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Research Article

Phenotypic Comparison of Culm Elongation Among Thirty -Two Nigerian Rice Genotypes under Rainfed and Deepwater Conditions

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Abstract

In rice production, culm elongation is a pivotal adaptive feature under deepwater conditions, as it enables the plant to rise above increasing flood levels and avoid complete submergence. When internodes extend sufficiently, the foliage remains exposed, allowing continued photosynthetic activity, energy production, and progression toward reproductive development even during prolonged flooding. This study was carried out using 32 selected Nigerian rice genotypes, to evaluate the phenotypic variation, heritability of culm elongation traits, yield components and select the best genotype for breeding purpose. The experiment was conducted in 2024, laid out in RCBD with three replications under rainfed and deep-water ecologies at Tokyo University of Agriculture, Setagaya campus, Japan. Physiological traits data were collected on the rice genotypes evaluated. Data collected were subjected to Analysis of variance using GenStat 64-bit (2.0) 2020. The Analysis of Variance (ANOVA) showed significant genotype, environment and genotype by environment interaction effects for all the traits, except 3rd and 5th Internodal Length. Under rainfed conditions, Culm Length (CL) ranged from 50.53-112.0 cm and Filled Grain per panicle (FGPP) from 81.00-288.67. TOX7-3-2-3B1-1-B-1 revealed highest values for Plant Height (173.94 cm) and CL (147.18cm). TOS 6949 exhibited highest value for Panicle Number - PN (14.00) under deep water condition. R studio software version 4.6.0 was used in calculating heritability. High variation among the genotypes was observed for Grain Weight Per Hill with PCV 46.63% and GCV 45.76%. Broad-sense heritability showed high values ranges from 0.82 to 0.99 % among the traits studied. Indication of high GA in TSPP (101.59). R studio software 4.6.0 was used in analysing correlation coefficient. A strong positive correlation was obtained between CL and PH($r=0.99$). In all, genotype 7-3-2-3-B1-1-B-1, IRESI-TORI, TOS6949 and IITA182 demonstrated superior culm length under deep water condition which may serve as a valuable accession for flood tolerant rice breeding programs.

Keywords: Rice genotypes, Culm length, Rainfed, Deep-water, Genetic Variability.

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Introduction

More than half of the world's population depend on rice (*Oryza sativa*) as daily food most especially in Asia, parts of Latin America and Africa (Zhu *et al.*, 2023). In Africa, rice consumption among urban and rural poor households has increased considerably (Mba *et al.*, 2021). It is a priority food security crop which is grown in Nigeria with over 183 million people

(Wudil *et al.*, 2023). Across different states and agroecological zones in Nigeria, rice is produced in diverse environments on approximately 4.2 million hectares, with yield range from of 1.93 tonnes/ha to 3.53 tonnes/ha (JICA, 2024). 47% of rice production in Nigeria were produced under rainfed ecology, 30% under upland ecology, 17% under irrigated lowland, 5% under deep water

ecology, 1% under mangrove ecology (Olohungbebe *et al.*, 2025). Nigeria as one of the largest producers of rice in Africa with diverse ecology for rice production, possess areas where water depths can surpass one meter for prolonged periods, frequently spanning several months (Mohammad *et al.*, 2020). This natural phenomenon is often caused by heavy downpour of rains, poor drainage, poor urban buildings plans, poor waste management, breaking of dam barriers and soil-terrain characteristics. This often led to yield losses which ranges from 10 -20% total crop loss (liu *et al.*, 2023; Wangum *et al.*, 2024). Rice genotypes suitable for this environment is called deepwater rice. Deepwater rice represents a unique ecology adapted to seasonal submergence exceeding one meter. Unlike varieties carrying SUB1A, which adopt a quiescence strategy to endure short-term submergence (Nagai & Ashikari, 2023). Deepwater rice employs an “escape” strategy through rapid culm elongation to maintain leaves above water with an average yield of 4-5 metric tonnes/ha. This adaptation is critical for survival, photosynthetic continuity, and reproductive success under long-duration floods (Ashikari *et al.*, 2025).

The process of escape secures the upper parts of the plant, including leaves and panicles, maintain its position above water, ensuring light interception, facilitating gas exchange, sustaining photosynthetic activity, and preventing carbohydrate starvation (Oladosu *et al.*, 2020). Internode elongation is fuelled by the activity of the intercalary meristem, which undergoes rapid cell division and elongation under hormonal control. Anatomically, deep water rice culms develop large aerenchyma and pith cavities that facilitate internal oxygen transport, sustaining metabolic activity in submerged tissues (Daisuke *et al.*, 2022; Gao *et al.*, 2022).

In order to increase rice sustainability, reduce costs of importation and meet the country demand for rice which will be about 584million tons or less towards 2050 according to (Sadiq., 2021). Nigerians, should consider deep water rice cultivation, with positive development in rice research towards increasing rice production. Therefore, the objective of this study is to

evaluates phenotypic variation and heritability of culm elongation traits among 32 Nigerian rice genotypes under rainfed and deepwater conditions; evaluate the variation in yield components of the rice genotypes under deep-water environment and rainfed ecology and to select the best genotype for breeding purpose in combating the deep-water challenges.

Materials and Methods

This study was carried out using 32 selected Nigerian rice genotypes obtained from National Agriculture and Food Research Organization (NARO) gene bank Japan. Table 1 showed all the genotypes used, their JP number and origin respectively. The selection was based on vigour, morphological characteristics and adaptability to lowland ecology. The experiment was conducted during normal rice growing season Spring and Autumn. The experimental field was at the Net house of Tokyo University of Agriculture NODAI, Setagaya campus in Japan, located at latitude: 35.6411° N, Longitude : 139.6321 ° E. Some Metrological data such as Temperature, Precipitation and Relative Humidity were taken during the experiment. The plot size was 2.8m x 1.9m. The experiment was laid in a Randomized complete block design with three replications under rainfed and deep-water ecologies. The rice seeds were sown in soil growth media mixtures in rice seedling tray. A total of 96 experimental pots (4 litres capacity, 19.8cm length x 17.5cm upper diameter x 16.0cm bottom diameter) were filled with alluvial clayey-loamy soil substrates of 3.6 kg and arranged in a randomized complete block design of 32 pots per block. The germinated seedlings were transplanted to the pots at 14 days old (four leaf seedling stage) at one seedling per pot.

