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Original Paper

The evaluation of drought-tolerance rice genetic resources

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***Abstract*— About 70% of the rice consumed in Ghana is imported. The state of self-insufficiency in rice production can be attributed to the lack of adequate or continuous water supply. Rice, being an aquatic plant, is not tolerant to drought, which is known as the most threatening abiotic factor causing as much as 64% yield reduction. Therefore, this study was conducted to identify drought-tolerance genotypes among 24 rice collections and to estimate their heritability. A total of 24 traits were assessed in this study, and three treatments were applied, including stress free, mild stress, and severe stress, each of which involved three replications. The results showed that most of the parameters under investigation, including panicle length, fertile panicle rate, shoot, and root dry weight, and maximum root depth, decreased considerably as the level of drought stress increased. In addition, five of the accessions showed considerable tolerance to drought, eight accessions were high yielding, and eight accessions combined high yields and drought tolerance. The study concluded that 80% of the rice accessions offer promising lines to be used as parents in the development of drought-tolerant varieties and in genetic improvement programs aimed at such a purpose. The study recommended that molecular studies and morphological characterization should be done on the collections to understand their genetic makeup, similarities, and differences.**

Keywords—genetic resources, drought tolerance, rice, stress

I. INTRODUCTION

Rice is a major food staple in Africa including Ghana and has become part of Ghana's local delicacies [1]. However, 70% of the rice consumed in Ghana is imported, constituting a huge drain on Ghana's scarce foreign exchange reserves [2]. The state of self-insufficiency in rice production in the country can be attributed to the lack of adequate or continuous water supply. Rice, being an aquatic plant, is not tolerant to drought, known as the most threatening abiotic factor to 64% reduction in yield [3]. Rice susceptibility to drought is more pronounced at the reproductive stage [4]. Depending on the severity and timing of drought incidence, low yields associated with drought have been recorded in previous studies.

Drought-related losses discourage rice farmers from making investments in inputs that can help to improve yield such as applying fertilizer, therefore resulting in poor production [3]. As a result, creating cultivars that efficiently use water will contribute to lowering irrigation costs, while increasing yield output and farmers' livelihoods in drought-prone areas [5,29]. The discovery of varied yet promising parents is critical to the success of breeding for a drought-tolerant cultivar. Drought-tolerance phenotypic investigations that include adequate germplasm screening present a chance for reaching such parents. Therefore, the relevance of screening rice germplasm for drought-tolerant genetic resources in increasing yield is crucial.

Hence, the study objectives were to (1) screen and select drought-tolerant cultivars among the rice germplasms collected and (2) to estimate their heritability of yield parameters including spikelet fertility, fertile panicle rate, spikelet length, number of grains, root dry weight, grain weight, dry root weight, maximum root length, total root length, panicle length, effective tillers, leaf rolling, and leaf drying.

II. LITERATURE REVIEW

A. Genetic and Phenotypic Diversity

Genetic diversity defines the differences in genes, nucleotides, chromosomes, or the complete genomes of living organisms [5]. The genome is the absolute complementary DNA (deoxyribonucleic acid)inside the cells or organelles of an organism. At the most basic level, genetic variability is represented by changes in the nucleotide sequences (guanine, cytosine, thymine, and adenine) that makeup DNA within the organism's cells. As a result, each gene provides a hereditary region of DNA that resides in a specific location on the chromosome and regulates a certain trait of a species [6].

Phenotypic diversity between individuals, populations, and species is usually described in terms of the variation in the external morphology of individuals [7]. Variations in physiological and biochemical characteristics of an organism are also important indicators of phenotypic diversity [5] [7]. Phenotypic characteristics represent how an organism interacts with its environment and are therefore the product of the anatomical, physiological, or biochemical traits that might be adapted to the environment. For example, the migration behavior of some birds or mammals, and the host specificity of parasites are closely linked with how the organisms use the environment to meet their physiological requirements [28]. As a result, behavioral variance can be utilized to characterize

phenotypic heterogeneity among individuals, groups, or species [6]. An organism's phenotypic variability is determined by its genetic makeup, but the magnitude to which genetic diversity varies across organisms is manifested in their phenotypes varies, greatly depending on the organism's features. Some phenotypic differences may be displayed as a result of genetic variability between some traits [6].

