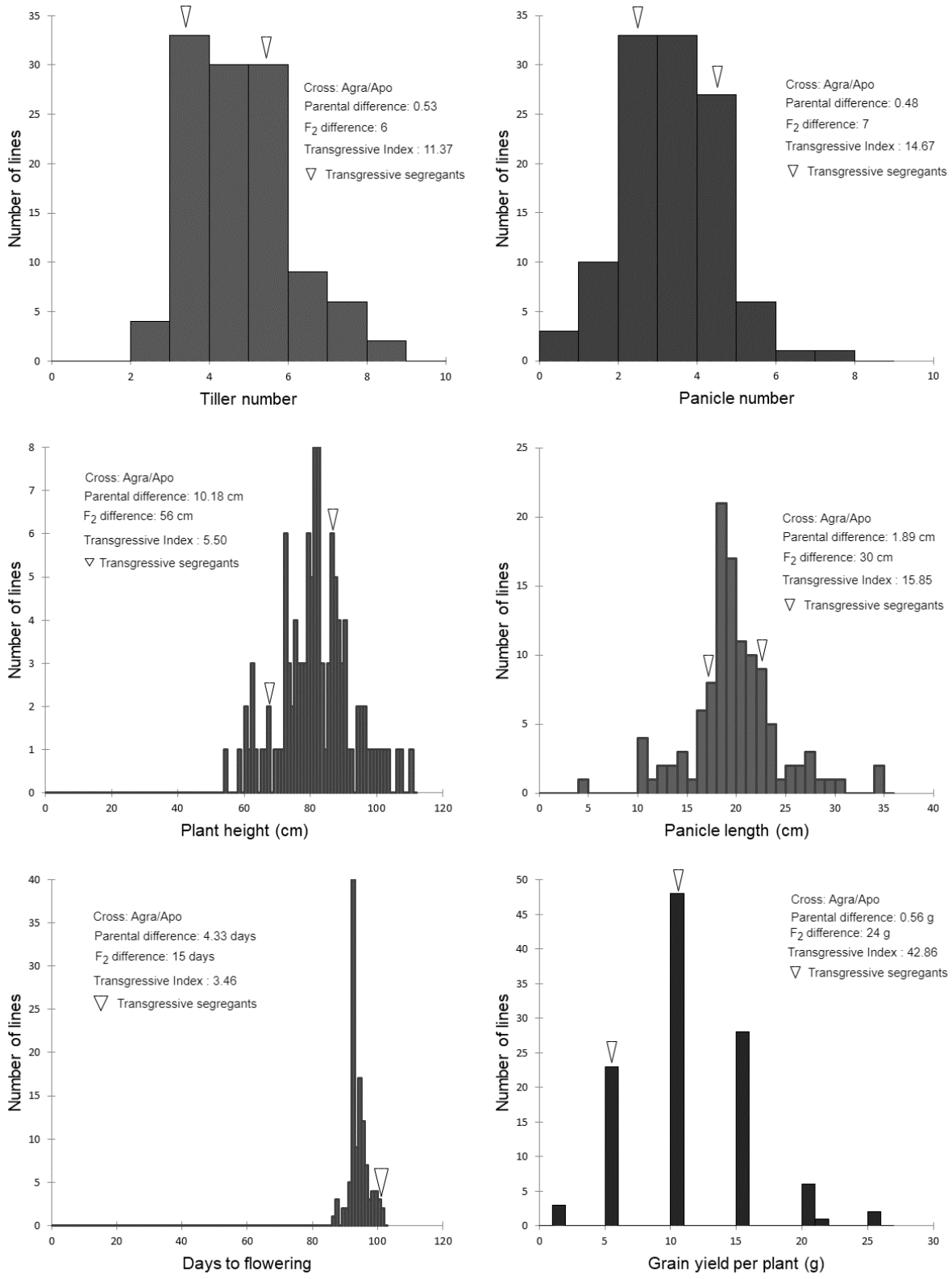


Figure 37B. Histogram showing the transgressive analysis in the F_2 population of Agra/Apo cross evaluated under drought conditions for tiller number, panicle number, plant height, panicle length, days to flowering and grain yield per plant at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

A

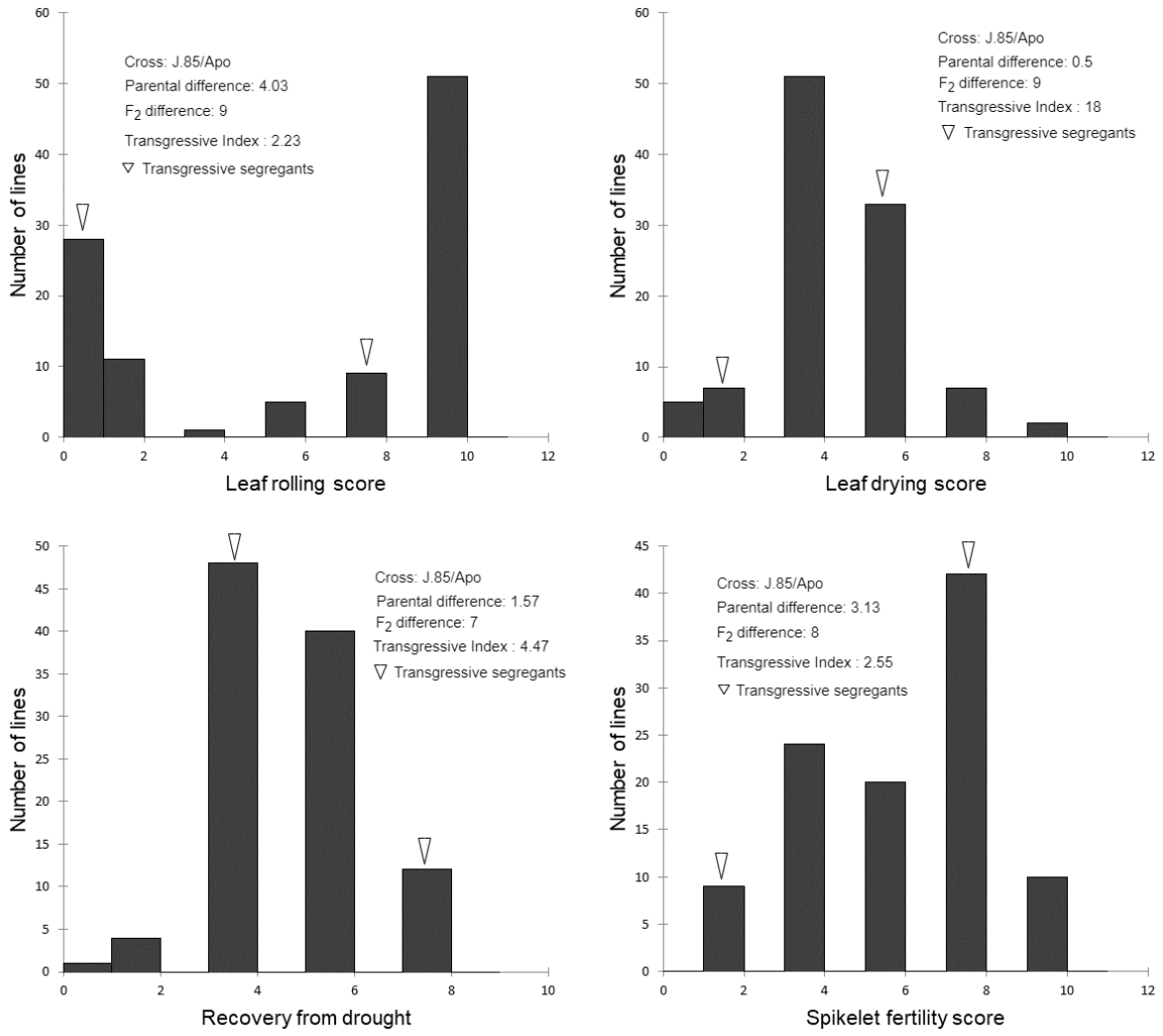


Figure 38A. Histogram showing the transgressive analysis in the F_2 population of J.85/Apo cross evaluated under drought stress for leaf rolling score, leaf drying score, recovery from drought and spikelet fertility score at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

B

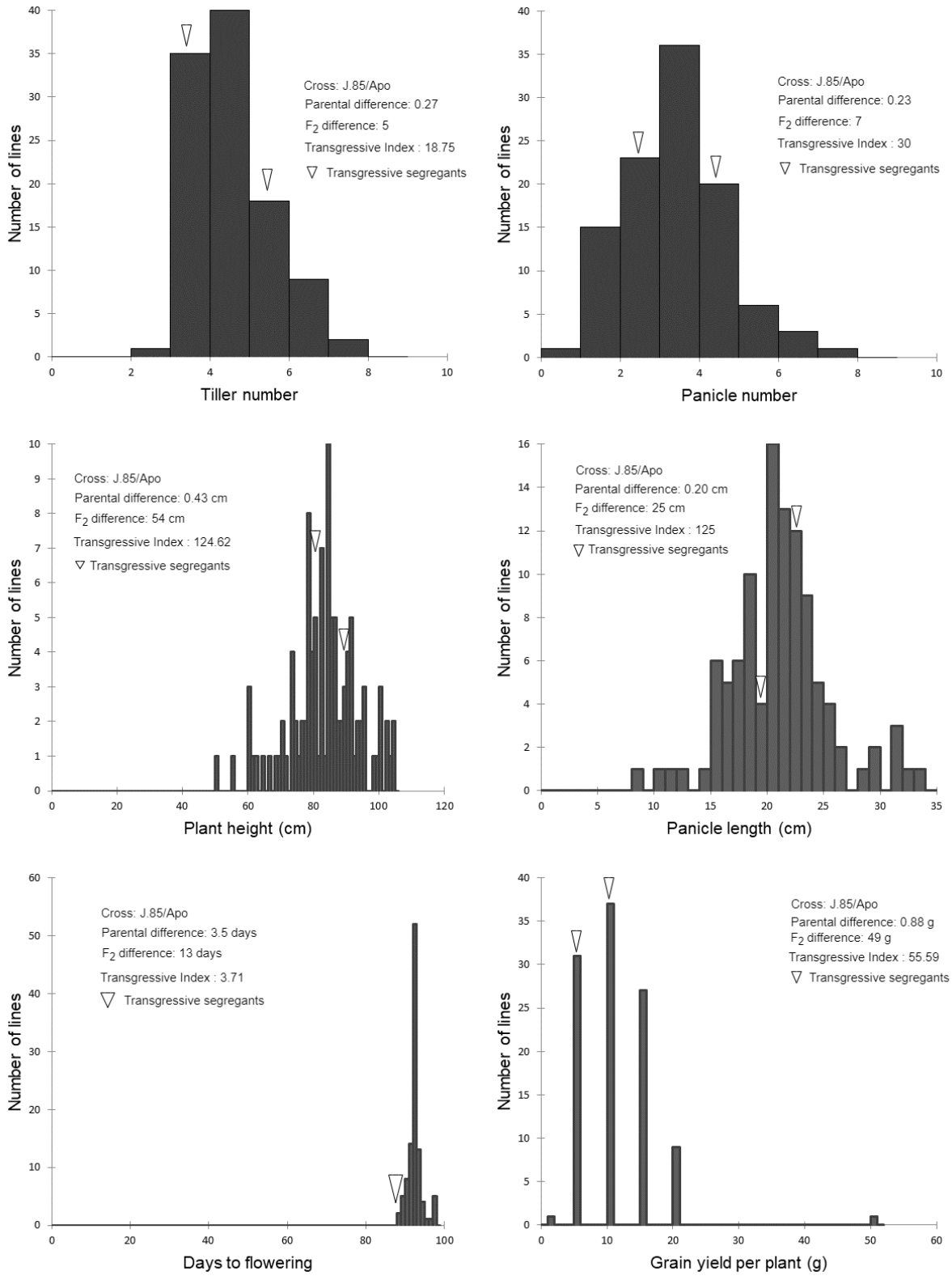


Figure 38B. Histogram showing the transgressive analysis in the F_2 population of J.85/Apo cross evaluated under drought conditions for tiller number, panicle number, plant height, panicle length, days to flowering and grain yield per plant at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Under non-drought conditions, despite the absence of significant difference in the two parental varieties namely Agra and Apo for tiller number, panicle number, panicle length and grain yield per plant, whereas J.85 and Apo for tiller number, panicle length and grain yield per plant, it was observed that transgressive phenotypes were however formed for these traits. On the other hand, no transgressive segregants were observed for DTF both in the F_2 progenies for Agra/Apo and J.85/Apo, despite the significant difference observed between J.85 and Apo, while no significance between Agra and Apo under non-drought conditions.

Under drought stress, at least one transgressive phenotype was produced for each trait whether there is a significant difference or not among the parental lines involved in the development of the F_2 populations.

4.1.4.4 Generation means analysis

4.1.4.4.1 Test for Epistasis

Under non-drought conditions, the scaling tests A and D of the trait DTF were significant out of the four (A, B, C, and D) for both crosses Agra/Apo (Scale A: t-cal= 7.52 > $t\text{-tab}_{0.05}$=2.01; Scale D: t-cal= |-3.13| > $t\text{-tab}_{0.05}$=1.96) and J.85/Apo (Scale A: t-cal= 5.06 > $t\text{-tab}_{0.05}$=2.01; Scale D: t-cal= |-3.69| > $t\text{-tab}_{0.05}$=1.96) indicating the presence of epistasis or gene interactions in particular additive × additive type of gene effects as per the significance of scale D for the days to flowering. The remaining traits namely tiller number, panicle number, plant height, panicle length and grain yield per plant showed no significance for all four scaling tests (A, B, C and D) for both crosses Agra/Apo and J.85/Apo indicating that the variation observed in these traits can be explained by simple additive and dominant model (Tables 36 and 37). Under drought stress, all four scaling tests showed non-significant for all the traits (LRS, LDS, DRR, SFPS, tiller number, panicle number, plant height, panicle length, DTF and grain yield per plant) in both crosses Apo/Agra and J.85/Apo indicating that the appropriate model to explain the variation observed in these traits is the simple additive and dominant model (Tables 36 and 37).

4.1.4.4.2 Genetic Effects

The partitioning of the generation means into six different genetic components namely direct genetic effects, mean effect (m), additive (d) and dominant (h), and interaction effects, additive × additive (i), additive × dominant (j), and dominant × dominant (l) showed that the mean effect was significant at 1% for the studied traits (LRS, LDS, DRR, SFPS, tiller number, panicle number, plant height, panicle length, DTF and grain yield per plant) in both crosses Apo/Agra

Table 36. Scaling tests for grain yield and yield-related traits of the Agra/Apo cross under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable		LRS	LDS	DRR	SFPS	TN		PN		PH		PL		DTF		GYP	
		UD	UD	UD	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
A	Scale A	-1.42	0.07	1.70	-0.35	-4.89	-0.76	-7.25	-0.32	17.68	0.24	4.80	-5.48	19.05	5.73	-6.82	2.86
	Var	80.89	10.57	10.12	28.69	30.83	5.04	26.96	5.88	914.54	581.89	133.77	85.52	6.41	78.21	130.68	68.61
	S.D.	8.99	3.25	3.18	5.36	5.55	2.25	5.19	2.42	30.24	24.12	11.57	9.25	2.53	8.84	11.43	8.28
	t-cal	-0.16	0.02	0.54	-0.07	-0.88	-0.34	-1.40	-0.13	0.58	0.01	0.42	-0.59	7.52**	0.65	-0.60	0.35
B	Scale B	0.40	1.90	0.13	5.80	-6.13	-0.91	-5.87	-1.05	16.67	-11.24	2.20	-10.31	3.67	4.34	-4.46	1.69
	Var	92.01	13.84	11.53	39.27	17.82	6.61	18.85	7.93	339.23	435.75	83.64	83.08	19.11	29.06	111.32	79.76
	S.D.	9.59	3.72	3.40	6.27	4.22	2.57	4.34	2.82	18.42	20.87	9.15	9.12	4.37	5.39	10.55	8.93
	t-cal	0.04	0.51	0.04	0.93	-1.45	-0.36	-1.35	-0.37	0.91	-0.54	0.24	-1.13	0.84	0.81	-0.42	0.19
C	Scale C	13.70	3.28	1.48	7.52	-0.24	2.24	-1.60	0.25	69.17	4.82	4.39	-11.41	-2.67	0.69	-1.19	12.79
	Var	237.59	47.51	35.19	105.60	114.99	35.87	129.05	32.17	3142.30	2328.46	589.60	390.05	70.20	151.69	631.28	464.54
	S.D.	15.41	6.89	5.93	10.28	10.72	5.99	11.36	5.67	56.06	48.25	24.28	19.75	8.38	12.32	25.13	21.55
	t-cal	0.89	0.48	0.25	0.73	-0.02	0.37	-0.14	0.04	1.23	0.10	0.18	-0.58	-0.32	0.06	-0.05	0.59
D	Scale D	7.36	0.65	-0.18	1.04	5.39	1.96	5.76	0.81	17.41	7.91	-1.31	2.19	-12.70	-4.69	5.05	4.12
	Var	79.62	12.69	10.39	38.80	30.89	7.99	32.37	7.77	960.44	640.27	182.40	114.00	16.47	54.43	154.50	114.26
	S.D.	8.92	3.56	3.22	6.23	5.56	2.83	5.69	2.79	30.99	25.30	13.51	10.68	4.06	7.38	12.43	10.69
	t-cal	0.82	0.18	-0.06	0.17	0.97	0.69	1.01	0.29	0.56	0.31	-0.10	0.21	-3.13**	-0.64	0.41	0.39

Scaling tests (A, B, C and D); Var-Variance, S.D-Standard deviation; t-cal- calculated t-value; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant in gram; UN-Under non-drought; UD-Under drought

Table 37. Scaling tests for grain yield and yield-related traits of the J.85/Apo cross under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable		LRS	LDS	DRR	SFPS	TN		PN		PH		PL		DTF		GYP
		UD	UD	UD	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	UD
A	Scale A	3.83	1.37	1.30	1.13	-0.73	-2.10	-6.73	-1.10	-35.80	-24.77	-18.27	-8.13	18.20	-0.10	5.83
	Var	60.18	15.29	11.12	23.47	14.28	5.09	17.02	5.49	1436.98	595.52	183.03	95.57	12.92	11.55	94.63
	S.D.	7.76	3.91	3.33	4.84	3.78	2.26	4.13	2.34	37.91	24.40	13.53	9.78	3.59	3.40	9.73
	t-cal	0.49	0.35	0.39	0.23	-0.19	-0.93	-1.63	-0.47	-0.94	-1.01	-1.35	-0.83	5.06**	-0.03	0.60
B	Scale B	8.94	2.45	-1.71	7.68	-0.52	0.31	-1.48	-1.50	13.45	-19.32	-1.95	-7.75	0.18	-1.07	2.19
	Var	66.41	13.30	9.53	25.43	19.41	4.95	21.39	6.83	423.24	786.63	114.19	218.73	20.49	13.66	124.58
	S.D.	8.15	3.65	3.09	5.04	4.41	2.23	4.63	2.61	20.57	28.05	10.69	14.79	4.53	3.70	11.16
	t-cal	1.10	0.67	-0.55	1.52	-0.12	0.14	-0.32	-0.57	0.65	-0.69	-0.18	-0.52	0.04	-0.29	0.20
C	Scale C	15.97	4.57	-0.63	11.39	7.57	1.68	9.00	0.72	54.82	-7.55	2.16	-4.18	-4.36	-8.83	12.72
	Var	278.33	60.31	45.37	95.74	100.43	22.92	100.56	35.17	2436.96	2436.85	325.59	365.92	49.48	61.95	666.60
	S.D.	16.68	7.77	6.74	9.78	10.02	4.79	10.03	5.93	49.37	49.36	18.04	19.13	7.03	7.87	25.82
	t-cal	0.96	0.59	-0.09	1.16	0.76	0.35	0.90	0.12	1.11	-0.15	0.12	-0.22	-0.62	-1.12	0.49
D	Scale D	1.60	0.38	-0.11	1.29	4.41	1.73	8.61	1.66	38.59	18.27	11.19	5.85	-11.37	-3.83	2.35
	Var	93.24	17.98	13.43	31.24	26.57	5.33	28.69	8.19	856.39	746.56	134.47	140.97	9.48	17.39	192.11
	S.D.	9.66	4.24	3.67	5.59	5.15	2.31	5.36	2.86	29.26	27.32	11.60	11.87	3.08	4.17	13.86
	t-cal	0.17	0.09	-0.03	0.23	0.86	0.75	1.61	0.58	1.32	0.67	0.96	0.49	-3.69**	-0.92	0.17

Scaling tests (A, B, C and D); Var-Variance, S.D-Standard deviation; t-cal- calculated t-value; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant in gram; UN-Under non-drought; UD-Under drought

and J.85/Apo under both non-drought and drought stress conditions except the mean effect of LRS and grain yield per plant in J.85/Apo cross under drought stress. In Agra/Apo cross under non-drought conditions, despite the absence of significance of all the four scaling tests indicating the absence of epistasis, among gene interaction effects, additive × additive effects showed significance at 1% for tiller number, panicle number, plant height, panicle length and grain yield per plant. In DTF where the scaling tests A and D were significant for Agra/Apo cross, all the six genetic effects, additive, dominant, additive × additive, additive × dominant and dominant × dominant, were significant at 1%. However, the magnitude of the dominance effect was 68.27% greater than that of the additive effect, while the magnitude of the additive × additive was 86.26% greater than that of the dominant × dominant gene interaction (Table 38). In J.85/Apo cross under non-drought conditions, despite the absence of significance of all four scaling tests indicating the absence of epistasis, among gene interaction effects, additive × additive effects showed significance at 1% for tiller number, plant height and panicle length. In the view of panicle number where all the scaling tests were non-significant too for J.85/Apo cross, the dominance effect and additive × additive gene interaction effect were significant. However, the magnitude of the additive × additive effect was 36.95% greater than that of the dominant genetic effect. In DTF where the scaling tests A and D were significant for J.85/Apo cross, all the six genetic effects, additive, dominant, additive × additive, additive × dominant and dominant × dominant, were significant at 1%. However, the magnitude of the dominant genetic effect was 57.38% greater than that of the additive effect, while the magnitude of the additive × additive was 88.11% greater than that of the dominant × dominant gene interaction (Table 39). In Agra/Apo cross under drought stress, despite the absence of significance of all four scaling tests indicating the absence of epistasis, the additive × additive gene interaction showed significance at 5% for all the studied traits (LDS, DRR, SFPS, tiller number, panicle number, plant height, panicle length, DTF and grain yield) except LRS (Table 40). In J.85/Apo cross under drought stress, despite the fact that all four scaling tests showed non-significance which indicates that epistasis is absent, however, the additive × additive gene interaction was found to be significant for all the studied traits (DRR, SFPS, tiller number, panicle number, plant height, panicle length and DTF) except LRS, LDS and grain yield per plant. Nonetheless, the magnitude of the additive × additive gene interaction was preponderant for these traits namely LRD, LDS and grain yield per plant as compared to the other genetic effects (Table 41). From the analysis of the direct genetic effects and inter-allelic interaction effects above, it was revealed that the additive × additive type of gene interaction was predominant in the two crosses Agra/Apo and J.85/Apo across both non-drought and drought stress conditions of this study.

Table 38. Generation mean analysis for grain yield and yield-related traits of the Agra/Apo cross under non-drought conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable		TN	PN	PH	PL	DTF	GYP
m	m	7.73	6.35	110.08	23.01	91.68	12.20
	var	5.75	6.40	174.74	34.35	3.37	29.91
	S.D.	2.40	2.53	13.22	5.86	1.84	5.47
	t-cal.	3.22**	2.51**	8.33**	3.93**	49.93**	2.23**
d	d	0.26	-1.26	-3.54	1.12	8.26	-1.89
	var	7.90	6.78	261.49	45.01	2.98	34.84
	S.D.	2.81	2.60	16.17	6.71	1.73	5.90
	t-cal.	0.09	-0.48	-0.22	0.17	4.78**	-0.32
h	h	-12.35	-13.02	-41.73	1.46	26.03	-15.09
	var	129.32	136.15	3928.39	739.60	69.95	656.16
	S.D.	11.37	11.67	62.68	27.20	8.36	25.62
	t-cal.	-1.09	-1.12	-0.67	0.05	3.11**	-0.59
i	i	-30.38	-27.92	-447.41	-89.79	-350.21	-52.59
	var	123.56	129.48	3841.77	729.59	65.88	618.00
	S.D.	11.12	11.38	61.98	27.01	8.12	24.86
	t-cal.	-2.73**	-2.45**	-7.22**	-3.32**	-43.15**	-2.12**
j	j	0.62	-0.69	0.51	1.30	7.69	-1.18
	var	10.66	9.45	278.77	53.68	5.71	48.00
	S.D.	3.27	3.07	16.70	7.33	2.39	6.93
	t-cal.	0.19	-0.22	0.03	0.18	3.22**	-0.17
l	l	21.80	24.63	0.46	-9.61	-48.11	21.37
	var	241.42	237.51	7326.10	1309.73	117.94	1188.73
	S.D.	15.54	15.41	85.59	36.19	10.86	34.48
	t-cal.	1.40	1.60	0.01	-0.27	-4.43**	0.62

**Significant at 0.01; Var-Variance, S.D-Standard deviation; t-cal- calculated t-value; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; d-additive gene effect; d-dominant gene effect; i- additive × additive gene interaction; j-additive × dominant gene interaction; l-dominant × dominant gene interaction

Table 39. Generation mean analysis for grain yield and yield-related traits of the J.85/Apo cross under non-drought conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable		TN	PN	PH	PL	DTF
m	m	7.89	7.03	106.73	23.94	91.39
	var	5.39	5.51	117.93	17.61	1.42
	S.D.	2.32	2.35	10.86	4.20	1.19
	t-cal.	3.40**	3.00**	9.83**	5.70**	76.78**
d	d	-0.71	-3.46	-27.21	-7.69	9.85
	var	5.03	6.66	384.69	64.02	3.82
	S.D.	2.24	2.58	19.61	8.00	1.95
	t-cal.	-0.31	-1.34	-1.39	-0.96	5.04**
h	h	-13.48	-22.11	-86.55	-21.84	23.11
	var	109.84	117.86	3563.09	548.83	44.63
	S.D.	10.48	10.86	59.69	23.43	6.68
	t-cal.	-1.29	-2.04**	-1.45	-0.93	3.46**
i	i	-32.97	-35.06	-481.33	-111.15	-345.87
	var	106.28	114.75	3425.55	537.88	37.93
	S.D.	10.31	10.71	58.53	23.19	6.16
	t-cal.	-3.20**	-3.27**	-8.22**	-4.79**	-56.16**
j	j	-0.11	-2.63	-24.62	-8.16	9.01
	var	8.25	9.44	407.89	73.64	6.19
	S.D.	2.87	3.07	20.20	8.58	2.49
	t-cal.	-0.04	-0.85	-1.22	-0.95	3.62**
l	l	10.07	25.43	99.52	42.59	-41.12
	var	180.83	207.10	8591.92	1349.93	110.53
	S.D.	13.45	14.39	92.69	36.74	10.51
	t-cal.	0.75	1.77	1.07	1.16	-3.91**

**Significant at 0.01; Var-Variance, S.D-Standard deviation; t-cal- calculated t-value; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; d-additive gene effect; d-dominant gene effect; i- additive × additive gene interaction; j-additive × dominant gene interaction; l-dominant × dominant gene interaction

Table 40. Generation mean analysis for grain yield and yield-related traits of the Agra/Apo cross under drought stress evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable		LRS	LDS	DRR	SFPS	TN	PN	PH	PL	DTF	GYP
m	m	6.82	3.29	3.44	5.65	4.28	2.86	81.49	19.22	93.64	10.89
	var	11.54	2.12	1.64	6.03	1.69	1.52	119.43	21.11	8.05	23.64
	S.D.	3.40	1.46	1.28	2.45	1.30	1.23	10.93	4.59	2.84	4.86
	t-cal.	2.01**	2.26**	2.69**	2.30**	3.29**	2.32**	7.46**	4.18**	33.01**	2.24**
d	d	-0.98	-0.95	0.32	-2.54	-0.19	0.12	0.65	1.47	2.86	0.86
	var	33.47	4.21	3.83	14.70	1.22	1.67	162.53	29.57	22.25	19.69
	S.D.	5.79	2.05	1.96	3.83	1.10	1.29	12.75	5.44	4.72	4.44
	t-cal.	-0.17	-0.46	0.16	-0.66	-0.17	0.10	0.05	0.27	0.61	0.19
h	h	-17.51	-2.24	-2.44	-7.61	-5.35	-1.88	-16.39	1.46	11.12	-10.29
	var	331.72	54.17	43.79	157.51	34.17	33.02	2665.46	469.10	223.47	478.62
	S.D.	18.21	7.36	6.62	12.55	5.85	5.75	51.63	21.66	14.95	21.88
	t-cal.	-0.96	-0.30	-0.37	-0.61	-0.92	-0.33	-0.32	0.07	0.74	-0.47
i	i	-29.25	-15.04	-13.11	-27.67	-17.48	-11.19	-324.68	-73.96	-368.83	-41.84
	var	318.47	50.77	41.54	155.22	31.98	31.08	2561.09	456.02	217.74	457.06
	S.D.	17.85	7.13	6.45	12.46	5.65	5.57	50.61	21.35	14.76	21.38
	t-cal.	-1.64	-2.11**	-2.03**	-2.22**	-3.09**	-2.01**	-6.42**	-3.46**	-25.00**	-1.96*
j	j	-0.91	-0.91	0.79	-3.08	0.08	0.36	5.74	2.42	0.69	0.58
	var	39.73	4.60	4.75	16.99	2.41	3.28	241.91	41.65	25.65	32.92
	S.D.	6.30	2.15	2.18	4.12	1.55	1.81	15.55	6.45	5.06	5.74
	t-cal.	-0.14	-0.43	0.36	-0.75	0.05	0.20	0.37	0.37	0.14	0.10
l	l	15.73	-0.67	-2.19	-3.37	5.59	2.99	26.82	20.18	-19.47	3.68
	var	773.15	114.85	96.52	340.75	55.37	58.93	4928.99	863.20	507.67	779.63
	S.D.	27.81	10.72	9.82	18.46	7.44	7.68	70.21	29.38	22.53	27.92
	t-cal.	0.57	-0.06	-0.22	-0.18	0.75	0.39	0.38	0.69	-0.86	0.13

**Significant at 0.01; Var-Variance, S.D-Standard deviation; t-cal- calculated t-value; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; d-additive gene effect; d-dominant gene effect; i- additive × additive gene interaction; j-additive × dominant gene interaction; l-dominant × dominant gene interaction

Table 41. Generation mean analysis for grain yield and yield-related traits of the J.85/Apo cross under drought stress evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable		LRS	LDS	DRR	SFPS	TN	PN	PH	PL	DTF	GYP
m	m	5.42	3.75	4.08	5.56	4.04	2.87	82.22	20.56	91.88	10.95
	var	16.40	3.11	2.40	5.37	1.05	1.72	123.10	19.11	3.28	37.47
	S.D.	4.05	1.76	1.55	2.32	1.03	1.31	11.10	4.37	1.81	6.12
	t-cal.	1.34	2.13**	2.64**	2.40**	3.93**	2.19**	7.41**	4.70**	50.73**	1.79
d	d	-4.57	-0.29	0.72	-4.84	-1.34	0.08	-2.51	-0.09	2.23	2.26
	var	27.65	5.52	3.85	9.76	1.11	1.30	254.17	64.53	4.27	42.21
	S.D.	5.26	2.35	1.96	3.12	1.05	1.14	15.94	8.03	2.07	6.50
	t-cal.	-0.87	-0.12	0.37	-1.55	-1.27	0.07	-0.16	-0.01	1.08	0.35
h	h	-6.04	-1.97	0.41	-6.01	-5.37	-4.04	-40.08	-8.91	11.48	-6.91
	var	376.94	74.53	55.49	127.41	22.82	34.66	3103.07	578.91	71.93	785.19
	S.D.	19.42	8.63	7.45	11.29	4.78	5.89	55.71	24.06	8.48	28.02
	t-cal.	-0.31	-0.23	0.06	-0.53	-1.12	-0.69	-0.72	-0.37	1.35	-0.25
i	i	-30.80	-15.58	-14.89	-31.94	-18.83	-11.32	-333.89	-82.40	-363.07	-39.29
	var	372.95	71.91	53.74	124.95	21.31	32.77	2986.25	563.87	69.56	768.44
	S.D.	19.31	8.48	7.33	11.18	4.62	5.72	54.65	23.75	8.34	27.72
	t-cal.	-1.60	-1.84	-2.03**	-2.86**	-4.08**	-1.98**	-6.11**	-3.47**	-43.53**	-1.42
j	j	-2.55	-0.54	1.50	-3.27	-1.21	0.20	-2.72	-0.19	0.48	1.82
	var	31.65	6.15	4.72	12.22	2.40	2.97	320.09	77.57	5.97	50.64
	S.D.	5.63	2.48	2.17	3.50	1.55	1.72	17.89	8.81	2.44	7.12
	t-cal.	-0.45	-0.22	0.69	-0.94	-0.78	0.12	-0.15	-0.02	0.20	0.26
l	l	-9.58	-3.06	0.18	-6.24	5.25	5.92	80.62	27.60	-6.50	-3.32
	var	720.74	148.68	106.95	251.94	40.67	55.89	6503.51	1398.42	130.26	1342.03
	S.D.	26.85	12.19	10.34	15.87	6.38	7.48	80.64	37.40	11.41	36.63
	t-cal.	-0.36	-0.25	0.02	-0.39	0.82	0.79	1.00	0.74	-0.57	-0.09

**Significant at 0.01; Var-Variance, S.D-Standard deviation; t-cal- calculated t-value; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; d-additive gene effect; d-dominant gene effect; i- additive × additive gene interaction; j-additive × dominant gene interaction; l-dominant × dominant gene interaction

4.1.4.5 Heterosis and degree of dominance

Under non-drought conditions, in Agra/Apo cross, negative heterosis over mid-parent (HMP) was recorded for all the traits except DTF which recorded a positive HMP with a relatively low magnitude compared to the other traits. The highest magnitude of HMP was recorded in grain yield per plant (-33.33), whereas the lowest in DTF (0.69). Negative mid-parent residual heterosis (MRH) was recorded for all the traits except plant height (14.37) and panicle length (2.31) which recorded a positive MRH with a high magnitude for plant height and low for panicle length compared to most of the other traits. The highest magnitude of MRH was recorded in grain yield per plant (-18.65), whereas the lowest in DTF (-0.38). The highest degree of dominance among the traits was observed in DTF (4.84), while the lowest value of 3.88 was in plant height (Table 42). In J.85/Apo cross under non-drought conditions, negative heterosis over mid-parent (HMP) was recorded for all the traits except the panicle length and DTF which recorded a positive HMP with a relatively low magnitude compared to the other traits. The highest magnitude of HMP was recorded in panicle number (-67.75), whereas the lowest in DTF (0.40). Negative mid-parent residual heterosis (MRH) was recorded for tiller number, panicle number and DTF, while positive MRH was recorded for plant height, panicle length and grain yield. The highest magnitude of MRH was recorded in plant height (9.22), whereas the lowest in DTF (-0.98). The highest degree of dominance among the traits was observed in tiller number (4.68) while the lowest value of 2.93 was in plant length (Table 43). Under drought stress, in Agra/Apo cross, negative heterosis over mid-parent (HMP) was recorded for all the traits except panicle length (30.52) and DTF (1.87). The highest magnitude of HMP was recorded in SPFS (-84.69), whereas the lowest in plant height (-0.71). Negative mid-parent residual heterosis (MRH) was recorded for DRR, SPFS, tiller number and panicle number, while positive MRH was observed for LRS, LDS, plant height, panicle length, DTF and grain yield per plant. The highest magnitude of MRH was recorded in LRS (42.22), whereas the lowest was in panicle length (0.37). The highest degree of dominance among the traits was observed in tiller number (5.29), while the lowest value of 3.15 was in LRS (Table 42). In J.85/Apo cross under drought stress, negative heterosis over mid-parent (HMP) was recorded for all the traits except panicle length (13.86) and DTF (4.14). The highest magnitude of HMP was recorded in LRS (-100) and the lowest in plant height (-4.13). Negative mid-parent residual heterosis (MRH) was recorded for DRR, SPFS, tiller number, panicle number, plant height and DTF, while positive MRH was observed for LRS, LDS, panicle length and grain yield per plant. The highest magnitude of MRH was recorded on LRS (90.21), whereas the lowest on DTF (-0.33).