For deepwater condition a set of 32 genotypes were randomly assigned within each block of deep-water ecology filled with water to 10cm high above soil surface then gradually increase the water level at two weeks interval up to 50cm as the crop grows. To maintain water level, a 50cm point was marked in a concrete submergence pond and maintained until harvesting. Similarly, for rain fed condition a set 32 genotypes were randomly assigned within

each block, the pots were placed on insulated platform on open space and water level in pots was maintained at 3cm mark.

At two weeks after transplanting, compound fertilizer N: P: K (14:14:14) was applied at the rate of (120: 80 :80) corresponding to N:42.86%, P₂O₅ 28.57%, K₂O 28.57%. Urea was used as an additional nitrogen source with two thirds applied as top dressing during booting stage to support grain fillings (Hossain *et al.*, 2021). The plots for both ecologies were maintained following the good agronomic practices and weeding was managed using hand as the need arises on the soil surfaces in the pots.

Among the traits measured were; days to 50% flowering time (number of days were counted), internodal length 3 and 5 was measured in (cm) from panicle initiation stage, culm length was measured in (cm) at maturity using a calibrated ruler, plant height was measured using a calibrated ruler in (cm) from the base of the plant to the highest leaf of each plant at vegetative, reproductive and maturation stage and yield components parameters was also measured. In order to avoid shattering of seeds, genotypes add mixtures, each genotype was harvested at harvest maturity using a sickle (Kanno *et al.*, 2023). The number of filled grains per panicle was determined following standard rice yield component evaluation procedures according to (Dong *et al.*, 2022). At physiological maturity, ten representative panicles were randomly sampled from each experimental plot. Panicles were air dried for three to five days and subsequently oven-dried at 40°C to 45 °C for 24 hours to ensure uniform moisture content. Each panicle was manually threshed, and all spikelets including filled, partially filled, and unfilled grains were collected for separation. Filled grains were identified using the specific gravity (salt-water flotation) method, which reliably distinguishes fully developed grains from unfilled spikelets. A sodium chloride (NaCl) solution with a density of approximately 1.06 to 1.08 g cm⁻³ was prepared, and the spikelets were gently poured into the solution. Filled grains sank, while unfilled and partially filled grains floated due to lower density. The sunken grains were removed, rinsed with

clean water to eliminate salt residue, and dried on absorbent paper. The total number of filled grains per panicle was then counted manually using a digital grain counter. The number of filled grains per panicle was calculated as the mean of all sampled panicles. Phenotypic, genotypic variance, broad-Sence heritability, genotypic coefficient of variation, phenotypic coefficient of variation, and genetic advance was calculated following the method used by (Vanipraveena *et al.*, 2022) given as follows:

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

$$\text{Genotypic variance } (\sigma^2 g) = (\text{Mean sum of squares due to treatment}); \sigma^2 e = \text{Mean sum of squares due to error), Number of replications}$$

$$\text{Broad Sense Heritability } h^2_{Bs} = \sigma^2 g / \sigma^2 p$$

$$\text{Genotypic Coefficient of Variation (GCV)} = (\sqrt{\sigma^2 g} / \bar{x}) \times 100\%$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = (\sqrt{\sigma^2 p} / \bar{x}) \times 100\%$$

GCV and GCV values were considered as low and low < 0 -10% (low), 10-20% (moderate), > 20% (High)

$$\text{Genetic Advance} = K.h_2$$

Where;

K is constant=2.06 at 5% selection intensity
 Heritability estimates were adjudged using random model; 0-30% (low), 30-60% (moderate), and 60% above as high.

Where;

$\sigma^2 g$ = genotypic variance, $\sigma^2 p$ = phenotypic variance, $\bar{x}$ = grand mean for the trait, h^2_{Bs} = broad sense heritability.

The data was analysed using R studio software software version 4.6.0 and important reference was drawn

Data Analysis

The data obtained from the study were subjected to analysis of Variance using GenStat 64-bit (2.0) 2020, where coefficient of variation (CV%) and least Significant difference at 5 % using two factor linear model : Factor 1=Genotype and Factor 2 = Environment.

$$Y_{ij} = \mu + G_i + E_j + (GE)_{ij} + E_{ij}$$

Where : Y_{ij} is the observed values of the trait, μ overall population mean, G_i genotypic effect, E_j environmental effect, $(GE)_{ij}$ interaction effect between genotype and environment, and E_{ij} experimental error effect, were evaluated to determine the interaction and variation between the genotypes and the environments. Also Mean separations of all the traits across the environment, Heritability variability where genotypic variation (GV), phenotypic variation (PV), environmental variation (EV), genotypic coefficient of variation, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance(GA), Generalized Additive Model(GAM), broad sense heritability (h^2_{Bs}) using R studio software version 4.6.0, following the formula as used in recent study by (Vanipraveena *et al.*, 2022). Correlations analysis among the traits across the environments was evaluated using RStudio software version 4.6.0 and Principal component analysis (PCA) was conducted using GenStat 64-bit (2.0) 2020 to estimate the influence of different genotypes under deep-water and rainfed ecology on plant grain yield, Culm elongation, Plant height, and tiller number to select the best genotype suitable for each environment.