B. Drought Stress

Drought is among the most severe constraints on crop production globally [8]. According to [9], crop growth forecasts have revealed that severe drought situations will intensify in the future. Drought wreaks havoc on normal growth, alters water exchanges, and reduces plant water use efficiency. Plants, on the other hand, have a diverse variety of physiological and biochemical reactions at the cellular and organismal levels, making the situation more complicated [9]. Water stress induces a variety of changes in the plant, including reduced stomatal opening, lower CO_2 assimilation, cause harmful impacts on photosynthetic activity, robustness, and height of the plant, decreased pollen grain fertility, and, among other things, decreased productivity [8]. Besides, water deficit lowers nutrient absorption, inflicts damage to rice producers, and causes year-to-year disruptions in production [10].

III. MATERIALS AND METHOD

A. Plant Material

Twenty-four genetic resources of rice were used in the study. These included seventeen genetic resources assembled from the Plant Genetic Resource Research Institute, PGRRI-Ghana, five genetic resources from African Rice Centre, ARC-Benin, and two genetic resources from the International Rice Research Institute, IRRI-Philippians. The accessions from PGRRI were collected from different parts of the country. Germplasm from IRRI and ARC are improved varieties for either drought tolerance or high yielding or both. They served as controls for the experiments.

B. Phenotypic characterization of collections for DT and HY

Screening and drought treatment of the rice accessions were carried out in a greenhouse following a modification of a protocol used by [11]. Pre-germinated rice seeds were sown directly in PVC pipes arranged in a completely randomized design (CRD) with three water regimes viz, stress free, mild stress, and severe stress as treatments. Rice seeds were grown in PVC pipes, with one plant per pipe. The pipe was 14 cm in diameter and 1 m in length with four holes at the base. Each pipe was loaded with 9.6 kg of thoroughly mixed soil composed of heavy clay and loose sandy soil. Five seeds were directly sown into each pipe and thinned down to two seeds per pipe three weeks after planting. Following a fertilizer recommendation of 45 kg NPK (15-15-15) and 150 kg sulfate of ammonia, each pipe received 0.16 g of NPK one week after planting and 0.5 g of sulfate of ammonia at the panicle initiation stage (8 weeks after planting). The plants were irrigated to field capacity by watering every day until the drought treatment was due. Drought stress was individually applied to each plant at the booting stage.

C. Drought treatment

The afternoon before the dry-down, all pots were fully watered to reach saturation. After allowing to drain overnight, the base of the plants was sealed with plastic bags to exclude any water loss due to evaporation. Pots were weighed after enclosing in plastic bags, and this value was recorded as the initial target pot weight. Thereafter, the pots were weighed every morning at around 9 am. Plant response to water stress related to soil water content was measured in the pots through daily weighing. The stress levels were expressed as a function of soil water content. For each stress treatment, the fraction of transpirable soil water criterion, FTSW (the fraction of transpirable soil water) left in the soil on each day was calculated as follows [12]:

$$\text{FTSW} = \frac{ATWS}{TTWS} = \frac{W_t - W_f}{W_i - W_f} \quad (1)$$

Where ATSW represents the actual transpirable soil water obtained for every individual pot weight at a particular day of measuring (W_t) subtracted from the final pot weight (W_f), that is, pot weight when daily transpiration rate decreases to < 0.1 of well-watered plants. The TTSW represents the total transpirable soil water estimated for every individual treatment as the difference between initial and final pot weight (W_i and W_f). The FTSW has an upper limit of one and decreases with time as soil water availability for transpiration decreases. The stress was held for 14 days when the FTSW was 0.1 in severely stressed pipes and 0.3 in mild stress pipes.

D. Traits and measurements

A total of 24 parameters were evaluated in this study where 14 parameters were taken from the above-ground part of the rice plant and 10 were root traits (see Table I). The above-ground part traits were linked to productivity and fitness, such as yield and yield component parameters, fertility, and biomass. Yield and components of yield traits were assessed for all plants under stressed and control conditions, including grain yield per plant (in grams), grain weight per plant (in grams), 1000-grain weight (in grams), spikelet number per plant, number of days to heading (in days), days to maturity (in days), fertile panicle rate (%), fertility of spikelet (%), harvest index (%), relative water content, and canopy temperature (ºC).