Table 42. Heritability/repeatability, genetic advance, heterosis and degree of dominance for grain yield and yield-related traits of the Agra/Apo cross under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable	LRS	LDS	DRR	SPFS	TN		PN		PH		PL		DTF		GYP	
	UD	UD	UD	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
HMP	-58.31	-31.82	-62.69	-84.69	-18.30	-32.37	-20.01	-8.93	-7.19	-0.71	-5.14	30.52	0.69	1.87	-33.33	-23.55
MRH	42.22	12.01	-23.05	-13.57	-9.84	-3.56	-15.35	-2.30	14.37	1.14	2.31	0.37	-0.38	1.12	-18.65	24.91
Vg	4.54	-0.88	0.30	6.03	2.75	0.69	2.40	1.19	105.41	94.43	33.01	20.11	2.04	5.71	4.91	15.31
h^2_{bs}	7.50	28.11	-	49.30	18.58	-	23.46	-	73.58	4.41	65.03	22.12	-	33.95	13.48	13.64
h^2_{ns}	-	1.57	-	-	62.51	-	94.04	90.27	50.35	63.91	68.96	59.91	-	-	83.53	-
GA	2.75	-	0.49	5.06	2.36	1.10	1.95	1.99	16.43	17.80	11.60	9.02	2.29	4.15	1.85	6.49
GAM	40.32	-	14.27	89.56	30.56	25.67	30.75	69.46	14.92	21.84	50.44	46.90	2.49	4.43	15.17	59.55
DD	3.15	3.59	3.38	3.27	4.05	5.29	4.48	4.44	3.88	4.05	4.05	3.98	4.84	3.17	4.34	4.93

HMP- Heterosis over mid-parent; MRH- Mid-parent residual heterosis; Vg- Genetic variance; h^2_{bs} - Broad-sense heritability; h^2_{ns} - Narrow-sense heritability; GA- Genetic advance; GAM- Genetic advance as percentage of mean; DD- Degree of dominance; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; ND-Under non-drought; UD-Under drought

Table 43. Heritability/repeatability, genetic advance, heterosis and degree of dominance for grain yield and yield-related traits of the J.85/Apo cross under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Variable	LRS	LDS	DRR	SFPS	TN		PN		PH		PL		DTF		GYP	
	UD	UD	UD	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
HMP	-100.00	-37.82	4.42	-77.44	-55.99	-41.61	-67.75	-23.50	-9.60	-4.13	2.31	13.86	0.40	4.14	-34.14	-24.93
MRH	90.21	16.58	-1.61	25.51	-5.28	-11.61	-2.79	-5.85	9.22	-4.27	3.49	1.76	-0.98	-0.33	1.70	23.33
Vg	16.40	1.11	1.51	5.37	5.05	0.83	5.17	1.50	3.59	72.21	16.28	17.11	-	2.61	-	29.14
h^2_{bs}	67.50	51.85	39.27	38.88	-	-	-	-	-	14.81	-	5.50	-	24.12	-	62.62
h^2_{ns}	31.36	22.61	39.41	18.16	18.00	94.74	30.71	-	41.45	-	24.67	-	-	69.87	-	87.35
GA	8.34	1.30	2.01	4.77	4.49	1.67	4.54	2.36	0.68	13.41	7.99	8.06	-	2.97	-	9.81
GAM	154.00	34.66	49.13	85.78	56.84	41.35	64.57	82.05	0.64	16.31	33.38	39.22	-	3.24	-	89.53
DD	3.69	3.67	3.80	3.61	4.68	4.53	4.21	5.17	3.04	3.49	2.93	3.00	3.42	4.10	-	4.31

HMP- Heterosis over mid-parent; MRH- Mid-parent residual heterosis; Vg- Genetic variance; h^2_{bs} - Broad-sense heritability; h^2_{ns} - Narrow-sense heritability; GA- Genetic advance; GAM- Genetic advance as percentage of mean; DD- Degree of dominance; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; ND-Under non-drought; UD-Under drought

The highest degree of dominance among the traits was observed on panicle number (5.17), while the lowest value of 3.00 was on panicle length (Table 43).

4.1.4.6 Heritability and Genetic Advance

Under non-drought conditions, in Agra/Apo cross, a high broad-sense heritability was observed for plant height (73.58%) and panicle length (65.03%), while other traits recorded low broad-sense heritability. Moreover, high narrow-sense heritability was observed among the traits with a magnitude ranging from 62.51% for tiller number to 94.04% for panicle number, whereas plant height recorded a moderate narrow-sense heritability of 50.35%. High genetic advance over a mean (GAM) in % was noted for tiller number (30.56%), panicle number (30.75%) and panicle length (50.44%), whereas the magnitude ranged from 2.49% for DTF to 50.44% for panicle length (Table 42). In J.85/Apo cross under non-drought conditions, a moderate broad-sense heritability was observed for plant height (41.45%) and panicle number (30.71%), while other traits recorded low broad-sense heritability. High genetic advance over a mean (GAM) in % was noted for tiller number (56.84%), panicle number (64.57%) and panicle length (33.38%), whereas the magnitude ranged from 0.64% for plant height to 64.57% for panicle number (Table 43).

Under drought stress, in Agra/Apo cross, a moderate broad-sense heritability was observed for SPFS (49.30%) and DTF (33.95%), while other traits recorded low broad-sense heritability. Moreover, high narrow-sense heritability was observed for panicle number (90.27%), plant height (63.91%) and panicle length (59.91%), whereas LDS recorded a low narrow-sense heritability of 1.57% (Table 42). High GAM (%) was noted for LRS (40.32%), SPFS (89.56%), tiller number (25.67%), panicle number (69.46%), panicle length (46.90%) and grain yield per plant (59.55%), whereas low to moderate magnitudes were observed for DTF (4.43%) and 14.27% for DRR (Table 42). Under drought stress, in J.85/Apo cross, a high broad-sense heritability was observed for LRS (67.50%) and grain yield per plant (62.62%), while other traits recorded low to moderate broad-sense heritability with the lowest broad-sense heritability of 5.50% on panicle length. Moreover, high narrow-sense heritability was observed for tiller number (94.74%), DTF (69.87%) and grain yield per plant (87.35%), whereas other traits recorded a moderate narrow-sense heritability with the lowest value of 18.16% for SFPS. High GAM (%) was noted for all the traits except plant height which recorded a moderate value of 16.31% and a DTF low value of 3.24% (Table 43).

4.1.4.7 Correlations among the grain yield and yield-related traits across the segregating populations (F_2, BC_1 and BC_2)

Pearson's correlation analysis was done to assess the relatedness of grain yield with other yield-related traits across the three segregating populations in each cross and water regime. Pearson's correlation analysis revealed significant positive correlations of grain yield per plant with most of the other traits studied in this evaluation among all crosses under non-drought and drought stress. Under non-drought conditions in Agra/Apo cross, grain yield per plant recorded a significant positive association with tiller number, panicle number, plant height, while non-significant positive correlation with panicle length and non-significant negative relation with DTF (Table 44). Under non-drought conditions in J.85/Apo cross, grain yield per plant recorded a significant positive association with panicle number and plant height, while non-significant positive correlation with tiller number and panicle length, and significant negative relation with DTF (Table 45). Under drought stress in Agra/Apo cross, grain yield per plant recorded a significant positive association with tiller number, panicle number, while non-significant positive correlation with panicle length and plant height, and non-significant negative relation with DTF and SPFS. The relationship of grain yield per plant with other traits are non-significant but positive values (Table 44). Under drought stress in J.85/Apo cross, grain yield per plant recorded a significant positive association with panicle number, while non-significant positive correlation with panicle length, plant height and LRS, and non-significant negative relation with DTF, tiller number and SPFS. The relationship of grain yield per plant with other traits are non-significant but negative values (Table 45).

Table 44. Pearson's correlation among grain yield with its related traits in the Agra/Apo cross under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

TRAITS		LRS	LDS	DRR	SFPS	TN		PN		PH		PL		DTF		GYP	
		UD	UD	UD	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
LRS	r	1	0.055	-0.037	0.113	-	0.271	-	0.094	-	0.126	-	0.047	-	-0.133	-	0.079
	p-value		0.459	0.614	0.128	-	0.000	-	0.224	-	0.101	-	0.538	-	0.076	-	0.311
LDS	r		1	0.417	0.150	-	0.125	-	0.145	-	-0.072	-	-0.070	-	-0.181	-	0.069
	p-value			<.0001	0.043	-	0.103	-	0.058	-	0.351	-	0.363	-	0.015	-	0.372
DRR	r			1	-0.099	-	0.161	-	0.194	-	0.083	-	-0.035	-	-0.073	-	0.076
	p-value				0.180	-	0.035	-	0.011	-	0.280	-	0.651	-	0.327	-	0.330
SFPS	r				1	-	0.041	-	-0.174	-	-0.172	-	-0.039	-	0.069	-	-0.081
	p-value					-	0.593	-	0.023	-	0.025	-	0.611	-	0.358	-	0.295
TN	r					1	1	0.608	0.655	0.107	0.079	-0.078	0.011	-0.372	-0.241	0.190	0.232
	p-value							<.0001	<.0001	0.179	0.303	0.327	0.881	<.0001	0.002	0.022	0.003
PN	r							1	1	0.278	0.116	0.078	0.066	-0.435	-0.181	0.221	0.327
	p-value									0.000	0.129	0.330	0.392	<.0001	0.019	0.008	<.0001
PH	r									1	1	0.646	0.461	-0.249	-0.073	0.226	0.086
	p-value											<.0001	<.0001	0.002	0.344	0.006	0.281
PL	r											1	1	-0.049	0.041	0.012	0.066
	p-value													0.541	0.600	0.890	0.413
DTF	r													1	1	-0.131	-0.150
	p-value															0.116	0.053

r- Pearson correlation coefficient; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; ND-Under non-drought; UD-Under drought

Table 45. Pearson's correlation among grain yield with its related traits in the J.85/Apo cross under non-drought and drought stress conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

TRAITS		LRS	LDS	DRR	SFPS	TN		PN		PH		PL		DTF		GYP	
		UD	UD	UD	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD	ND	UD
LRS	r	1	0.311	0.131	0.256	-	0.089	-	0.047	-	0.101	-	0.070	-	-0.131	-	0.041
	p-value		<.0001	0.086	0.001	-	0.284	-	0.572	-	0.227	-	0.402	-	0.086	-	0.617
LDS	r		1	0.252	0.003	-	0.119	-	0.184	-	0.095	-	0.037	-	0.003	-	-0.054
	p-value			0.001	0.967	-	0.153	-	0.026	-	0.255	-	0.656	-	0.965	-	0.509
DRR	r			1	-0.095	-	-0.020	-	-0.010	-	-0.058	-	0.034	-	-0.052	-	-0.004
	p-value				0.217	-	0.814	-	0.901	-	0.490	-	0.685	-	0.493	-	0.958
SFPS	r				1	-	0.136	-	-0.118	-	0.007	-	-0.014	-	-0.258	-	-0.137
	p-value					-	0.106	-	0.159	-	0.938	-	0.865	-	0.001	-	0.094
TN	r					1	1	0.815	0.594	0.017	0.135	0.049	0.064	-0.168	-0.102	0.017	-0.012
	p-value							<.0001	<.0001	0.834	0.104	0.555	0.446	0.039	0.223	0.860	0.889
PN	r							1	1	0.217	0.190	0.109	0.084	-0.405	-0.089	0.187	0.275
	p-value									0.007	0.021	0.188	0.314	<.0001	0.286	0.044	0.001
PH	r									1	1	0.689	0.389	-0.371	-0.094	0.332	0.086
	p-value											<.0001	<.0001	<.0001	0.260	0.000	0.317
PL	r											1	1	-0.106	-0.125	0.086	0.067
	p-value													0.201	0.131	0.360	0.436
DTF	r													1	1	-0.262	-0.012
	p-value															0.004	0.879

r- Pearson correlation coefficient; LRS-Leaf rolling score; LDS-Leaf drying score; DRR-Recovery from drought; SPFS-Spikelet fertility score; TN-Tiller number; PN-Panicle number; PH-Plant height; PL-Panicle length; DTF-Days to flowering; GYP- Grain yield per plant; ND-Under non-drought; UD-Under drought

4.2 Discussions

4.2.1 Combination of phenotyping and SNP-based drought-tolerant QTLs for the selection of drought-tolerant genotypes

The volumetric soil moisture content of a saturated topsoil at the depth of 15 cm is 35% to 40% in general. When it is under 20%, the ground starts to crack and top rice leaves start to die. Obvious cracks in the ground are observed when the volumetric soil moisture content is less than 15%, at this point leaf death becomes obvious. Severe damage in the plant growth is observed when the volumetric soil moisture content is lower than 10% (Kato & Katsura, 2014). The 2.05% volumetric soil moisture content observed in this study at 10 cm soil depth showed that the drought stress imposed is extremely severe and consistent with the data observed under drought experiments in 2015 and 2016 by Zu et al. (2017), and in 2012 and 2013 by Huang et al. (2019). Consistent observations were observed during the evaluation of 2030 rice accessions under continuous drought stress with days to flowering as main secondary screening traits in 2017 and 2018 under field conditions (Ahmad et al., 2020).

The significance of the Mann-Whitney U test observed for chlorophyll content index, spikelet fertility score, grain yield per plant (g), days to flowering, tiller number per plant, panicle number per plant, plant height (cm), panicle length (cm) and hundred grains weight (g) in this study indicates that a complete difference in performance under both water regimes and genotype by environment (G×E) effects will play a large role in the expression of these traits. This is also reflected by the huge variation recorded in the heritability of these traits under drought and non-drought conditions. For all the investigated traits in this study, a general reduction was observed among the genotypes under drought compared to the non-drought conditions. Several studies have recorded grain yield reduction of rice genotypes under drought stress compared to non-drought conditions, where the drought-tolerant controls yielded better results than most of the landraces and the susceptible controls under the reproductive stage drought stress (Iseki et al., 2014; Luo, 2010; Pantuwan et al., 2002; Yue et al., 2006, Anyaoha et al., 2018). In this study under field conditions, 19% of the genotypes showed a low relative spikelet fertility score of 1.00, implying that 81% of the genotypes used in this study are severely affected by drought stress regarding to spikelet fertility and, by extension, to grain yield, since grain yield and spikelet fertility showed positive correlation. Similar performance for spikelet fertility was reported by Afiukwa et al. (2016), who obtained up to a 40.1% reduction in spikelet fertility in more than 78% of the 30 genotypes under drought compared to the non-drought conditions during eight days drought treatment. On the other hand, the low

relative grain yield recorded by G11 in this study despite its best performance in the secondary traits can be explained by the fact that this genotype is known to be a short-term drought-tolerant genotype. In fact, the yield of this genotype might be harshly affected after 15 days of severe drought stress. Even though, delay in 50% flowering date was observed in almost all the genotypes, 5% of the genotypes in the present study flowered 1 to 17 days earlier under drought compared to non-drought conditions. Drought escape is the ability of a plant to complete its life cycle before severe drought stress occurs (Yadav & Sharma, 2016). These genotypes that flowered earlier under drought stress might apply this mechanism to escape the upcoming severe drought stress and therefore can be suitable candidate genetic resources to be used in the development of drought-escaping rice genotypes (Ahmad et al., 2020). However, it is important to note that, the effectiveness of a delay in DTF in breeding for drought tolerance is proven only during a short drought stress period (Afiukwa et al., 2016; Lamo, 2010).

Based on the drought risk index, the relative grain yield was correlated with the relative grain length, grain width (Haider et al., 2015), hundred grains weight and relative spikelet fertility score (Gaballah et al., 2022) making these traits desirable in prediction and selection of drought-tolerant rice genotypes under drought conditions. The low spikelet sterility score implied a high spikelet fertility percentage. The negative correlation observed by Gaballah et al. (2022) between spikelet sterility score and grain yield, and leaf rolling confirms our findings that the increase in grain yield is directly attributable to high spikelet fertility with low reduced leaf rolling and high recovery from drought. In this study, one of the genotypes performed better than G100, and two genotypes performed better than G99 based on the MGIDI index ranking, while 5 genotypes performed better than the two tolerant genotypes based on relative grain yield alone, confirming that it is possible to select tolerant genotypes by directly using relative grain yield. These results agree with Kumar et al. (2008), where breeding lines were found to be superior to the tolerant parental by 2 to 2.5 times.

Effective selection requires the association of secondary traits. A couple of secondary traits have been used in breeding and as selection criteria for the selection of drought-tolerant cultivars. Some of these traits are leaf rolling and leaf drying at the vegetative growth drought stage (Farooq et al., 2010; Thanh et al., 2006; Umego et al., 2020) and spikelet fertility at the reproductive drought stress stage, which is the most important determinant of yield under drought stress (Lafitte et al., 2003; Yue et al., 2006). A couple of breeding efforts for drought tolerance have been reported by monitoring chlorophyll content (Monteoliva et al., 2021). On the other hand, grain yield has been used as the main criteria for the successful development of

high-yielding drought-tolerant rice varieties in Asia and Africa (Dixit et al., 2014; Kumar et al., 2014). It was derived from this current study that, relative spikelet fertility score, relative grain yield, relative plant height, relative grain length, relative leaf rolling, relative leaf drying, relative recovery from drought, relative chlorophyll content index, relative days to flowering and relative tiller number were used to compute the MGIDI index, which was used to select 15 genotypes with tolerance to drought. Similar to our results, other scientists reported QTL profiling results under drought stress that revealed the presence of the of *qDTY1.1*, in 22% of the evaluated genotypes, *qDTY2-2_1* (in 53%), *qDTY3.1* (in 85%) and *qDTY12.1* in 90% (Ndikuryayo et al., 2023). Other studies introgressed two known drought-tolerant QTLs of grain yield, *qDTY12.1* and *qDTY2.3,* into FUNAABOR-2 using marker-assisted selection under drought conditions (Anyaoha et al., 2019).

4.2.2 Physiological and biochemical characterization of selected West Africa rice genotypes in response to drought stress

A progressive and rapid decrease in transpiration rate (E) and stomatal conductance was recorded from 5D to 27D on all the genotypes except on the two drought-tolerant genotypes G100 and G99 implying increase in water use efficiency in these genotypes as observed by Khan et al. (2017) in evaluating two contrasting rice cultivars for their tolerance to drought where the water use efficiency increased in drought-tolerant PR-115, while it rapidly decreased in a drought-sensitive Super-7 at 4, 7 and 10 days of drought stress. While other genotypes were continuing to decrease at 18 days after the stress initiation, G100 and G99 recorded an increase of 89.97% and 20.33% for transpiration rate, from the 18D to 27D, respectively. For stomatal conductance G100 recorded an increase of 29.28%, while G99 recorded the lowest reduction of 17.89% from the 18D to 27D. These results indicate that after 18 days of drought stress where the average moisture content of the soil dropped from 60.78 vol/vol to 32.80 vol/vol, rice plant started to feel the severity of the imposed drought stress. At these points, the tolerant varieties like G100 and G99 could start producing some phytohormones and compounds such as proline, ABA to trigger their tolerance mechanisms and maintain their photosynthesis rate and stomatal conductance relatively high in order to improve their water use efficiency. Similar observations were reported by other authors in evaluating two contrasting rice cultivars for their tolerance to drought where stomatal conductance, transpiration rate and photosynthesis rate decreased in both drought-tolerant PR-115 and drought-sensitive Super-7 at 4, 7 and 10 days of drought stress initiation (Khan et al., 2017). In this study, CRI1 and CRI2, physiological parameters such as stomatal conductance, transpiration rate, electron transport rate and PhiPS

II exhibited enough variation and pattern for tolerance to drought among the genotypes and therefore can be used as a selection criterion at vegetative stage drought stress. Tiwari et al. (2021) reported similar observation of increased performance of physiological parameters such as photosynthesis rate, stomatal conductance and transpiration rate, and increased carotenoids production in drought-tolerant genotype Heena than the sensitive Kiran indicating better performance of Heena under drought stress over Kiran.

Under both non-drought and drought stress conditions, all the leaf reflectance parameters (NDVI, RDVI, CRI1 and CRI2) and PhiPS II recorded low to moderate C.V. and moderate to high heritability at 5, 11, 18 and 27 days after the drought stress initiation. High C.V. and moderate to high heritability were recorded for stomatal conductance, transpiration rate, ETR and tiller number under both drought stress and non-drought conditions at 5, 11, 18 and 27 days after the drought stress initiation. Moderate to high C.V. and heritability indicate the presence of enough variability among the genotypes for these traits (Asante et al., 2019) and therefore, suitable for selection. But, the combination of low C.V. with low heritability like in case of NDVI at 27 days after drought stress initiation doesn't give room for selection in population improvement. Furthermore, no consistent reductions in heritability under drought stress were visible across the entire stress period, in some cases, the heritability increased under drought stress. Proximal heritability estimates for stomatal conductance, transpiration rate, ETR and tiller number under drought stress and non-drought conditions indicate that selection for these traits under drought stress at the vegetative stage in rice will be rewarding with the same level of accuracy as that under non-drought conditions, as suggested by Kumar et al. (2008) for grain yield.

In general, the mean performance of all the genotypes has been reduced notably under 11, 18 and 27 days drought stress compared to the non-drought conditions for stomatal conductance and transpiration rate for all the genotypes except G99, G100 and G6 which were previously identified as drought-tolerant based on the field experiment. It has been reported that drought stress has induced a significant decrease in photosynthetic rate, stomatal conductance, transpiration rate, and significant genotypic variations were observed among different rice genotypes for these leaf gas exchange parameters (Mumtaz et al., 2020). Similar reductions in the physiological performances of these genotypes under drought and spotted that the drought effect on the physiological parameters such as stomatal conductance, transpiration rate and PhiPS II were more pronounced in Super-7 (a drought-sensitive cultivar) than in PR-115 identified as a drought-tolerant one (Khan et al., 2017). When the soil moisture content reached

18.14 vol/vol and the stress became severe at 27 days after the drought stress initiation, significative difference in the mean performance were observed between G99 (best performing) and G22 (waste performing), and between G100 (best performing) and G22 (waste performing) for stomatal conductance and transpiration rate under drought stress, respectively. Gaballah et al. (2022) reported similar mean performance for stomatal conductance and transpiration rate among 17 rice genotypes evaluated under drought stress with 12 days interval exposition to irrigation starting from 15 days after transplanting. These authors reported that the following cultivars ET1444, Egyptian Yasmine, and Giza177 exhibited similar performance under both non-drought and drought stress conditions for stomatal conductance and transpiration rate implying their ability to tolerate drought stress (Gaballah et al., 2022) like G99 and G100 in this current study.

At 5 days after drought stress initiation, the genotype G63 (waste performing) showed a difference in the mean performance with G6 (best performing) for NDVI. On the other hand, under non-drought conditions G11 (best performing) showed a statistically difference in the mean performance with G6, G2 and G78 (best performing). At 27 days after drought stress initiation, under both water regimes no statistical difference was observed among the worst performing genotypes (G11 and G63) with the best performing genotypes (G53, G5 and G99). Other authors such as Phyu et al. (2020) reported similar results for NDVI in evaluation of 36 genotypes under non-drought conditions and suggested that NDVI can be used in screening for high yield rice genotypes in tropical agriculture. These authors reported that NDVI at active tillering stage showed significant differences among the genotypes in dry season with heritability of 76%. Till date, few works have been reported about the screening of genotypes using NDVI under drought stress in rice, however it has been demonstrated that NDVI can be used for high yield wheat genotypes selection under mild drought stress (Naser et al., 2020), while it is not recommended under severe drought stress (Thapa et al., 2019).

Under 11 and 27 days drought stress, Pearson correlation analysis revealed under both water regimes, strong positive significant correlation between stomatal conductance and transpiration rate, and between CRI1 and CRI2. These explained the fact that, G100, G6 and G99 managed to maintain high stomatal conductance and transpiration rate as compared to the non-drought conditions, while all others genotypes have registered a notable decrease. It has been reported under drought stress that the reduction in stomatal conductance resulted in photosynthetic rate and transpiration rate decreases (Begna, 2022). In contrary to the findings of this current study under 5, 11, 18 and 27 days drought stress, Gaballah et al. (2022) reported a non-significant

negative correlation between stomatal conductance and transpiration rate during the evaluation of 17 rice genotypes for morpho-physiological traits for identifying best genotypes under drought stress.

At 27 days after drought stress initiation, the results revealed significant variability among the rice genotypes for MDA and proline content under drought stress, confirming the existence of large segregation among the genotypes for these traits (Asante et al., 2019), which can be rewarding in selection. The MDA is used as a drought indicator to evaluate the degree of lipid peroxide in plasma membrane (Zhang et al., 2021), implying that higher MDA concentration under drought stress more sensitive the genotype is. On the other hand, the accumulation of proline in plants is considered in several species as a physiological response to withstand drought stress (Mafakheri et al., 2010). In this study, proline content of all the seven genotypes notably increased by more than 50% under drought stress compared to non-drought conditions. A non-increase in MDA concentration and an increase in proline content is associated with a protective role in tolerant rice cultivars against drought stress (Nahar et al., 2018), implying that the genotypes G99, G100, G11 and G78 exhibited good tolerance to drought stress. Other studies reported that drought stress induced an increase in proline accumulation in leaf samples by 1.3 to 10.2 times from 9 to 18 days after drought stress initiation in the rice variety BRRI Dhan-24 (Nasrin et al., 2020). The mean performance of all the genotypes was reduced notably under drought stress compared to the non-drought conditions for RWC (%), except G11, G99 and G100. Similar variations in RWC (%) were reported by several studies, confirming the results of this study (Sahoo et al., 2020; Afiukwa et al., 2016; Bunnag et al., 2013; Umego et al., 2020; Gaballah et al., 2022).

The results revealed significant variability among the rice genotypes for all the grain yield and yield-related traits under both drought and non-drought conditions, indicating the presence of large variability among the genotypes (Asante et al., 2019) at the reproductive stage, which can be used for effective selection for tolerance to drought among the genotypes used in this study. The approximate heritability values of biomass and grain yield obtained under drought stress and non-drought conditions in this study show that selection for biomass and grain yield under drought stress in rice will give outcomes with the same level of precision as under non-drought conditions (Kumar et al., 2008) provided that the screening process is well managed.

In general, the flowering date of all the genotypes was delayed for more than 5 days under drought stress compared to that under non-drought conditions, except in G99, G100 and G11, which flowered earlier under drought than under non-drought conditions. These three

genotypes that flowered earlier seem to have exhibited drought escape ability to produce grain before the drought became severe at the late maturing stage. Additionally, these three genotypes G99, G100 and G11 exhibited a typical characteristic of drought escape by maintaining high stomatal conductance and transpiration rates associated with effective photosynthesis and high RWC under drought, resulting in rapid plant development to produce early flowers, as suggested by Kooyers (2015) and Shavrukov et al. (2017). Furthermore, similar observations were made by Sahoo et al. (2020), where at the reproductive stage, DTF were delayed in all genotypes, except Anjali and N22, which flowered earlier. Moreover, the low leaf drying score obtained for these traits confirmed their predisposition to tolerate drought stress. A notable reduction in the mean performance for all the genotypes was registered under drought stress compared to the non-drought conditions for the aboveground biomass and grain yield, except G100, which recorded a similar biomass under non-drought and drought stress. Similar results for grain yield and other yield-related traits were reported by Yang et al. (2019), Huang et al. (2019), Sahoo et al. (2020), Gaballah et al. (2021) and Gaballah et al., (2022).

The negative correlation obtained between grain yield and delay in DTF tended to prove that the genotypes with early flowering under drought stress compared to the non-drought conditions manifested drought escape abilities rather than 100% tolerance capacities. The LDS, DTF and delay in DTF showed positive correlations among themselves, whereas these three traits showed significant correlations with RWC (%), confirming that the genotypes with early flowering under drought stress and low leaf drying are better able to maintain their leaf water status to withstand drought stress by effectively fine adjusting their transpiration rate and stomatal conductance. Grain yield showed a positive correlation with NDVI and RDVI, as reported by Phyu et al. (2020) in a wet season drought-free trial, and concluded that NDVI can be used as a screening criterion in varietal selection for high yield. However, in the present study, RDVI has shown more promising results to be used as a screening criterion for selecting high-yielding genotypes under drought stress. This is confirmed by the regression analysis using grain yield as dependent variable and RDVI where close to 34% of the variability in grain yield is explained by RDVI. The correlation analysis between LDS, DTF, RWC (%) and RDVI implied that these traits can be used as predictors of grain yield and drought-tolerant genotypes.