Results and Discussion

Interaction between rice genotypes and environments

In this study, analysis of variance (ANOVA) was performed to examine the physiological responses of the thirty-two selected genotypes to different environments i.e. rainfed and deepwater ecology. The Analysis of Variance (ANOVA) showed significant genotype, environment and genotype by environment interaction effects for all the traits, except 3rd and 5th Internodal Length (Table 2). These results demonstrate that the genotypes expressed substantial phenotypic variability across both rainfed and deep-water ecologies. Such wide variation in performance is consistent with previous studies that emphasized the influence of genotype-specific adaptations under contrasting ecological conditions (Lin *et*

al., 2024; Zhu *et al.*, 2023). The non significant difference observed for 3rd internodal length and 5th internodal length suggests that the stem breaking strength of internodes across the environments. This study corroborates with the findings of (Shan *et al.*, 2021) who found out similar trait performance on soybean internode elongation and drew an assertion that GA₃ Content in stem is an important factor affecting stem elongation. The coefficient of variation (CV) of number of D50%F, CL, PH, 1000GW, TSPP, TTPH, PN and GWPH indicate variability in the traits' stability ranges from 0.08 to 13.17 (Table 2). This agrees with reports of (Nagai *et al.*, 2023) that reproductive traits including spikelet fertility and panicle architecture are often environment-dependent, particularly under stress conditions such as prolonged flooding.

Influence of deep-water and rainfed ecology on culm elongation

The influence of ecology among the thirty-two genotypes compared under rainfed and deep-water Table 3 showed that genotype TOX7-3-2-3B1-1-B-1 exhibited highest values of PH (139.32cm), CL (112.00cm) and EX GANYE had the maximum value of PN (15.67) and TTPH (17.67). Also, the Highest values of FGPP (288.67) were obtained in Genotype IRESI ABEOKUTA followed by R66(78160) with the value of 258.33 and TOS6949 (285.33). Meanwhile, under the deep-water condition in Table 4, the expression of these traits differs per varieties although genotype TOX7-3-2-3B1-1-B-1 still revealed maximum values for PH (173.94 cm) and CL (147.18cm). This finding recorded low plasticity in internode elongation or alternative adaptive traits that support survival without excessive elongation and confirms the past research by (Nagai *et al.*, 2023) stipulates that irrespective of the ecology, elongation remains the same. Genotype TOS 6949, exhibited highest value for PN (14.00) and TTPH (17.00) while TOS 6928 had the maximum value of FGPP. This result implies that only a subset of genotypes typically exhibits exceptional differences when exposed to varying water regimes, reflecting strong genotype by environment interactions. The results corroborate with previous findings by (Lin *et al.*, 2024). Also, the results confirmed that under deepwater

ecology, flood tolerance rice genotypes exhibited significant earliness in days to flowering, increase tillering and increase in filled grain per panicle. (Hu *et al.*, 2023) stated that an increase in panicle number and grain weight of rice cultivars is an approach to achieve increase in rice yield potential. Table 4 also showed that most genotypes can be considered tolerant to the deep-water; considering their ability to elongate even in the presence of more water except for genotypes like IITA 186, IITA 185, IITA 118 and EXMANGU with shorter plant height and culm length. This result revealed that short-statured varieties are vulnerable to flood-prone ecologies and it corroborate with the research carried out by (Wang *et al.*, 2024).

Genetic variability for culm elongation and yield related traits

Coefficient of variation is a critical tool for plant breeders in effective selection where population is enough. The genetic variability for culm elongation and yield related traits entailing genotypic variance, phenotypic variance, environmental variance, phenotypic coefficient of variation, genotypic coefficient of variation, genetic advance, and broad sense heritability showed that there was high significant variability amidst the traits evaluated (Table 5). Genotypic coefficient of variation (GCV) explains the importance of genetic potential of traits under study in crop improvement through selection as recorded by (Barde *et al.*, 2021). The genetic coefficient of variation was high for traits such as filled grain per panicle, grain weight per hill, total spikelet per panicle with values between 35.84%, 45.76% and 30.68% respectively. Moderate GCV on the other hand estimated for 1000 grain weight, culm length, panicle length, panicle number and total tiller per hill (13.64% to 18.42%) except for days to 50% flowering that recorded the lowest value (5.82%). Slightly high parallel trajectory values were observed in phenotypic coefficient of variation (PCV) results. This shows that there was little effect of environment on the genotypes whereby the genetic factors were predominance in their expression. The genetic implication is that there are good prospects for yield improvement through phenotypic selection. These results were similar to the results obtained by (Prakash *et al.*,

2021). Results from PCV and GCV would not be adequate enough for plant breeders without considering heritability and genetic advance results since heritability is dependent on phenotypic variability. High broad sense heritability was recorded in this present study in traits such as CL, D50F, PH, PL, TTPH, TSPP, GWPH, FGPP from 0.94 to 0.99. The analyzed traits were associated with yield potentials thereby suggesting selection for future breeding. These results substantiate the findings by (Jiban *et al.* 2021; Chamar *et al.*, 2021), who recorded highly heritable results with a range of 0.55 to 0.74 broad sense heritability and assert that high heritability estimates is an indication for traits selection. There was record of high genetic advance (GA%) in TSPP, FGPP and PH indicating that heritability is due to additive gene effects in the traits' expression. Lower genetic advance was observed in 1000gw, PN and TTPH this means that there were few chances of improvement in these traits. The traits with lower environmental variance suggest stability of genotypes in the ecology (Susmi *et al.*, 2025). Also, there is high genotypic variation value for traits such as CL, FGPP, GWPH, PH and TSPP which connotes strong genetic control and stability across rainfed and deep-water environments. Even though, traits such like 3IL and 5IL showed negligible genetic variance which is said to be influenced by environmental effects. This result is similar to the findings of (Mamidi *et al.*, 2024) whose research showed that strong culm is reliant on internode length of primary internodes.