In addition, two traits related to the water status of the plants viz leaf-drying score and number of days to leaf rolling were also recorded. Leaf-drying score was recorded based on the degrees of leaf drying immediately after re-watering as 0 (no leaf drying) to 4 (>20% of the leaf area drying). The number of days to leaf rolling of each plant was recorded as the number of days from the application of drought stress to the day when all leaves became rolled at noon. The root traits were scored at the seed maturity of the plants. To measure these traits, the plastic bag containing the soil and roots was pulled out from the PVC pipe and laid out on a 2-mm sieve screen frame. The lowest visible root in the soil after removing the plastic bag was scored as the maximum root depth (in centimeters). The body of soil and roots was cut into two parts at 30 cm from the basal node of the plant, and the soil was washed carefully to collect roots. The volumes (in milliliters) of roots from the two parts were measured in a cylinder using the water-replacing method [13]. The root mass below 30 cm was considered to be deep root, from which some

measurements were derived. Root growth rate in-depth and root growth rate in volume were calculated by dividing the maximum root depth and the total root volume, respectively, by the root growth period (number of days from sowing to the heading of the plant). Drought-induced root growth was evaluated by two traits: drought-induced root growth in depth and drought-induced deep-root rate in volume, which were calculated as the differences of maximum root depth and deep-root rate in volume between the measurements obtained under drought stress and control conditions. The abbreviations for and descriptions of these traits are listed in Table I and used hereafter.

TABLE I. DROUGHT-TOLERANCE TRAITS AND THEIR DESCRIPTION

Abbreviation	Trait	Description
FPR	Fertile Panicle Rate	The proportion of the number of fertile panicles (with 5 grains or more on each panicle) in all the panicles of a plant
NSP	Number of Spikelet per Plant	Total number of spikelets borne on each plant
SF	Spikelet Fertility	The number of grains divided by the total number of spikelets of a plant
DF	Days to Heading (days)	The number of days from sowing when plants have attained 50% flowering
DM	Days to Maturity (days)	The number of days from sowing to maturity
LD	Leaf Drying	The degrees of leaf drying immediately after re-watering scored 1 (no drying) to 5 (.20% area dried)
LA	Leaf Area	Area of leaves taken by a leaf area meter
NDLR	Number of Days to Leaf Rolling	The number of days to leaf rolling starting from day of drought treatment
CT	Canopy Temperature (ºC)	The temperature around leaf canopy measured by an infrared thermometer at noon during vegetative growth.
SDW	Shoot Dry Weight (grams)	Weight of dried shoot from each plant
GYP	Grain Yield per Plant (in grams)	Total weight of grain yield as recorded from each plant
GW	1000-grain weight (in grams)	Weight of approximately 1000 seed from each plant.
RDW	Root Dry Weight	Weight of dried roots from each plant.
MRL	Maximum Root Length	The lowest visible root at the soil surface after removing the plastic bag
RDWTNR	Root Dry Weight/Tiller Number Ratio	Ratio of root dry weight to tiller number
RN	Root Number	The total number of roots per plant
DIRGD	Drought-induced root growth in depth (cm)	The difference of maximum root depth under drought and control conditions
RGRD	Root growth rate in depth (cm/day)	Maximum root depth divided by root growth periods
RV	Root volume (ml)	Total root volume divided by root growth period
DRR	Deep root rate in volume (%)	Percentage of root volume ,30 cm in the total root volume
RGR	Root growth rate in volume (ml/day)	Total root volume divided by root growth period
DRRD	Deep root rate in volume induced by drought conditions (%)	The difference in deep-root rate in volume under drought and control conditions
HI	Harvest Index	Grain yield divided by the total dry matter of the above-ground part

Source; http://www.iris.irri.org:8080/drought/traits.html. Assessed; January 15, 2011

E. Statistical Analysis

The GENSTATS package version 19.1 was used to examine the data on shoot, yield, and root characteristics. ANOVA with the LSD was used to find differences between the means of assessed traits, while pairwise correlation coefficients were used to establish the association between the traits. The principal components were then created and utilized as predictor variables to determine how much each principal component contributed to DT among the genotypes (using Principal Component Analysis, and PCA in R stats). The calculation of heritability was performed by computing phenotypic, genotypic, and environmental coefficients of variation (PCV, GCV, and ECV).

IV. RESULTS AND DISCUSSION

A. Analysis of variance

For all variables, there were substantial differences in mean performance between accessions, indicating that the performance investigated in this study is accession-specific (Table II). This demonstrates the potential for genetic enhancement of these features through the identification of promising lines for crop improvement programs from the current gene pool. The high level of diversity could be attributable to the many sources of materials used as well as environmental influences on the phenotypes. These findings are consistent with those of [14], [15], [16], and [17], who found significant heterogeneity in rice yield and its components.