4.2.3 Transcriptome analysis of four contrasting genotypes selected out of 100 West Africa rice germplasms in response to drought stress

The drought-tolerant genotype G99 behaved as expected by inducing by more than 2x higher transcripts abundance under drought stress compared to the non-drought conditions for all the

tested drought response genes. The significant upregulation of the transcription factor, *LOC_Os04g23550, Basic-helix-loop helix family protein, BHLH6* in G99 (drought-tolerant) as compared to other genotypes under drought conditions implied its positive role in drought tolerance by enhancing signalling pathways under drought stress, as previously stated by Huang et al. (2014). Similar upregulation of *LOC_Os04g23550, Basic-helix-loop helix family protein, BHLH6* was registered in Nagina 22 (drought-tolerant variety) under reproductive stage drought, highlighting the importance of this gene in regulating tolerance to drought stress (Kaur et al., 2023). In both tolerant (G99 and G11) and sensitive (G36 and G1) rice genotypes, the gene *LOC_Os05g08480 (cytokinin-O-glucosyltransferase-1)* was upregulated. However, this was not the case in the results reported by Bhattacharjee et al. (2023) in 15 days old leaves and Ahmad et al. (2022) at the pre-anthesis stage of drought-tolerant/sensitive rice genotypes. These studies reported that, in drought-sensitive genotypes, *LOC_Os05g08480 (cytokinin-O-glucosyltransferase-1)* showed upregulation, while downregulated in the drought-tolerant genotypes (Ahmad et al., 2022; Bhattacharjee et al., 2023). *LOC_Os07g43560 (DUF26 kinases, DUF26K)*, which encode cysteine-rich receptor kinases (CRK), was upregulated in G99 (drought-tolerant) and G36 (drought-sensitive), while it was downregulated in G11 (drought-tolerant) and G1 (drought-sensitive). This was not the case in a study conducted by Ahmad et al. (2022), where *LOC_Os07g43560 (DUF26 kinases, DUF26K)* was downregulated in all the genotypes evaluated under drought stress. The drought-tolerant genotype G11 behaved as expected by maintaining the same level of induction of transcripts abundance under both drought stress compared to the non-drought conditions for all the tested drought response genes. This behaviour can also be matched with the shoot weight which showed no significant difference between drought and non-drought conditions. The drought-sensitive genotype G36 showed an unexpected behaviour as all the tested drought response genes were upregulated, but their levels of induction were significantly lower as compared to the tolerant genotype G99. The drought-sensitive genotype G1 showed an unexpected behaviour since two of the tested drought response genes (*LOC_Os04g23550, Basic-helix-loop helix family protein, transcription factor, BHLH6,* and *LOC_Os05g08480, Cytokinin-O-glucosyltransferase-1*) were upregulated, while *LOC_Os07g43560 (DUF26 kinases, DUF26K)* was repressed under drought as compared to the non-drought conditions.

4.2.4 Genetic basis behind the expression of tolerance to drought stress among the rice breeding lines using generation mean analysis

Mean performance and heritability

Several authors have confirmed the results of this study indicating in both crosses under non-drought and drought stress conditions enough degree of genetic variability for these traits among the segregating populations in this study (Adjah et al., 2020; Asante et al., 2019; Pujar et al., 2022). In addition to that, most of these traits combined moderate to high heritability and genetic advance as percentage of mean indicating possible effective selection in early generation for these traits (Asante et al., 2019). Grain yield per plant has combined high broad-sense and narrow-sense heritability with high genetic advance as percentage of mean in J.85/Apo cross under drought stress indicating that direct selection for grain yield in this population will be rewarding. Such high heritability (>60%) for grain yield and its related traits were also reported by several authors (Solis et al., 2018; Swamy et al., 2017; Venkateshwarlu et al., 2022; Vikram et al., 2011). The relatively identical narrow-sense heritability estimates for panicle number, plant height and panicle length and their positive association with grain yield under drought stress and non-drought conditions imply that selection for these traits as indirect contributors for grain yield under drought stress in rice lines might be rewarding with the same precision as that under non-drought conditions (Kumar et al., 2008) provided that the appraisals are well conducted. Overall, the mean performance of the six populations has decreased significantly under drought stress compared to the non-drought conditions for both crosses Agra/Apo and J.85/Apo for all the studied traits indicating the effectiveness of the stress imposed. Severe decrease in grain yield of rice under drought stress has been reported by Maisura et al. (2014) and Torres & Henry (2018), while Singh et al. (2010) observed in six generations of six crosses of rice under drought and non-drought conditions a reduction in many phenological traits including grain yield under drought conditions. Yield decreases are combined results of the detrimental effect of drought on plant height, number of tillers, leaf area, root length, root thickness and root depth, spikelet fertility, panicle exertion, leaf greenness, leaf temperature, days to flowering, leaf drying and leaf rolling (Bocco et al., 2012; Ndjiondjop et al., 2010).

Transgressive segregation analysis

Unlike heterosis, transgressive segregation is the formation of transgressive phenotypes (extreme phenotypes) in a segregating population (F_2, BC, RILs) towards a negative or positive direction outside the range of the two parental lines and the heritability of these extreme phenotypes are stable (Nirubana et al., 2021). It provides an opportunity for the development of new hybrid species, that are more fit when compared to their ancestors. It is helpful to create varieties that are more adaptable and resilient in stress environments than their counterpart

parents, therefore useful in robust hybrids production (Nirubana et al., 2021). In the view to check whether extreme phenotypes can be produced when both parents in a cross have similar phenotypes, it is observed in this current study that under non-drought conditions, despite the absence of significant difference in the two parental varieties namely Agra and Apo for tiller number, panicle number, panicle length, DTF and grain yield per plant, whereas J.85 and Apo for tiller number, panicle length and grain yield per plant, transgressive phenotypes were however formed for these traits. Under drought stress, at least one transgressive phenotype was produced for each trait whether there is a significant difference or no among the parental lines involved in the development of the F_2 populations. While the progenies from parents with the proximal phenotypes are expected to exhibit a very narrow phenotypic variation (Kim & Rieseberg, 1999; Mansur et al., 1993), the presence of transgressive phenotypes in the F_2 progenies in this current study despite the similarity of the two parents in most traits, can be explained by various reasons among which a high mutation rate in hybrids, low developmental stability, epistasis, overdominance, the expression of unexpressed rare recessive heterozygous alleles in the parents genome, variation in chromosome number or complementary action of dispersed additive alleles between the parental lines. Based on a genome-wide SNP analysis, Koide et al. (2019) deciphered that the transgressive phenotypes for DTF were formed through the exchange of complementary alleles of a few minor QTL in a cross of two identical parental phenotypes. No transgressive phenotypes were observed for DTF in both F_2 progenies for Agra/Apo with a transgressive index (TI) of 7.86 and no significance between Agra and Apo, whereas J.85/Apo with a TI of 4.19 and significant difference observed between J.85 and Apo under non-drought conditions. On the other hand, under drought stress, lower TI of 3.46 and 3.71 for Agra/Apo and J.85/Apo, respectively resulted into the production of transgressive phenotypes. Such a relatively low transgressive segregation was not noted in the F_2 progenies of six crosses between the genotype A58 and the other varieties where the TIs ranged from 0.91 to 2.12 (Ota et al., 2014), while a strong transgressive segregation of 25.7 in the cross A58/Kitaake indicating that DTF of several progenies of F_2 population surpassed the range between their parents (Koide et al., 2019). Across both water regimes, tiller number recorded an identical phenotype performance between the recipient's parents (Agra and J.85) with the donor parent (Apo), but both crosses Agra/Apo and J.85/Apo resulted into strong transgressive segregation with TI ranging from 10.04 under non-drought to 18.75 under drought stress. Such a high transgressive segregation was not seen in any of the evaluation of 378 and 425 progenies of the F_2 population obtained from the crosses between Aikawa1 and Shuho and Shuho and Aikawa1, respectively. It turned out that Aikawa1 and Shuho had the same low-tiller gene based

on alleles tests in F_2 progenies obtained from reciprocal crosses between Aikawa1 and Shuho (Fukuta et al., 2003). Moreover, such high transgressive segregation observed in this study, was also reported by other authors in F_2 progenies of both crosses between BPT5204/NLR33892 and BPT5204/NLR33892 for plant height, panicle number, panicle length, spikelet fertility and grain yield per plant. High density of desirable transgressive phenotypes was obtained for plant height in BPT5204/NLR33892 cross, while BPT5204/NLR33892 cross exhibited many favorable transgressive phenotypes for spikelet fertility. This high frequencies of desirable transgressive segregants associated with polygenic inheritance for grain yield and its related traits indicates the presence of a large scope for transferring favorable alleles into a single line through adequate selection in later generations (Reddyyamini et al., 2019).

Genetic effects

Epistasis is defined as any form of non-allelic interaction (Gaoh et al., 2020) making the expression of gene interaction more complex. This complexity can be overcome when the intensity of the epistasis is relatively low but when epistasis is the primary source of genetic variation no measure of additive or dominance variation is possible (Hayman, 1960). The non-significance of the four scaling tests for most of the grain yield and yield-related traits in both Agra/Apo and J.85/Apo crosses under both non-drought and drought stress conditions indicate that epistatic interaction effects is not the primary source of genetic variation in the inheritance genes governing the grain yield and yield-related traits in this rice lines, therefore additive or dominance effect are more likely to express themselves.

In this current study, among the direct gene effect, the magnitude of dominance effect was preponderant as compared to the additive in both crosses under non-drought and drought stress conditions providing the evidence that the dominance gene effect is predominant in the inheritance of these traits. Dominance gene effect was in the negative direction for most of the traits except days to flowering which showed consistent positive direction across all crosses and water regimes. The predominance of dominant effect is further emphasized by the high values of degree of dominance calculated for all the traits in this study under both crosses and water regimes. Such level of dominance is also observed by Yogameenakshi et al. (2019) and Gobu et al. (2021) for agronomic traits including grain yield, hundred grains weight, panicle number, filled grains per panicle, harvest index, flag leaf width, spikelet fertility.

In this current study, among the interaction effect, additive x additive gene interaction was significant for most of the traits despite the fact that the scaling tests were not significant. Other

authors reported similar significance of the additive x additive gene interaction in panicle length and number of filled grains panicle (Yogameenakshi et al., 2019). Moreover, the magnitude of additive x additive gene interaction was higher than the dominance x dominance gene interaction which was also higher than additive x dominance type of gene interaction for most of the studied traits in both crosses, and in both non-drought and drought conditions independent of the – or + signs. The predominance of significant additive × additive gene action for most traits in this study across both water regimes indicates that selection could be effective in early generations since additive gene effect and additive × additive gene interaction effects constitute the fixable genetic variance (Pujar et al., 2022).

Apart from the significance of all the six types of gene actions (mean effect, additive effect, dominance effect, additive × additive effect, additive × dominance effect and dominance × dominance effect) for days to flowering under non-drought conditions in both crosses, and the dominance gene effects and dominance x dominance gene effect were having opposite sign for days to flowering which indicate the presence of duplicate epistasis, clearly explain the complex nature of this trait, making early generation selection a difficult task since super lines development could only be achieved through population improvement using pedigree selection in the later generation. Similar duplicate epistasis is reported by Gobu et al. (2021) and Pujar et al. (2022), while Yogameenakshi et al. (2019) reported additive x dominance and dominance x dominance gene interaction effects in days to flowering.

Under both non-drought and drought stress conditions, all the F_1 hybrid lines obtained in the present study did not exceed the mean of the better parent for all the traits except panicle length and days to flowering which showed consistent across the crosses and water regimes. This indicates that there was no heterosis over the better-parent. Moreover, the predominance of additive × additive type of gene interaction for these traits' inheritance would render it difficult to obtain better parent heterosis. Most of the heterosis over mid-parent (HMP) and residual heterosis over mid-parent (HRM) were in negative direction implying that most of the HMP obtained in F_1 generation are retained in F_2 generation.

Correlation analysis among the segregating populations

In general, the correlation between grain yield per plant and its related traits were positive and significant except for DTF and SPFS which recorded consistent negative correlation across all both crosses in these segregating populations in the present study, shows that these traits are co-segregating. Thus, these results tend to indicate that indirect selection of grain yield in rice

could be effective in improving grain yield under drought using secondary traits such as tiller number, panicle number, plant height, panicle length and SPFS. Nevertheless, it was not the case in the evaluation of 156 breeding lines derived from $F_{2:4}$ where all the secondary traits recorded negative association with grain yield except harvest index and biomass, indicating that indirect selection using the secondary traits could not be effective in grain yield improvement under drought (Venkateshwarlu et al., 2022). Secondary traits such leaf rolling and leaf drying were not able to select for rice grain yield under drought stress (Kumar et al., 2008). In Agra/Apo cross, no significant correlation between DTF and grain yield per plant was established in both non-drought and drought stress conditions, it is evident that the drought tolerance registered in some segregating lines might largely due to the drought tolerance rather than drought escape. One cannot also conclude about the grain yield advantage under drought stress as a result of rice plant tallness, dwarfness or semi-dwarfness since there is no established correlation between plant height and grain yield per plant in both crosses under drought condition in this study. These findings are consisted with the results of Venkateshwarlu et al. (2022). It is well established that drought stress significantly decreases grain yield as results of low spikelet fertility % or high spikelet fertility score (the lower the spikelet fertility %, the higher the spikelet fertility score) as reported by Salleh et al. (2022). In this study, no significant correlation was registered between spikelet fertility score (SPFS) and grain yield per plant under drought stress and crosses indicating the presence of several low-yielding lines in the three segregating populations (F_2, BC_1 and BC_2) with high SPFS. These low yielding lines actually are having few grains but have this ability to translocate the photosynthates to most of its grains to keep them filled.

CHAPTER 5 CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

One of the major challenges is to increase rice production under increasing drought as result of climate change, however, the use of drought-tolerant rice cultivars can be one of the solutions as they have the ability to secure high yield under drought. This study aimed to assess the impact of drought stress on morphological, physiological, biochemical traits and transcripts abundance of drought responsive genes among the rice genotypes and select the genotypes that are tolerant to drought stress. Furthermore, this study sought to understand the genetic basis and inheritance behind the expression of tolerance of the rice breeding lines to drought stress.

Under field screening conditions, using relative grain yield as the main selection criterion followed by other secondary traits and the genotyping results of the nine known drought tolerance QTLs, eight out of the 100 genotypes evaluated, were selected as potential drought-tolerant genotypes in the chronological order: G6, G62, G731, G79, G100, G99, G65 and G11. Using the multi-trait genotype-ideotype distance index (MGIDI), the following genotypes were selected in the chronological order: G60, G100, G77, G99, G79, G66, G6, G74, G65, G44, G81, G21, G89, G14 and G10.

Under greenhouse screening conditions, a progressive decrease in transpiration rate and stomatal conductance was recorded from 5 to 27 days after the drought stress initiation on all the genotypes except on G100 and G99 implying increase in water use efficiency in these genotypes. In this experiment, five (G11, G73, G99, G100 and G78) out the 14 genotypes which showed consistent signs of tolerance during the vegetative stage drought were selected using the relative value of the leaf gas exchange attributes and leaf reflectance parameters and were used in screening for further biochemical characterisation. At 27 days after the drought stress initiation, the mean performance of all the genotypes has been increased notably under drought stress compared to the non-drought conditions for MDA concentration for all the genotypes except G11, G99 and G100, while the proline content of G78 and G100 has notably increased under drought stress compared to that of Jasmine 85 which is considered as drought-sensitive variety based on the field experiment. In general, the mean performance of all the genotypes has been reduced notably under drought stress compared to the non-drought conditions for stomatal conductance, transpiration rate and PhiPS2 for all the genotypes except G11 for stomatal conductance and PhiPS2, and G100 for transpiration rate indicating the tolerance ability of these genotypes to drought at the reproductive stage. Under the reproductive stage

drought, results revealed significant differences among the rice genotypes for all the grain yield and yield-related traits namely days to flowering, leaf drying score, aboveground biomass and grain yield per plant under both drought stress and non-drought conditions. Based on the above results from grain yield and relative yield-related traits analysis and using relative grain yield as a main selection criterion followed by other relative yield-related traits, G100, G99, G73 and G11 were selected as showing tolerance under the reproductive stage drought.

Under growth chambers screening conditions, in the drought-tolerant genotype G99, there was an induction by more than 2x of specific drought-associated genes (*BHLH6*, *Cytokinin-O-glucosyltransferase-1* and *DUF26K*) under drought conditions. However, in the case of the drought-tolerant genotype G11, it was observed that a similar induction level was maintained for all the tested genes under drought compared to the non-drought conditions. This behaviour can also be matched with their shoot weight which showed no significant difference between drought and non-drought conditions. Interestingly, in the drought-sensitive genotype G36, it was found that all the tested drought response genes were upregulated, but their level of induction was significantly lower when compared with the tolerant genotype G99. The drought-sensitive genotype G1 showed upregulation of two of the tested drought response genes (*BHLH6* and *Cytokinin-O-glucosyltransferase-1*), whereas *DUF26K* was repressed under drought as compared to the non-drought conditions. Together our results showed that different drought-tolerant genotypes might engage into specific molecular responses. By characterising the transcriptome of these plants, we can better understand the mechanisms behind their tolerance/sensitivity and improve our toolkit to address this abiotic stress in crops.

Under the screenhouse evaluation of the six populations (P_1, P_2 F_1, F_2, BC_1 and BC_2) of rice lines developed from each of Agra/Apo and J.85/Apo crosses, overall, the mean performance of the six populations has decreased significantly under drought stress compared to the non-drought conditions for both crosses Agra/Apo and J.85/Apo for all the studied traits indicating the effectiveness of the stress imposed. To check whether extreme phenotypes can be produced when both parents in a cross have similar phenotypes, it is observed that under drought stress, at least one transgressive phenotype was produced for each trait whether there is a significant difference or no among the parental lines involved in the development of the F_2 populations. The non-significance of the four scaling tests for most of the grain yield and yield-related traits in both Agra/Apo and J.85/Apo crosses under both non-drought and drought stress conditions indicate that epistatic interaction effects is not the primary source of genetic variation in the

inheritance of genes governing the grain yield and yield-related traits in this rice lines, therefore additive or dominance effect are more likely to express themselves. In this study, among the direct gene effects, the magnitude of dominance effect was preponderant as compared to the additive in both crosses under non-drought and drought stress conditions providing the evidence that the dominance gene effect is predominant in the inheritance of these traits.

In this current study, among the interaction effect, additive x additive gene interaction was significant for most of the traits despite the fact that the scaling tests were not significant. The predominance of significant additive × additive gene action for most traits in this study across both water regimes indicates that selection could be effective in early generations. Moreover, the dominance gene effect and dominance x dominance gene effect were having opposite sign for days to flowering which indicate the presence of duplicate epistasis, clearly indicates that superior lines development could only be achieved through population improvement using pedigree selection in the later generation.

5.2 Recommendations

The results in this dissertation can be used in improving breeding efforts, especially in selection processes and also improving the livelihoods of the households of rice producers. Therefore, our recommendations are as follow:

1. The genotypes Apo (G99) and UPLR-17 (G100) can be used as drought-tolerant donors' parents in the breeding of drought-tolerant rice genotypes under tropical agriculture conditions.
2. The genotype CRI-Enapa (G11) can now be recommended for farmers as short-term drought-tolerant genotype to be cultivated in Ghana. Genotype G11 can tolerant drought stress up to 15 days after drought initiation under both the vegetative and the reproductive stage drought. This genotype has been released in Ghana by CSIR-Crops Research under the national code GH/Os/006/19 in the Catalogue of Crop Varieties Released & Registered in Ghana in 2019 and it has been widely cultivated countrywide.
3. The genotypes Viwonor short (G60), SA68-SARI (G78) and SR35266-2-12-1-1 (G73) can be released as drought-tolerant genotypes to improve the cropping index of rice in Ghana, while further studies need to be conducted and subsequently released in Togo and any other west Africa country. These genotypes must go through multilocational trials in order to verify their performance under various environments before their release.

4. The formation of extremes phenotypes or transgressive segregants for most traits in this study, despite the similarities of phenotypes between the parents involved in the crosses, led us to question how the transgressive segregants are formed. Further molecular studies need to be done to help decipher this mechanism. In this era of advanced technological application in genomics analysis, it is advisable to analyse a larger proportion of the progenies obtained from these crosses to help decipher gene function and interaction of genes and understand how these extremes phenotypes are formed despite the similarities of their parental lines.
5. With the predominance of the additive × additive type of gene interaction among these segregating populations, selection for grain yield using secondary traits can be done in early generations using whether forward breeding or backcross breeding.

REFERENCES

Adeboye, K. A., Semon, M., Oyetunde, O. A., Oduwaye, O. A., Adebambo, A. O., Fofana, M., & Daniel, I. O. (2021). Diversity array technology (DArT)-based mapping of phenotypic variations among recombinant inbred lines of WAB638-1/PRIMAVERA under drought stress. *Euphytica*, *217*(6), 130. https://doi.org/10.1007/s10681-021-02860-6

Adjah, K. L., Abe, A., Adetimirin, V. O., & Asante, M. D. (2020). Genetic variability, heritability and correlations for milling and grain appearance qualities in some accessions of rice (*Oryza sativa* L.). *Physiology and Molecular Biology of Plants*. https://doi.org/10.1007/s12298-020-00826-x

Adnane, B., Mainassara, Z. A., Mohamed, F., Mohamed, L., Jean-Jacques, D., T. Rim, M., & Georg, C. (2015). Physiological and Molecular Aspects of Tolerance to Environmental Constraints in Grain and Forage Legumes. *International Journal of Molecular Sciences*, *16*(8), 18976. https://doi.org/10.3390/IJMS160818976

Affortit, P., Effa-Effa, B., Ndoye, M. S., Moukouanga, D., Luchaire, N., Cabrera-Bosquet, L., Perálvarez, M., Pilloni, R., Welcker, C., Champion, A., Gantet, P., Diedhiou, A. G., Manneh, B., Aroca, R., Vadez, V., Laplaze, L., Cubry, P., & Grondin, A. (2022). Physiological and genetic control of transpiration efficiency in African rice, Oryza glaberrima Steud. *Journal of Experimental Botany*, *73*(15), 5279–5293. https://doi.org/10.1093/jxb/erac156

Afiukwa, C. A., Faluyi, O. J., Atkinson, J. C., Ubi, E. B., Igwe, O. D., & Akinwale, O. R. (2016). Screening of some rice varieties and landraces cultivated in Nigeria for drought tolerance based on phenotypic traits and their association with SSR polymorphism. *African Journal of Agricultural Research*, *11*(29), 2599–2615. https://doi.org/10.5897/ajar2016.11239

AGRA. (2018). *Africa Agriculture Status Report: Catalyzing Government Capacity to Drive Agricultural Transformation*. https://agra.org/news/agras-2018-annual-report-a-green-revolution-in-africa-a-fitting-tribute-to-its-visionary-founder/

Ahmad, H., Zafar, S. A., Naeem, M. K., Shokat, S., Inam, S., Rehman, M. A. ur, Naveed, S. A., Xu, J., Li, Z., Ali, G. M., & Khan, M. R. (2022). Impact of Pre-Anthesis Drought Stress on Physiology, Yield-Related Traits, and Drought-Responsive Genes in Green Super Rice. *Frontiers in Genetics*, *13*, 832542. https://doi.org/10.3389/FGENE.2022.832542/BIBTEX

Ahmad, M. S., Wu, B., Wang, H., & Kang, D. (2020). Field Screening of Rice Germplasm (*Oryza sativa* L. ssp. japonica) Based on Days to Flowering for Drought Escape. *Plants*, *9*(5). https://doi.org/10.3390/PLANTS9050609

Allard, R. W. (1960). Principles of Plant Breeding. *John Wiley and Sons Inc., New York, USA*, 485.

Anyaoha, C. O., Fofana, M., Gracen, V. E., Tongoona, P. B., Blay, E. T., Semon, M., & Popoola, B. (2018). Yield potential of upland rice varieties under reproductive-stage drought and optimal water regimes in Nigeria. *Plant Genetic Resources: Characterisation and Utilisation*, *16*(4), 378–385. https://doi.org/10.1017/S1479262118000060

Anyaoha, C. O., Fofana, M., Gracen, V., Tongoona, P., & Mande, S. (2019). Introgression of Two Drought QTLs into FUNAABOR-2 Early Generation Backcross Progenies Under

Drought Stress at Reproductive Stage. *Rice Science*, *26*(1), 32–41. https://doi.org/10.1016/j.rsci.2018.04.006

Arifuzzaman, Md., Kabir, Md. S., Hossain, Md. M., Hoque, Md. A., Baki, M. A., Kabir, Md. H., Hossain, Md. S., Rahman, M., Mohamud, M. A., Azad, Md. A. K., Mollah, Md. D. A., Shumsun, N., & Rahman, Md. H. (2022). Analysis of Genetic Diversity in Some Rice Varieties and Their Performance in Bangladesh. *International Journal of Advances in Agricultural Science and Technology*, *9*(12), 59–80. https://doi.org/10.47856/ijaast.2022.v09i12.003

Arouna, A., Lokossou, J. C., Wopereis, M. C. S., Bruce-Oliver, S., & Roy-Macauley, H. (2017). Contribution of improved rice varieties to poverty reduction and food security in sub-Saharan Africa. In *Global Food Security* (Vol. 14, pp. 54–60). Elsevier B.V. https://doi.org/10.1016/j.gfs.2017.03.001

Asante, M. D., Adjah, K. L., & Annan-Afful, E. (2019). Assessment of Genetic Diversity for Grain Yield and Yield Component Traits in Some Genotypes of Rice (*Oryza Sativa* L.). *Journal of Crop Science and Biotechnology*, *22*(2), 123–130. https://doi.org/10.1007/S12892-019-0008-0/METRICS

Atkinson, N. J., & Urwin, P. E. (2012). The interaction of plant biotic and abiotic stresses: from genes to the field. *Journal of Experimental Botany*, *63*(10), 3523–3544. https://doi.org/10.1093/JXB/ERS100

Atlin G. (2003). Improving drought tolerance by selecting for yield. Breeding Rice for Drought-prone Environments. *International Rice Research Institute*, 14.

Baisakh, N., Yabes, J., Gutierrez, A., Mangu, V., Ma, P., Famoso, A., & Pereira, A. (2020). Genetic mapping identifies consistent quantitative trait loci for yield traits of rice under greenhouse drought conditions. *Genes*, *11*(1). https://doi.org/10.3390/genes11010062

Barik, S. R., Pandit, E., Mohanty, S. P., Nayak, D. K., & Pradhan, S. K. (2020). Genetic mapping of physiological traits associated with terminal stage drought tolerance in rice. *BMC Genetics*, *21*(1). https://doi.org/10.1186/s12863-020-00883-x

Barik, S. R., Pandit, E., Pradhan, S. K., Mohanty, S. P., & Mohapatra, T. (2019). Genetic mapping of morpho-physiological traits involved during reproductive stage drought tolerance in rice. *PLOS ONE*, *14*(12), e0214979. https://doi.org/10.1371/JOURNAL.PONE.0214979

Bates, B. C., Kundzewicz. Z.W., Wu, S., & Palutikof, J. P. (2008, June). *Climate Change and Water — IPCC*. Technical Paper of the Intergovernmental Panel on Climate Change, IPCC Secretariat, Geneva,. https://www.ipcc.ch/publication/climate-change-and-water-2/

Bates, L. S., Waldren, R. P., & Teare, I. D. (1973). Rapid determination of free proline for water-stress studies. *Plant and Soil 1973 39:1*, *39*(1), 205–207. https://doi.org/10.1007/BF00018060

Bazrkar-Khatibani, L., Fakheri, B. A., Hosseini-Chaleshtori, M., Mahender, A., Mahdinejad, N., & Ali, J. (2019). Genetic mapping and validation of Quantitative Trait Loci (QTL) for the grain appearance and quality traits in rice (Oryza sativa L.) by using Recombinant Inbred Line (RIL) population. *International Journal of Genomics*, *2019*. https://doi.org/10.1155/2019/3160275

Begna, T. (2022). Breeding Strategies for Improvement of Drought Tolerant in Crops. *Adv Crop Sci Tech, an Open Access Journal*, *2022*(7), 1000523. https://doi.org/10.4172/2329-8863.1000523

Benjamins, R., Quint, A., Weijers, D., Hooykaas, P., & Offringa, R. (2001). The PINOID protein kinase regulates organ development in Arabidopsis by enhancing polar auxin transport. *Development (Cambridge, England)*, *128*(20), 4057–4067. https://doi.org/10.1242/dev.128.20.4057

Bernier, J., Kumar, A., Ramaiah, V., Spaner, D., & Atlin, G. (2007). A Large-Effect QTL for Grain Yield under Reproductive-Stage Drought Stress in Upland Rice. *Crop Science*, *47*(2), 507–516. https://doi.org/10.2135/cropsci2006.07.0495

Bhandari, A., Sandhu, N., Bartholome, J., Cao-Hamadoun, T.-V., Ahmadi, N., Kumari, N., & Kumar, A. (2020). Genome-Wide Association Study for Yield and Yield Related Traits under Reproductive Stage Drought in a Diverse indica-aus Rice Panel. *Rice 2020 13:1*, *13*(1), 1–22. https://doi.org/10.1186/S12284-020-00406-3

Bhat, J. A., & Yu, D. (2021). High-throughput NGS-based genotyping and phenotyping: Role in genomics-assisted breeding for soybean improvement. In *Legume Science* (Vol. 3, Issue 3). John Wiley and Sons Inc. https://doi.org/10.1002/leg3.81

Bhattacharjee, B., Ali, A., Rangappa, K., Choudhury, B. U., & Mishra, V. K. (2023). A detailed study on genetic diversity, antioxidant machinery, and expression profile of drought-responsive genes in rice genotypes exposed to artificial osmotic stress. *Scientific Reports 2023 13:1*, *13*(1), 1–19. https://doi.org/10.1038/s41598-023-45661-8

Bhattarai, U., & Subudhi, P. K. (2018). Genetic analysis of yield and agronomic traits under reproductive-stage drought stress in rice using a high-resolution linkage map. *Gene*, *669*, 69–76. https://doi.org/10.1016/j.gene.2018.05.086

Bimpong, I. K., Manneh, B., Sander, Z., Futakuchi, K., & Kumashiro, T. (2011). *Climate change Impacts and Strategies on Rice Production in Africa "Developing Climate-Smart Crops for a 2030 World" Workshop ILRI, Addis Ababa Ethiopia, December 6-8 2011*.