Environmental effects observed on plant height, culm elongation, and grain weight per hill in (Figure 1a) showed that rice genotypes under deep-water environment exhibited significantly longer culm length and plant height compared to rice genotypes under rainfed conditions. This increase in stem elongation is an adaptive response mechanism of rice to flooding stress with internodes rapidly elongate to maintain foliage above water surface. This is essential for continued photosynthesis and survival. In contrast, rice genotypes under rainfed condition maintained shorter stature due to absence of submergence stress this result is in conformity with the research by (Zhu *et al.*, (2023).

Grain weight per hill is higher and more variable in deepwater conditions compared to rainfed environment (Figure1b) showed that light interception and biomass production can be enhanced by plant height and culm length elongation under deepwater thereby supporting greater assimilate accumulation for grain filling (Sakagami, *et al.*, 2024; Weng *et al.*, 2025). Additionally, the genotypes under deep water exhibited wide distribution in grain weight suggesting variation in genotypic adaptability. These results agree with recent study by (Liao *et al.*, 2023) whose findings suggests that some rice genotypes are capable of high grain yield and reduction in lodging risk.

Phenotypic linkages between genotypes environment, and selection of the best genotypes

The results of Table 6 showed strong positive correlation coefficient between culm length and plant height ($r = 0.99^{**}$). This indicates that among the Nigeria genotypes, a longer plant height results in maximum culm length. This relationship is expected, as culm elongation directly contributes to overall plant stature, particularly under flood-prone environments where elongation plays an important adaptive role (Saran *et al.*, 2023; Lin *et al.*, 2024). Also, there positive correlation between culm length and panicle length ($r = 0.48^*$) indicating that genotypes with elongated culms tend to support longer panicles, a trait that may enhance reproductive potential under favourable conditions. Similar trade-offs between panicle number and spikelet fertility have been written in studies by (Zhu *et al.*, 2023; Wang *et al.*, 2024; Gautam *et al.*, 2023) on rice productivity under different ecologies, where resource allocation tends to favour either panicle abundance or panicle size rather than maximizing both simultaneously. A moderate positive correlation was found between filled grain and 1000grain weight. This corroborates with the research carried out by (Zhao *et al.*, 2020) whose finding showed positive correlation between grain weight

and grain yield.

The GGE biplot in Figure 2 (A, B and C), describe the principal component analysis of culm elongation, total tiller per hill and number of days to 50% flowering. The result *Figure a* revealed more genotypes tend towards having longer culm elongation under deep-water ecology PC1(66.01%) compared to rainfed ecology PC2(33.9%). This explained that most genotypes under deep-water ecology activate an internode elongation response that lengthens the culm in a rapid way which enables the rice photosynthetic tissues keeps its tissues above the water surface thereby preventing death and enables escape from sub-emergence. This result corroborates with findings of (Susmi *et al.*, 2025), who described the relationship between culm elongation and rice as interconnection between physiological and genetic basis for plant stature. Meanwhile, Fig 2b showed that genotypes under rainfed ecology produced more tillers PC1 (61.62%) than genotypes under deep water ecology PC2(38.38 %) This implies that tillering is highly sensitive to genetic, and environment which gives room for environment specific breeding as suggested by (Meher *et al.*, 2025). Although flooding is an environmental stress that disrupt oxygen availability, metabolism and growth. It had been reported earlier by several authours that flood tolerant genotypes activate the specialized adaptation hormone that influence early flowering as a mode of escape for growth, reproduction, completion of lifecycle and maturity (Bu *et al.*, 2025; Jegadeeswaran *et al.*, 2017 and Vangaru *et al.*, 2017). Also, in this research Figure2C) attributed early flowering to genotype under deepwater ecology. PC1(82.33%) compared to genotypes under rainfed PC2 (17.67%). which is in conformity with the result of this research The findings of the authors explained the variability exhibited by genotypes scattered across two ecologies with high level of genetic variation in the population.

Conclusion and Recommendation

The findings of the study would aid in selecting genotypes that had significant longer culm to avoid submergence while maintaining structural stability and efficient photosynthesis to sustain higher grain production. These genotypes 7-3-2-3-B1-1-B-1, IRESI ITORI, TOS 6949 and IITA 182 can be further look into by Plant breeders, as they demonstrated superior culm length under deep water condition and these may serve as a valuable accession for flood tolerant rice breeding programs. Thus, future research should focus on the traits evaluated to enhance rice production and productivity. However, in breeding rice that is adapted to deep water and longtime flood resistance genotypes, improvement strategies should prioritize molecular evaluation by looking into genotypic variability, location of gene responsible for culm elongation. Also consider these genotypes for post - harvest seed quality.

Authors' Contributions

All authors contributed equally to this research, such as data curation, formal analysis, funding acquisition, investigation, methodology, software supervision, validation, writing review and editing. All authors read and approved the manuscript.

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Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

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Table 1: The list of lowland genotypes used in the experiment, their JP number, and their Origin

JP Number	Genotype Name	Origin
45132	TOX7-3-2-3B1-1-B-1	Nigeria
45133	MAIMANJA	Nigeria
45141	EXZARIA	Nigeria
45143	EXSOKOTO 1	Nigeria
45144	EX ARGUNGUN	Nigeria
45145	EX SOKOTO	Nigeria
45146	EX MANGU	Nigeria
45149	EXKASTINA ALA	Nigeria
45151	IRESI ILARO 1	Nigeria
50280	IRESI ILARO2	Nigeria
45153	IRESI SWAMP	Nigeria
45154	IRESI ITORI	Nigeria
45155	EX SHANA	Nigeria
45156	EX GBANGBASHOFO(BIDA)	Nigeria
45157	EX GANYE	Nigeria
45160	IRESI ABEOKUTA	Nigeria
45161	IRESI 3	Nigeria
45162	IRESI 4	Nigeria
45424	IITA 182	Nigeria
45425	IITA 183	Nigeria
45427	IITA 186	Nigeria
45428	IITA 185	Nigeria
45429	IITA 220	Nigeria
48765	EXGBIKO WILD	Nigeria
49223	IITA 118	Nigeria
49225	TOS 5303-1	Nigeria
53913	TOS 5865	Nigeria
53914	TOS 6900	Nigeria
53915	TOS 6928	Nigeria
53916	TOS 6949	Nigeria
53917	LAC 23	Nigeria
67301	R66(78160)	Nigeria

Table 2: Analysis of Variance Showing Interaction Between Rice Genotypes and Environments.

