

# Genetic Variability and Correlation of Agronomic Traits in Rice Landraces Subjected to Flash Flooding at Seedling Stage

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## Abstract

Flash flooding at early seedling stage, is one of the major abiotic stresses that pose threat on rice productivity worldwide, it is a common feature in Nigeria and has been linked to considerable yield loss in rice. This study was therefore aimed at determining the genetic variability and correlation of agronomic traits in rice landraces subjected to flash flood at vegetative stage. The study was conducted at the Botanical Garden, Department of Botany, Ahmadu Bello University, Zaria. Rice genotypes were obtained from local farmers across savanna agro-ecological zones of Nigeria and Africa Rice Centre. The rice genotypes were sown in labelled polythene bags containing surface loamy soil. The experiment was arranged in Randomized Complete Block Design with two replicates. Thirty-day old seedlings of the two replicates were submerged completely in plastic tanks at a water depth of 100cm for a period of 14 days after which the rice genotypes were then de-submerged. A non-submerged treatment was maintained as a control. Parameters such as plant height, chlorophyll content, number of tillers, number of leaves, days to fifty percent flowering, hundred-seed weight and yield were taken according to standard procedures. The result indicated that there is genetic variation in the traits of the rice genotypes as observed in the greater phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) in all the traits. Highest PCV, GCV and heritability values of 90.34%, 89.26% and 97.63% respectively were obtained in Hundred-seed weight. Low heritability estimates were observed in most of the traits which is an evidence of influence by the environment. A strong positive correlation was observed between the morphological traits and yield of the rice genotypes ( $P = 0.001$ ). In conclusion, the rice landraces possess adequate genetic variability and could be improved via recurrent and mass selection in breeding programmes.

**Keywords:** Correlation, Genetic variability, Genotypes, Heritability, Rice

## INTRODUCTION

Rice is a major staple food crop for people living in the tropics and sub-tropics, the knowledge of nature and magnitude of genetic variation of agronomic traits of rice under submergence stress is essential for genetic improvement (Babu *et al.*, 2012). Information on genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability are prerequisites in formulating breeding methods necessary

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to develop high yielding crops in the course of genetic improvement (Saha *et al.*, 2019). Genetic variability is one of the primary factors considered during selection in an efficient breeding programme (Saha *et al.*, 2019). Rice is a semiaquatic plant but generally does not tolerate complete submergence, even the deep water rice that is tolerant to submergence by rapid internode elongation usually die within few days of complete submergence (Wassmann *et al.*, 2009). Interestingly, enormous diversity and plasticity exist in terms of rice adaptation to myriad of hydrological conditions and that makes it one of the suitable candidate crops for genetic manipulations especially in developing varieties suitable for excess water environments (Ismail & Mackill, 2013; Miro & Ismail, 2013; Kirk *et al.*, 2014). Several studies were conducted on the phenotypic response of rice to submergence, Akinwale *et al.* (2012) conducted a phenotypic screening of some Nigerian rice varieties and landraces for submergence tolerance and reported variations in response of rice genotypes based on percentage survival, stem elongation, days to 50% flowering, number of tillers, number of panicles per plant and grain yield. Limited stem elongation growth was found to be associated with cultivars ability to survive flash flooding (Goswamil *et al.*, 2015). Rice submergence can result in yellow leaf discoloration, a decrease in the number of green leaves and white roots, a decrease in root absorption, impaired growth and development, and a decrease in lodging tolerance, which can result in underproduction or even a complete lack of yield (Zhang *et al.*, 2015). Also, Elanchezian *et al.* (2013) reported various phenotypic responses such as survival, growth and yield attributing traits of rice genotypes and landraces including the most widely studied landrace, FR13A during kharif season in India, with significant differences in yield attributing traits.