Bimpong, I. K., Serraj, R., Chin, J. H., Mendoza, E. M. T., Hernandez, J., & Mendioro, M. S. (2018). Determination of genetic variability for physiological traits related to drought tolerance in African rice (*Oryza glaberrima*). In *African Journal of Crop Science* (Vol. 6, Issue 8). www.internationalscholarsjournals.org

Bocco, R., Lorieux, M., Seck, P. A., Futakuchi, K., Manneh, B., Baimey, H., & Ndjiondjop, M. N. (2012). Agro-morphological characterization of a population of introgression lines derived from crosses between IR 64 (*Oryza sativa* indica) and TOG 5681 (Oryza glaberrima) for drought tolerance. *Plant Science*, *183*, 65–76. https://doi.org/10.1016/j.plantsci.2011.09.010

Boubacar Gaoh, B. S., Gangashetty, P. I., Mohammed, R., Dzidzienyo, D. K., & Tongoona, P. (2020). Generation mean analysis of pearl millet [Pennisetum glaucum (L.) R. Br.] grain iron and zinc contents and agronomic traits in West Africa. *Journal of Cereal Science*, *96*, 103066. https://doi.org/10.1016/J.JCS.2020.103066

Bouman, B. A. M., Humphreys, E., Tuong, T. P., & Barker, R. (2007). Rice and Water. *Advances in Agronomy*, *92*, 187–237. https://doi.org/10.1016/S0065-2113(04)92004-4

Bouman, B. A. M., Kropff, M. J., Wopereis, M. C. S., ten Berge, H. F. M., & van Laar, H. H. (2001). ORYZA2000: modeling lowland rice. *IRRI Books*. https://doi.org/10.22004/AG.ECON.281825

Boyer, J. S., & Westgate, M. E. (2004). Grain yields with limited water. *Journal of Experimental Botany*, *55*(407), 2385–2394. https://doi.org/10.1093/JXB/ERH219

Bunnag, S., Pongthai, P., Bunnag, S., & Pongthai, P. (2013). Selection of Rice (Oryza sativa L.) Cultivars Tolerant to Drought Stress at the Vegetative Stage under Field Conditions. *American Journal of Plant Sciences*, *4*(9), 1701–1708. https://doi.org/10.4236/AJPS.2013.49207

Cazzola, F., Bermejo, C. J., & Cointry, E. (2020). Transgressive segregations in two pea F2 populations and their respective F2:3 families. *Pesquisa Agropecuária Brasileira*, *55*. https://doi.org/10.1590/S1678-3921.PAB2020.V55.01623

Centritto, M., Lauteri, M., Monteverdi, M. C., & Serraj, R. (2009). Leaf gas exchange, carbon isotope discrimination, and grain yield in contrasting rice genotypes subjected to water deficits during the reproductive stage. *Journal of Experimental Botany*, *60*(8), 2325–2339. https://doi.org/10.1093/JXB/ERP123

Chandra Babu, R., Gomez, S. M., Kumar, S. S., Jeyaprakash, P., Suresh, R., Biji, K. R., Boopathi, N. M., & Price, A. H. (2006). Mapping QTLs Linked to Physio-Morphological and Plant Production Traits under Drought Stress in Rice (Oryza sativa L.) in the Target Environment. *American Journal of Biochemistry and Biotechnology*, *2*(4), 161–169.

Chen, H., Xie, W., He, H., Yu, H., Chen, W., Li, J., Yu, R., Yao, Y., Zhang, W., He, Y., Tang, X., Zhou, F., Deng, X. W., & Zhang, Q. (2014). A high-density snp genotyping array for rice biology and molecular breeding. *Molecular Plant*, *7*(3), 541–553. https://doi.org/10.1093/mp/sst135

Choi, J. Y., Zaidem, M., Gutaker, R., Dorph, K., Singh, R. K., & Purugganan, M. D. (2019). The complex geography of domestication of the African rice oryza glaberrima. *PLoS Genetics*, *15*(3). https://doi.org/10.1371/journal.pgen.1007414

Ciarmiello, L. F., Woodrow, P., Fuggi, A., Pontecorvo, G., Carillo, P., Ciarmiello, L. F., Woodrow, P., Fuggi, A., Pontecorvo, G., & Carillo, P. (2011). Plant Genes for Abiotic Stress. *Abiotic Stress in Plants - Mechanisms and Adaptations*. https://doi.org/10.5772/22465

Cruz De Carvalho, M. H. (2008). Drought stress and reactive oxygen species: Production, scavenging and signaling. *Plant Signaling & Behavior*, *3*(3), 156–165. https://doi.org/10.4161/PSB.3.3.5536

de Souza, T. C., de Castro, E. M., César Magalhães, P., De Oliveira Lino, L., Trindade Alves, E., & de Albuquerque, P. E. P. (2013). Morphophysiology, morphoanatomy, and grain yield under field conditions for two maize hybrids with contrasting response to drought stress. *Acta Physiologiae Plantarum*, *35*(11), 3201–3211. https://doi.org/10.1007/S11738-013-1355-1/TABLES/4

Dingkuhn, M., Audebert, A. Y., Jones, M. P., Etienne, K., & Sow, A. (1999). Control of stomatal conductance and leaf rolling in O. sativa and O. glaberrima upland rice. *Field Crops Research*, *61*(3), 223–236. https://doi.org/10.1016/S0378-4290(98)00165-8

Dixit, S., Singh, A., & Kumar, A. (2014). Rice breeding for high grain yield under drought: A strategic solution to a complex problem. *International Journal of Agronomy*, *2014*. https://doi.org/10.1155/2014/863683

Du, H., Wu, N., Fu, J., Wang, S., Li, X., Xiao, J., & Xiong, L. (2012). A GH3 family member, OsGH3-2, modulates auxin and abscisic acid levels and differentially affects drought and cold tolerance in rice. *Journal of Experimental Botany*, *63*(18), 6467–6480. https://doi.org/10.1093/JXB/ERS300

Efisue, A. A., Tongoona, P., Derera, J., Ubi, B. E., & Oselebe, H. O. (2009). Genetics of Morpho-Physiological Traits in Segregating Populations of Interspecific Hybrid Rice Under Stress and Non-Stress Conditions. *Journal of Crop Improvement*, *23*(4), 383–401. https://doi.org/10.1080/15427520902976471

Fan, M., Gao, Y., Wu, Z., & Zhang, Q. (2020). Linkage map development by EST-SSR markers and QTL analysis for inflorescence and leaf traits in chrysanthemum (Chrysanthemum morifolium ramat.). *Plants*, *9*(10), 1–20. https://doi.org/10.3390/plants9101342

Fang, Y., & Xiong, L. (2015). General mechanisms of drought response and their application in drought resistance improvement in plants. *Cellular and Molecular Life Sciences: CMLS*, *72*(4), 673–689. https://doi.org/10.1007/S00018-014-1767-0

FAOSTAT. (2023). *FAOSTAT*. Production Quantities of Rice, Paddy by Country. Food and Agriculture Organization of the United Nations (FAO), Statistics. http://www.fao.org/faostat/en/#data/QC/visualize

Farooq, M., Kobayashi, N., Ito, O., Wahid, A., & Serraj, R. (2010). Broader leaves result in better performance of indica rice under drought stress. *Journal of Plant Physiology*, *167*(13), 1066–1075. https://doi.org/10.1016/J.JPLPH.2010.03.003

Farooq, M., Wahid, A., & Lee, D. J. (2009). Exogenously applied polyamines increase drought tolerance of rice by improving leaf water status, photosynthesis and membrane properties. *Acta Physiologiae Plantarum*, *31*(5), 937–945. https://doi.org/10.1007/s11738-009-0307-2

Foley, J. A., Ramankutty, N., Brauman, K. A., Cassidy, E. S., Gerber, J. S., Johnston, M., Mueller, N. D., O'Connell, C., Ray, D. K., West, P. C., Balzer, C., Bennett, E. M., Carpenter, S. R., Hill, J., Monfreda, C., Polasky, S., Rockström, J., Sheehan, J., Siebert, S., … Zaks, D. P. M. (2011). Solutions for a cultivated planet. *Nature*, *478*(7369), 337–342. https://doi.org/10.1038/nature10452

Fonseca, S., & Patterson, F. L. (1968). Hybrid Vigor in a Seven-Parent Diallel Cross in Common Winter Wheat (*Triticum aestivum* L.)1. *Crop Science*, *8*(1), 85–88. https://doi.org/10.2135/CROPSCI1968.0011183X000800010025X

Frimpong, F., Windt, C. W., van Dusschoten, D., Naz, A. A., Frei, M., & Fiorani, F. (2021). A Wild Allele of Pyrroline-5-Carboxylate Synthase1 Leads to Proline Accumulation in Spikes and Leaves of Barley Contributing to Improved Performance Under Reduced Water Availability. *Frontiers in Plant Science*, *12*, 633448. https://doi.org/10.3389/FPLS.2021.633448/BIBTEX

Fukuta, Y., Araki, E., Ebron, L. A., Cuevas, P. R., Mercado-Escueta, D., Khush, G. S., Sheehy, J. E., Tsunematsu, H., & Kato, H. (2003). Identification of the low-tillering gene in rice (*Oryza sativa* L.). In *JIRCAS Research Highlights*.

Gaballah, M. M., Ghoneim, A. M., Ghazy, M. I., Mohammed, H. M., Sakran, R. M., Rehman, H. U., & Shamsudin, N. A. A. (2021). Root Traits Responses to Irrigation Intervals in Rice (Oryza sativa). *International Journal of Agriculture and Biology*, *26*(1), 22–30. https://doi.org/10.17957/IJAB/15.1804

Gaballah, M. M., Ghoneim, A. M., Rehman, H. U., Shehab, M. M., Ghazy, M. I., El-Iraqi, A. S., Mohamed, A. E., Waqas, M., Shamsudin, N. A. A., & Chen, Y. (2022). Evaluation of Morpho-Physiological Traits in Rice Genotypes for Adaptation under Irrigated and Water-Limited Environments. *Agronomy*, *12*(8). https://doi.org/10.3390/agronomy12081868

Ghimire, K. H., Quiatchon, L. A., Vikram, P., Swamy, B. P. M., Dixit, S., Ahmed, H., Hernandez, J. E., Borromeo, T. H., & Kumar, A. (2012). Identification and mapping of a QTL (qDTY 1.1) with a consistent effect on grain yield under drought. *Field Crops Research*, *131*, 88–96. https://doi.org/10.1016/j.fcr.2012.02.028

Gilevaei, M. D. (2020). Mapping genomic regions associated with yield and drought tolerance indices in recombinant inbred lines of rice. *IRANIAN JOURNAL of GENETICS and PLANT BREEDING*, *9*(2). https://doi.org/10.30479/ijgpb.2021.13558.1273

Gitelson, A. A., Kaufman, Y. J., Stark, R., & Rundquist, D. (2002). Novel algorithms for remote estimation of vegetation fraction. *Remote Sensing of Environment*, *80*(1), 76–87. https://doi.org/10.1016/S0034-4257(01)00289-9

Gobu, R., Lal, J. P., & Anandan, A. (2021). Generation Mean Analysis for Yield and Drought Tolerant Traits under Rainfed and Irrigated Conditions in Rice (*Oryza sativa* L.). *International Journal of Environment and Climate Change*, *11*(11), 170–178. https://doi.org/10.9734/IJECC/2021/V11I1130530

Haefele, S. M., Nelson, A., & Hijmans, R. J. (2014). Soil quality and constraints in global rice production. *Geoderma*, *235–236*, 250–259. https://doi.org/10.1016/J.GEODERMA.2014.07.019

Haider, Z., Farooq, U., Naseem, I., Zia, S., & Alamgeer, M. (2015). Impact of Drought Stress on Some Grain Quality Traits in Rice (*Oryza sativa*). *Agricultural Research*, *4*(2), 132–138. https://doi.org/10.1007/s40003-015-0148-8

Hayat, S., Hayat, Q., Alyemeni, M. N., Wani, A. S., Pichtel, J., & Ahmad, A. (2012). Role of proline under changing environments: A review. In *Plant Signaling and Behavior* (Vol. 7, Issue 11). https://doi.org/10.4161/psb.21949

Hayman, B. I. (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity*, *12*, 371–390.

Hayman, B. I. (1960). The separation of epistatic from additive and dominance variation in generation means. II. *Genetica 1960 31:1*, *31*(1), 133–146. https://doi.org/10.1007/BF01984430

Hodges, D. M., DeLong, J. M., Forney, C. F., & Prange, R. K. (1999). Improving the thiobarbituric acid-reactive-substances assay for estimating lipid peroxidation in plant tissues containing anthocyanin and other interfering compounds. *Planta*, *207*(4), 604–611. https://doi.org/10.1007/S004250050524/METRICS

Huang, J., Gu, M., Lai, Z., Fan, B., Shi, K., Zhou, Y. H., Yu, J. Q., & Chen, Z. (2010). Functional analysis of the Arabidopsis PAL gene family in plant growth, development, and response to environmental stress. *Plant Physiology*, *153*(4), 1526–1538. https://doi.org/10.1104/PP.110.157370

Huang, L., Zhang, F., Zhang, F., Wang, W., Zhou, Y., Fu, B., & Li, Z. (2014). Comparative transcriptome sequencing of tolerant rice introgression line and its parents in response to drought stress. *BMC Genomics*, *15*(1), 1–16. https://doi.org/10.1186/1471-2164-15-1026/FIGURES/6

HUANG, M., XU, Y. hui, & WANG, H. qi. (2019). Field identification of morphological and physiological traits in two special mutants with strong tolerance and high sensitivity to drought stress in upland rice (*Oryza sativa* L.). *Journal of Integrative Agriculture*, *18*(5), 970–981. https://doi.org/10.1016/S2095-3119(18)61909-4

IRRI (International Rice Research Institute). (2009). *Introduction to Seed Management*. Http//Www.Knowledgebank.Irri.Org/Qualityseed.

Iseki, K., Homma, K., Shiraiwa, T., Jongdee, B., & Mekwatanakarn, P. (2014). The effects of cross-tolerance to oxidative stress and drought stress on rice dry matter production under aerobic conditions. *Field Crops Research*, *163*, 18–23. https://repository.kulib.kyoto-u.ac.jp

Izquierdo, P., Astudillo, C., Blair, M. W., Iqbal, A. M., Raatz, B., & Cichy, K. A. (2018). Meta-QTL analysis of seed iron and zinc concentration and content in common bean (Phaseolus vulgaris L.). *Theoretical and Applied Genetics*, *131*(8), 1645–1658. https://doi.org/10.1007/s00122-018-3104-8

Jarvis, A., Upadhyaya, H., Aggarwal, P. K., Fujisaka, S., & Anderson, B. (2010). *Climate Change and its Eect on Conservation and Use of Plant Genetic Resources for Food and Agriculture and Associated Biodiversity for Food Security CLL Gowda International Centre for Research in the Semi-Arid Tropics (ICRISAT)*. Food and Agriculture Organisation of the United Nations. https://cgspace.cgiar.org/handle/10568/33384

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of Genetic and Environmental Variability in Soybeans1. *Agronomy Journal*, *47*(7), 314–318. https://doi.org/10.2134/AGRONJ1955.00021962004700070009X

Joseph, L., Kuriachan, P., & Thomas, G. (2008). Is Oryza malampuzhaensis Krish. et Chand. (Poaceae) a valid species? Evidence from morphological and molecular analyses. *Plant Systematics and Evolution*, *270*(1–2), 75–94. https://doi.org/10.1007/S00606-007-0606-2/METRICS

Kaiser, H. F. (1958). The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, *23*(3), 187–200. https://doi.org/10.1007/BF02289233/METRICS

Kato, Y., & Katsura, K. (2014). Rice adaptation to aerobic soils: Physiological considerations and implications for agronomy. *Plant Production Science*, *17*(1), 1–12. https://doi.org/10.1626/pps.17.1

Kaur, S., Seem, K., Duhan, N., Kumar, S., Kaundal, R., & Mohapatra, T. (2023). Transcriptome and Physio-Biochemical Profiling Reveals Differential Responses of Rice Cultivars at Reproductive-Stage Drought Stress. *International Journal of Molecular Sciences*, *24*(2). https://doi.org/10.3390/IJMS24021002/S1

Kearsey, M. J. (1998). The principles of QTL analysis (a minimal mathematics approach). *Journal of Experimental Botany*, *49*(327), 1619–1623. https://doi.org/10.1093/jxb/49.327.1619

Kellogg, E. A. (2009). The evolutionary history of Ehrhartoideae, Oryzeae, and Oryza. In *Rice* (Vol. 2, Issue 1, pp. 1–14). https://doi.org/10.1007/s12284-009-9022-2

Khahani, B., Tavakol, E., Shariati, V., & Rossini, L. (2021). Meta-QTL and ortho-MQTL analyses identified genomic regions controlling rice yield, yield-related traits and root architecture under water deficit conditions. *Scientific Reports*, *11*(1), 6942. https://doi.org/10.1038/s41598-021-86259-2

Khan, F., Upreti, P., Singh, R., Shukla, P. K., & Shirke, P. A. (2017). Physiological performance of two contrasting rice varieties under water stress. *Physiology and Molecular Biology of Plants*, *23*(1), 85–97. https://doi.org/10.1007/s12298-016-0399-2

Khowaja, F. S., Norton, G. J., Courtois, B., & Price, A. H. (2009). Improved resolution in the position of drought-related QTLs in a single mapping population of rice by meta-analysis. *BMC Genomics*, *10*(1), 276. https://doi.org/10.1186/1471-2164-10-276

Kim, S. C., & Rieseberg, L. H. (1999). Genetic architecture of species differences in annual sunflowers: implications for adaptive trait introgression. *Genetics*, *153*(2), 965. https://doi.org/10.1093/GENETICS/153.2.965

Koide, Y., Sakaguchi, S., Uchiyama, T., Ota, Y., Tezuka, A., Nagano, A. J., Ishiguro, S., Takamure, I., & Kishima, Y. (2019). Genetic Properties Responsible for the Transgressive Segregation of Days to Heading in Rice. *G3 Genes|Genomes|Genetics*, *9*(5), 1655–1662. https://doi.org/10.1534/G3.119.201011

Kooyers, N. J. (2015). The evolution of drought escape and avoidance in natural herbaceous populations. *Plant Science: An International Journal of Experimental Plant Biology*, *234*, 155–162. https://doi.org/10.1016/J.PLANTSCI.2015.02.012

Kumar, A., Bernier, J., Verulkar, S., Lafitte, H. R., & Atlin, G. N. (2008). Breeding for drought tolerance: Direct selection for yield, response to selection and use of drought-tolerant donors in upland and lowland-adapted populations. *Field Crops Research*, *107*(3), 221–231. https://doi.org/10.1016/J.FCR.2008.02.007

Kumar, A., Dixit, S., Ram, T., Yadaw, R. B., Mishra, K. K., & Mandal, N. P. (2014). Breeding high-yielding drought-tolerant rice: genetic variations and conventional and molecular approaches. *Journal of Experimental Botany*, *65*(21), 6265. https://doi.org/10.1093/JXB/ERU363

Kumar, R., Venuprasad, R., & Atlin, G. N. (2007). Genetic analysis of rainfed lowland rice drought tolerance under naturally-occurring stress in eastern India: Heritability and QTL effects. *Field Crops Research*, *103*(1), 42–52. https://doi.org/10.1016/J.FCR.2007.04.013

Kumar Verma, S., Saxena, R. R., Ratna Saxena, R., Xalxo, M. S., & Balkrishna Verulkar, S. (2014). QTL for grain yield under water stress and non-stress conditions over years in rice (Oryza sativa L.). In *AJCS* (Vol. 8, Issue 6).

Lafitte, H. R., Blum, A., & Atlin, G. (2003). Using Secondary Traits to Help Identify Drought-Tolerant Genotypes. In K. S. Fischer, R. H. Lafitte, S. Fukai, G. Atlin, & B. Hardy (Eds.), *Breeding Rice for Drought-Prone Environments* (pp. 37–48). International Rice Research Institute.

Lagos, J., Osinski, J., & Sylla, F. (2018). *Senegal Grain and Feed Annual :2018 West Africa Rice Annual*. https://gain.fas.usda.gov/#/home

Lamo, J. (2010). *Genetic Studies on Drought Tolerance and Grain Shattering in Rice* [PhD, University of KwaZulu-Natal]. https://researchspace.ukzn.ac.za/handle/10413/735?show=full

Lanceras, J. C., Pantuwan, G., Jongdee, B., & Toojinda, T. (2004). Quantitative trait loci associated with drought tolerance at reproductive stage in rice. *Plant Physiology*, *135*(1), 384–399. https://doi.org/10.1104/pp.103.035527

Lang, N. T., & Buu, B. C. (2008). FINE MAPPING FOR DROUGHT TOLERANCE IN RICE (Oryza sativa L.). *Omonrice*, *16*, 9–15.

Larkin, D. L., Lozada, D. N., & Mason, R. E. (2019). Genomic selection—considerations for successful implementation in wheat breeding programs. In *Agronomy* (Vol. 9, Issue 9). MDPI AG. https://doi.org/10.3390/agronomy9090479

Lei, L., Zheng, H. L., Wang, J. G., Liu, H. L., Sun, J., Zhao, H. W., Yang, L. M., & Zou, D. T. (2018). Genetic dissection of rice (*Oryza sativa* L.) tiller, plant height, and grain yield based on QTL mapping and metaanalysis. *Euphytica*, *214*(7), 1–17. https://doi.org/10.1007/s10681-018-2187-2

Lisar, S., Seyed Y., Motafakkerazad, R., M., M., & M. Rahm, I. M. (2012). Water Stress in Plants: Causes, Effects and Responses. In *Water Stress*. InTech. https://doi.org/10.5772/39363

Liu, H., Mei, H., Yu, X., Zou, G., Liu, G., & Luo, L. (2006). Towards improving the drought tolerance of rice in China. *Plant Genetic Resources*, *4*(1), 47–53. https://doi.org/10.1079/PGR2006111

Liu, N., Xue, Y., Guo, Z., Li, W., & Tang, J. (2016). Genome-wide association study identifies candidate genes for starch content regulation in Maize Kernels. *Frontiers in Plant Science*, *7*(JULY2016), 1046. https://doi.org/10.3389/FPLS.2016.01046/BIBTEX

Liu, W. Y., Wang, M. M., Huang, J., Tang, H. J., Lan, H. X., & Zhang, H. S. (2009). The OsDHODH1 Gene is Involved in Salt and Drought Tolerance in Rice. *Journal of Integrative Plant Biology*, *51*(9), 825–833. https://doi.org/10.1111/J.1744-7909.2009.00853.X

Londo, J. P., Chiang, Y.-C., Hung, K.-H., Chiang, T.-Y., & Schaal, B. A. (2006). *Phylogeography of Asian wild rice, Oryza rufipogon, reveals multiple independent domestications of cultivated rice, Oryza sativa*. www.pnas.orgcgidoi10.1073pnas.0603152103

Lu, G., Gao, C., Zheng, X., & Han, B. (2009). Identification of OsbZIP72 as a positive regulator of ABA response and drought tolerance in rice. *Planta*, *229*(3), 605–615. https://doi.org/10.1007/S00425-008-0857-3/FIGURES/7

Luo, L. J. (2010). Breeding for water-saving and drought-resistance rice (WDR) in China. *Journal of Experimental Botany*, *61*(13), 3509–3517. https://doi.org/10.1093/JXB/ERQ185

Mafakheri, A., Siosemardeh, A., Bahramnejad, B., Struik, P. C., & Sohrabi, Y. (2010). *Effect of drought stress on yield, proline and chlorophyll contents in three chickpea cultivars*.

Maisura, Chozin, M., Lubis, I., Junaedi, A., & Ehara, H. (2014). SOME PHYSIOLOGICAL CHARACTER RESPONSES OF RICE UNDER DROUGHT CONDITIONS IN A PADDY SYSTEM. *Undefined*.

Manickavelu, A., Nadarajan, N., Ganesh, S. K., Gnanamalar, R. P., & Babu, R. C. (2006). Drought tolerance in rice: morphological and molecular genetic consideration. *Plant Growth Regulation 2006 50:2*, *50*(2), 121–138. https://doi.org/10.1007/S10725-006-9109-3

Mansur, L. M., Lark, K. G., Kross, H., & Oliveira, A. (1993). Interval mapping of quantitative trait loci for reproductive, morphological, and seed traits of soybean (Glycine max L.). *Theoretical and Applied Genetics*, *86*(8), 907–913. https://doi.org/10.1007/BF00211040/METRICS

Mather, K. (1949). *Biometrical Genetics: The Study of Continuous Variation* (1st Edition). Metuen and Co.Ltd. https://www.abebooks.com/first-edition/Biometrical-Genetics-Study-Continuous-Variation-Mather/30685509296/bd

McCouch, S. R., Teytelman, L., Xu, Y., Lobos, K. B., Clare, K., Walton, M., Fu, B., Maghirang, R., Li, Z., Xing, Y., Zhang, Q., Kono, I., Yano, M., Fjellstrom, R., DeClerck, G., Schneider, D., Cartinhour, S., Ware, D., & Stein, L. (2002). Development and mapping of 2240 new SSR markers for rice (*Oryza sativa* L.). *DNA Research*, *9*(6), 199–207. https://doi.org/10.1093/dnares/9.6.199

McCouch, S. R., Zhao, K., Wright, M., Tung, C.-W., Ebana, K., Thomson, M., Reynolds, A., Wang, D., DeClerck, G., Ali, Md. L., McClung, A., Eizenga, G., & Bustamante, C. (2010). Development of genome-wide SNP assays for rice. *Breeding Science*, *60*(5), 524–535. https://doi.org/10.1270/jsbbs.60.524

Melandri, G., AbdElgawad, H., Floková, K., Jamar, D. C., Asard, H., Beemster, G. T. S., Ruyter-Spira, C., & Bouwmeester, H. J. (2021). Drought tolerance in selected aerobic and upland rice varieties is driven by different metabolic and antioxidative responses. *Planta*, *254*(1). https://doi.org/10.1007/S00425-021-03659-4

Mendez del Villar, P., & Lançon, F. (2015). West African rice development: Beyond protectionism versus liberalization? *Global Food Security*, *5*, 56–61. https://doi.org/10.1016/J.GFS.2014.11.001

Mitra, J. (2001). Genetics and Genetic Improvement of Drought Tolerance in Crop Plants. *Current Science*, *80*, 758–762.

Mohidem, N. A., Hashim, N., Shamsudin, R., & Man, H. C. (2022). Rice for Food Security: Revisiting Its Production, Diversity, Rice Milling Process and Nutrient Content. In *Agriculture (Switzerland)* (Vol. 12, Issue 6). MDPI. https://doi.org/10.3390/agriculture12060741

Monteoliva, M. I., Guzzo, M. C., & Posada, G. A. (2021). Breeding for Drought Tolerance by Monitoring Chlorophyll Content. *Gene Technology*, *10*(3), 1–11. https://doi.org/10.35248/2329-6682.21.10.165

Morinaga, T. (1968). Origin and Geographical Distribution of Japanese Rice. *Jarq-Japan Agricultural Research Quarterly*.

Mumtaz, M. Z., Saqib, M., Abbas, G., Akhtar, J., & Ul-Qamar, Z. (2020). Drought Stress Impairs Grain Yield and Quality of Rice Genotypes by Impaired Photosynthetic Attributes and K Nutrition. *Rice Science*, *27*(1), 5–9. https://doi.org/10.1016/J.RSCI.2019.12.001

Munns, R., & Richards, R. A. (2007). Recent advances in breeding wheat for drought and salt stresses. *Advances in Molecular Breeding Toward Drought and Salt Tolerant Crops*, 565–585. https://doi.org/10.1007/978-1-4020-5578-2_22/COVER

Nadarajan, N., Manivannan, N., & Gunasekaran, M. (2016). *Quantitative genetics and Biometrical Techniques in Plant breeding* (1st ed.). Kalyani Publishers. http://kalyanipublishers.co.in/index.php/welcome/searchbook

Nahar, S., Sahoo, L., & Tanti, B. (2018). Screening of drought tolerant rice through morpho-physiological and biochemical approaches. *Biocatalysis and Agricultural Biotechnology*, *15*, 150–159. https://doi.org/10.1016/J.BCAB.2018.06.002

Namuco, O. S., Cairns, J. E., & Johnson, D. E. (2009). Investigating early vigour in upland rice (Oryza sativa L.): Part I. Seedling growth and grain yield in competition with weeds. *Field Crops Research*, *113*(3), 197–206. https://doi.org/10.1016/J.FCR.2009.05.008

Naser, M. A., Khosla, R., Longchamps, L., & Dahal, S. (2020). Using NDVI to Differentiate Wheat Genotypes Productivity Under Dryland and Irrigated Conditions. *Remote Sensing 2020, Vol. 12, Page 824*, *12*(5), 824. https://doi.org/10.3390/RS12050824

Nasrin, S., Saha, S., Hena, H., And, B., & Samad, R. (2020). Impacts of drought stress on growth, protein, proline, pigment content and antioxidant enzyme activities in rice (Oryza sativa L. var. BRRI dhan-24). *Dhaka University Journal of Biological Sciences*, *29*(1), 117–123. https://doi.org/10.3329/DUJBS.V29I1.46537

Ndikuryayo, C., Ndayiragije, A., Kilasi, N. L., & Kusolwa, P. (2023). Identification of Drought Tolerant Rice (*Oryza Sativa* L.) Genotypes with Asian and African Backgrounds. *Plants*, *12*(4), 922. https://doi.org/10.3390/PLANTS12040922/S1

Ndjiondjop, M. N., Cisse, F., Girma, G., Sow, M., Bocco, R., Djedatin, G., & Blandine, F. (2010). Morpho-agronomic and molecular characterisation of Oryza glaberrima germplasm from Mali. *African Journal of Biotechnology*, *9*(44), 7409–7417. http://www.academicjournals.org/AJB

Ndjiondjop, M. N., Futakuchi, K., Cisse, F., Baimey, H., & Bocco, R. (2012). Field Evaluation of Rice Genotypes from the Two Cultivated Species (*Oryza sativa* L. and *Oryza glaberrima* Steud.) and Their Interspecifics for Tolerance to Drought. *Crop Science*, *52*(2), 524–538. https://doi.org/10.2135/CROPSCI2011.05.0287

Ndjiondjop, M. N., Wambugu, P. W., Sangare, J. R., & Gnikoua, K. (2018). The effects of drought on rice cultivation in sub-Saharan Africa and its mitigation: A review. *African Journal of Agricultural Research*, *13*(25), 1257–1271. https://doi.org/10.5897/ajar2018.12974

Ning, J., Li, X., Hicks, L. M., & Xiong, L. (2010). A Raf-Like MAPKKK Gene DSM1 Mediates Drought Resistance through Reactive Oxygen Species Scavenging in Rice. *Plant Physiology*, *152*(2), 876–890. https://doi.org/10.1104/PP.109.149856

Nirubana, V., Palaniyappan, S., Ramamoorthy, P., Karthikeyan, M., & Deepika, C. (2021). *Transgressive segregation and its importance in crop improvement*. https://ssrn.com/abstract=3800538

Nishimura, K., Motoki, K., Yamazaki, A., Takisawa, R., Yasui, Y., Kawai, T., Ushijima, K., Nakano, R., & Nakazaki, T. (2022). MIG-seq is an effective method for high-throughput genotyping in wheat (Triticum spp.). *DNA Research*, *29*(2). https://doi.org/10.1093/dnares/dsac011

OECD (Organisation for Economic Co-operation and Development). (2022). *Revised Consensus Document on the Biology of Rice (Oryza sativa L.)*. www.oecd.org/env/ehs/biotrack/

Olivoto, T., & Nardino, M. (2021). MGIDI: toward an effective multivariate selection in biological experiments. *Bioinformatics*, *37*(10), 1383–1389. https://doi.org/10.1093/BIOINFORMATICS/BTAA981

Ota, Y., Ishiguro, S., Aoyama, E., Aiba, R., Iwashiro, R., Tanabata, T., Takamure, I., Fujino, K., & Kishima, Y. (2014). Isolation of a major genetic interaction associated with an extreme phenotype using assorted F2 populations in rice. *Molecular Breeding*, *33*(4), 997–1003. https://doi.org/10.1007/s11032-013-9998-6

Palanog, A. D., Swamy, B. P. M., Shamsudin, N. A. A., Dixit, S., Hernandez, J. E., Boromeo, T. H., Cruz, P. C. S., & Kumar, A. (2014). Grain yield QTLs with consistent-effect under reproductive-stage drought stress in rice. *Field Crops Research*, *161*, 46–54. https://doi.org/10.1016/J.FCR.2014.01.004

Pantalião, G., Narciso, M., Guimarães, C., Castro, A., Colombari, J., Breseghello, F., Rodrigues, L., Vianello, R., Borba, T., & Brondani, C. (2016). Genome wide association study (GWAS) for grain yield in rice cultivated under water deficit. *Genetica*, *144*(6), 651–664. https://doi.org/10.1007/S10709-016-9932-Z

Pantuwan, G., Fukai, S., Cooper, M., Rajatasereekul, S., & O'Toole, J. C. (2002). Yield response of rice (*Oryza sativa* L.) genotypes to different types of drought under rainfed lowlands: Part 1. Grain yield and yield components. *Field Crops Research*, *73*(2–3), 153–168. https://doi.org/10.1016/S0378-4290(01)00187-3

Park, S. Y., & Jeong, D. H. (2023). Comprehensive Analysis of Rice Seedling Transcriptome during Dehydration and Rehydration. *International Journal of Molecular Sciences*, *24*(9). https://doi.org/10.3390/IJMS24098439/S1

Phyu, P., Islam, M. R., Sta Cruz, P. C., Collard, B. C. Y., & Kato, Y. (2020). Use of NDVI for indirect selection of high yield in tropical rice breeding. *Euphytica*, *216*(5), 1–9. https://doi.org/10.1007/S10681-020-02598-7/TABLES/5

Price, A. H., Steele, K. A., Gorham, J., Bridges, J. M., Moore, B. J., Evans, J. L., Richardson, P., & Jones, R. G. W. (2002). Upland rice grown in soil-filled chambers and exposed to contrasting water-deficit regimes: I. Root distribution, water use and plant water status. *Field Crops Research*, *76*(1), 11–24. https://doi.org/10.1016/S0378-4290(02)00012-6

Pujar, M., Govindaraj, M., Gangaprasad, S., Kanatti, A., Gowda, T. H., Dushyantha Kumar, B. M., & Satish, K. M. (2022). Generation Mean Analysis Reveals the Predominant Gene Effects for Grain Iron and Zinc Contents in Pearl Millet. *Frontiers in Plant Science*, *12*, 3269. https://doi.org/10.3389/FPLS.2021.693680/BIBTEX

Qiu, D., Xiao, J., Xie, W., Liu, H., Li, X., Xiong, L., & Wang, S. (2008). Rice Gene Network Inferred from Expression Profiling of Plants Overexpressing OsWRKY13, a Positive Regulator of Disease Resistance. *Molecular Plant*, *1*(3), 538–551. https://doi.org/10.1093/MPLANT/SSN012

Rajurkar, A. B., Muthukumar, C., Bharathi, A., Thomas, H. B., & Babu, R. C. (2019). Saturation mapping of consistent QTLs for yield and days to flowering under drought using locally adapted landrace in rice (*Oryza sativa* L.). *NJAS - Wageningen Journal of Life Sciences*, *88*, 66–75. https://doi.org/10.1016/j.njas.2018.10.002

Rao, N. G. (1980). *Statistics for Agricultural Sciences Second Edition* (Second Edition). New Delhi: Oxford and IBH Publishing Co. Pvt. Ltd.