Source of Variation	Df	1000GW(g)	3IL (cm)	5IL (cm)	CL (cm)	D50F	FGPP	GWPH (g)	PL (cm)	PN	PH (cm)	TSPP	TTPH
Environment	1	833.33***	802.17***	984.19***	32358.36***	0.005208***	23941.33***	14356.87***	531.77***	8.76*	41196.09***	18585.01***	8.33*
Genotype	31	85.84***	42.17ns	58.35ns	1170.43***	168.26***	14445.29***	4333.80***	76.06***	20.73***	1576.20***	15071.4***	26.44***
R x E	4	15.43***	112.69ns	77.18ns	3.98*	0.01ns	313.07	160.61*	1.40ns	1.79ns	5.67ns	241.30ns	1.66ns
G x E	31	14.53***	22.34ns	35.54ns	621.01***	44.94***	44932.78***	2105.77***	37.37***	15.30***	657.87***	6870.53***	17.05***
Error	124	1.54	31.8	40.71	1.52	0.01	188.83	57.62	1.19	1.51	2.64	164.71	1.23
LSD _{0.05}		1.54	NS	NS	1.41	0.08	15.70	8.67	1.25	1.41	1.86	14.67	1.27
CV%		4.94	NS	NS	1.37	0.08	10.15	13.17	5.7	11.52	1.49	7.92	8.36

Key: ***, **, * significant at P0.001,0.01,0.05 level of probability. ^{ns} not significance
Key: 3IL: 3rd Internodal Length (cm), 5IL: 5th Internodal Length (cm), CL: Culm Length (cm), D50F: Days_50%_Flowering, FGPP: Filled Grain per panicle, GWPH: Grain weight per Hill (g), PL: Panicle Length (cm), PN: Panicle Number, PH: Plant Height (cm), TSPP: Total spikelet per panicle, TTPH: Total Tiller per Hill

Table 3: The Mean Values of Phenotypic Traits, and Yield Components of 32 Nigeria Rice Genotypes Under Rainfed

Genotypes	1000GW (g)	3IL (cm)	5IL (cm)	CL (cm)	D50F	FGPP	GWPH (g)	PL (cm)	PN	PH (cm)	TSPP	TTPH
TOX7-3-2-3B1-1-B-1	22.33	13.50	28.83	112.00	77.27	81.67	36.47	27.32	10.00	139.32	116.67	14.00
EX SOKOTO	19.00	18.56	20.63	105.14	95.40	81.00	29.87	20.02	10.33	125.16	114.00	13.33
TOS 6900	19.00	8.73	19.23	104.07	94.20	153.00	61.57	20.33	14.00	124.40	187.00	17.33
TOS 6928	23.67	14.63	14.80	103.23	94.20	99.00	24.30	15.33	7.33	118.56	109.33	9.33
MAIMANJA	18.67	16.83	19.00	100.97	92.33	93.67	21.61	20.07	8.00	123.03	112.00	10.33
EXGBANGBASHOFO(BIDA)	20.00	10.47	19.23	99.00	85.30	115.67	64.91	17.43	11.33	116.43	211.67	15.33
IRESI 4	20.00	14.26	19.90	97.99	100.37	96.67	20.62	23.36	7.33	121.36	110.00	9.33
IRESI SWAMP	21.33	6.34	10.40	86.87	99.20	82.33	19.77	13.33	6.67	100.20	103.00	9.00
IITA 182	26.33	12.50	17.76	83.10	82.37	161.67	57.52	11.72	9.33	94.82	185.33	11.67
EXZARIA	22.00	14.25	22.20	81.87	90.47	88.33	24.64	20.04	8.33	101.90	112.00	10.00
R66(78160)	24.33	13.70	19.80	80.74	83.50	285.33	90.68	18.55	11.00	99.29	265.67	14.00
IRESI ABEOKUTA	27.00	12.43	17.10	79.31	99.00	288.67	73.01	21.23	13.00	100.53	181.00	15.00
LAC 23	24.00	15.30	23.03	78.45	101.33	111.33	116.81	16.03	13.33	94.49	304.33	16.00
TOS 5303-1	28.00	13.93	16.70	76.28	98.10	126.00	63.72	19.83	10.33	96.11	170.67	13.33
IITA 118	25.00	16.10	22.80	74.53	86.27	120.33	39.66	15.63	9.67	90.17	132.00	15.00
EX ARGUNGUN	21.00	18.57	15.17	73.33	85.30	99.33	37.17	19.53	12.67	92.86	118.00	15.00
EX GANYE	24.00	13.13	17.10	73.22	98.30	126.33	68.18	20.47	15.67	93.69	161.00	17.67
EXSOKOTO 1	10.33	15.8	24.67	72.93	93.43	89.33	17.68	20.01	10.00	92.94	122.33	14.00
IITA 220	27.67	17.90	25.25	72.00	100.57	108.00	53.90	14.37	10.67	86.37	154.00	12.67
EXGBIKO WILD	28.00	14.06	18.03	71.27	90.07	88.00	46.37	11.72	12.67	82.99	108.00	15.33
TOS 5865	29.67	12.63	17.67	70.75	104.40	109.33	43.06	14.37	9.00	82.52	127.33	11.33
IITA 183	28.00	12.45	22.97	67.33	94.30	111.33	36.62	14.60	8.67	81.93	125.33	10.33
IITA 185	20.00	14.50	20.63	67.06	87.23	122.33	33.18	16.25	8.33	83.31	182.33	10.67
IRESI ITORI	25.00	14.75	18.03	64.26	91.47	144.33	77.49	26.07	14.33	90.32	182.33	17.00
IITA 186	18.67	17.47	20.10	63.46	91.33	222.33	95.91	16.23	15.00	79.69	245.33	17.00
EX MANGU	19.00	9.40	17.20	62.67	99.30	99.00	33.91	19.00	10.67	81.67	130.67	13.67
TOS 6949	26.00	11.43	18.83	61.80	93.57	285.33	146.43	19.80	13.67	81.60	318.67	17.67
IRESI ILARO 1	22.67	13.33	19.40	60.43	104.30	87.00	30.90	15.87	10.00	76.30	106.67	12.67
IRESI 3	25.00	15.65	18.90	58.37	97.53	86.67	27.03	7.67	8.00	66.03	110.67	9.67
IRESI ILARO2	20.33	11.30	16.30	57.40	84.23	84.00	17.84	15.87	7.00	73.80	91.33	9.67
EXKASTINA ALA	22.00	12.73	16.17	55.57	90.13	85.00	35.25	11.05	11.33	66.61	108.33	14.67
EX SHANA	24.00	13.43	19.50	50.53	92.20	93.67	21.24	16.43	7.00	66.96	98.33	9.00
LSD _{0.05}	2.13	NS	NS	1.21	0.24	24.03	11.28	2.53	1.96	2.77	23.98	1.77
Grand mean	23.03	13.75	19.10	77.06	92.82	124.24	48.99	17.48	10.45	94.54	152.20	13.06
CV%	5.65	NS	NS	0.96	0.16	11.85	14.11	8.88	11.50	1.8	9.66	8.31