The life cycle of rice is categorized into different stages as seedling, tillering, jointing and booting, heading- flowering, milk and maturation stages (Zhang *et al.*, 2015) and the ability of rice to endure water logging varies according to the growth stage, submergence duration and depth. Zhang *et al.* (2015) in their study on short- term complete submergence of rice at different submergence depth and at tillering stage reported increase in plant height and yield. Complete submergence at seedling establishment and maximum tillering stages cause reduction in number of ear-bearing tillers and grain yield. However, the decrease is more conspicuous at seedling establishment than at maximum tillering. Rice submergence at seedling establishment leads to rapid increase in height and affects tillering adversely. Damage at maximum tillering is comparatively less because of complete formation of tillers with adequate carbohydrates to withstand submergence for short periods (Akinwale *et al.*, 2012). Complete submergence at all stages of reproductive growth is detrimental to rice, when the plants are submerged at booting stage, a considerable number of young panicles failed to emerge out of the flag leaf even after removal from water (Sinha & Mishra, 2013). Complete submergence at seedling, maximum tillering and flowering stages affects grain yield adversely especially at flowering due to impaired anthesis thereby causing high sterility. Moreover, the growth of the endosperm is suppressed after fertilization and this finally leads to abortive kernels with underdeveloped endosperm. Improper grain filling under submergence was reported to be due to reduction in carbohydrate content and its less translocation (Jackson & Ram, 2003). Leaf expansion, leaf number and tillering ability vary with rice genotypes during submergence, submergence tolerant genotypes show reduced plant growth, with reduction in all morphological parameters for conservation of energy. Negative correlation exists between elongation ability and submergence tolerance as well as survival percentage after de-submergence. Rapid shoot elongation and leaf width expansion may compete for energy required for maintenance processes for survival. Shoot elongation during submergence depends on the genetic character of the genotype and may be affected by the submergence environment. In small seedlings, rapid elongation is restricted to

emerging leaves (Aliyu *et al.*, 2015; Goswamil *et al.*, 2015). Percentage survival, tiller number, plant height, and most of the grain yield-attributing traits have strong correlation with grain yield under deep stagnant flood and may suggest the importance of the proportion of leaf area exposed above water as a source of photosynthate and oxygen supply (Singh *et al.*, 2010). This study was therefore conducted to determine the genetic variability and correlation of agronomic traits of rice landraces subjected to flash flooding at seedling stage.

## **MATERIALS AND METHODS**

### **Study Area**

Phenotypic screening of the rice landraces subjected to flash flooding was conducted at the Botanical Garden, Department of Botany, Ahmadu Bello University, Zaria, Nigeria (Lat. 11 ° N, Long. 70 ° 42' E and Altitude 660m).

### **Sources of Plant Materials**

Healthy seeds of seventy five (75) genotypes were used for the study. These comprised of seventy three (73) rice landraces collected from local farmers across savanna zones from the nineteen (19) northern states of Nigeria and submergence tolerant lines (L- 19 SUB1 and Futia-12) obtained from Africa Rice Centre, Ibadan Station, Nigeria. The traditional names of the landraces were identified by the farmers.

### **Phenotyping rice landraces to flash flooding**

Surface loamy soil from the Botanical Garden was used for phenotyping. Five rice seeds of each landrace were sown in a 1.54m<sup>2</sup> labelled polythene bags containing 3.5kg of the soil (Panda *et al.*, 2006). The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replicates (Kawano *et al.*, 2002). The seedlings were thinned to three seedlings per bag after germination (Kawano *et al.*, 2009) and watered daily, weeds were controlled by combination of hoeing and hand weeding (Akinwale *et al.*, 2012). Fertilizer was applied at 50 N, 25 P and 25 K mg/kg of soil before the seeds were planted (Wazed, 2014). Six plastic tanks of 1m x 1m x 1m dimension and 1000litres capacity each were used for submergence with three tanks per replicate. Thirty (30) day- old plants from emergence were submerged at a water depth of Hundred (100) cm (IRRI, 2006; NICRA, 2012) according to International Rice Research Institute protocol for submergence. The seedlings were then de-submerged after fourteen (14) days of submergence. Seedling height (cm) was measured with meter rule immediately before submergence. A non-submerged control was maintained with two submergence tolerant checks.

Plant height (cm) and percentage (%) survival were also taken immediately after de-submergence according to IRRI protocol (Wazed, 2014; Duttarganvi *et al.*, 2016). The length (cm) and maximum width (cm) of longest leaf of each hill were also measured with meter rule from the base to the tip of the leaf and from one leaf margin to the other, respectively (IRRI, 2013). Number of tillers per plant (NTPP), Days to Maturity (DTM) and Number of leaves per plant (NLPP) were counted, 100- Seed weight (HSWT) and yield per plant (YLPP) were also recorded at maturity with sensitive weighing balance. The plant parameters for flash flood were recorded according to International Rice Research Institute (IRRI) standard protocol of 2013.

**Plant height (cm):** Plant height was taken from the ground level to the tip of the flag leaf before and after de-submergence (IRRI, 2013).

**Survival percentage (%):** Survival percentage was taken by counting the number of plants before submergence and immediately after de-submergence and survival percentage then calculated (Sarkar and Bhattacharjee, 2011).

**Number of leaves per plant:** Number of leaves of three plants were counted for each landrace and average was taken (Wazed, 2014).

**Number of tillers per plant:** Number of tillers of three plants for each landrace were counted after de-submergence and average taken (Wazed, 2014).

**Number of panicles per plant:** Number of panicles of three plants for each landrace were counted after de-submergence and average was taken (Wazed, 2014).