Rasheed, A., Hao, Y., Xia, X., Khan, A., Xu, Y., Varshney, R. K., & He, Z. (2017). Crop Breeding Chips and Genotyping Platforms: Progress, Challenges, and Perspectives. In *Molecular Plant* (Vol. 10, Issue 8, pp. 1047–1064). Cell Press. https://doi.org/10.1016/j.molp.2017.06.008

Ravindra Babu, V., Shreya, K., Singh Dangi, K., Usharani, G., & Nagesh, P. (2012). Genetic Variability Studies for Qualitative and Quantitative traits in Popular Rice (*Oryza sativa* L.) Hybrids of India. *International Journal of Scientific and Research Publications*, *2*(6). www.ijsrp.org

Ray, D. K., Gerber, J. S., Macdonald, G. K., & West, P. C. (2015). Climate variation explains a third of global crop yield variability. *Nature Communications*, *6*(1), 1–9. https://doi.org/10.1038/ncomms6989

Rebolledo, M., Dingkuhn, M., Courtois, B., Gibon, Y., Clément-Vidal, A., Cruz, D., Duitama, J., Lorieux, M., & Luquet, D. (2015). Phenotypic and genetic dissection of component traits for early vigour in rice using plant growth modelling, sugar content analyses and association mapping. *Journal of Experimental Botany*, *66*(18), 5555–5566. https://doi.org/10.1093/JXB/ERV258

Reddyyamini, B., Hariprasad Reddy, K., Narayana Reddy, V. L., Ramesh Babu, P., & Sudhakar, P. (2019). Transgressive Segregation for Yield and Its Component Traits in Rice (Oryza sativa L.). *International Journal of Current Microbiology and Applied Sciences*, *8*(06), 2450–2455. https://doi.org/10.20546/ijcmas.2019.806.292

Reynolds, M., Molero, G., Mollins, J., & Braun, H. (2015). *TRIGO (Wheat) Yield Potential WORKSHOP 2015 Proceedings of the International*. www.cimmyt.org

RICOWAS. (2021). *Scaling-up climate-resilient rice production in West Africa*. https://www.adaptation-fund.org/wp-content/uploads/2021/05/OSS_RIE-Regional_Full_Proposal-RICOWAS_Project-Benin-al-26April2021.pdf

Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of Heritability and the Degree of Dominance in Corn1. *Agronomy Journal*, *41*(8), 353–359. https://doi.org/10.2134/AGRONJ1949.00021962004100080005X

Rouf Mir, R., Zaman-Allah, M., Sreenivasulu, N., Trethowan, R., Varshney, R. K., Mir Á M Zaman-Allah Á R K Varshney, R. R., Mir, R. R., Zaman-Allah, M., Sreenivasulu, N., Trethowan, R., & Varshney, R. K. (2012). Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. *Theoretical and Applied Genetics 2012 125:4*, *125*(4), 625–645. https://doi.org/10.1007/S00122-012-1904-9

Roujean, J. L., & Breon, F. M. (1995). Estimating PAR absorbed by vegetation from bidirectional reflectance measurements. *Remote Sensing of Environment*, *51*(3), 375–384. https://doi.org/10.1016/0034-4257(94)00114-3

Rouse, J. W. , Jr., Haas, R. H., Schell, J. A., Deering, D. W., Haas, R. H., Schell, J. A., & Deering, D. W. (1974). Monitoring vegetation systems in the Great Plains with ERTS. *NASA. Goddard Space Flight Center 3d ERTS-1 Symp., Vol. 1, Sect. A*.

Sabar, M., Shabir, G., Shah, S. M., Aslam, K., Naveed, S. A., & Arif, M. (2019). Identification and mapping of QTLs associated with drought tolerance traits in rice by a cross between super Basmati and IR55419-04. *Breeding Science*, *69*(1), 169–178. https://doi.org/10.1270/jsbbs.18068

Saddique, M. A. B., Ali, Z., Sher, M. A., Farid, B., Ikram, R. M., & Ahmad, M. S. (2020). Proline, Total Antioxidant Capacity, and OsP5CS Gene Activity in Radical and Plumule of Rice are Efficient Drought Tolerance Indicator Traits. *International Journal of Agronomy, 2020*. https://doi.org/10.1155/2020/8862792

Sahoo, S. K., Dash, G. K., Guhey, A., Baig, M. J., Barik, M., Parida, S., & Swain, P. (2020). Phenological, Physiological and yield markers as efficient tools to identify drought tolerant rice genotypes in Eastern India. *BioRxiv*, 2020.05.29.122929. https://doi.org/10.1101/2020.05.29.122929

Saijo, Y., Hata, S., Kyozuka, J., Shimamoto, K., & Izui, K. (2000). Over-expression of a single Ca2+-dependent protein kinase confers both cold and salt/drought tolerance on rice plants. *The Plant Journal*, *23*(3), 319–327. https://doi.org/10.1046/J.1365-313X.2000.00787.X

Saikumar, S., Kalmeshwer Gouda, P., Saiharini, A., Varma, C. M. K., Vineesha, O., Padmavathi, G., & Shenoy, V. V. (2014). Major QTL for enhancing rice grain yield under lowland reproductive drought stress identified using an *O. sativa/O. glaberrima* introgression line. *Field Crops Research*, *163*, 119–131. https://doi.org/10.1016/J.FCR.2014.03.011

Salleh, M. S., Nordin, M. S., Puteh, A., Shahari, R., Zainuddin, Z., Ab-Ghaffar, M. B., & Shamsudin, N. A. A. (2022). Drought-Induced Changes in The Flowering Capacity, Anthesis Quality and Seed Set in Rice (*Oryza sativa* L.). *Tropical Life Sciences Research*, *33*(2), 239. https://doi.org/10.21315/TLSR2022.33.2.11

Sandhu, N., & Kumar, A. (2017). Bridging the rice yield gaps under drought: QTLs, genes, and their use in breeding programs. In *Agronomy* (Vol. 7, Issue 2). MDPI AG. https://doi.org/10.3390/agronomy7020027

Sangodele, E. A., Hanchinal, R. R., Hanamaratti, N. G., Shenoy, V., & Kumar, V. M. (2014). Analysis of drought tolerant QTL linked to physiological and productivity component traits under water-stress and non-stress in rice (*Oryza sativa* L.). *International Journal of Current Research and Academic Review*, *2*(5), 108–113. www.ijcrar.com

Sautter, C., Poletti, S., Zhang, P., & Gruissem, W. (2006). Biofortification of essential nutritional compounds and trace elements in rice and cassava. *Proceedings of the Nutrition Society*, *65*(2), 153–159. https://doi.org/10.1079/PNS2006488

Scheben, A., Batley, J., & Edwards, D. (2017). Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. In *Plant Biotechnology Journal* (Vol. 15, Issue 2, pp. 149–161). Blackwell Publishing Ltd. https://doi.org/10.1111/pbi.12645

Selamat, N., & Nadarajah, K. K. (2021). Meta-Analysis of Quantitative Traits Loci (QTL) Identified in Drought Response in Rice (*Oryza sativa* L.). *Plants 2021, Vol. 10, Page 716*, *10*(4), 716. https://doi.org/10.3390/PLANTS10040716

Sellamuthu, R., Ranganathan, C., & Serraj, R. (2015). Mapping QTLs for reproductive-stage drought resistance traits using an advanced backcross population in upland rice. *Crop Science*, *55*(4), 1524–1536. https://doi.org/10.2135/cropsci2014.05.0344

Serraj, R., Kumar, A., McNally, K. L., Slamet-Loedin, I., Bruskiewich, R., Mauleon, R., Cairns, J., & Hijmans, R. J. (2009). Chapter 2 Improvement of Drought Resistance in Rice. In *Advances in Agronomy* (Vol. 103, pp. 41–99). Academic Press Inc. https://doi.org/10.1016/S0065-2113(09)03002-8

SES. (2002). Standard Evaluation System for Rice. In *Standard Evaluation System for Rice*. http://www.knowledgebank.irri.org/images/docs/rice-standard-evaluation-system.pdf.

Seyoum, M., Alamerew, S., & Bantte, K. (2012). Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Sciences*, *7*(1), 13–22. https://doi.org/10.3923/JPS.2012.13.22

Shahryari, R., Gurbanov, E., Gadimov, A., & Hassanpanah, D. (2008). Tolerance of 42 bread wheat genotypes to drought stress after anthesis. *Pakistan Journal of Biological Sciences*, *11*(10), 1330–1335. https://doi.org/10.3923/pjbs.2008.1330.1335

Shavrukov, Y., Kurishbayev, A., Jatayev, S., Shvidchenko, V., Zotova, L., Koekemoer, F., De Groot, S., Soole, K., & Langridge, P. (2017). Early Flowering as a Drought Escape Mechanism in Plants: How Can It Aid Wheat Production? *Frontiers in Plant Science*, *8*. https://doi.org/10.3389/FPLS.2017.01950

Singh, A. K., Mall, A. K., Singh, P. K., & Verma, O. P. (2010). Interrelationship of genetics parameters for quantitative and physiological traits in rice under irrigated and drought conditions. In *Oryza* (Vol. 47, Issue 2). SHORT COMMUNICATION. www.pdffactory.com

Singh, N., Jayaswal, P. K., Panda, K., Mandal, P., Kumar, V., Singh, B., Mishra, S., Singh, Y., Singh, R., Rai, V., Gupta, A., Raj Sharma, T., & Singh, N. K. (2015). Single-copy gene based 50 K SNP chip for genetic studies and molecular breeding in rice. *Scientific Reports*, *5*(1), 11600. https://doi.org/10.1038/srep11600

Solis, J., Gutierrez, A., Mangu, V., Sánchez Timm, E., Bedre, R., Linscombe, S., & Baisakh, N. (2018). Genetic mapping of quantitative trait loci for grain yield under drought in rice under controlled greenhouse conditions. *Frontiers in Chemistry*, *5*, 129. https://doi.org/10.3389/fchem.2017.00129

Soullier, G., Demont, M., Arouna, A., Lançon, F., & Mendez del Villar, P. (2020). The state of rice value chain upgrading in West Africa. *Global Food Security*, *25*, 100365. https://doi.org/10.1016/J.GFS.2020.100365

Srividhya, A., Vemireddy, L. R., Sridhar, S., Jayaprada, M., Ramanarao, P. V., Hariprasad, A. S., Reddy, H. K., Anuradha, G., & Siddiq, E. (2011). Molecular mapping of QTLs for yield and its components under two water supply conditions in rice (Oryza sativa L.). *Journal of Crop Science and Biotechnology 2011 14:1*, *14*(1), 45–56. https://doi.org/10.1007/S12892-010-0023-X

Suji, K. K., Biji, K. R., Poornima, R., Prince, K. S. J., Amudha, K., Kavitha, S., Mankar, S., & Babu, R. C. (2011). Mapping QTLs for Plant Phenology and Production Traits Using Indica Rice (*Oryza sativa* L.) Lines Adapted to Rainfed Environment. *Molecular Biotechnology 2011 52:2*, *52*(2), 151–160. https://doi.org/10.1007/S12033-011-9482-7

Swamy, B. M., Vikram, P., Dixit, S., Ahmed, H. U., & Kumar, A. (2011). Meta-analysis of grain yield QTL identified during agricultural drought in grasses showed consensus. *BMC Genomics*, *12*(1), 319. https://doi.org/10.1186/1471-2164-12-319

Swamy, B. P. M., Shamsudin, N. A. A., Rahman, S. N. A., Mauleon, R., Ratnam, W., Sta. Cruz, M. T., & Kumar, A. (2017). Association Mapping of Yield and Yield-related Traits Under Reproductive Stage Drought Stress in Rice (Oryza sativa L.). *Rice*, *10*(1), 1–13. https://doi.org/10.1186/s12284-017-0161-6

Thanh, P. T., Sripichitt, P., Chanprame, S., & Peyachoknagul, S. (2006). Transfer of Drought Resistant Character from Wild Rice (*Oryza meridionalis* and *Oryza nivara*) to Cultivated Rice (*Oryza sativa* L.) by Backcrossing and Immature Embryo Culture. *Agriculture and*

Natural Resources, *40*(3), 582–594. https://li01.tci-thaijo.org/index.php/anres/article/view/243709

Thapa, S., Rudd, J. C., Xue, Q., Bhandari, M., Reddy, S. K., Jessup, K. E., Liu, S., Devkota, R. N., Baker, J., & Baker, S. (2019). Use of NDVI for characterizing winter wheat response to water stress in a semi-arid environment. *Journal of Crop Improvement*, *33*(5), 633–648. https://doi.org/10.1080/15427528.2019.1648348

Thomson, M. J., Singh, N., Dwiyanti, M. S., Wang, D. R., Wright, M. H., Perez, F. A., DeClerck, G., Chin, J. H., Malitic-Layaoen, G. A., Juanillas, V. M., Dilla-Ermita, C. J., Mauleon, R., Kretzschmar, T., & McCouch, S. R. (2017). Large-scale deployment of a rice 6 K SNP array for genetics and breeding applications. *Rice*, *10*(1), 40. https://doi.org/10.1186/s12284-017-0181-2

Tiwari, D., & Pandey, P. (2011). Studies on genetic variability for yield components in rice (*Oryza sativa* L.) CSIR Arom Mission View project Fast-Track Translational Project FTT-5 (Calliterpenone for enhancing crop yields) View project. *Advances in Agriculture & Botanics-International Journal of the Bioflux Society*, *3*(1). http://www.aab.bioflux.com.ro

Tiwari, P., Srivastava, D., Chauhan, A. S., Indoliya, Y., Singh, P. K., Tiwari, S., Fatima, T., Mishra, S. K., Dwivedi, S., Agarwal, L., Singh, P. C., Asif, M. H., Tripathi, R. D., Shirke, P. A., Chakrabarty, D., Chauhan, P. S., & Nautiyal, C. S. (2021). Root system architecture, physiological analysis and dynamic transcriptomics unravel the drought-responsive traits in rice genotypes. *Ecotoxicology and Environmental Safety*, *207*, 111252. https://doi.org/10.1016/J.ECOENV.2020.111252

Tong, S., Ashikari, M., Nagai, K., & Pedersen, O. (2023). Can the Wild Perennial, Rhizomatous Rice Species *Oryza longistaminata* be a Candidate for De Novo Domestication? In *Rice* (Vol. 16, Issue 1). Springer. https://doi.org/10.1186/s12284-023-00630-7

Torres, R. O., & Henry, A. (2018). Yield stability of selected rice breeding lines and donors across conditions of mild to moderately severe drought stress. *Field Crops Research*, *220*, 37–45. https://doi.org/10.1016/J.FCR.2016.09.011

Trijatmiko, K. R., Supriyanta, Prasetiyono, J., Thomson, M. J., Vera Cruz, C. M., Moeljopawiro, S., & Pereira, A. (2014). Meta-analysis of quantitative trait loci for grain yield and component traits under reproductive-stage drought stress in an upland rice population. *Molecular Breeding*, *34*(2), 283–295. https://doi.org/10.1007/s11032-013-0012-0

Tung, C. W., Zhao, K., Wright, M. H., Ali, M. L., Jung, J., Kimball, J., Tyagi, W., Thomson, M. J., McNally, K., Leung, H., Kim, H., Ahn, S. N., Reynolds, A., Scheffler, B., Eizenga, G., McClung, A., Bustamante, C., & McCouch, S. R. (2010). Development of a research platform for dissecting phenotype-genotype associations in rice (Oryza spp.). *Rice*, *3*(4), 205–217. https://doi.org/10.1007/s12284-010-9056-5

Turral, H., Burke, J., & Faurès, J. M. (2011). *Climate change, water and food security*. FAO Water Reports No. 36, Food and Agriculture Organization of the United Nations. http://www.fao.org/3/i2096e/i2096e00.htm

Tuteja, N. (2007). Abscisic Acid and abiotic stress signaling. *Plant Signaling & Behavior*, *2*(3), 135–138. https://doi.org/10.4161/PSB.2.3.4156

Udvardi, M. K., Czechowski, T., & Scheible, W. R. (2008). Eleven Golden Rules of Quantitative RT-PCR. *The Plant Cell*, *20*(7), 1736–1737. https://doi.org/10.1105/TPC.108.061143

Umego, C., Ntui, V. O., Ita, E. E., Opara, C., & Uyoh, E. A. (2020). Screening of Rice Accessions for Tolerance to Drought and Salt Stress Using Morphological and Physiological Parameters. *American Journal of Plant Sciences*, *11*(12), 2080–2102. https://doi.org/10.4236/ajps.2020.1112147

Van, K., & McHale, L. (2017). Meta-Analyses of QTLs Associated with Protein and Oil Contents and Compositions in Soybean [Glycine max (L.) Merr.] Seed. *International Journal of Molecular Sciences*, *18*(6), 1180. https://doi.org/10.3390/ijms18061180

van Oort, P. A. J. (2018). Mapping abiotic stresses for rice in Africa: Drought, cold, iron toxicity, salinity and sodicity. *Field Crops Research*, *219*, 55–75. https://doi.org/10.1016/J.FCR.2018.01.016

Van Oort, P. A. J., Saito, K., Tanaka, A., Amovin-Assagba, E., Van Bussel, L. G. J., Van Wart, J., De Groot, H., Van Ittersum, M. K., Cassman, K. G., & Wopereis, M. C. S. (2015). Assessment of rice self-sufficiency in 2025 in eight African countries. In *Global Food Security* (Vol. 5, pp. 39–49). Elsevier B.V. https://doi.org/10.1016/j.gfs.2015.01.002

Varshney, R. K., Singh, V. K., Kumar, A., Powell, W., & Sorrells, M. E. (2018). Can genomics deliver climate-change ready crops? In *Current Opinion in Plant Biology* (Vol. 45, Issue Pt B, pp. 205–211). Elsevier Ltd. https://doi.org/10.1016/j.pbi.2018.03.007

Venkateshwarlu, C., Kole, P. C., Paul, P. J., Singh, A. K., Singh, V. K., & Kumar, A. (2022). Capturing Genetic Variability and Identification of Promising Drought-Tolerant Lines in Exotic Landrace Derived Population Under Reproductive Drought Stress in Rice. *Frontiers in Plant Science*, *13*, 115. https://doi.org/10.3389/FPLS.2022.814774/BIBTEX

Venuprasad, R., Dalid, C. O., Del Valle, M., Zhao, D., Espiritu, M., Sta Cruz, M. T., Amante, M., Kumar, A., & Atlin, G. N. (2009). Identification and characterization of large-effect quantitative trait loci for grain yield under lowland drought stress in rice using bulk-segregant analysis. *Theoretical and Applied Genetics*, *120*(1), 177–190. https://doi.org/10.1007/s00122-009-1168-1

Verma, R. K., Chetia, S. K., Dey, P. C., Baruah, A. R., & Modi, M. K. (2017). Mapping of QTLs for Grain Yield and its Component Traits under Drought Stress in Elite Rice Variety of Assam. *International Journal of Current Microbiology and Applied Sciences*, *6*(6), 1443–1455. https://doi.org/10.20546/ijcmas.2017.606.169

Veyrieras, J. B., Goffinet, B., & Charcosset, A. (2007). MetaQTL: A package of new computational methods for the meta-analysis of QTL mapping experiments. *BMC Bioinformatics*, *8*(1), 49. https://doi.org/10.1186/1471-2105-8-49

Vigueira, C. C., Qi, X., Song, B. K., Li, L. F., Caicedo, A. L., Jia, Y., & Olsen, K. M. (2019). Call of the wild rice: *Oryza rufipogon* shapes weedy rice evolution in Southeast Asia. *Evolutionary Applications*, *12*(1), 93–104. https://doi.org/10.1111/eva.12581

Vikram, P., Swamy, B. P. M., Dixit, S., Ahmed, H. U., Teresa Sta Cruz, M., Singh, A. K., & Kumar, A. (2011). QDTY1.1, a major QTL for rice grain yield under reproductive-stage drought stress with a consistent effect in multiple elite genetic backgrounds. *BMC Genetics*, *12*. https://doi.org/10.1186/1471-2156-12-89

Wang, C. J., Yang, W., Wang, C., Gu, C., Niu, D. D., Liu, H. X., Wang, Y. P., & Guo, J. H. (2012). Induction of Drought Tolerance in Cucumber Plants by a Consortium of Three Plant Growth-Promoting Rhizobacterium Strains. *PLoS ONE*, *7*(12), 52565. https://doi.org/10.1371/journal.pone.0052565

Wang, M., Yu, Y., Haberer, G., Marri, P. R., Fan, C., Goicoechea, J. L., Zuccolo, A., Song, X., Kudrna, D., Ammiraju, J. S. S., Cossu, R. M., Maldonado, C., Chen, J., Lee, S., Sisneros, N., De Baynast, K., Golser, W., Wissotski, M., Kim, W., … Wing, R. A. (2014). The genome sequence of African rice (*Oryza glaberrima*) and evidence for independent domestication. *Nature Genetics*, *46*(9), 982–988. https://doi.org/10.1038/NG.3044

Wang, W., Mauleon, R., Hu, Z., Chebotarov, D., Tai, S., Wu, Z., Li, M., Zheng, T., Fuentes, R. R., Zhang, F., Mansueto, L., Copetti, D., Sanciangco, M., Palis, K. C., Xu, J., Sun, C., Fu, B., Zhang, H., Gao, Y., … Leung, H. (2018). Genomic variation in 3,010 diverse accessions of Asian cultivated rice. *Nature*, *557*(7703), 43–49. https://doi.org/10.1038/s41586-018-0063-9

Wang, X., Yang, X., Yao, J., Li, Q., Lu, C., & Duan, D. (2023). Genetic linkage map construction and QTL mapping of blade length and width in Saccharina japonica using SSR and SNP markers. *Frontiers in Marine Science*, *10*. https://doi.org/10.3389/fmars.2023.1116412

Warner, J. N. (1952). A Method for Estimating Heritability1. *Agronomy Journal*, *44*(8), 427–430. https://doi.org/10.2134/AGRONJ1952.00021962004400080007X

Wassmann, R., Jagadish, S. V. K., Sumfleth, K., Pathak, H., Howell, G., Ismail, A., Serraj, R., Redona, E., Singh, R. K., & Heuer, S. (2009). Chapter 3 Regional Vulnerability of Climate Change Impacts on Asian Rice Production and Scope for Adaptation. In *Advances in Agronomy* (Vol. 102, pp. 91–133). Academic Press Inc. https://doi.org/10.1016/S0065-2113(09)01003-7

Wing, R. A., Purugganan, M. D., & Zhang, Q. (2018). The rice genome revolution: from an ancient grain to Green Super Rice. *Nature Reviews. Genetics*, *19*(8), 505–517. https://doi.org/10.1038/S41576-018-0024-Z

Wu, L. B., Feng, Y., Zeibig, F., Alam, M. S., & Frei, M. (2021). High throughput analyses of ascorbate-turnover enzyme activities in rice (Oryza sativa L.) seedlings. *Bio-Protocol*, *11*(20). https://doi.org/10.21769/BIOPROTOC.4190

Xiang, Y., Huang, Y., & Xiong, L. (2007). Characterization of Stress-Responsive CIPK Genes in Rice for Stress Tolerance Improvement. *Plant Physiology*, *144*(3), 1416. https://doi.org/10.1104/PP.107.101295

Xiao, J., Cheng, H., Li, X., Xiao, J., Xu, C., & Wang, S. (2013). Rice WRKY13 Regulates Cross Talk between Abiotic and Biotic Stress Signaling Pathways by Selective Binding to Different cis-Elements. *Plant Physiology*, *163*(4), 1868–1882. https://doi.org/10.1104/PP.113.226019

Xing, W., Zhao, H., & Zou, D. (2014). Detection of main-effect and epistatic QTL for yield-related traits in rice under drought stress and normal conditions. *Canadian Journal of Plant Science*, *94*(4), 633–641. https://doi.org/10.4141/CJPS2013-297

Xiong, L. (2013). Abiotic stress resistance. *Genetics and Genomics of Rice*, 193–215. https://doi.org/10.1007/978-1-4614-7903-1_13/COVER

Yadav, S., Sandhu, N., Singh, V. K., Catolos, M., & Kumar, A. (2019). Genotyping-by-sequencing based QTL mapping for rice grain yield under reproductive stage drought stress tolerance. *Scientific Reports*, *9*(1). https://doi.org/10.1038/s41598-019-50880-z

Yadav, S., & Sharma, K. D. (2016). Molecular and Morphophysiological Analysis of Drought Stress in Plants. *Plant Growth*. https://doi.org/10.5772/65246

Yaish, M. W., El-Kereamy, A., Zhu, T., Beatty, P. H., Good, A. G., Bi, Y. M., & Rothstein, S. J. (2010). The APETALA-2-Like Transcription Factor OsAP2-39 Controls Key Interactions between Abscisic Acid and Gibberellin in Rice. *PLOS Genetics*, *6*(9), e1001098. https://doi.org/10.1371/JOURNAL.PGEN.1001098

Yamanaka, S., Nakamura, I., Nakai, H., & Sato, Y. I. (2003). Dual origin of the cultivated rice based on molecular markers of newly collected annual and perennial strains of wild rice species, *Oryza nivara* and *O. rufipogon*. *Genetic Resources and Crop Evolution*, *50*(5), 529–538. https://doi.org/10.1023/A:1023926802198/METRICS

Yang, S., Xu, K., Chen, S., Li, T., Xia, H., Chen, L., Liu, H., & Luo, L. (2019). A stress-responsive bZIP transcription factor OsbZIP62 improves drought and oxidative tolerance in rice. *BMC Plant Biology*, *19*(1), 1–15. https://doi.org/10.1186/S12870-019-1872-1/FIGURES/8

Yang, X., Wang, B., Chen, L., Li, P., & Cao, C. (2019). The different influences of drought stress at the flowering stage on rice physiological traits, grain yield, and quality. *Scientific Reports 2019 9:1*, *9*(1), 1–12. https://doi.org/10.1038/s41598-019-40161-0

Yogameenakshi, P., Vivekanandan, P., & Nadarajan, N. (2019). Genetic effects of yield and root parameters in rice (*Oryza sativa* L.) at reproductive stage drought stress as apportioned by generation mean analysis. *Oryza-An International Journal on Rice*, 175–184. https://doi.org/10.35709/ory.2019.56.2.1

Yu, H., Xie, W., Li, J., Zhou, F., & Zhang, Q. (2014). A whole-genome SNP array (RICE6K) for genomic breeding in rice. *Plant Biotechnology Journal*, *12*(1), 28–37. https://doi.org/10.1111/pbi.12113

Yue, B., Xue, W., Xiong, L., Yu, X., Luo, L., Cui, K., Jin, D., Xing, Y., & Zhang, Q. (2006). Genetic Basis of Drought Resistance at Reproductive Stage in Rice: Separation of Drought Tolerance From Drought Avoidance. *Genetics*, *172*(2), 1213–1228. https://doi.org/10.1534/GENETICS.105.045062

Zhang, J., Zhang, S., Cheng, M., Jiang, H., Zhang, X., Peng, C., Lu, X., Zhang, M., & Jin, J. (2018). Effect of drought on agronomic traits of rice and wheat: A meta-analysis. *International Journal of Environmental Research and Public Health*, *15*(5). https://doi.org/10.3390/ijerph15050839

Zhang, Y., Luan, Q., Jiang, J., & Li, Y. (2021). Prediction and Utilization of Malondialdehyde in Exotic Pine Under Drought Stress Using Near-Infrared Spectroscopy. *Frontiers in Plant Science*, *12*, 2261. https://doi.org/10.3389/FPLS.2021.735275/BIBTEX

Zhang, Z. F., Li, Y. Y., & Xiao, B. Z. (2016). Comparative transcriptome analysis highlights the crucial roles of photosynthetic system in drought stress adaptation in upland rice. *Scientific Reports 2016 6:1*, *6*(1), 1–13. https://doi.org/10.1038/srep19349

Zhao, K., Tung, C. W., Eizenga, G. C., Wright, M. H., Ali, M. L., Price, A. H., Norton, G. J., Islam, M. R., Reynolds, A., Mezey, J., McClung, A. M., Bustamante, C. D., & McCouch, S. R. (2011). Genome-wide association mapping reveals a rich genetic architecture of

complex traits in Oryza sativa. *Nature Communications*, *2*(1), 1–10. https://doi.org/10.1038/ncomms1467

Zhao, L., Hu, Y., Chong, K., & Wang, T. (2010). ARAG1, an ABA-responsive DREB gene, plays a role in seed germination and drought tolerance of rice. *Annals of Botany*, *105*(3), 401–409. https://doi.org/10.1093/AOB/MCP303

Zhao, T., & Dai, A. (2017). Uncertainties in historical changes and future projections of drought. Part II: model-simulated historical and future drought changes. *Climatic Change*, *144*(3), 535–548. https://doi.org/10.1007/S10584-016-1742-X/FIGURES/6

Zhao, X., Peng, Y., Zhang, J., Fang, P., & Wu, B. (2018). Identification of QTLs and Meta-QTLs for Seven Agronomic Traits in Multiple Maize Populations under Well-Watered and Water-Stressed Conditions. *Crop Science*, *58*(2), 507–520. https://doi.org/10.2135/cropsci2016.12.0991

Zu, X., Lu, Y., Wang, Q., Chu, P., Miao, W., Wang, H., & La, H. (2017). A new method for evaluating the drought tolerance of upland rice cultivars. *The Crop Journal*, *5*(6), 488–498. https://doi.org/10.1016/J.CJ.2017.05.002

Zuo, Z. W., Zhang, Z. H., Huang, D. R., Fan, Y. Y., Yu, S. Bin, Zhuang, J. Y., & Zhu, Y. J. (2022). Control of thousand-grain weight by osmads56 in rice. *International Journal of Molecular Sciences*, *23*(1). https://doi.org/10.3390/IJMS23010125/S1