Key: 3IL: 3rd Internodal Length (cm), 5IL: 5th Internodal Length (cm), CL: Culm Length (cm), D50F: Days_50%_Flowering, FGPP: Filled Grain per panicle, GWPH: Grain weight per Hill (g), PL: Panicle Length (cm), PN: Panicle Number, PH: Plant Height (cm), TSPP: Total spikelet per panicle, TTPH: Total Tiller per Hill.

TABLE 4: The Mean Values of Phenotypic Traits, and Yield Components of 32 Nigeria Rice Genotypes Under Deep- Water Ecology

Genotypes	1000GW (g)	3IL (cm)	5IL (cm)	CL (cm)	D50F	FGPP	GWPH (g)	PL (cm)	PN	PH (cm)	TSPP	TTPH
TOX7-3-2-3B1-1-B-1	25.66	21.07	22.07	147.18	78.00	103.00	45.28	26.76	12.33	173.94	126.00	14.00
EX SOKOTO	24.33	14.10	23.70	109.00	95.00	150.00	76.46	21.25	13.00	130.25	185.00	17.00
TOS 6900	29.33	14.73	12.97	103.88	94.00	186.00	109.30	34.12	11.30	138.00	253.00	14.67
TOS 6928	27.00	16.34	23.1	115.43	92.00	281.00	85.93	22.86	9.67	138.29	289.33	11.00
MAIMANJA	20.00	18.67	30.53	108	86.00	103.67	33.32	23.61	11.00	131.61	125.00	13.33
EXGBANGBASHOFO(BIDA)	22.00	19.83	28.33	103.13	86.00	115.33	33.08	16.00	9.67	119.13	125.33	12.00
IRESI 4	31.33	22.23	22.23	102.23	85.00	126.33	58.21	18.77	10.33	121.00	142.33	13.00
IRESI SWAMP	25.00	10.50	17.40	75.96	89.00	107.33	42.92	17.7	9.33	93.66	131.67	13.00
IITA 182	31.00	24.23	34.60	108.07	90.00	188.00	102.46	22.73	12.33	93.66	216.00	15.33
EXZARIA	25.00	20.50	27.86	99.41	83.00	103.00	57.13	20.83	12.67	120.33	152.33	15.00
R66(78160)	25.00	22.73	24.80	116.13	96.00	93.67	28.33	20.87	8.00	137.00	113.33	10.00
IRESI ABEOKUTA	27.00	25.83	31.77	108.92	98.00	134.00	58.21	23.50	12.33	132.42	154.00	14.00
LAC 23	30.00	19.86	25.93	87.40	95.00	263.00	112.36	20.37	11.00	107.77	280.33	13.33
TOS 5303-1	29.00	16.27	21.87	123.77	86.00	198.00	97.22	22.56	12.67	146.33	218.67	15.33
IITA 118	34.44	17.93	22.60	74.53	85.00	265.00	156.20	15.93	12.67	90.46	297.00	15.33
EX ARGUNGUN	23.33	16.23	24.83	99.70	95.00	114.00	32.29	21.23	8.33	120.93	125.67	11.00
EX GANYE	30.33	16.21	20.68	132.54	89.00	133.00	92.57	25.36	15.00	157.91	160.67	19.00
EXSOKOTO 1	14.00	20.77	26.86	123.77	95.00	88.67	15.89	18.14	8.00	134.81	100.00	11.33
IITA 220	31.67	16.16	18.67	85.33	87.00	132.00	71.21	14.73	13.33	100.06	147.33	15.33
EXGBIKO WILD	33.33	17.2	20.40	109.06	89.00	94.67	33.24	17.86	7.00	126.92	105.67	9.33
TOS5865	31.00	13.23	19.40	106.09	94.00	168.00	103.29	10.39	12.33	116.49	217.00	15.33
IITA 183	29.00	15.70	25.20	84.90	86.00	94.67	30.74	19.67	7.00	104.57	106.00	10.00
IITA 185	25.00	18.33	23.50	81.04	88.33	226.00	119.85	16.53	14.33	97.57	282.00	17.00
IRESI ITORI	30.00	18.77	21.13	139.00	87.00	127.33	55.58	19.05	10.00	158.05	132.33	14.00
IITA 186	29.33	20.00	23.83	82.00	86.00	168.33	51.39	23.73	7.67	105.73	181.00	9.67
EX MANGU	20.00	11.77	20.34	70.67	99.00	128.00	57.35	28.28	13.33	122.36	187.00	15.33
TOS 6949	26.00	16.67	26.77	105.70	84.00	249.67	118.16	18.25	14.00	88.92	267.33	17.00
IRESI ILARO 1	30.00	17.40	25.97	105.70	87.00	101.33	42.49	20.63	8.67	126.33	132.67	10.67
IRESI 3	28.33	24.50	31.43	115.44	97.00	112.67	43.85	21.20	9.00	136.64	136.00	10.00
IRESI ILARO2	29.33	12.17	19.33	102.30	87.00	108.33	42.70	20.77	9.67	123.07	121.33	12.00
EXKASTINA ALA	29.67	14.77	19.93	88.67	89.00	123.67	86.10	23.47	14.33	112.14	174.00	16.67
EX SHANA	24.00	16.20	17.93	100.67	85.00	102.67	86.10	18.80	8.00	119.47	114.67	10.00
LSD _{0.05}	1.92	NS	NS	2.58	0.17	20.66	13.37	0.25	2.04	2.58	17.13	1.84
Grand Mean	27.2	17.84	23.63	103.02	89.45	146.57	66.28	20.81	10.89	123.84	171.88	13.48
CV%	4.32	NS	NS	1.54	0.11	8.64	12.36	0.72	11.49	1.28	6.11	8.35