**Days to Maturity:** Days to maturity was recorded when 80% of the grain attained golden yellow colour (IRRI, 2013).

**Hundred-Seed weight (g):** One hundred clean sun-dried seeds were counted from each landrace for both submerged and non-submerged samples, weighed on a sensitive weighing balance at 14% moisture content and expressed in grams (IRRI, 2013).

**Yield per plant (g):** The total grains harvested from each landrace for both submerged and non-submerged samples were sun-dried, weighed on a sensitive weighing balance and expressed in grams (IRRI, 2013).

Genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated according to Ahsan *et al.* (2015). Heritability was also calculated using the formulae below:

$$GCV = \sqrt{\frac{Vg}{x}} \times 100 \quad PCV = \sqrt{\frac{Vp}{x}} \times 100 \quad H^2 = \frac{Vp}{Vg}$$

Where GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, Vg = Genotypic variance, Vp = Phenotypic variance, H<sup>2</sup> = Broad sense heritability, x = mean

## RESULTS AND DISCUSSION

The estimation of variance components, phenotypic coefficient of variation, genotypic coefficient of variation and heritability for traits of rice landraces subjected to flash flooding are presented in table 1. Phenotypic variance was highest in days to maturity (277.86), genotypic variance was highest in number of tillers per plant (16.46). Highest phenotypic coefficient of variation and genotypic coefficient of variation of 90.34% and 89.26% respectively were observed in hundred-seed weight. Traits that showed high broad sense heritability are hundred-seed weight (97.63%), number of tillers (92.34%) and leaf width (66.37%). High heritability, which is an indication of high response to selection, can be used to predict effect of selection on crop (Harsha *et al.*, 2017). When heritability and GCV are high, selection based on phenotypic performance of traits will be effective (Ogunbayo *et al.*, 2014). However, if heritability is low, rice genotypes can only be bred for specific environments because they will respond differently due to environments (Ogunbayo *et al.*, 2014). There was positive correlation for yield of the rice landraces with number of panicles ( $r = 0.372$ ), number of leaves ( $r = 0.422$ ), number of tillers ( $r = 0.495$ ), leaf length ( $r = 0.464$ ), leaf width ( $r = 0.471$ ) and hundred-seed weight ( $r = 0.781$ ). There was correlation for chlorophyll content with days to maturity ( $r = 0.245$ ) and leaf width ( $r = 0.229$ ) under submerged treatment (Table 2). The trend under non-submerged condition was that there was positive correlation for yield of the rice landraces with number of tillers ( $r = 0.235$ ) and hundred-seed weight ( $r = 0.272$ ). Chlorophyll content showed positive with number of tillers ( $r = 0.236$ ) and negative correlation

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to both days to maturity ( $r = -0.319$ ) and leaf length ( $r = -0.417$ ) under non-submerged condition (Table 2).

Table 1: The genetic variation and trait heritability of rice landraces subjected to flash flooding

TRAIT	Grand mean	Phenotypic variance	Genotypic variance	Error variance	PCV	GCV	H <sub>B</sub>
NPPP	25.08	90.09	1.92	176.35	37.85	5.52	2.13
CCAD	26.15	25.18	2.00	46.35	19.19	5.41	7.96
NLPP	25.08	143.34	0.98	288.63	47.74	3.94	0.68
NTPP	9.82	17.82	16.46	2.73	42.99	41.31	92.34
PHEL	18.46	107.69	1.16	217.70	56.22	5.82	1.07
DTM	128.53	277.86	3.36	562.45	12.97	1.43	1.21
LFLG	44.75	64.96	0.82	131.56	18.01	2.02	1.26
LFWD	1.36	0.16	0.11	0.11	29.73	24.22	66.37
HSWT	1.97	3.17	3.09	0.15	90.34	89.26	97.63
YLPP	6.17	3.25	0.15	6.21	29.24	6.27	4.59

NPPP- Number of Panicles/Plant, CCAD- Chlorophyll Content after De-submergence, NLPP- Number of Leaves/Plant, NTPP- Number of Tillers/Plant, PHEL- Plant Height Elongation, DTM- Days to Maturity, LFLG- Leaf Length, LFWD- Leaf Width, HSWT- Hundred-Seed Weight, YLPP- Yield/Plant, PCV (%)- Phenotypic coefficient of variation, GCV (%)- Genotypic coefficient of variation, H<sub>B</sub>- Broad sense heritability (%)

Table 2: Correlation matrix of agronomic traits of rice landraces under flash flood and control conditions