ANNEXES

Annex I: R scripts used for the scaling tests analysis during the generation means analysis

```
#Programme for scaling test – Modified programme of Nadarajan et al (2016)
#rm(list=ls()) removes variable and values in the programme memory
rm(list=ls())
#Scaling test scripts
meanp1<-10.5
meanp2<-8.5
meanf1<-11.22
meanf2<-10.50
meanb1<-10.06
meanb2<-9.04
vp1<-0.078
vp2<-0.013
vf1<-0.057
vf2<-0.018
vb1<-0.014
vb2<-0.017
scalea<-2*meanb1-meanp1-meanf1
scaleb<-2*meanb2-meanp2-meanf1
scalec<-4*meanf2-2*meanf1-meanp1-meanp2
scaled<-2*meanf2-meanb1-meanb2
va<-4*vb1+vp1+vf1
vb<-4*vb2+vp2+vf1
vc<-16*vf2+4*vf1+vp1+vp2
vscaled<-4*vf2+vb1+vb2
sea<-va^0.5
seb<-vb^0.5
sec<-vc^0.5
sescaled<-vscaled^0.5
ta<-scalea/sea
tb<-scaleb/seb
tc<-scalec/sec
tscaled<-scaled/sescaled
cat("Scale","Value", "SE","t", "\n")
# "\n" helps to start from new line
cat("A",scalea,va,sea,ta,"\n")
cat("B",scaleb,vb,seb,tb,"\n")
cat("C",scalec,vc,sec,tc,"\n")
cat("D",scaled,vscaled,sescaled,tscaled,"\n")
```

Annex II: R scripts used for the six parameters model's analysis during the generation means analysis

```
# Programme for GMA - 6 parameters model – Modified programme of Nadarajan et al (2016)
# rm(list=ls()) removes variable and values in the programme memory
rm(list=ls())
# Generation mean analysis
meanp1<-11
meanp2<-9
meanf1<-10.7
meanf2<-10.9
meanb1<-11.1
meanb2<-9.22
vp1<-0.100
vp2<-0.050
vf1<-0.021
vf2<-0.024
vb1<-0.041
vb2<-0.040
m<-meanf2
d<-meanb1-meanb2
h<-meanf1-4*meanf2-1/2*meanp1-1/2*meanp2+2*meanb1+2*meanb2
i<-2*meanb1-2*meanb2-4*meanf2
j<-meanb1-1/2*meanp1-meanb2+1/2*meanp2
l<-meanp1+meanp2+2*meanf1+4*meanf2-4*meanb1-4*meanb2
vm<-vf2
vd<-vb1+vb2
vh<-vf1+16*vf2+1/4*vp1+1/4*vp2+4*vb1+4*vb2
vi<-4*vb1+4*vb2+16*vf2
vj<-vb1+1/4*vp1+vb2+1/4*vp2
vl<-vp1+vp2+4*vf1+16*vf2+16*vb1+16*vb2
sem<-vm^0.5
sed<-vd^0.5
seh<-vh^0.5
sei<-vi^0.5
sej<-vj^0.5
sel<-vl^0.5
tm<-m/sem
td<-d/sed
th<-h/seh
ti<-i/sei
tj<-j/sej
tl<-l/sel
cat("Parameter","Value", "SE","t", "\n")
# "\n" helps to start from new line
cat("m",m,vm,sem,tm,"\n")
cat("d",d,vd,sed,td,"\n")
cat("h",h,vh,seh,th,"\n")
cat("i",i,vi,sei,ti,"\n")
cat("j",j,vj,sej,tj,"\n")
cat("l",l,vl,sel,tl,"\n")
```

Annex III. The mean performance of 100 rice genotypes evaluated for 11 morpho-physiological traits under non-drought conditions at Fumesua-Kumasi, Ghana in 2021-2022

ID	GENOTYPE NAME	CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW
G1	CRI-AMANKWATIA	21.34	1.00	24.13	83.00	11.00	10.00	108.75	25.55	8.63	1.77	3.41
G2	CRI-AgraRice	19.18	1.00	19.89	82.00	11.00	10.00	84.53	28.80	8.99	2.32	2.94
G3	Obolo	23.00	1.00	20.42	81.00	12.00	11.00	148.40	38.60	7.59	1.90	2.26
G4	Jasmine 85-CRI	20.03	1.00	19.08	82.00	8.00	7.00	92.20	24.27	8.69	2.31	3.30
G5	ARICA 3	19.37	1.00	16.62	83.00	11.00	10.00	103.87	26.88	8.86	2.42	3.14
G6	Togo Marshall	14.41	1.00	17.14	84.00	13.00	12.00	91.47	22.20	8.68	2.36	3.05
G7	CRI-Kantinka	17.59	1.00	16.60	84.00	10.00	9.00	105.40	21.73	8.85	2.14	2.89
G8	CRI-Oboafo	17.57	3.00	8.00	78.00	16.00	14.00	106.20	25.00	10.13	2.16	2.83
G9	CRI-Emopa	19.38	3.00	9.48	84.00	10.00	9.00	114.67	17.47	8.99	2.38	3.23
G10	CRI-Mpuntuo	25.97	3.00	11.22	71.00	6.00	5.00	110.00	21.20	7.56	2.27	3.48
G11	CRI-Enapa	18.38	1.00	39.09	89.00	11.00	10.00	100.60	23.80	9.51	2.33	3.21
G12	AGRA-CRI-LOL-2-7	21.69	1.00	29.00	80.00	11.00	10.00	90.00	22.67	8.58	2.35	3.48
G13	SA54-SARI	19.04	1.00	17.25	90.00	12.00	12.00	111.00	26.87	7.67	1.94	2.26
G14	AGRA-CRI-LOL-1-11	17.19	1.00	13.77	83.00	8.00	8.00	93.45	19.25	7.03	1.38	3.16
G15	AGRA-CRI-LOL-1-21	16.59	1.00	18.62	84.00	13.00	12.00	100.13	25.00	7.68	2.06	3.02
G16	SA25-SARI	15.99	1.00	22.78	80.00	13.00	11.00	100.05	22.70	8.40	2.54	3.28
G17	SAHEL 177	20.56	1.00	31.78	79.00	13.00	13.00	102.13	25.75	6.89	2.14	3.08
G18	SR34590-HB 3433-5-1-1	16.54	1.00	19.47	85.00	16.00	14.00	95.10	19.30	8.51	2.33	3.22
G19	SR35266-2-16-1-1	21.69	1.00	9.45	82.00	8.00	7.00	80.80	36.90	6.82	2.00	3.18
G20	SR35266-2-18-2-1	18.81	3.00	30.00	94.00	10.00	9.00	84.87	22.40	7.74	2.42	3.09
G21	SR35266-2-12-4-1	21.01	1.00	9.17	82.00	8.00	8.00	93.73	27.00	8.70	1.93	2.63
G22	Jasmine 85-SARI	20.69	1.00	17.63	87.00	11.00	10.00	79.53	23.20	9.25	1.85	3.14
G23	ART216-149-B-1-B-B	18.16	1.00	25.00	95.00	8.00	7.00	80.00	20.28	8.38	1.17	2.90
G24	ART216-187-B-1-B-B	21.17	3.00	24.54	89.00	11.00	10.00	79.33	19.69	8.25	2.45	2.91
G25	SA29-SARI	15.64	1.00	13.97	86.00	12.00	12.00	113.60	21.85	7.30	2.24	2.83
G26	ART314-14-B-1-B-B	16.18	3.00	20.81	85.00	8.00	8.00	123.40	30.73	8.41	1.88	2.80
G27	SA7-SARI	16.72	3.00	14.35	84.00	9.00	9.00	113.57	22.65	7.48	1.53	2.71
G28	ART387-9-1-1-1-B	20.68	3.00	36.60	83.00	11.00	10.00	118.73	21.13	8.84	2.38	3.41
G29	ART397-12-1-1-1-B	18.18	3.00	36.21	86.00	10.00	9.00	104.90	19.90	9.14	1.85	3.05
G30	ART430-16-1-1-1-5	21.46	1.00	16.61	82.00	13.00	12.00	103.73	23.27	7.62	2.08	2.48
G31	ART1005-21-1-1-1-B	20.19	1.00	29.61	86.00	13.00	12.00	119.53	23.93	8.89	2.34	3.29
G32	SA26-SARI	19.66	1.00	18.45	82.00	10.00	10.00	94.90	24.50	8.45	2.22	3.35
G33	ART478-13-8-1-1-B***	21.38	3.00	23.13	87.00	9.00	8.00	100.73	18.87	8.78	2.14	3.50
G34	ART478-8-1-1-1-B	23.68	1.00	24.60	83.00	11.00	11.00	96.40	17.70	9.29	2.64	3.17
G35	ART493-16-1-1-1-B	18.06	1.00	12.68	84.00	11.00	10.00	112.20	31.47	9.20	2.32	2.05
G36	ART132-35-1-1-B-B	16.77	3.00	19.44	82.00	11.00	10.00	119.27	26.87	8.10	2.41	2.16
G37	SA41-SARI	20.03	1.00	12.08	83.00	13.00	12.00	103.30	25.60	8.15	2.18	3.15
G38	SA50-SARI	17.58	1.00	17.60	85.00	11.00	10.00	106.20	19.80	9.18	2.65	3.14
G39	ART174-2-1-1-B-B	12.93	1.00	14.35	81.00	12.00	11.00	121.93	24.40	8.01	2.36	2.78
G40	SA38-SARI	19.12	1.00	12.81	84.00	11.00	10.00	82.50	19.60	8.22	2.29	2.90
G41	SA9-SARI	20.62	3.00	35.00	81.00	11.00	10.00	101.20	22.20	9.83	2.42	3.54
G42	ART68-12-1-1-B-B	20.26	1.00	30.17	83.00	12.00	11.00	109.73	21.47	7.35	2.22	2.72
G43	ART75-14-1-2-B-B	19.82	1.00	19.87	84.00	8.00	8.00	106.00	26.67	9.05	2.15	3.15
G44	ART75-33-1-1-B-B	18.38	3.00	28.89	76.00	14.00	13.00	81.00	21.87	9.63	2.20	3.27
G45	ART90-9-1-1-B-B	19.24	1.00	10.20	83.00	11.00	10.00	127.13	25.00	7.74	1.93	2.57

ID	GENOTYPE NAME	CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW
G46	ART73-69-1-2-B-B	15.54	1.00	13.52	85.00	12.00	11.00	113.33	24.40	9.05	2.39	2.79
G47	ART98-147-1-1-B-B	19.56	3.00	15.27	84.00	14.00	13.00	89.93	24.07	8.59	2.56	2.65
G48	SA21-SARI	17.77	1.00	17.90	85.00	12.00	12.00	113.30	22.10	8.87	2.58	2.97
G49	SA20-SARI	23.90	1.00	26.10	79.00	13.00	13.00	90.20	22.80	8.70	2.10	3.33
G50	ART100-57-1-2-B-B	22.13	1.00	16.23	86.00	12.00	12.00	111.60	18.20	8.94	2.48	3.15
G51	ART112-74-1-1-B-B	13.38	1.00	12.78	87.00	12.00	11.00	109.80	22.40	6.01	1.44	2.91
G52	ART350:2-6-1-B	21.96	1.00	25.83	85.00	10.00	9.00	120.47	26.60	7.91	2.43	2.74
G53	WAB 2085-TGR2-WAT4-1-1	23.44	3.00	33.04	90.00	7.00	6.00	128.07	24.07	9.31	2.05	2.88
G54	WAB 2135-WAC B-2-TGR3-WAT8-3	22.27	1.00	18.88	85.00	11.00	11.00	141.50	35.20	7.43	2.30	2.90
G55	WAB 2099-WAC1.FKR3-1-TGR1-2	19.04	3.00	15.26	82.00	17.00	15.00	94.40	20.30	9.31	2.60	3.42
G56	AGRA-CRI-LOL-2-29	16.96	1.00	21.60	85.00	9.00	8.00	112.80	21.50	8.87	1.90	3.36
G57	NERICA-L 41	17.18	1.00	33.83	86.00	13.00	13.00	123.50	35.70	9.45	2.65	2.65
G58	CRI-1-21-5-12	16.31	3.00	7.84	86.00	12.00	11.00	106.00	28.33	8.33	1.99	2.63
G59	SA64-SARI	23.43	3.00	26.22	86.00	11.00	10.00	113.87	26.67	8.13	2.32	3.23
G60	Viwornor short	17.12	3.00	23.89	76.00	14.00	11.00	107.37	22.70	9.03	2.34	2.52
G61	BETIA	14.52	1.00	11.86	84.00	11.00	10.00	98.00	21.87	8.19	1.99	2.84
G62	KE40	13.17	1.00	12.45	78.00	9.00	8.00	111.90	29.90	7.89	1.87	3.12
G63	ARICA 2	22.42	1.00	30.60	83.00	11.00	10.00	93.80	23.87	8.78	2.05	2.96
G64	SA14-SARI	20.00	1.00	11.65	82.00	10.00	9.00	90.07	22.20	9.17	2.32	3.23
G65	GR18-SARI	18.33	1.00	11.20	85.00	9.00	8.00	88.47	16.47	9.02	2.43	2.83
G66	UPL 32	12.37	1.00	34.93	84.00	12.00	11.00	106.07	25.00	8.69	2.20	3.16
G67	Awarema	16.32	1.00	8.00	88.00	16.00	15.00	66.63	20.13	9.26	2.29	2.74
G68	Oreire	13.62	3.00	24.00	84.00	9.00	8.00	118.90	21.90	9.62	2.44	2.93
G69	AGRA-SARI	19.07	1.00	29.22	80.00	12.00	11.00	73.03	21.00	9.59	2.48	3.34
G70	Ex-Baike (Asutware)	18.80	3.00	20.98	82.00	15.00	13.00	115.53	25.53	9.40	2.32	3.19
G71	SR34590-HB 3433-8-3-1	27.26	1.00	11.89	83.00	10.00	9.00	97.63	25.90	7.80	2.13	2.97
G72	SR34590-HB3433-8-2-1	22.76	1.00	17.86	86.00	13.00	12.00	107.62	25.98	7.90	2.06	2.73
G73	SR35266-2-12-1-1	27.60	1.00	5.44	81.00	10.00	9.00	91.10	25.60	7.45	2.53	3.38
G74	SR35266-2-12-4-1	22.30	3.00	12.38	86.00	9.00	8.00	85.07	22.60	8.58	2.22	2.40
G75	SR35266-2-17-2-1	24.72	1.00	10.60	80.00	8.00	8.00	101.20	23.00	8.30	1.77	2.72
G76	SR35266-2-18-1-1	25.76	1.00	18.24	85.00	8.00	7.00	89.20	22.80	8.66	2.44	2.92
G77	SR35250-2-4-2-3	15.52	1.00	6.89	83.00	10.00	9.00	86.55	19.30	8.27	1.73	3.55
G78	SA68-SARI	20.39	1.00	14.60	83.00	9.00	8.00	88.05	20.25	8.06	1.91	3.26
G79	SA69-SARI	15.70	3.00	18.33	83.00	11.00	10.00	103.87	24.67	7.99	2.40	2.76
G80	SA24-SARI	16.19	1.00	18.59	86.00	15.00	14.00	70.47	26.40	9.01	2.47	3.24
G81	SR34590-HB3433-6-2-1	20.59	1.00	6.93	87.00	9.00	9.00	91.67	25.87	8.39	2.45	2.60
G82	SAHEL 134	20.93	1.00	8.77	78.00	15.00	14.00	79.53	23.93	8.10	2.39	2.66
G83	SAHEL 210	18.43	1.00	22.83	85.00	8.00	8.00	101.73	26.73	8.33	1.93	3.39
G84	SR34796-1-4-6-3-2-1	18.98	1.00	19.58	86.00	17.00	16.00	75.73	19.67	8.56	2.41	2.75
G85	SR35278-1-7-2-2	20.36	1.00	29.43	83.00	11.00	9.00	100.60	24.27	7.79	2.37	3.16
G86	SR33705F2-61-1-3-HV-1-1	22.07	1.00	10.70	80.00	9.00	8.00	84.62	25.62	7.72	2.40	2.88
G87	SR35278-1-7-3-2	19.48	1.00	8.72	83.00	12.00	10.00	71.13	17.30	8.35	1.94	2.38
G88	SR35266-2-11-4-1-1	19.19	1.00	23.02	85.00	19.00	17.00	81.47	22.73	8.72	2.60	2.41
G89	SR35311-HB3497-87	19.18	1.00	18.13	81.00	11.00	9.00	105.67	24.57	7.24	2.46	2.52
G90	HR32067F1-2-14-1	20.88	1.00	15.72	87.00	11.00	10.00	88.48	20.50	7.23	2.01	2.98

ID	GENOTYPE NAME	CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW
G91	SA60-SARI	20.96	1.00	23.52	81.00	9.00	8.00	99.30	22.60	8.86	2.37	2.99
G92	Gigante	18.08	3.00	29.62	62.00	12.00	11.00	106.73	23.13	8.33	2.33	2.31
G93	DigJas-61	22.01	1.00	12.59	81.00	12.00	11.00	96.50	21.80	9.21	2.30	2.85
G94	DigJas-78	16.72	1.00	30.50	80.00	9.00	8.00	102.60	23.03	9.63	2.33	3.18
G95	AgKE99-26	22.13	1.00	11.84	78.00	12.00	11.00	88.07	29.60	8.50	2.06	3.47
G96	JKE56-12	13.48	3.00	9.92	83.00	14.00	13.00	94.20	24.80	8.52	2.14	3.25
G97	KBR 10	17.80	1.00	7.96	76.00	7.00	6.00	97.33	24.60	8.30	2.24	2.41
G98	ORYLUX 6	18.89	1.00	11.84	78.00	11.00	10.00	87.80	21.80	9.27	2.41	2.69
G99	APO	18.71	1.00	11.55	82.00	9.00	7.00	95.73	27.22	8.18	2.47	2.73
G100	UPLR-17	19.04	1.00	8.70	82.00	9.00	8.00	96.33	21.47	7.72	2.39	3.48

CCI- Chlorophyll Content Index; SPFS-Spikelet Fertility Score; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm); GL-Grain Length(mm); GW-Grain width(mm); HGW-Hundred Grains Weight(g); ID-Genotype Identity

Annex IV. The mean performance of 100 rice genotypes evaluated for 14 morpho-physiological traits under drought stress at Fumesua-Kumasi, Ghana in 2021-2022

ID	GENOTYPE	CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW	LRS	LDS	DRR
G1	CRI-AMANKWATIA	15.74	3.00	3.33	93.00	5.00	3.00	71.47	21.67	5.96	2.62	2.62	3.87	1.00	1.00
G2	CRI-AgraRice	16.98	1.00	1.53	92.00	4.00	4.00	81.27	21.85	8.74	2.41	2.74	3.47	1.00	1.00
G3	Obolo	18.68	1.00	0.77	98.00	5.00	4.00	78.80	19.20	7.44	2.34	3.44	4.67	1.00	1.00
G4	Jasmine 85-CRI	14.43	7.00	0.83	98.00	6.00	5.00	67.00	19.13	-	-	-	4.87	1.00	1.00
G5	ARICA 3	16.43	5.00	5.00	71.00	4.00	3.00	88.40	21.73	8.33	2.14	2.98	6.33	2.87	3.00
G6	Togo Marshall	14.22	1.00	15.00	96.00	5.00	4.00	66.93	14.07	10.25	3.15	4.02	8.47	1.00	1.00
G7	CRI-Kantinka	8.98	5.00	1.00	98.00	5.00	4.00	70.60	19.52	7.29	1.31	3.57	6.60	1.67	1.67
G8	CRI-Oboafo	15.65	-	0.00	92.00	4.00	0.00	92.00	-	-	-	-	1.00	0.67	0.67
G9	CRI-Emopa	19.71	7.00	0.00	87.00	5.00	4.00	74.13	15.47	-	-	-	5.13	1.00	1.00
G10	CRI-Mpuntuo	19.69	5.00	2.75	88.00	6.00	6.00	74.04	19.58	8.14	1.49	3.64	1.73	0.80	1.00
G11	Enapa	12.89	1.00	2.89	92.00	6.00	5.00	77.23	19.10	9.35	2.33	2.42	4.73	1.00	1.00
G12	AGRA-CRI-LOL-2-7	21.18	5.00	5.00	89.00	4.00	4.00	74.67	19.93	4.79	2.51	2.15	4.53	1.00	1.00
G13	SA54-SARI	11.07	5.00	0.74	94.00	4.00	4.00	96.13	18.60	7.57	1.44	2.26	6.33	1.00	1.00
G14	AGRA-CRI-LOL-1-11	16.14	1.00	1.97	91.00	5.00	4.00	87.60	24.67	8.06	1.83	2.24	3.73	0.67	1.00
G15	AGRA-CRI-LOL-1-21	12.38	7.00	2.14	94.00	5.00	5.00	85.87	23.20	9.25	1.77	2.41	4.93	0.67	1.67
G16	SA25-SARI	11.79	3.00	10.00	94.00	6.00	4.00	56.00	22.13	-	-	2.56	5.53	1.00	2.33
G17	SAHEL 177	10.10	3.00	5.00	90.00	5.00	4.00	61.27	22.93	8.77	1.88	2.18	7.53	2.47	2.33
G18	SR34590-HB 3433-5-1-1	15.86	7.00	1.74	94.00	4.00	4.00	68.80	11.87	-	-	-	5.27	1.00	1.00
G19	SR35266-2-16-1-1	11.33	5.00	3.33	98.00	4.00	3.00	77.13	19.67	8.27	2.78	2.31	7.67	1.67	2.33
G20	SR35266-2-18-2-1	14.84	5.00	6.67	96.00	6.00	5.00	77.13	18.53	7.81	2.10	2.31	5.40	1.00	1.67
G21	SR35266-2-12-4-1	10.98	5.00	1.61	93.00	5.00	4.00	63.67	22.80	7.35	1.56	2.46	6.07	1.00	1.00
G22	Jasmine 85-SARI	13.98	7.00	0.83	100.00	6.00	5.00	70.67	16.76	8.30	1.43	2.40	5.00	1.67	3.00
G23	ART216-149-B-1-B-B	16.16	3.00	2.83	94.00	5.00	4.00	78.87	17.70	8.18	2.35	3.20	5.67	0.87	1.00
G24	ART216-187-B-1-B-B	14.38	3.00	1.89	96.00	7.00	6.00	69.62	17.32	8.66	2.49	2.60	4.40	0.67	1.00
G25	SA29-SARI	13.89	7.00	2.00	97.00	5.00	5.00	72.10	20.00	8.33	1.91	2.64	6.73	1.00	3.00
G26	ART314-14-B-1-B-B	11.72	7.00	2.50	94.00	4.00	4.00	85.40	19.93	7.35	2.18	2.60	8.33	4.07	3.00
G27	SA7-SARI	13.22	9.00	0.00	90.00	6.00	4.00	81.20	20.00	-	-	-	7.40	1.67	2.33
G28	ART387-9-1-1-1-B	10.50	3.00	3.67	90.00	7.00	7.00	105.93	19.27	9.50	2.35	2.25	7.40	1.67	1.67
G29	ART397-12-1-1-1-B	5.99	5.00	3.33	95.00	5.00	5.00	86.40	20.27	8.17	1.12	1.74	7.80	1.00	2.33
G30	ART430-16-1-1-1-5	9.70	5.00	3.33	90.00	8.00	6.00	75.40	22.00	7.04	2.16	2.21	7.40	1.27	2.33
G31	ART1005-21-1-1-1-B	19.07	1.00	3.50	83.00	5.00	4.00	83.20	19.73	7.70	2.02	2.50	4.60	0.80	1.00
G32	SA26-SARI	19.58	5.00	0.81	95.00	6.00	5.00	65.67	10.70	10.15	2.15	2.98	3.93	1.00	1.00
G33	ART478-13-8-1-1-B***	17.02	3.00	2.93	97.00	6.00	5.00	75.40	19.40	9.33	2.42	2.60	6.20	1.00	1.00
G34	ART478-8-1-1-1-B	18.07	1.00	1.69	97.00	5.00	4.00	84.80	24.03	9.61	2.27	3.60	4.87	1.00	1.67
G35	ART493-16-1-1-1-B	12.44	7.00	1.67	90.00	7.00	7.00	76.95	20.02	12.06	4.11	2.17	5.93	1.00	1.67
G36	ART132-35-1-1-B-B	7.86	9.00	0.00	89.00	6.00	6.00	60.73	19.90	-	-	-	8.87	3.00	5.00
G37	SA41-SARI	16.61	3.00	5.50	92.00	7.00	6.00	64.27	19.27	8.33	2.36	3.14	4.67	1.00	1.00
G38	SA50-SARI	14.16	1.00	2.50	95.00	6.00	5.00	68.93	18.20	7.11	1.35	2.26	6.33	1.00	1.00
G39	ART174-2-1-1-B-B	8.37	9.00	0.00	94.00	4.00	3.00	78.33	20.10	9.26	1.70	1.85	7.00	1.40	1.67
G40	SA38-SARI	14.38	3.00	2.06	95.00	7.00	4.00	62.27	18.73	8.34	1.87	2.15	4.07	0.67	1.00
G41	SA9-SARI	7.03	9.00	5.00	81.00	4.00	4.00	91.13	19.53	-	-	-	8.20	1.67	3.00
G42	ART68-12-1-1-B-B	18.53	5.00	6.67	100.00	4.00	3.00	84.07	23.33	7.52	2.69	2.58	3.20	0.67	1.67
G43	ART75-14-1-2-B-B	19.34	3.00	2.08	91.00	4.00	3.00	75.13	16.73	8.42	2.43	2.97	4.27	1.00	2.33
G44	ART75-33-1-1-B-B	20.13	1.00	9.67	85.00	4.00	4.00	64.73	18.67	8.56	1.85	2.52	3.60	0.67	1.00
G45	ART90-9-1-1-B-B	13.99	9.00	0.00	96.00	5.00	4.00	89.40	28.27	-	-	-	5.80	2.47	2.33
G46	ART73-69-1-2-B-B	14.18	9.00	5.00	99.00	5.00	4.00	78.33	16.40	-	-	-	6.73	1.00	1.00

ID	GENOTYPE	CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW	LRS	LDS	DRR
G47	ART98-147-1-1-B-B	10.41	7.00	1.00	92.00	4.00	3.00	85.60	18.40	-	-	-	6.87	1.27	3.00
G48	SA21-SARI	9.57	7.00	3.33	91.00	6.00	5.00	93.07	20.27	7.35	2.40	2.58	4.80	0.67	1.00
G49	SA20-SARI	17.94	7.00	7.50	95.00	5.00	4.00	73.40	16.68	9.33	2.03	2.14	5.80	2.07	1.67
G50	ART100-57-1-2-B-B	19.54	9.00	0.00	87.00	4.00	4.00	81.53	20.63	8.40	2.20	3.34	4.87	1.00	1.00
G51	ART112-74-1-1-B-B	18.71	7.00	3.33	97.00	4.00	4.00	77.07	18.27	8.12	1.84	3.10	5.93	1.00	1.00
G52	ART350:2-6-1-B	19.09	5.00	2.50	96.00	6.00	6.00	81.07	21.87	9.41	2.11	-	4.40	1.00	1.00
G53	WAB 2085-TGR2-WAT4-1-1	12.84	9.00	0.00	101.00	4.00	4.00	82.00	17.89	8.40	2.47	2.81	8.87	4.07	3.00
G54	WAB 2135-WAC B-2-TGR3-WAT8-3	12.21	7.00	2.50	101.00	6.00	5.00	101.93	20.60	8.53	2.57	2.22	7.40	2.47	2.33
G55	WAB 2099-WAC1.FKR3-1-TGR1-2	14.19	5.00	0.67	95.00	5.00	4.00	65.40	22.47	9.99	2.08	2.81	5.67	1.40	1.67
G56	AGRA-CRI-LOL-2-29	14.11	7.00	2.22	95.00	5.00	4.00	62.80	17.53	6.55	1.64	2.06	9.00	3.27	1.67
G57	NERICA-L 41	12.78	9.00	0.00	89.00	5.00	4.00	64.73	16.40	-	-	-	5.40	1.67	1.67
G58	CRI-1-21-5-12	13.44	9.00	0.00	88.00	4.00	4.00	91.07	30.07	8.38	2.09	-	4.80	1.00	1.00
G59	SA64-SARI	16.78	5.00	10.00	87.00	5.00	4.00	91.35	23.02	9.59	2.28	2.70	4.40	1.00	1.00
G60	Viwornor short	14.18	3.00	8.33	88.00	7.00	6.00	85.73	24.53	9.20	2.21	1.53	5.80	1.00	1.00
G61	BETIA	13.20	7.00	0.00	95.00	5.00	4.00	67.40	15.30	-	-	-	5.40	1.67	1.00
G62	KE40	9.60	5.00	10.00	81.00	6.00	5.00	63.80	20.73	6.45	2.59	1.68	7.13	1.67	3.00
G63	ARICA 2	20.78	5.00	3.33	86.00	5.00	4.00	77.70	20.60	-	-	-	4.13	1.00	1.00
G64	SA14-SARI	16.94	3.00	5.00	91.00	5.00	4.00	73.40	21.27	9.40	1.89	2.76	1.47	1.00	1.00
G65	GR18-SARI	19.84	7.00	5.00	99.00	5.00	4.00	72.53	18.47	8.12	2.31	2.18	5.93	1.00	2.33
G66	UPL 32	17.73	7.00	0.00	88.00	5.00	5.00	76.93	16.53	9.19	2.15	2.57	4.47	1.00	1.00
G67	Awarema	17.47	9.00	0.00	71.00	6.00	5.00	72.40	19.97	5.84	1.34	2.54	5.20	3.00	3.00
G68	Oreire	7.76	7.00	3.75	86.00	6.00	6.00	81.75	15.35	10.14	2.37	2.24	6.20	1.00	1.00
G69	AGRA-SARI	15.07	3.00	5.63	93.00	5.00	4.00	79.53	22.98	7.55	2.18	2.96	4.53	1.00	1.00
G70	Ex-Baike (Asutware)	17.16	3.00	3.50	92.00	6.00	5.00	77.87	22.35	8.82	3.08	2.47	5.27	1.00	3.00
G71	SR34590-HB 3433-8-3-1	11.86	1.00	2.89	93.00	5.00	5.00	71.33	19.13	9.32	2.40	2.84	7.67	2.07	2.33
G72	SR34590-HB3433-8-2-1	21.60	1.00	4.76	93.00	4.00	3.00	87.27	21.75	8.82	2.12	2.39	7.67	2.47	2.33
G73	SR35266-2-12-1-1	8.37	5.00	3.27	92.00	5.00	4.00	91.87	17.65	7.13	2.05	2.31	5.60	1.80	1.67
G74	SR35266-2-12-4-1	15.39	1.00	5.00	92.00	5.00	5.00	73.00	19.27	7.79	2.54	2.00	4.60	1.00	1.00
G75	SR35266-2-17-2-1	16.72	3.00	3.65	90.00	7.00	7.00	73.73	18.33	8.27	2.11	2.35	4.73	1.00	1.00
G76	SR35266-2-18-1-1	15.46	3.00	1.35	93.00	6.00	5.00	70.73	15.20	6.93	2.01	2.56	6.87	1.00	1.67
G77	SR35250-2-4-2-3	21.39	3.00	3.00	83.00	5.00	4.00	62.60	19.47	4.58	1.71	2.48	3.53	0.67	1.00
G78	SA68-SARI	8.11	9.00	0.00	94.00	6.00	5.00	65.80	29.30	-	-	-	7.53	1.27	1.67
G79	SA69-SARI	16.68	3.00	10.00	86.00	7.00	7.00	82.12	31.88	8.24	2.03	2.35	4.13	1.27	1.67
G80	SA24-SARI	14.68	3.00	6.30	91.00	6.00	5.00	66.67	19.27	8.52	2.34	2.87	7.00	0.67	2.33
G81	SR34590-HB3433-6-2-1	15.82	5.00	4.13	93.00	4.00	3.00	78.22	18.22	8.44	2.28	2.29	7.13	1.00	1.00
G82	SAHEL 134	12.90	7.00	3.00	96.00	4.00	4.00	72.00	19.47	7.13	1.42	1.16	5.40	1.67	2.33
G83	SAHEL 210	13.22	3.00	2.86	91.00	7.00	6.00	80.73	22.30	8.27	2.63	2.72	6.07	1.13	1.67
G84	SR34796-1-4-6-3-2-1	15.99	3.00	2.00	98.00	5.00	5.00	69.67	16.87	7.25	2.54	2.52	7.00	2.07	1.67
G85	SR35278-1-7-2-2	18.79	9.00	0.00	92.00	5.00	4.00	72.60	21.70	-	-	-	6.20	1.00	1.00
G86	SR33705F2-61-1-3-HV-1-1	16.18	3.00	3.06	84.00	5.00	4.00	81.40	18.20	7.80	2.06	1.91	5.67	1.00	1.00
G87	SR35278-1-7-3-2	10.50	3.00	1.00	80.00	7.00	6.00	74.40	20.47	5.51	2.16	1.59	6.07	1.00	1.67
G88	SR35266-2-11-4-1-1	8.59	1.00	3.17	90.00	9.00	3.00	71.87	21.30	8.31	2.36	3.14	5.40	3.00	3.00
G89	SR35311-HB3497-87	17.87	5.00	0.17	95.00	5.00	5.00	85.73	20.53	8.00	2.70	-	5.07	1.00	1.00
G90	HR32067F1-2-14-1	12.28	1.00	2.32	95.00	4.00	3.00	76.40	23.15	8.24	2.11	2.93	5.33	1.80	2.33
G91	SA60-SARI	13.47	5.00	2.58	97.00	6.00	5.00	61.07	19.33	9.23	1.85	2.30	7.13	3.00	3.00
G92	Gigante	9.93	5.00	4.17	96.00	7.00	5.00	83.47	19.93	8.57	2.24	2.26	6.53	2.33	4.33
G93	DigJas-61	16.42	3.00	2.60	89.00	4.00	3.00	87.27	25.00	9.12	2.44	3.49	4.20	1.13	1.67
G94	DigJas-78	10.80	3.00	3.00	81.00	6.00	4.00	71.73	19.64	7.05	2.13	3.18	5.00	3.00	3.00