Key: 3IL: 3rd Internodal Length (cm), 5IL: 5th Internodal Length (cm), CL: Culm Length (cm), D50F: Days_50%_Flowering, FGPP: Filled Grain per panicle, GWPH: Grain weight per Hill (g), PL: Panicle Length (cm), PN: Panicle Number, PH: Plant Height (cm), TSPP: Total spikelet per panicle, TTPH: Total Tiller per Hill.

Table 5: Genetic Variability for Culm Elongation and Yield Related Traits of 32 Nigeria Rice Genotypes

Traits	σ^2_g	σ^2_p	σ^2_e	Heritability (h^2_{BS})	GCV%	PCV%	GA%	GAM%
1000GW(g)	11.74	14.31	1.54	0.82	13.64	15.06	6.39	25.44
CL (cm)	194.41	195.07	1.53	0.98	15.48	15.51	28.67	31.85
D50F	28.04	28.04	0.01	0.99	5.82	5.82	10.91	11.99
FGPP	2355.37	2407.55	188.82	0.97	35.84	36.24	98.88	73.03
GWPH (g)	695.533	722.30	57.61	0.96	45.76	46.63	53.31	92.50
PL (cm)	12.44	12.68	1.19	0.98	18.42	18.60	7.20	37.60
PN	3.16	3.45	1.51	0.91	16.65	17.42	3.50	32.78
PH (cm)	261.76	262.69	2.64	0.99	14.82	14.84	33.27	30.47
TSPP	2355.37	2511.90	164.71	0.98	30.68	30.93	101.59	62.70
TTPH	4.13	4.41	1.23	0.94	15.31	15.82	4.05	30.54

Key: σ^2_g : Genetic variance, σ^2_p : Phenotypic Variance, σ^2_e : Environmental variance, CL: Culm Length (cm), D50F: Days 50%Flowering, FGPP: Filled Grain per panicle, GWPH: Grain weight per Hill (g), PL: Panicle Length (cm), PN: Panicle Number, PH: Plant Height (cm), TSPP: Total spikelet per panicle, TTPH: Total Tiller per Hill, Broad Sense Heritability (h^2_{BS}), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), GA: Genetic Advance, GAM Generalized Additive Model.

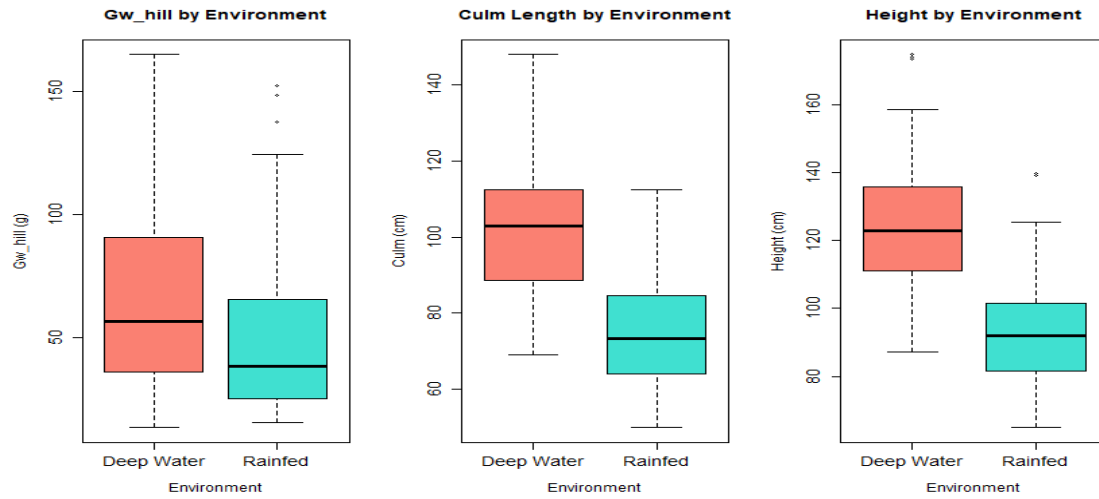


Figure 1a. Environment Boxplots for Grain weight per hill, Culm length, and plant height.