For all examined characteristics, there were significant variations among treatments as well as accessions by treatment interaction (Table II). With a probability of 0.1274 and 0.0478, spikelet length did not follow that pattern. This demonstrates that the various drought treatment levels, as well as accession and the drought treatment level interaction, can explain variation in trait-based performance to a substantial extent. However, there was no significant variation in spikelet length between treatments or the combination between accession and treatment. The length of spikelets was likely unaffected by drought stress or the combined effect of accession and drought stress.

TABLE II. ANALYSIS OF VARIANCE

Trait	Source	DF	SS	MS	F Value	Pr > F
Spkfrt	Vars	23	16373	7119.1	1305	<.0001
	Trts	2	9.47	2	5.9	<.0001
	Vars*Trts	46	26533	3266.9	2433	<.0001
	Reps	2	.91	6	0.5	<.0001
	Error	96	28063	610.08	1118.	
			.82	11.15	84	
			22.30	0.55	20.45	

			52.35			
fepanrt	Vars	23	11094	4823.5	2794	<.0001
	Trts	2	2.67	9	34	<.0001
	Vars*Trts	46	9712.	4856.1	2813	<.0001
	Reps	2	22	1	17	0.0363
	Error	96	22210	4828.2	2797	
			0.15	6	04	
			0.12	0.06	3.43	
			1.66	0.02		
spklnt	Vars	23	7.04	0.31	40.66	<.0001
	Trts	2	0.03	0.02	2.11	0.1274
	Vars*Trts	46	0.52	0.01	1.50	0.0478
	Reps	2	0.01	0.01	0.15	0.8588
	Error	96	0.72	0.01		
unflgrn	Vars	23	10790	46914.	9326.	<.0001
	Trts	2	42.20	88	84	<.0001
	Vars*Trts	46	79437	39718.	7896.	<.0001
	Reps	2	.82	91	26	0.6280
	Error	96	68470	14884.	2959.	
			5.30	90	17	
			4.70	2.35	0.47	
			482.8	5.03		
			9			
rdwtrat	Vars	23	76.45	3.32	1909.	<.0001
	Trts	2	11.52	5.76	79	<.0001
	Vars*Trts	46	15.36	0.33	3310.	<.0001
	Reps	2	0.025	0.01	54	0.0014
	Error	96	0.17	0.002	191.8	
					4	
					7.05	
grnwgt	Vars	23	9015.	391.98	682.1	<.0001
	Trts	2	53	1957.9	0	<.0001
	Vars*Trts	46	3915.	4	3407.	<.0001
	Reps	2	87	165.54	10	0.0716
	Error	96	7614.	1.56	288.0	
			71	0.57	6	
			3.12		2.71	
			55.17			
dryrtwt	Vars	23	406.3	17.67	120.2	<.0001
	Trts	2	9	112.14	1	<.0001
	Vars*Trts	46	224.2	3.13	762.9	<.0001
	Reps	2	8	0.48	1	0.0426
	Error	96	143.9	0.15	21.29	
			6		3.26	
			0.96			
			14.11			
maxrtln	Vars	23	38618	1679.0	5292.	<.0001
	Trts	2	.25	5	22	<.0001
	Vars*Trts	46	9240.	4620.1	1456	<.0001
	Reps	2	28	4	2.20	0.3077
	Error	96	23367	507.99	1601.	
			.56	0.38	14	
			0.76	0.32	1.19	
			30.47			
totrtlt	Vars	23	40712	17701.	2966.	<.0001
	Trts	2	5.97	13	80	<.0001
	Vars*Trts	46	78240	39120.	6556.	<.0001
	Reps	2	.83	41	77	0.7880
	Error	96	17821	3874.2	649.3	
			4.92	4 1.43	4	
			2.85	5.97	0.24	
			572.7			
			8			
panlnt	Vars	23	4656.	202.47	136.8	<.0001
	Trts	2	85	55.69	4	<.0001
	Vars*Trts	46	111.3	59.97	37.64	<.0001
	Reps	2	7	4.85	40.53	0.0420
	Error	96	2758.	1.48	3.28	
			82			
			9.70			
			142.0			
			4			
efftils	Vars	23	593.9	25.82	253.5	<.0001
	Trts	2	3	69.73	3	<.0001
	Vars*Trts	46	139.4	1.54	684.5	<.0001
	Reps	2	5	47.56	9	<.0001
	Error	96	70.77	0.10	15.10	
			95.12		466.9	
			9.78		5	
lfroln	Vars	23	1965.	85.45	117.1	<.0001
	Trts	2	33	3146.3	9	<.0001
	Vars*Trts	46	6292.	5	4314.	<.0001
	Reps	2	69	26.68	99	<.0001
	Error	96	1227.	24.01	36.59	
			31	0.73	32.93	
			48.03			
			70.00			
lfdryn	Vars	23	119.0	5.18	13.23	<.0001
	Trts	2	4	356.81	912.0	<.0001
	Vars*Trts	46	713.6	2.45	8	<.0001
	Reps	2	2	22.81	6.27	<.0001
	Error	96	112.8	0.39	58.31	
			2			
			45.62			
			37.56			