ID	GENOTYPE	CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW	LRS	LDS	DRR
G95	AgKE99-26	9.84	3.00	1.63	93.00	5.00	4.00	74.80	22.20	8.68	1.91	2.65	4.27	0.73	1.00
G96	JKE56-12	11.97	3.00	0.63	94.00	8.00	6.00	78.13	18.40	6.56	1.72	2.74	5.40	1.00	1.67
G97	KBR 10	14.18	9.00	0.00	78.00	5.00	4.00	70.00	19.00	-	-	-	4.33	1.67	1.67
G98	ORYLUX 6	13.39	7.00	3.00	94.00	6.00	4.00	78.53	31.87	7.07	1.94	2.34	4.87	1.00	2.33
G99	APO	16.42	1.00	5.33	88.00	4.00	3.00	69.47	18.00	8.80	2.18	2.38	1.80	1.00	1.00
G100	UPLR-17	17.54	3.00	4.75	89.00	4.00	3.00	71.27	20.53	8.28	2.38	2.95	5.67	1.00	1.00

CCI- Chlorophyll Content Index; SPFS-Spikelet Fertility Score; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm); GL-Grain Length(mm); GW-Grain width(mm); HGW-Hundred Grains Weight(g); LRS-Leaf Rolling Score; LDS-Leaf Drying Score; DRR-Drought Recovery; ID-Genotype Identity

Annex V: Estimate of Pearson correlations of 100 rice genotypes evaluated under non-drought conditions at Fumesua-Kumasi, Ghana in 2021-2022

TRAITS		CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW
CCI	r	1	-0.068	0.011	-0.082	-0.226	-0.209	-0.071	0.065	-0.088	0.099	0.096
	p-value		0.500	0.911	0.417	0.024	0.037	0.480	0.520	0.384	0.326	0.342
SPFS	r		1	0.187	-0.079	0.024	-0.021	0.181	-0.105	0.208	0.067	0.001
	p-value			0.063	0.435	0.810	0.838	0.071	0.298	0.038	0.508	0.995
GYP	r			1	0.101	0.068	0.072	0.207	-0.016	0.269	0.131	0.215
	p-value				0.316	0.504	0.478	0.039	0.878	0.007	0.194	0.032
DTF	r				1	-0.024	0.017	-0.029	-0.076	-0.013	-0.156	0.006
	p-value					0.810	0.866	0.776	0.451	0.896	0.120	0.949
TN	r					1	0.972	-0.152	-0.057	0.179	0.315	-0.117
	p-value						<.0001	0.132	0.572	0.075	0.001	0.245
PN	r						1	-0.119	-0.021	0.153	0.279	-0.113
	p-value							0.239	0.837	0.130	0.005	0.262
PH	r							1	0.407	-0.118	-0.050	-0.171
	p-value								<.0001	0.244	0.623	0.090
PL	r								1	-0.206	-0.047	-0.249
	p-value									0.040	0.646	0.013
GL	r									1	0.369	0.164
	p-value										0.000	0.103
GW	r										1	0.010
	p-value											0.919

r-correlation value; p-value- Significant value; CCI- Chlorophyll Content Index; SPFS-Spikelet Fertility Score; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm); GL-Grain Length(mm); GW-Grain width(mm); HGW-Hundred Grains Weight(g);

Annex VI. Estimate of Pearson correlations of 100 rice genotypes evaluated under drought stress at Fumesua-Kumasi, Ghana in 2021-2022

TRAITS		CCI	SPFS	GYP	DTF	TN	PN	PH	PL	GL	GW	HGW	LRS	LDS	DRR
CCI	r	1	-0.214	0.097	-0.059	-0.263	-0.152	-0.070	-0.095	-0.028	0.110	0.280	-0.507	-0.300	-0.431
	p-value		0.033	0.339	0.561	0.008	0.130	0.486	0.348	0.802	0.322	0.011	<.0001	0.002	<.0001
SPFS	r		1	-0.391	0.000	-0.159	-0.004	0.083	-0.008	-0.019	-0.144	-0.219	0.297	0.255	0.242
	p-value			<.0001	0.996	0.117	0.972	0.413	0.934	0.864	0.193	0.050	0.003	0.011	0.016
GYP	r			1	-0.097	0.055	0.054	-0.072	0.066	0.117	0.242	-0.022	0.008	-0.131	-0.032
	p-value				0.338	0.590	0.596	0.477	0.514	0.292	0.027	0.848	0.940	0.194	0.755
DTF	r				1	-0.038	-0.037	-0.025	-0.097	0.228	0.059	0.069	0.170	-0.054	-0.051
	p-value					0.711	0.715	0.808	0.341	0.039	0.598	0.542	0.091	0.596	0.614
TN	r					1	0.690	-0.159	0.062	0.025	0.092	-0.111	0.045	-0.007	0.136
	p-value						<.0001	0.114	0.544	0.826	0.408	0.323	0.653	0.942	0.179
PN	r						1	-0.059	0.001	0.139	0.097	-0.215	0.171	-0.065	0.048
	p-value							0.563	0.994	0.209	0.383	0.054	0.090	0.518	0.634
PH	r							1	0.269	0.148	0.118	-0.053	-0.010	-0.011	-0.038
	p-value								0.007	0.181	0.288	0.638	0.924	0.915	0.705
PL	r								1	-0.056	-0.028	-0.065	-0.115	-0.016	0.114
	p-value									0.615	0.802	0.562	0.256	0.872	0.263
GL	r									1	0.354	0.189	0.020	-0.081	-0.068
	p-value										0.001	0.093	0.855	0.465	0.543
GW	r										1	0.148	0.062	-0.068	-0.016
	p-value											0.190	0.580	0.541	0.886
HGW	r											1	-0.193	-0.025	-0.117
	p-value												0.084	0.822	0.296
LRS	r												1	0.539	0.519
	p-value													<.0001	<.0001
LDS	r													1	0.675
	p-value														<.0001

r-correlation value; p-value- Significant value; CCI- Chlorophyll Content Index; SPFS-Spikelet Fertility Score; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm); GL-Grain Length(mm); GW-Grain width(mm); HGW-Hundred Grains Weight(g); LRS-Leaf Rolling Score; LDS-Leaf Drying Score; DRR-Drought Recovery

Annex VII. Estimate of Pearson correlations of 100 rice genotypes evaluated under drought stress based on drought risk index or relative value of the traits at Fumesua-Kumasi, Ghana in 2021-2022

Traits	Relative chlorophyll content index	Relative spikelet fertility score	Relative grain yield per plant	Relative days to flowering	Relative tiller number	Relative panicle number	Relative plant height	Relative panicle length	Relative grain length	Relative grain width	Relative hundred grains weight	Leaf rolling score	Leaf drying score	Recovery score
Relative chlorophyll content index	1	0.080	0.123	-0.182	-0.246*	-0.152	-0.078	-0.005	0.012	0.082	0.012	-0.400**	-0.021	-0.309**
Relative spikelet fertility score		1	-0.205*	0.006	-0.092	-0.104	-0.135	-0.070	-0.337**	-.352**	-0.370**	0.095	-0.057	-0.005
Relative grain yield			1	0.023	-0.041	-0.011	0.067	-0.043	0.269**	.284**	.277**	-0.076	0.101	-0.023
Relative days to flowering				1	0.072	0.042	-0.188	-0.014	0.100	-0.015	0.040	-0.013	0.150	0.150
Relative tiller number					1	0.847**	-0.172	-0.010	0.038	0.106	0.033	-0.003	0.049	-0.023
Relative panicle number						1	-0.157	-0.006	0.065	0.098	-0.049	-0.010	-0.061	-0.124
Relative plant height							1	0.274**	0.144	0.161	0.104	-0.150	0.030	-0.074
Relative panicle length								1	-0.022	-0.049	0.019	-0.137	0.084	-0.016
Relative grain length									1	0.842**	0.737**	-0.143	0.030	-0.077
Relative grain width										1	0.721**	-0.116	0.008	-0.082
Relative hundred grains weight											1	-0.102	0.104	0.001
Leaf rolling score												1	-0.150	0.405**
Leaf drying score													1	0.041
Recovery score														1

*. Correlation is significant at the 0.05 level (2-taile); **. Correlation is significant at the 0.01 level (2-tailed)

Annex VIII. Relative values of 100 rice genotypes for the 14 morpho-physiological traits evaluated under drought stress at Fumesua-Kumasi, Ghana in 2021-2022

ID	GENOTYPE	CCI-R	SPFS-R	GYP-R	DTF-R	TN-R	PN-R	PH-R	PL-R	GL-R	GW-R	HGW-R	LRS	LDS	DRR
G6	Togo Marshall	0.99	1.00	0.88	1.15	0.38	0.33	0.73	0.63	1.18	1.33	1.32	9	1	1
G62	KE40	0.73	5.00	0.80	1.04	0.67	0.63	0.57	0.69	0.82	1.33	0.54	7	1	3
G73	SR35266-2-12-1-1	0.30	5.00	0.60	1.14	0.50	0.44	1.01	0.69	0.96	0.81	0.68	5	1	1
G81	SR34590-HB3433-6-2-1	0.77	5.00	0.60	1.07	0.44	0.33	0.85	0.70	1.01	0.93	0.88	7	1	1
G79	SA69-SARI	1.06	1.00	0.55	1.03	0.64	0.70	0.79	1.29	1.03	0.85	0.85	5	1	1
G100	UPLR-17	0.92	3.00	0.55	1.09	0.44	0.38	0.74	0.96	1.07	1.00	0.85	5	5	1
G99	APO	0.88	1.00	0.46	1.07	0.44	0.43	0.73	0.66	1.08	0.88	0.87	1	3	1
G37	SA41-SARI	0.83	3.00	0.46	1.11	0.54	0.50	0.62	0.75	1.02	1.08	1.00	5	1	1
G65	GR18-SARI	1.08	7.00	0.45	1.16	0.56	0.50	0.82	1.12	0.90	0.95	0.77	5	1	3
G16	SA25-SARI	0.74	3.00	0.44	1.18	0.46	0.36	0.56	0.98	0.00	0.00	0.78	6	1	3
G77	SR35250-2-4-2-3	1.38	3.00	0.44	1.00	0.50	0.44	0.72	1.01	0.55	0.98	0.70	3	1	1
G64	SA14-SARI	0.85	3.00	0.43	1.10	0.50	0.44	0.81	0.96	1.02	0.81	0.86	1	1	1
G74	SR35266-2-12-4-1	0.69	0.33	0.40	1.07	0.56	0.63	0.86	0.85	0.91	1.14	0.83	5	1	1
G59	SA64-SARI	0.72	1.67	0.38	1.01	0.45	0.40	0.80	0.86	1.18	0.98	0.84	5	1	1
G46	ART73-69-1-2-B-B	0.91	9.00	0.37	1.16	0.42	0.36	0.69	0.67	0.00	0.00	0.00	7	1	1
G19	SR35266-2-16-1-1	0.52	5.00	0.35	1.20	0.50	0.43	0.95	0.53	1.21	1.39	0.73	7	1	3
G60	Viwornor short	0.83	1.00	0.35	1.15	0.50	0.55	0.80	1.08	1.02	0.95	0.61	5	1	1
G75	SR35266-2-17-2-1	0.68	3.00	0.34	1.13	0.88	0.88	0.73	0.80	1.00	1.19	0.86	5	1	1
G82	SAHEL 134	0.62	7.00	0.34	1.22	0.27	0.29	0.91	0.81	0.88	0.60	0.44	5	1	3
G80	SA24-SARI	0.91	3.00	0.34	1.06	0.40	0.36	0.95	0.73	0.95	0.95	0.89	7	1	3
G44	ART75-33-1-1-B-B	1.10	0.33	0.33	1.12	0.29	0.31	0.80	0.85	0.89	0.84	0.77	3	1	1
G5	ARICA 3	0.85	5.00	0.30	0.86	0.36	0.30	0.85	0.81	0.94	0.88	0.95	7	1	3
G49	SA20-SARI	0.75	7.00	0.29	1.20	0.38	0.31	0.81	0.73	1.07	0.97	0.64	5	1	1
G86	SR33705F2-61-1-3-HV-1-1	0.73	3.00	0.29	1.05	0.56	0.50	0.96	0.71	1.01	0.86	0.66	5	1	1
G72	SR34590-HB3433-8-2-1	0.95	1.00	0.27	1.08	0.31	0.25	0.81	0.84	1.12	1.03	0.88	7	1	3
G51	ART112-74-1-1-B-B	1.40	7.00	0.26	1.11	0.33	0.36	0.70	0.82	1.35	1.28	1.07	5	1	1
G98	ORYLUX 6	0.71	7.00	0.25	1.21	0.55	0.40	0.89	1.46	0.76	0.80	0.87	5	3	3
G10	CRI-Mpuntuo	0.76	1.67	0.25	1.24	1.00	1.20	0.67	0.92	1.08	0.66	1.05	1	1	1
G71	SR34590-HB 3433-8-3-1	0.43	1.00	0.24	1.12	0.50	0.56	0.73	0.74	1.19	1.13	0.95	7	1	3
G20	SR35266-2-18-2-1	0.79	1.67	0.22	1.02	0.60	0.56	0.91	0.83	1.01	0.87	0.75	5	1	1
G42	ART68-12-1-1-B-B	0.91	5.00	0.22	1.20	0.33	0.27	0.77	1.09	1.02	1.21	0.95	3	1	1
G93	DigJas-61	0.75	3.00	0.21	1.10	0.33	0.27	0.90	1.15	0.99	1.06	1.22	5	3	1
G30	ART430-16-1-1-1-5	0.45	5.00	0.20	1.10	0.62	0.50	0.73	0.95	0.92	1.04	0.89	7	1	3
G69	AGRA-SARI	0.79	3.00	0.19	1.16	0.42	0.36	1.09	1.09	0.79	0.88	0.89	5	1	1

ID	GENOTYPE	CCI-R	SPFS-R	GYP-R	DTF-R	TN-R	PN-R	PH-R	PL-R	GL-R	GW-R	HGW-R	LRS	LDS	DRR
G48	SA21-SARI	0.54	7.00	0.19	1.07	0.50	0.42	0.82	0.92	0.83	0.93	0.87	5	1	1
G21	SR35266-2-12-4-1	0.52	5.00	0.18	1.13	0.63	0.50	0.68	0.84	0.85	0.81	0.93	7	1	1
G12	AGRA-CRI-LOL-2-7	0.98	5.00	0.17	1.11	0.36	0.40	0.83	0.88	0.56	1.07	0.62	5	1	1
G70	Ex-Baike (Asutware)	0.91	1.00	0.17	1.13	0.40	0.38	0.67	0.88	0.94	1.33	0.77	5	1	3
G40	SA38-SARI	0.75	3.00	0.16	1.13	0.64	0.40	0.75	0.96	1.01	0.82	0.74	5	1	1
G17	SAHEL 177	0.49	3.00	0.16	1.14	0.38	0.31	0.60	0.89	1.27	0.88	0.71	7	1	3
G68	Oreire	0.57	2.33	0.16	1.02	0.67	0.75	0.69	0.70	1.05	0.97	0.76	7	1	1
G90	HR32067F1-2-14-1	0.59	1.00	0.15	1.09	0.36	0.30	0.86	1.13	1.14	1.05	0.99	5	1	3
G25	SA29-SARI	0.89	7.00	0.14	1.13	0.42	0.42	0.63	0.92	1.14	0.85	0.93	7	1	3
G14	AGRA-CRI-LOL-1-11	0.94	1.00	0.14	1.10	0.63	0.50	0.94	1.28	1.15	1.32	0.71	3	1	1
G41	SA9-SARI	0.34	3.00	0.14	1.00	0.36	0.40	0.90	0.88	0.00	0.00	0.00	9	1	3
G38	SA50-SARI	0.81	1.00	0.14	1.12	0.55	0.50	0.65	0.92	0.77	0.51	0.72	7	1	1
G92	Gigante	0.55	1.67	0.14	1.54	0.58	0.45	0.78	0.86	1.03	0.96	0.98	7	3	5
G1	CRI-AMANKWATIA	0.74	3.00	0.14	1.11	0.45	0.30	0.66	0.85	0.69	1.48	0.77	3	1	1
G88	SR35266-2-11-4-1-1	0.45	1.00	0.14	1.06	0.47	0.18	0.88	0.94	0.95	0.91	1.30	5	1	3
G95	AgKE99-26	0.44	3.00	0.14	1.19	0.42	0.36	0.85	0.75	1.02	0.92	0.77	5	3	1
G54	WAB 2135-WAC B-2-TGR3-WAT8-3	0.55	7.00	0.13	1.18	0.55	0.45	0.72	0.59	1.15	1.12	0.76	7	1	3
G35	ART493-16-1-1-1-B	0.69	7.00	0.13	1.07	0.64	0.70	0.69	0.64	1.31	1.77	1.06	5	1	1
G33	ART478-13-8-1-1-B***	0.80	1.00	0.13	1.11	0.67	0.63	0.75	1.03	1.06	1.13	0.74	7	1	1
G83	SAHEL 210	0.72	3.00	0.13	1.07	0.88	0.75	0.79	0.83	0.99	1.36	0.80	6	1	1
G26	ART314-14-B-1-B-B	0.72	2.33	0.12	1.11	0.50	0.50	0.69	0.65	0.87	1.16	0.93	9	1	3
G31	ART1005-21-1-1-1-B	0.94	1.00	0.12	0.97	0.38	0.33	0.70	0.82	0.87	0.86	0.76	5	1	1
G15	AGRA-CRI-LOL-1-21	0.75	7.00	0.12	1.11	0.38	0.42	0.86	0.93	1.20	0.86	0.80	5	1	1
G87	SR35278-1-7-3-2	0.54	3.00	0.11	0.96	0.58	0.60	1.05	1.18	0.66	1.12	0.67	7	1	1
G23	ART216-149-B-1-B-B	0.89	3.00	0.11	0.99	0.63	0.57	0.99	0.87	0.98	2.01	1.10	5	1	1
G91	SA60-SARI	0.64	5.00	0.11	1.19	0.67	0.63	0.61	0.86	1.04	0.78	0.77	7	1	3
G63	ARICA 2	0.93	5.00	0.11	1.03	0.45	0.40	0.83	0.86	0.00	0.00	0.00	5	1	1
G43	ART75-14-1-2-B-B	0.98	3.00	0.10	1.08	0.50	0.38	0.71	0.63	0.93	1.13	0.94	5	1	3
G56	AGRA-CRI-LOL-2-29	0.83	7.00	0.10	1.12	0.56	0.50	0.56	0.82	0.74	0.86	0.61	9	1	1
G84	SR34796-1-4-6-3-2-1	0.84	3.00	0.10	1.14	0.29	0.31	0.92	0.86	0.85	1.05	0.92	7	1	1
G28	ART387-9-1-1-1-B	0.51	1.00	0.10	1.09	0.64	0.70	0.89	0.91	1.07	0.99	0.66	7	1	1
G94	DigJas-78	0.65	3.00	0.10	1.01	0.67	0.50	0.70	0.85	0.73	0.91	1.00	5	3	3
G52	ART350:2-6-1-B	0.87	5.00	0.10	1.13	0.60	0.67	0.67	0.82	1.19	0.87	0.00	5	1	1
G29	ART397-12-1-1-1-B	0.33	1.67	0.09	1.10	0.50	0.56	0.82	1.02	0.89	0.61	0.57	7	1	3
G18	SR34590-HB 3433-5-1-1	0.96	7.00	0.09	1.11	0.25	0.29	0.72	0.61	0.00	0.00	0.00	5	1	1

ID	GENOTYPE	CCI-R	SPFS-R	GYP-R	DTF-R	TN-R	PN-R	PH-R	PL-R	GL-R	GW-R	HGW-R	LRS	LDS	DRR
G2	CRI-AgraRice	0.89	1.00	0.08	1.13	0.36	0.40	0.96	0.76	0.97	1.04	0.93	3	1	1
G24	ART216-187-B-1-B-B	0.68	1.00	0.08	1.08	0.64	0.60	0.88	0.88	1.05	1.02	0.89	5	1	1
G76	SR35266-2-18-1-1	0.60	3.00	0.07	1.09	0.75	0.71	0.79	0.67	0.80	0.82	0.88	7	1	1
G11	Enapa	0.70	1.00	0.07	1.03	0.55	0.50	0.77	0.80	0.98	1.00	0.75	5	1	1
G34	ART478-8-1-1-1-B	0.76	1.00	0.07	1.17	0.45	0.36	0.88	1.36	1.04	0.86	1.14	5	1	1
G47	ART98-147-1-1-B-B	0.53	2.33	0.07	1.10	0.29	0.23	0.95	0.76	0.00	0.00	0.00	7	1	3
G96	JKE56-12	0.89	1.00	0.06	1.13	0.57	0.46	0.83	0.74	0.77	0.81	0.84	5	3	1
G7	CRI-Kantinka	0.51	5.00	0.06	1.17	0.50	0.44	0.67	0.90	0.82	0.61	1.24	7	1	1
G22	Jasmine 85-SARI	0.68	7.00	0.05	1.15	0.55	0.50	0.89	0.72	0.90	0.78	0.76	5	1	3
G32	SA26-SARI	1.00	5.00	0.04	1.15	0.60	0.50	0.69	0.44	1.20	0.97	0.89	3	1	1
G55	WAB 2099-WAC1.FKR3-1-TGR1-2	0.75	1.67	0.04	1.16	0.29	0.27	0.69	1.11	1.07	0.80	0.82	5	1	1
G4	Jasmine 85-CRI	0.72	7.00	0.04	1.19	0.75	0.71	0.73	0.79	0.00	0.00	0.00	5	1	1
G13	SA54-SARI	0.58	5.00	0.04	1.05	0.33	0.33	0.87	0.69	0.99	0.74	1.00	7	1	1
G3	Obolo	0.81	1.00	0.04	1.21	0.42	0.36	0.53	0.50	0.98	1.23	1.53	5	1	1
G89	SR35311-HB3497-87	0.93	5.00	0.01	1.18	0.45	0.56	0.81	0.84	1.11	1.10	0.00	5	1	1
G50	ART100-57-1-2-B-B	0.88	9.00	0.00	1.02	0.33	0.33	0.73	1.13	0.94	0.89	1.06	5	1	1
G53	WAB 2085-TGR2-WAT4-1-1	0.55	3.00	0.00	1.12	0.57	0.67	0.64	0.74	0.90	1.20	0.97	9	1	3
G67	Awarema	1.07	9.00	0.00	0.81	0.38	0.33	1.09	0.99	0.63	0.59	0.93	5	1	3
G66	UPL 32	1.43	7.00	0.00	1.05	0.42	0.45	0.73	0.66	1.06	0.98	0.81	5	1	1
G39	ART174-2-1-1-B-B	0.65	9.00	0.00	1.16	0.33	0.27	0.64	0.82	1.16	0.72	0.67	7	1	1
G58	CRI-1-21-5-12	0.82	3.00	0.00	1.03	0.33	0.36	0.86	1.06	1.01	1.05	0.00	5	1	1
G9	CRI-Emopa	1.02	2.33	0.00	1.04	0.50	0.44	0.65	0.89	0.00	0.00	0.00	5	1	1
G27	SA7-SARI	0.79	3.00	0.00	1.07	0.67	0.44	0.71	0.88	0.00	0.00	0.00	7	1	3
G36	ART132-35-1-1-B-B	0.47	3.00	0.00	1.09	0.55	0.60	0.51	0.74	0.00	0.00	0.00	9	1	5
G45	ART90-9-1-1-B-B	0.73	9.00	0.00	1.16	0.45	0.40	0.70	1.13	0.00	0.00	0.00	5	1	3
G57	NERICA-L 41	0.74	9.00	0.00	1.04	0.38	0.31	0.52	0.46	0.00	0.00	0.00	5	1	1
G61	BETIA	0.91	7.00	0.00	1.13	0.45	0.40	0.69	0.70	0.00	0.00	0.00	5	1	1
G78	SA68-SARI	0.40	9.00	0.00	1.13	0.67	0.63	0.75	1.45	0.00	0.00	0.00	7	1	1
G85	SR35278-1-7-2-2	0.92	9.00	0.00	1.11	0.45	0.44	0.72	0.89	0.00	0.00	0.00	7	1	1
G97	KBR 10	0.80	9.00	0.00	1.03	0.71	0.67	0.72	0.77	0.00	0.00	0.00	5	3	1
G8	CRI-Oboafo	0.89	-	-	1.17	0.25	-	0.87	-	0.00	0.00	0.00	5	1	1

CCI-R- Relative Chlorophyll Content Index; SPFS-R-Relative Spikelet Fertility Score; GYP-R-Relative Grain Yield per Plant; DTF-R-Relative Days to flowering; TN-R-Relative Tiller Number per Plant; PN-R-Relative Panicle Number per Plant; PH-R-Relative Plant Height(cm); PL-R-Relative Panicle Length(cm); GL-R-Relative Grain Length(mm); GW-R-Relative Grain width(mm); HGW-R-Relative Hundred Grains Weight(g); LRS-Leaf Rolling Score ; LDS-Leaf Drying Score; DRR-Drought Recovery

Annex IX. The outputs of the MGIDI index computation among the 100 rice genotypes evaluated for 14 morphophysiological traits across both non-drought and drought stress water regimes under field conditions at the CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2021-2022

```
> View(Kossia)
> df <- Kossia %>% mutate_at(c('REP', 'BLOCK','GENOTYPE'), as.factor)
> str(df)
tibble [300 × 13] (S3: tbl_df/tbl/data.frame)
 $ REP     : Factor w/ 3 levels "1","2","3": 1 2 3 1 2 3 1 2 3 1 ...
 $ BLOCK   : Factor w/ 10 levels "1","2","3","4",..: 1 1 1 1 1 1 10 10 10 2 ...
 $ GENOTYPE: Factor w/ 100 levels "G1","G10","G100",..: 1 1 1 2 2 2 3 3 3 4 ...
 $ LRS     : num [1:300] 3.2 4.2 4.2 0.2 2.4 2.6 3.8 4.2 9 6.6 ...
 $ LDS     : num [1:300] 1 1 1 0.4 1 1 1 1 1 1 ...
 $ DRR     : num [1:300] 1 1 1 1 1 1 1 1 1 1 ...
 $ SPFS    : num [1:300] 0.65 0 NA NA 1.15 ...
 $ CC      : num [1:300] 0.778 0.531 0.952 NA 0.82 ...
 $ GYP     : num [1:300] 0.0548 0 0.2 0.1042 0.2 ...
 $ DTF     : num [1:300] 1.12 0 1.11 1.29 1.37 ...
 $ TN      : num [1:300] 0.339 0.66 NA NA 1.75 ...
 $ PH      : num [1:300] 0.58 0.713 NA NA 0.765 ...
 $ GL      : num [1:300] 0.609 0 NA NA 1.341 ...
> mod <- gamem(df,
+              gen = GENOTYPE,
+              rep = REP,
+              block = BLOCK,
+              resp = everything())

Method: REML/BLUP
Random effects: GEN, BLOCK(REP)
Fixed effects: REP
Denominador DF: Satterthwaite's method
---------------------------------------------------------------------------
P-values for Likelihood Ratio Test of the analyzed traits
---------------------------------------------------------------------------
     model     LRS    LDS   DRR     SPFS   CC     GYP   DTF   TN    PH
  Complete      NA     NA    NA       NA  NA      NA    NA   NA    NA
  Genotype 0.00175 0.0277 0.647 0.000761 0.75 0.06010 0.581 0.29 0.950
 rep:block 1.00000 1.0000 1.000 1.000000 0.82 0.00289 1.000 1.00 0.393
    GL
    NA
 0.689
 0.892
---------------------------------------------------------------------------
Variables with nonsignificant Genotype effect
DRR CC GYP DTF TN PH GL
---------------------------------------------------------------------------
> blups <- gmd(mod, "blupg")
Class of the model: gamem
Variable extracted: blupg
> res <- c(rep(0, 4), rep(100, 6))
> for (i in 2:ncol(blups)) {
+   blups[i] <- resca(values = blups[i], new_max = res[i], new_min = 100 - res[i])
+ }
> str(blups)
tibble [100 × 11] (S3: tbl_df/tbl/data.frame)
 $ GEN : chr [1:100] "G1" "G10" "G100" "G11" ...
 $ LRS : num [1:100] 68.1 96.5 44.2 56.6 59.3 ...
 $ LDS : num [1:100] 92.1 96.8 92.1 92.1 92.1 ...
 $ DRR : num [1:100] 100 100 100 100 100 ...
 $ SPFS: num [1:100] 31.9 77.5 73.4 85.7 18.5 ...
 $ CC  : num [1:100] 14.2 18 20.4 12.7 22.8 ...
 $ GYP : num [1:100] 21.7 41.4 71.4 24.9 26.3 ...
 $ DTF : num [1:100] 34 69.9 58.5 28.8 60.5 ...
 $ TN  : num [1:100] 27 84.8 25.3 14.8 15.7 ...
 $ PH  : num [1:100] 35.2 47.5 41.6 43 53.7 ...
 $ GL  : num [1:100] NA NA NA NA NA NA NA NA NA NA ...
> mgidi_index <-
```

```
+   mgidi(mod,
+         ideotype = c(rep("l", 4), rep("h", 6)),
+         SI = 15)

-------------------------------------------------------------------------------
Principal Component Analysis
-------------------------------------------------------------------------------
# A tibble: 10 × 4
   PC    Eigenvalues `Variance (%)` `Cum. variance (%)`
   <chr>       <dbl>          <dbl>               <dbl>
 1 PC1          2.71          27.1                27.1
 2 PC2          1.82          18.2                45.3
 3 PC3          1.1           11                  56.3
 4 PC4          1.07          10.7                67.0
 5 PC5          0.81           8.08               75.1
 6 PC6          0.8            7.96               83.1
 7 PC7          0.52           5.22               88.3
 8 PC8          0.45           4.54               92.8
 9 PC9          0.39           3.9                96.7
10 PC10         0.33           3.28              100
-------------------------------------------------------------------------------
Factor Analysis - factorial loadings after rotation-
-------------------------------------------------------------------------------
# A tibble: 10 × 7
   VAR     FA1   FA2   FA3   FA4 Communality Uniquenesses
   <chr> <dbl> <dbl> <dbl> <dbl>       <dbl>        <dbl>
 1 LRS   -0.86  0.11 -0.07  0          0.76         0.24
 2 LDS   -0.81  0.08  0.15 -0.01       0.68         0.32
 3 DRR   -0.77  0.02  0.2   0.01       0.63         0.37
 4 SPFS   0.26 -0.77 -0.03  0.11       0.68         0.32
 5 CC    -0.26 -0.17  0.72  0.26       0.69         0.31
 6 GYP   -0.05  0.66  0.47  0.15       0.68         0.32
 7 DTF   -0.08  0.31  0.57 -0.35       0.55         0.45
 8 TN    -0.02 -0.02 -0.06 -0.88       0.77         0.23
 9 PH    -0.16  0.55 -0.35  0.29       0.54         0.46
10 GL     0.1   0.84  0    -0.09       0.72         0.28
-------------------------------------------------------------------------------
Comunalit Mean: 0.6702168
-------------------------------------------------------------------------------
Selection differential
-------------------------------------------------------------------------------
# A tibble: 10 × 11
   VAR   Factor    Xo    Xs       SD  SDperc     h2       SG   SGperc sense
   <chr> <chr>  <dbl> <dbl>    <dbl>   <dbl>  <dbl>    <dbl>    <dbl> <chr>
 1 LRS   FA1    5.60  5.26  -3.40e-1 -6.07   0.415  -1.41e-1 -2.52e+0 decr…
 2 LDS   FA1    1.29  1.18  -1.12e-1 -8.64   0.313  -3.50e-2 -2.70e+0 decr…
 3 DRR   FA1    1.70  1.65  -4.30e-2 -2.54   0.0763 -3.28e-3 -1.93e-1 decr…
 4 SPFS  FA2    0.445 0.584  1.38e-1 31.1    0.483   6.69e-2  1.50e+1 decr…
 5 GYP   FA2    0.158 0.212  5.42e-2 34.4    0.270   1.47e-2  9.29e+0 incr…
 6 PH    FA2    0.787 0.787  9.06e-5  0.0115 0.0110  9.93e-7  1.26e-4 incr…
 7 GL    FA2    0.448 0.462  1.36e-2  3.02   0.0677  9.18e-4  2.05e-1 incr…
 8 CC    FA3    0.844 0.861  1.72e-2  2.03   0.0551  9.44e-4  1.12e-1 incr…
 9 DTF   FA3    0.921 0.938  1.72e-2  1.87   0.0908  1.57e-3  1.70e-1 incr…
10 TN    FA4    0.515 0.522  7.85e-3  1.53   0.174   1.37e-3  2.66e-1 incr…
# ℹ 1 more variable: goal <dbl>
-------------------------------------------------------------------------------
Selected genotypes
-------------------------------------------------------------------------------
G60 G100 G77 G99 G79 G66 G6 G74 G65 G44 G81 G21 G89 G14 G10
-------------------------------------------------------------------------------
```