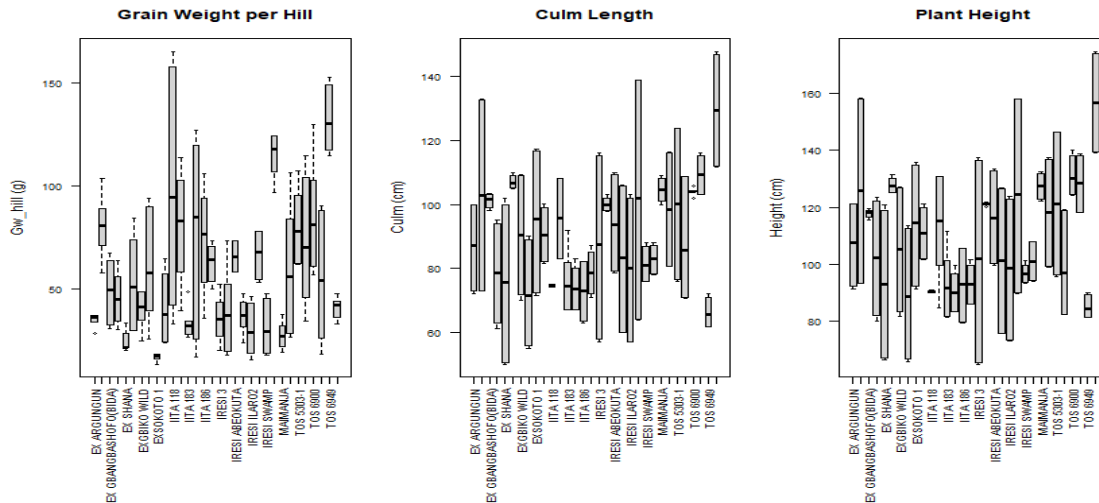


Figure 1b. Genotype Boxplots for Grain weight per hill, Culm length, and plant height

Table 6: Correlation analysis showing culm elongation and yield parameters traits

TRAITS	Plant Height	Total Tiller	Culm Length	D50% Flowering	Panicle Length	Panicle Number	Spikelet Number	Filled Grain	3IL	5IL	1000 Grain Weight	Grain Weight /Hill
Plant Height	1	0.061	0.985	-0.205	0.623	0.033	-0.021	-0.032	0.279	0.227	0.138	0.020
Total Tiller		1	0.022	0.151	0.212	0.939	0.549	0.445	0.020	0.006	0.095	0.698
Culm Length			1	-0.208	0.481	-0.006	-0.052	-0.053	0.280	0.228	0.158	-0.008
D50% Flowering				1	-0.098	0.139	0.105	0.05	-0.060	-0.057	-0.224	0.028
Panicle Length					1	0.197	0.132	0.078	0.149	0.123	-0.012	0.137
Panicle Number						1	0.557	0.463	0.058	0.033	0.142	0.692
Spikelet Number							1	0.959	0.035	0.077	0.280	0.922
Filled Grain								1	0.085	0.121	0.313	0.875
3IL									1	0.776	0.136	0.072
5IL										1	0.068	0.076
1000 Grain Weight											1	0.486
Grain Weight /Hill												1

Key: ***, **, * significant at $P \leq 0.001$, $P \leq 0.01$, $P \leq 0.05$ level of probability. ^{ns} not significance

Key: 3IL: 3rd Internodal Length (cm), 5IL: 5th Internodal Length (cm), CL: Culm Length (cm), D50F: Days_50%_Flowering, FGPP: Filled Grain per panicle, GWPH: Grain weight per Hill (g), PL: Panicle Length (cm), PN: Panicle Number, PH: Plant Height (cm), TSPP: Total spikelet per panicle, TTPH: Total Tiller per Hill.

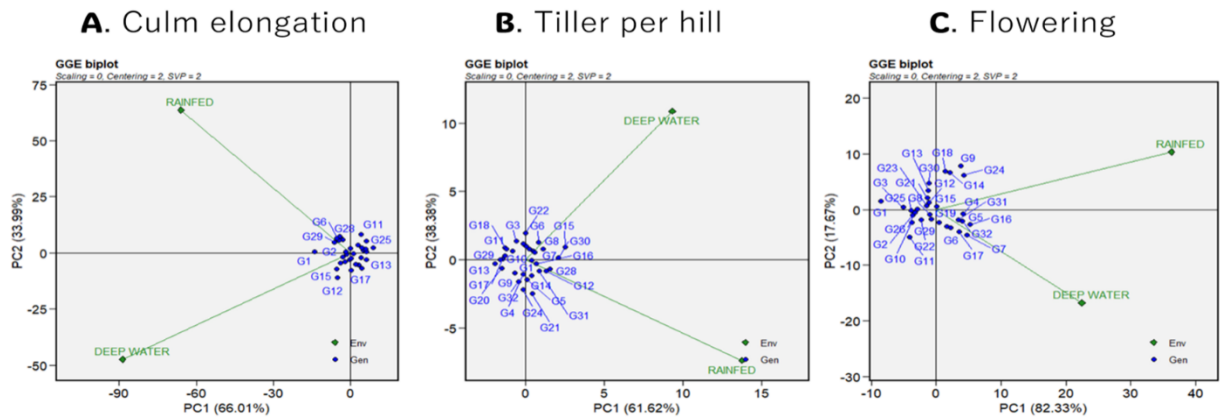


Figure 2: GGE biplot showing Culm Elongation, Total Tiller per Hill traits and Days to 50% Flowering traits across rainfed and deep- water ecology.