TRAIT	NPPP	CCAD	NLPP	NTPP	PHEL	DTM	LFLG	LFWD	HSWT	YLPP
NPPP	1.000									
CCAD	0.166	1.000								
NLPP	0.629*	0.185	1.000							
NTPP	0.596*	0.067	0.704*	1.000						
PHEL	0.187	0.187	0.173	0.071	1.000					
DTM	0.330*	0.245*	0.175	0.250*	0.317*	1.000				
LFLG	0.626*	0.224	0.473*	0.505*	0.244*	0.601*	1.000			
LFWD	0.711*	0.229*	0.526*	0.440*	0.203	0.375*	0.755*	1.000		
HSWT	0.313*	-0.048	0.336*	0.424*	-0.127	-0.111	0.422*	0.476*	1.000	
YLPP	0.372*	-0.080	0.422*	0.495*	-0.054	-0.082	0.464*	0.471*	0.781*	1.000

\* = Significant at  $p \leq 0.05$

     flood      = Control

NPPP- Number of Panicles/Plant, CCAD- Chlorophyll Content after De-submergence, NLPP- Number of Leaves/Plant, NTPP- Number of Tillers/Plant, PHEL- Plant Height Elongation, DTM- Days to Maturity, LFLG- Leaf Length, LFWD- Leaf Width, HSWT- Hundred-Seed Weight, YLPP- Yield/Plant

There is adequate genetic variability present in the rice landraces studied and therefore the genotypes could be used for submergence tolerance breeding purposes. Phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits studied, the difference between PCV and GCV could be as a result of environmental effects (Afrin *et al.*, 2018; Ibrahim and Hussein, 2006). High heritability estimates obtained for number of tillers, leaf width and hundred-seed weight suggest that the traits are governed by genetic control and could be as a result of additive gene action (Ogunbayo *et al.*, 2014) hence their improvement can be done through mass selection as reported by Ibrahim and Hussein (2006). The low broad sense heritability recorded for number of panicles, chlorophyll content, number of leaves, height elongation, days to maturity, leaf length and yield could be due to non-additive gene action suggesting that the traits were responsive to environmental influences and therefore could be as a result of the submergence stress imposed on the rice landraces hence their improvement could be effected via recurrent selection. Murtadha *et al.* (2004) and Ibrahim and Hussein (2006) suggested that traits with high heritability estimates could be good predictors of seed yield in crops. Ogunbayo *et al.* (2014) and Afrin *et al.* (2018) also recorded higher PCV (33.42% and 57.86% respectively) than GCV (22.32% and 54.92% respectively) for yield and all the traits they studied in rice due to submergence. Harsha *et al.* (2017) however recorded small differences between PCV (48.62%) and GCV (47.79%), high heritability (96.60%) for yield and other traits in rice genotypes. They opined that number of tillers, panicle length, yield and other yield related traits were less influenced by environment and had a high heritability (93.41%, 83.83% and 96.60% respectively). The coefficient of variations and heritability estimates observed are in agreement with the report of Singh *et al.* (2018) on genetic variability in rice genotypes under control and complete flash flood

environments. They reported higher PCV (20.27%, 54.90%) than GCV (18.52%, 52.63%) values for yield and all the traits, however, their study reported high heritability estimates in all the traits (98.68% in days to 50% flowering) in contrast to the current study where most of the heritability estimates are low (Yield-0.68%, Number of leaves- 4.59%). The positive correlation between number of panicles, number of leaves, number of tillers, leaf length and leaf width traits of rice and yield is similar to the work of Singh *et al.* (2011) who reported a strong positive correlation ( $r= 0.85$ ) between number of tillers and grain yield in Swarna-sub1 subjected to partial stagnant flooding. Wazed (2014) also reported a combination of positive and negative correlations between morphological and yield contributing characters of submerged and unsubmerged rice. The negative correlation is however in contrast to the work of Azeez (2017) who reported only positive correlations between survival and morphological traits of rice varieties after submergence. Singh *et al.* (2011) also reported negative correlation between yield and percentage survival, tiller number, stem elongation and grain yield-attributing traits. Stem elongation has been reported in deep-water rice cultivar completely submerged when water depth increase daily was more than 10cm. The observed reduction in morphological traits such as number of leaves and number of tillers in this study could be due to the fast depletion of energy for utilization in elongation growth.

## CONCLUSION

The rice landraces evaluated had adequate genetic variability. Phenotypic coefficient of variation were greater than genotypic coefficient of variation for all the traits studied. Highest heritability recorded was 98%. There was also positive correlation between yield and agromorphological traits. The study provides information for breeders on the responses of rice landraces under flood conditions. Genetic variability and heritability of traits obtained are good predictors of crop yield. The information could be useful in developing flood tolerant rice varieties for flood-prone areas. Rice landraces could also be subjected to genetic improvement via recurrent and mass selection approach.

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