Annex X. Genotyping results of 100 rice genotypes evaluated under drought stress based on known drought-tolerant QTLs for grain yield at Fumesua-Kumasi, Ghana in 2021-2022

ID	QTL ID	DTY1.1	DTY1.1	DTY1.1	DTY12.1	DTY12.1	DTY2.2	DTY2.2	DTY2.2	DTY2.2
	SNP ID	snpOS00400	snpOS00402	snpOS00408	snpOS00483	snpOS00484	snpOS00412	snpOS00413	snpOS00414	snpOS00415
	FAVORABLE ALLELE	G	A	G	C	T	A	C	G	A
	Genotype									
G1	CRI-AMANKWATIA	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G2	CRI-AgraRice	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G3	Obolo	G:G	G:G	G:G	G:G	G:G	C:C	T:T	A:A	C:C
G4	Jasmine 85- CRI	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G5	ARICA 3	C:C	G:G	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G6	TogoMarshall	C:C	G:G	T:T	C:C	G:A	C:C	A:A	A:A	T:T
G7	CRI-Kantinka	G:G	A:A	G:G	C:C	G:G	C:C	A:A	G:G	T:T
G8	CRI-Oboafo	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G9	CRI-Emopa	G:G	G:G	T:T	G:G	G:G	A:A	A:A	A:A	T:T
G10	CRI-Mpuntuo	C:C	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G11	CRI-Enapa	G:G	G:G	T:T	G:G	G:G	A:A	A:A	A:A	T:T
G12	AGRA-CRI-LOL-2-7	C:C	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G13	SA54-SARI	G:G	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G14	AGRA-CRI-LOL-1-11	G:G	A:A	G:G	C:C	G:G	C:C	A:A	G:G	T:T
G15	AGRA-CRI-LOL-1-21	G:G	A:A	G:G	C:C	G:G	C:C	A:A	G:G	T:T
G16	SA25-SARI	G:G	A:A	G:G	C:C	G:G	C:C	A:A	G:G	T:T
G17	SAHEL 177	C:C	G:G	T:T	G:G	A:A	A:A	A:A	G:G	C:C
G18	SR34590-HB3433-5-1-1	C:C	G:G	T:T	G:G	A:A	A:A	A:A	A:A	T:T
G19	SR35266-2-16-1-1	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G20	SR35266-2-18-2-1	G:G	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G21	SR35266-2-12-4-1	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G22	Jasmine 85- SARI	C:C	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G23	ART216-149-B-1-B-B	G:G	A:A	T:T	C:C	G:G	C:C	A:A	A:A	T:T
G24	ART216-187-B-1-B-B	C:C	G:G	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G25	SA29-SARI	C:C	G:G	T:T	G:G	A:A	C:C	A:A	G:G	T:T
G26	ART314-14-B-1-B-B	G:G	G:G	T:T	G:G	G:G	A:A	A:A	G:G	T:T

ID	QTL ID SNP ID FAVORABLE ALLELE Genotype	DTY1.1 snpOS00400	DTY1.1 snpOS00402	DTY1.1 snpOS00408	DTY12.1 snpOS00483	DTY12.1 snpOS00484	DTY2.2 snpOS00412	DTY2.2 snpOS00413	DTY2.2 snpOS00414	DTY2.2 snpOS00415
		G	A	G	C	T	A	C	G	A
G27	SA7-SARI	C:G	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G28	ART387-9-1-1-1-B									
G29	ART397-12-1-1-1-B	G:G	G:G	T:T	G:G	A:A	A:A	A:A	G:G	T:T
G30	ART430-16-1-1-1-B	G:G	A:A	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G31	ART1005-21-1-1-1-B	G:G	A:A	T:T	G:G	G:G	A:A	A:A	A:A	T:T
G32	SA26-SARI	C:C	G:G	T:T	C:C	G:A	C:C	A:A	G:G	T:T
G33	ART478-13-8-1-1-B***	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G34	ART478-8-1-1-1-B	C:C	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G35	ART493-16-1-1-1-B	C:C	G:G	G:G	G:G	G:G	A:A	A:A	G:G	T:T
G36	ART132-35-1-1-B-B	G:G	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G37	SA41-SARI	C:C	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G38	SA50-SARI	C:C	G:G	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G39	ART174-2-1-1-B-B	G:G	A:A	G:G	G:G	A:A	C:C	A:A	A:A	T:T
G40	SA38-SARI	C:C	G:G	T:T	G:G	G:G	A:A	A:A	A:A	T:T
G41	SA9-SARI	G:G	A:A	G:G	C:C	G:G	C:C	A:A	A:A	C:C
G42	ART68-12-1-1-B-B**	G:G	G:G	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G43	ART75-14-1-2-B-B	G:G	A:A	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G44	ART75-33-1-1-B-B	C:C	G:G	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G45	ART90-9-1-1-B-B									
G46	ART73-69-1-2-B-B	G:G	G:G	T:T	G:G	A:A	C:C	A:A	G:G	T:T
G47	ART98-147-1-1-B-B	G:G	A:A	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G48	SA21-SARI	G:G	G:G	T:T	G:G	G:G	A:A	A:A	A:A	T:T
G49	SA20-SARI	C:C	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G50	ART100-57-1-2-B-B	G:G	A:A	G:G	C:C	G:G	C:C	A:A	G:G	T:T
G51	ART112-74-1-1-B-B	G:G	G:G	G:G	C:G	G:G	C:C	A:T	G:A	T:C
G52	ART350:2-6-1-B	C:C	G:G	G:G	G:G	A:A	C:C	A:A	G:G	T:T
G53	WAB 2085-TGR2-WAT4-1-1	G:G	G:G	T:T	C:C	G:G	A:A	A:A	A:A	T:T

ID	QTL ID SNP ID FAVORABLE ALLELE Genotype	DTY1.1 snpOS00400 G	DTY1.1 snpOS00402 A	DTY1.1 snpOS00408 G	DTY12.1 snpOS00483 C	DTY12.1 snpOS00484 T	DTY2.2 snpOS00412 A	DTY2.2 snpOS00413 C	DTY2.2 snpOS00414 G	DTY2.2 snpOS00415 A
G54	WAB 2135-WAC B-2-TGR3-WAT8-3	G:G	A:A	G:G	C:C	G:G	C:C	A:A	A:A	C:C
G55	WAB 2099-WAC1.FKR3-1-TGR1-2	C:C	G:G	G:G	G:G	G:G	A:A	A:A	G:G	T:T
G56	AGRA-CRI-LOL-2-29	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G57	NERICA-L 41	G:G	A:A	G:G	C:C	G:G	C:C	A:A	G:G	T:T
G58	CRI-1-21-5-12	G:G	G:G	T:T	G:G	G:G	A:A	A:A	A:A	T:T
G59	SA64-SARI	G:G	A:A	G:G	G:G	A:A	A:A	A:A	A:A	C:C
G60	Viwonor short	C:G	A:A	G:G	G:G	G:G	A:A	A:A	G:G	T:T
G61	BETIA	C:C	G:G	T:T	C:C	G:G	C:C	A:A	A:A	T:T
G62	KE40	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G63	ARICA 2	C:C	G:G	T:T	G:G	A:A	C:C	A:A	G:G	T:T
G64	SA14-SARI	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G65	GR18-SARI	C:C	G:G	T:T	G:G	A:A	A:A	A:A	G:G	T:T
G66	UPL 32	G:G	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G67	Awarema									
G68	Oreire	G:G	G:G	T:T	C:C	G:G	C:C	A:A	A:A	T:T
G69	AGRA-SARI									
G70	Ex- Baike (Asutware)	C:C	G:G	T:T	C:C	G:G	C:C	A:A	A:A	T:T
G71	SR34590-HB3433-8-3-1	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G72	SR34590-HB3433-8-2-1	C:C	G:G	T:T	G:G	G:A	A:A	A:A	A:A	T:T
G73	SR35266-2-12-1-1	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G74	SR35266-2-12-4-1-SARI	C:C	G:G	T:T	G:G	A:A	A:C	A:A	A:A	T:T
G75	SR35266-2-17-2-1	C:C	G:G	T:T	G:G	G:G	A:A	A:A	G:G	T:T
G76	SR35266-2-18-1-1	C:C	G:G	T:T	G:G	G:G	A:A	A:A	G:G	T:T
G77	SR35250-2-4-2-3	C:C	G:G	T:T	G:G	A:A	C:C	A:A	G:G	T:T
G78	SA68-SARI	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G79	SA69-SARI	G:G	A:A	G:G	G:G	A:A	C:C	A:A	G:G	T:T

ID	QTL ID	DTY1.1	DTY1.1	DTY1.1	DTY12.1	DTY12.1	DTY2.2	DTY2.2	DTY2.2	DTY2.2
	SNP ID	snpOS00400	snpOS00402	snpOS00408	snpOS00483	snpOS00484	snpOS00412	snpOS00413	snpOS00414	snpOS00415
	FAVORABLE ALLELE	G	A	G	C	T	A	C	G	A
	Genotype									
G80	SA24-SARI	C:C	G:G	T:T	C:C	G:G	C:C	A:A	A:A	T:T
G81	SR34590-HB3433-6-2-1	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G82	SAHEL134	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	C:C
G83	SAHEL210	C:C	G:G	T:T	G:G	A:A	A:A	A:A	A:A	T:T
G84	SR34796-1-4-6-3-2-1	G:G	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G85	SR35278-1-7-2-2	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G86	SR33705F2-61-1-3-HV-1-1	C:C	G:G	T:T	G:G	A:A	C:C	A:A	A:A	T:T
G87	SR35278-1-7-3-2	C:C	G:G	T:T	G:G	G:G	C:C	A:A	G:G	T:T
G88	SR35266-2-11-4-1-1	C:C	G:G	T:T	G:G	A:A	A:A	A:A	G:G	T:T
G89	SR35311-HB3497-87									
G90	HR32067F1-2-14-1	G:G	G:G	T:T	G:G	G:A	C:C	A:A	A:A	T:T
G91	SA60-SARI	G:G	G:G	T:T	G:G	G:G	C:C	A:A	A:A	T:T
G92	Gigante	G:G	G:G	G:G	G:G	G:G	A:A	T:T	A:A	C:C
G93	DigJas-61	G:G	A:A	G:G	C:C	G:G	C:C	A:A	A:A	C:C
G94	DigJas-78	G:G	A:A	G:G	C:C	G:G	C:C	A:A	A:A	C:C
G95	AgKE99-26	C:C	G:G	T:T	G:G	A:A	A:A	A:A	G:G	T:T
G96	JKE56-12	C:C	G:G	G:G	G:G	A:A	A:A	A:A	G:G	T:T
G97	KBR 10	C:C	G:G	T:T	G:G	A:A	A:A	A:A	G:G	T:T
G98	ORYLUX 6	C:C	G:G	G:G	G:G	G:G	A:A	A:A	G:G	T:T
G99	APO	G:G	A:A	G:G	C:C	G:G				
G100	UPL R17	G:G	A:A	G:G	C:C	G:G				

Genotypes highlighted in yellow are the selected genotypes with tolerance to drought based on MGIDI index; The highlighted in deep green, are the favorable alleles for each QTL present in each selected genotype; ID-Genotype identity; QTL ID-Quantitative Trait Locus Identity; SNP ID-Single Nucleotide Polymorphism Marker Identity

Annex XI. Pearson correlations among 14 rice genotypes evaluated under non-drought conditions for eight physiological and leaf reflectance traits at 5 days after starting of the drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.9601	-0.0945	0.3382	-0.0657	-0.1712	-0.2411	0.1528
	p-value		<.0001	0.4075	0.0023	0.5651	0.1314	0.0323	0.1787
E	r		1	-0.027	0.325	-0.011	-0.141	-0.211	0.181
	p-value			0.8167	0.0035	0.9265	0.2153	0.0622	0.1107
PhiPS2	r			1	-0.4249	-0.0202	0.1235	0.1490	-0.0568
	p-value				<.0001	0.8601	0.2784	0.19	0.6188
ETR	r				1	0.0892	0.0737	0.0193	0.0016
	p-value					0.4343	0.5185	0.8661	0.9886
NDVI	r					1	0.5998	0.5417	0.2303
	p-value						<.0001	<.0001	0.0411
CRI1	r						1	0.9783	-0.4203
	p-value							<.0001	0.0001
CRI2	r							1	-0.4326
	p-value								<.0001

r-correlation value; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XII. Pearson correlations among 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 5 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.9387	-0.0691	0.0066	-0.0965	-0.2587	-0.3311	0.1503
	p-value		<.0001	0.545	0.9538	0.3974	0.0213	0.0029	0.1863
E	r		1	-0.0106	-0.0474	-0.0899	-0.1880	-0.2585	0.0474
	p-value			0.9262	0.6781	0.4307	0.0971	0.0214	0.6781
PhiPS2	r			1	-0.4892	0.2030	0.1799	0.1617	-0.0654
	p-value				<.0001	0.0728	0.1127	0.1546	0.567
ETR	r				1	-0.1927	-0.0187	-0.0063	-0.1109
	p-value					0.0888	0.8698	0.956	0.3307
NDVI	r					1	0.3076	0.2424	0.3673
	p-value						0.0058	0.0314	0.0009
CRI1	r						1	0.9774	-0.6927
	p-value							<.0001	<.0001
CRI2	r							1	-0.699
	p-value								<.0001

r-correlation value; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XIII. Pearson correlations among 14 rice genotypes evaluated under non-drought conditions for eight physiological and leaf reflectance traits at 11 days after starting of the drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.9282	-0.0872	0.1322	0.1858	-0.1085	-0.1115	0.1643
	p-value		<.0001	0.4448	0.2455	0.1011	0.3414	0.3279	0.148
E	r		1	-0.1955	0.2345	0.1875	-0.1484	-0.1406	0.1335
	p-value			0.0843	0.0375	0.098	0.1917	0.2165	0.2407
PhiPS2	r			1	-0.6493	-0.1691	-0.0511	-0.0586	-0.0602
	p-value				<.0001	0.1362	0.6549	0.6078	0.598
ETR	r				1	0.0582	0.0505	0.1091	-0.0503
	p-value					0.6105	0.6583	0.3385	0.6599
NDVI	r					1	0.0350	0.0202	0.5405
	p-value						0.7596	0.8595	<.0001
CRI1	r						1	0.9809	-0.6121
	p-value							<.0001	<.0001
CRI2	r							1	-0.6031
	p-value								<.0001

r-correlation value; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XIV. Pearson correlations among 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 11 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.9361	-0.1720	0.3916	0.0087	-0.2059	-0.2032	0.1550
	p-value		<.0001	0.1296	0.0004	0.9392	0.0687	0.0725	0.1727
E	r		1	-0.1908	0.4452	-0.0422	-0.2310	-0.2269	0.1254
	p-value			0.0921	<.0001	0.7122	0.0406	0.0444	0.2708
PhiPS2	r			1	-0.5628	-0.0834	0.1754	0.2156	-0.2231
	p-value				<.0001	0.465	0.1221	0.0564	0.0482
ETR	r				1	0.0624	-0.0838	-0.0836	0.1206
	p-value					0.5852	0.4626	0.4639	0.2897
NDVI	r					1	0.1103	0.0465	0.5851
	p-value						0.3332	0.6838	<.0001
CRI1	r						1	0.9641	-0.5095
	p-value							<.0001	<.0001
CRI2	r							1	-0.5328
	p-value								<.0001

r-correlation value; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XV. Pearson correlations among 14 rice genotypes evaluated under non-drought conditions for eight physiological and leaf reflectance traits at 18 days after starting of the drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.9283	-0.0103	0.0731	0.0792	0.0276	0.0362	0.0387
	p-value		<.0001	0.928	0.5222	0.488	0.8093	0.7518	0.7351
E	r		1	-0.0407	0.1898	0.0595	-0.0356	-0.0303	0.1131
	p-value			0.7216	0.0938	0.6023	0.7558	0.7907	0.321
PhiPS2	r			1	-0.4107	-0.2675	0.0456	0.1156	-0.2098
	p-value				0.0002	0.0172	0.6897	0.3102	0.0635
ETR	r				1	-0.0503	-0.0259	-0.0167	0.0512
	p-value					0.6595	0.821	0.8839	0.6538
NDVI	r					1	0.0536	-0.0117	0.4121
	p-value						0.6391	0.9182	0.0002
CRI1	r						1	0.9694	-0.7020
	p-value							<.0001	<.0001
CRI2	r							1	-0.6841
	p-value								<.0001

r-correlation value; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XVI. Pearson correlations among 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 18 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.8659	-0.0095	-0.0084	0.0149	-0.0181	-0.0179	-0.0820
	p-value		<.0001	0.906	0.9163	0.853	0.8215	0.8234	0.3057
E	r		1	-0.0175	0.1004	-0.0236	-0.0662	-0.0609	-0.0531
	p-value			0.8271	0.2095	0.7686	0.4089	0.447	0.5079
PhiPS2	r			1	-0.3076	-0.2419	0.1333	0.1955	-0.2274
	p-value				<.0001	0.0022	0.0951	0.0138	0.0041
ETR	r				1	0.0322	-0.0244	-0.0232	0.0563
	p-value					0.6884	0.7608	0.7725	0.4821
NDVI	r					1	0.0599	0.0152	0.4307
	p-value						0.4548	0.8495	<.0001
CRI1	r						1	0.9770	-0.7027
	p-value							<.0001	<.0001
CRI2	r							1	-0.6954
	p-value								<.0001

r-correlation value; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XVII. Pearson correlations among 14 rice genotypes evaluated under non-drought conditions for eight physiological and leaf reflectance traits at 27 days after starting of the drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.5341	-0.0368	-0.0602	-0.1658	0.0588	0.0865	-0.0787
	p-value		0.0006	0.8265	0.7196	0.3197	0.7259	0.6057	0.6387
E	r		1	0.1796	0.0540	0.0199	-0.1224	-0.1363	0.1452
	p-value			0.2806	0.7475	0.9056	0.4642	0.4147	0.3845
PhiPS2	r			1	-0.2721	-0.0525	-0.2310	-0.2039	0.1765
	p-value				0.0984	0.7544	0.1629	0.2195	0.2893
ETR	r				1	-0.2665	0.2101	0.2156	-0.3200
	p-value					0.1058	0.2054	0.1935	0.0502
NDVI	r					1	0.1400	0.0500	0.3681
	p-value						0.3271	0.7278	0.0079
CRI1	r						1	0.9752	-0.7321
	p-value							<.0001	<.0001
CRI2	r							1	-0.7924
	p-value								<.0001

r-correlation coefficient; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XVIII. Pearson correlations among 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 27 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

TRAITS		gsw	E	PhiPS2	ETR	NDVI	CRI1	CRI2	RDVI
gsw	r	1	0.9772	0.2550	-0.1105	0.0117	0.1782	0.1975	-0.0425
	p-value		<.0001	0.1076	0.4915	0.9421	0.2651	0.2159	0.792
E	r		1	0.2778	-0.1067	0.0246	0.1537	0.1736	-0.0229
	p-value			0.0787	0.5068	0.8788	0.3372	0.2779	0.8868
PhiPS2	r			1	0.1770	0.8378	0.7945	0.8040	0.7884
	p-value				0.2683	<.0001	<.0001	<.0001	<.0001
ETR	r				1	0.2801	0.1829	0.1437	0.3144
	p-value					0.0762	0.2525	0.3702	0.0453
NDVI	r					1	0.7448	0.8171	0.9411
	p-value						<.0001	<.0001	<.0001
CRI1	r						1	0.9593	0.5188
	p-value							<.0001	<.0001
CRI2	r							1	0.6188
	p-value								<.0001

r-correlation coefficient; gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XIX. Relative values of 14 rice genotypes evaluated for eight physiological and leaf reflectance traits under 5, 11, 18 and 27 days drought stress at the Institute for Agronomy and Plant Breeding of Justus-Liebig-University of Giessen, Germany in 2022

ID	Genotype	Relative gsw	Relative E	Relative PhiPS2	Relative ETR	Relative NDVI	Relative CRI	Relative CRI2	Relative RDVI
5 days drought stress									
G11	CRI-Enapa	1.286	1.259	0.988	0.787	1.024	1.138	1.167	0.981
G62	KE40	0.764	0.959	1.011	1.035	1.020	1.128	1.124	0.975
G99	APO	0.738	0.916	1.003	0.842	0.989	1.102	1.117	0.914
G6	Togo Marshall	0.886	0.875	0.999	1.081	1.000	1.080	1.081	0.978
G73	SR35266-2-12-1-1	1.020	1.076	0.962	0.932	1.011	1.062	1.080	1.011
G36	ART132-35-1-1-B-B	0.717	0.812	1.049	1.468	0.992	1.070	1.068	0.943
G5	ARICA 3	1.039	0.998	1.001	0.821	0.997	1.068	1.060	0.987
G22	Jasmine 85	1.258	1.208	1.001	1.071	1.011	1.062	1.032	1.030
G65	GR18-SARI	0.929	1.018	0.964	1.274	1.005	1.004	0.982	0.983
G63	ARICA 2	1.018	1.039	1.009	1.038	0.991	0.980	1.016	1.017
G2	CRI-Agrarice	1.349	1.298	1.037	0.909	0.998	0.970	0.969	1.000
G78	SA68-SARI	0.789	0.840	1.025	0.756	0.984	0.955	0.951	0.990
G53	WAB 2085-TGR2-WAT4-1-1	0.657	0.785	0.990	0.916	0.988	0.933	0.956	0.999
G100	UPLR-17	1.095	1.074	0.978	0.851	0.992	0.928	0.925	1.014
11 days drought stress									
G6	Togo Marshall	1.484	1.290	1.027	0.830	1.003	0.963	0.962	1.023
G100	UPLR-17	1.103	1.043	1.042	0.443	1.005	1.008	1.005	1.004
G5	ARICA 3	0.822	0.897	1.035	1.031	1.009	1.017	1.011	1.007
G2	CRI-Agrarice	0.736	0.785	1.042	0.682	0.989	0.983	0.996	0.967
G11	CRI-Enapa	0.731	0.825	0.945	1.308	1.028	1.029	1.025	1.025
G22	Jasmine 85	0.609	0.706	0.990	1.215	1.012	0.958	0.966	1.039
G99	APO	0.599	0.731	0.996	0.842	0.991	0.993	0.998	0.979
G53	WAB 2085-TGR2-WAT4-1-1	0.581	0.627	1.104	0.350	1.000	0.986	0.997	0.993
G73	SR35266-2-12-1-1	0.578	0.780	1.005	0.972	0.992	0.940	0.940	0.996
G78	SA68-SARI	0.578	0.633	1.059	0.917	0.979	1.030	1.036	0.973
G62	KE40	0.517	0.696	1.005	1.035	1.018	0.999	1.004	1.015
G63	ARICA 2	0.453	0.649	1.001	0.962	0.993	1.000	1.009	0.988
G65	GR18-SARI	0.401	0.522	1.032	0.699	1.004	0.995	1.000	1.014
G36	ART132-35-1-1-B-B	0.312	0.503	1.037	0.988	1.014	1.087	1.075	0.992
18 days drought stress									
G99	APO	0.502	0.685	0.992	1.067	1.007	1.008	1.010	1.024
G100	UPLR-17	0.435	0.617	0.987	1.031	1.001	1.011	1.010	1.011
G22	Jasmine 85	0.418	0.571	0.953	0.957	0.994	1.012	1.023	1.006
G36	ART132-35-1-1-B-B	0.412	0.562	1.005	1.605	0.997	1.065	1.083	0.973
G11	CRI-Enapa	0.406	0.564	0.994	0.941	1.004	1.070	1.076	0.983
G2	CRI-AgraRice	0.397	0.550	0.996	1.241	1.000	0.988	0.993	1.013
G6	Togo Marshall	0.317	0.474	1.084	0.838	0.995	1.028	1.022	0.978
G65	GR18-SARI	0.308	0.479	0.941	1.083	1.008	0.970	0.959	1.035
G53	WAB 2085-TGR2-WAT4-1-1	0.293	0.399	0.985	0.871	1.004	1.014	1.012	0.994
G5	ARICA 3	0.242	0.397	0.983	1.009	1.009	0.942	0.930	1.047

ID	Genotype	Relative gsw	Relative E	Relative PhiPS2	Relative ETR	Relative NDVI	Relative CRI	Relative CRI2	Relative RDVI
G62	KE40	0.226	0.399	0.994	0.820	1.004	0.938	0.931	1.038
G73	SR35266-2-12-1-1	0.222	0.357	0.996	1.017	1.000	0.957	0.935	1.030
G78	SA68-SARI	0.209	0.410	1.007	0.886	0.991	0.981	0.962	1.023
G63	ARICA 2	0.150	0.305	1.098	1.020	1.004	1.004	1.011	1.019
				27 days drought stress					
G99	APO	0.439	0.699	1.062	0.963	1.006	0.867	0.827	1.131
G100	UPLR-17	0.401	0.725	1.039	0.794	0.977	0.937	0.945	1.003
G22	CRI-Agrarice	0.182	0.304	0.923	1.200	0.950	0.851	0.891	0.958
G36	ART132-35-1-1-B-B	0.141	0.271	0.959	1.292	0.988	0.931	0.890	1.029
G6	Togo Marshall	0.127	0.238	0.890	0.872	0.985	0.957	1.007	1.008
G11	CRI-Enapa	0.123	0.328	1.296	1.251	0.969	0.883	0.893	1.026
G78	SA68-SARI	0.118	0.288	1.006	0.998	0.978	1.077	1.073	0.955
G73	SR35266-2-12-1-1	0.112	0.252	0.889	1.048	0.980	0.912	0.887	1.032
G53	WAB 2085-TGR2-WAT4-1-1	0.102	0.182	0.965	0.997	0.996	0.923	0.914	1.048
G62	KE40	0.100	0.202	0.996	0.946	0.970	0.842	0.902	1.001
G63	ARICA 2	0.082	0.234	1.026	0.913	0.956	0.844	0.898	0.984
G5	ARICA 3	0.070	0.164	0.917	0.712	1.007	0.931	0.923	1.051
G65	GR18-SARI	0.070	0.168	0.989	0.987	0.983	0.900	0.904	1.032
G22	Jasmine 85	0.035	0.105	0.985	1.223	0.993	0.906	0.887	1.020

gsw-Stomatal conductance; E-transpiration rate; PhiPS II-Quantum yield of fluorescence; ETR-Electron transport rate; NDVI-Normalized difference vegetative index; CRI1-Carotenoid reflectance index 1; CRI1-Carotenoid reflectance index 2; RDVI-Renormalized difference vegetative index

Annex XX. Mean square from the analysis of variance among the six populations derived from the crosses Agra/Apo for all the traits under non-drought conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Source	DF	TN	PN	PH	PL	DTF	GYP
Model	7	50.60**	68.44**	1505.02**	19.31	272.21**	97.64**
Replication	2	18.40*	30.62**	554.09	35.87	9.74	3.84
Generation	5	64.76**	85.20**	1878.36**	13.49	378.79**	133.85
Residual	211	5.21	5.34	185.71	102.52	3.50	27.27
C.V. (%)	218	30.64	37.67	13.11	45.68	2.02	41.58

***-Significant at 0.01; *-Significant at 0.05; DF-Degree of freedom; C.V.- Coefficient of variation; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm)*

Annex XXI. Mean square from the analysis of variance among the six populations derived from the crosses J.85/Apo for all the traits under non-drought conditions evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Source	DF	TN	PN	PH	PL	DTF	GYP
Model	7	36.71**	66.94**	1430.64**	45.52	101.10**	68.40*
Replication	2	28.39**	11.91	677.14**	71.13	7.73*	7.79
Generation	5	39.10**	86.70**	1695.63**	29.94	138.08**	91.54*
Residual	211	5.05	5.14	137.73	68.91	2.37	27.89
C.V. (%)	-	29.38	34.72	11.52	36.21	1.67	35.01

***-Significant at 0.01; *-Significant at 0.05; DF-Degree of freedom; C.V.- Coefficient of variation; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm)*

Annex XXII. Mean square from the analysis of variance among the six populations derived from the crosses Agra/Apo for all the traits under drought stress evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Source	DF	LRS	LDS	DRR	SPFS	TN	PN	PH	PL	DTF	GYP
Model	7	96.79**	9.17**	11.27**	38.25**	8.73**	2.64	498.67**	47.64	120.48**	58.88**
Replication	2	12.83	19.11**	3.30	4.81	3.00	3.40	675.37**	26.06	0.10	64.72*
Generation	5	130.10**	5.28**	14.48**	51.54**	10.65**	2.26	412.16**	55.67	168.63**	56.23*
Residual	238	13.07	1.65	1.74	5.97	1.59	1.76	114.26	36.87	8.78	20.00
C.V. (%)	-	68.24	41.56	35.72	43.29	31.01	47.77	13.31	31.50	3.15	45.54

***-Significant at 0.01; *-Significant at 0.05; DF-Degree of freedom; C.V.- Coefficient of variation; SPFS-Spikelet Fertility Score; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm); LRS-Leaf Rolling Score; LDS-Leaf Drying Score; DRR-Drought Recovery*

Annex XXIII. Mean square from the analysis of variance among the six populations derived from the crosses J.85/Apo for all the traits under drought stress evaluated at CSIR-Crops Research Institute, Fumesua-Kumasi, Ghana in 2022

Source	DF	LRS	LDS	DRR	SPFS	TN	PN	PH	PL	DTF	GYP
Model	7	135.05**	4.45	7.46**	75.68**	7.57	4.01	693.99**	51.82	48.94**	43.69
Replication	2	52.09*	3.79	4.56	4.96	0.12	0.19	626.08**	21.97	3.96	13.04
Generation	5	169.00**	4.70	8.65**	103.97**	10.56**	5.48	707.06**	62.54	66.96**	54.28
Residual	227	13.20	2.55	2.05	5.06	1.40	2.01	122.33	29.72	2.99	28.65
C.V. (%)	-	75.76	44.73	35.17	41.90	29.21	51.23	13.53	27.09	1.87	53.70

***-Significant at 0.01; *-Significant at 0.05; DF-Degree of freedom; C.V.- Coefficient of variation; SPFS-Spikelet Fertility Score; GYP-Grain Yield per Plant(g); DTF-Days to flowering; TN-Tiller Number per Plant; PN-Panicle Number per Plant; PH-Plant Height(cm); PL-Panicle Length(cm); LRS-Leaf Rolling Score; LDS-Leaf Drying Score; DRR-Drought Recovery*