The results from the principal component analysis revealed that accessions 1514, 1539, 1593, 1596, Vandana, NERICA 8, NERICA 5, NERICA 6, and IR 64 were the best performers in terms of yield. Moroberekan, IR64, 1552, 1520, 1541, and CG14 were the best performers based on drought tolerance. However, CG14, IR64, 1541, 1593, 1580, NERICA 5, and NERICA 8 combined drought tolerance with high yielding. These accessions offer promising lines to be used as parents in the development of drought-tolerant varieties and hence may be used in genetic improvement programs.

The results showed that phenotypic variance was higher than the genotypic variance for all the yields and root traits, indicating the influence of environmental factors on these traits. Similar findings were reported in different rice genotypes by [18] and [19]. Also, the estimation of the phenotypic coefficient of variation and genotypic coefficient variation for all the characters showed higher PCV than GCV. The results are in agreement with the findings of [18] and [20]. These values alone, however, do not help determine the heritable portion of variation [21].

TABLE III. HERITABILITY, GV, PV, GCV, PCV ANALYSIS

Parameters	**GV**	**PV**	**GCV**	**PCV**	**H^2**
spkfrt	723.23	926.89	55.8	63.2	0.78
fepanrt	-0.52	1608.9	13.4	74.8	-0.0003
spklnt	0.03	0.04	22.5	26.0	0.75
nogrns	1449	9990.23	23.6	62.0	0.15
rdwtrat	0.33	0.44	95.7	111.0	0.75
grnwgt	25.16	80.40	26.4	46.5	0.31
dryrtwt	1.62	2.68	60.0	77.2	0.60
maxrtln	130.12	299.47	32.9	49.9	0.43

totrtlt	1536.32	2828.39	40.0	52.9	0.54
panlnt	15.83	35.98	16.9	25.5	0.44
efftils	2.70	3.22	71.4	78.0	0.84
lfroln	6.53	15.50	35.9	55.4	0.42
lfdryn	0.30	2.05	22.5	58.9	0.15

The heritability estimated for 12 quantitative characters under study ranged from 0 % (fertile panicle rate) to 84 % (the number of effective tillers) (Table I). In order for a parameter to be considered highly heritable, the heritability value must be above 50%. The number of effective tillers, spikelet fertility, spikelet length, and dry root weight to tiller number ratio had high heritability. According to [21], such characters with high heritability are governed predominantly by additive gene action and could be improved through individual plant selection. In a related study, [22] recorded high heritability for plant height. However, [23], [24] and [25] reported high estimates of heritability for grain yield per plant.

Upon breeding, careful consideration needs to be applied to the selection based on heritability as it includes both additive and non-additive gene actions [26]. In the present study, the number of effective tillers, spikelet fertility, dry root weight to tiller number ratio, and dry root weight exhibited high heritability. These characters show additive gene action and provide ample scopes for selection. The results are in accordance with [21], [22], and [27]. Moderate estimate was observed in maximum root length with a corresponding moderate GA as a percent of mean. High heritability was registered for dry root weight, the number of effective tillers, spikelet fertility, and dry root weight suggesting a preponderance of additive gene action in the expression of these characters. These character types could be improved by mass selection and other breeding methods based on progeny testing [21].

V. CONCLUSION AND RECOMMENDATION

Rice collections including CG14, IR64, 1541, 1593, 1580, NERICA 5, and NERICA 8 have been proven drought tolerant with high yielding. These accessions offer promising lines to be used as parents in the development of drought-tolerant varieties which may be used in genetic improvement programs aimed at such a purpose.

The study recommends that molecular studies, such as DNA analysis, should be done on these accessions to understand their genetic makeup, and morphological characterization should be done to determine the similarities and differences among the accessions. Also, accessions with considerable tolerance to drought, those with high yield, and those with combined high yield and drought tolerance need to be screened in further experiments.

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