

Combining Ability and Heritability of Yield Components of Segregating Population of Rice (*Oryza sativa* L.)

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Abstract: Combining ability analysis aids in identifying parents with good trait in the desired direction for various targeted traits, and provides information on the relative importance and magnitude of additive and non-additive types of gene action in trait expression. This study was carried out to determine the combining abilities and heritability for grain yield and grain yield components of segregating population of rice. A total of 78 genotypes of rice were used in this experiment, which included 59 F₁ hybrids developed through North Carolina II mating design together with their parents, and adapted check. The experiment was conducted using alpha lattice design, with two replications. Analysis of variance revealed highly significant differences between genotypes, indicating the presence of genotype variation. The GCA exhibited high significance with the days to 50% flowering, leaf area, leaf area index, and all the traits under study, while SCA showed significant effects with the number of days to 50% flowering and 1000 grain weight. Broad-sense heritability showed higher results for days to 50% flowering at 0.97, and narrow-sense heritability showed the highest value of 0.81 for panicle length. The cross UPN 349 × NERICA 2 recorded 57.5 days very early. FARO 52 displayed a positive significant GCA effect when used as male parent under grain yield. Panicle weight (0.39489) and number of grains per panicle (0.64909) showed positive significant correlation with the grain yield. For grain yield and the majority of studied traits, non-additive genetic variance was found to be greater in magnitude than the corresponding additive variance.

Keywords: General Combining Ability, Specific Combining Ability, Heritability, Rice

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in terms of human nutrition and caloric intake [1]. Rice provides more than 70% of human caloric intake [2]. It is primarily grown for its grain, which contains approximately 80% starch, 7% protein, and 12% water [3, 4]. In addition, rice grain is also rich in fiber, vitamins, has low cholesterol, and contains minerals such as copper, iron, calcium, magnesium, manganese, zinc and sodium [2, 4]. This therefore suggests that rice is an excellent source of energy and health, particularly for hypertensive individuals [2]. The global rice demand by 2050 will be 943.6 million tonnes,

requiring an annual increase of about 5.8 million tonnes from current production levels [5, 6].

In Africa, rice is a staple food for millions of people, and it accounts for a significant portion of daily diet in the African region [7]. Rice consumption in Sub-Saharan Africa (SSA) is expected to increase significantly at a rate of 6% annually as the population grows at a rate of 3 to 4% per year, and rice consumption is growing faster than that of any other major food [8]. The average rice production in West Africa is showing irregular pattern, probably due to unreliable rainfall which is as a result of climate change, limitation on the availability of water for irrigation and low fertilizer input [9].

In Nigeria, the three main rice production ecologies are

lowland rice, upland rice, and irrigated rice. Among these, lowland rice has the highest priority due to its importance in terms of ecology, as it accounts for the largest share of rice area and production [10]. However, the traditional rice genotypes that are still present in Nigeria's upland rice ecosystems can provide the genetic diversity required to develop improved high yielding rice varieties with farmer-preferred traits [11].

Yield component does not act independently, and in general, they are interconnected with each other to produce grain yield in rice. Furthermore, majority of the yield component traits are quantitative in nature, with both heritable and non-heritable variability [12].

The crossing of parental lines known to have desirable qualities such as combining ability and heritability is the first step in breeding to improve grain yield in rice and its related traits [13]. However, the quality attributes of rice varieties in West Africa, including those commonly used as parental lines are poorly documented. Combining ability analysis provides information on the relative significance and magnitude of additive and non-additive types of gene action in trait expression. Therefore, this study was carried out to determine the combining abilities and heritability for grain yield and grain yield components of segregating population of rice.

2. Materials and Methods

2.1. Location of Study

The field experiment was conducted at the experimental field (plot EN6 Puddy) of African Rice Centre at the International Institute of Tropical Agriculture (IITA), Old Oyo Road, Ibadan, Oyo state, Nigeria, starting November 21, 2021. IITA is located at longitude 7°30'8"N, latitude 3°54'37"E and at an elevation of 243m above sea level. It has an annual rainfall range of 1300-2000 mm and a bimodal rainfall distribution pattern. During the dry season, the annual mean temperature is 27.2°C, and during the rainy season, it is 25.6°C [14].

2.2. Experimental Materials

A total of 78 genotypes of rice were used in this experiment, which included 59 F₁ hybrids derived through the North Carolina II (NCD II) mating design at IITA, Ibadan [15]. The materials also included 18 parental lines and a commercial check. In generating the crosses, each line was used as a male in one set and as a female parent in another set.

2.3. Experimental Design and Procedure

The experiment was conducted using alpha lattice design (rows × columns), with two replications. Each plot measured 3m × 0.6 m in dimension, with a plant spacing of 0.2m x 0.2 m gap between and within rows respectively, thus resulted to three rows per plot with a total of 45 planting hills. An alley of 1m between the replicates and 0.6m between the blocks was observed. Nursery beds for the irrigated plots were

prepared, and seedlings transplanted at 18 days old, with each planting hill having one seedling. N:P:K 15:15:15 fertilizer was applied 2 days after transplanting as a basal application at a rate of 200 kg per hectare, and urea was later applied as a top dressing 30 days after transplanting, at a rate of 65 kg hectare. All other agronomic practices, such as gap filling, weeding, irrigation and drainage, top dressing, and plant protection measures, were carried out as considered necessary.

2.4. Data Collection

Data were collected at the appropriate stage of crop development. The agronomic character traits were measured by selecting three plants at random from each experimental plot. Except where otherwise specified, the International Rice Research Institute's (IRRI) Standard Evaluation System (SES), 2002 for Rice reference manual was used for all the morphological and yield trait measurements [16]. Data were collected for parameters which included; number of plants per plot, number of days to 50% flowering, number of tillers per plant at vegetative stage, number of effective tillers per plant, plant height (cm), flag leaf length (cm), leaf width (cm), leaf area (cm²), leaf area index, panicle length (cm), panicle weight (g), number of grains per panicle, 1000 grain weight (g), and grain yield per plot (g).

The leaf length and leaf width were used to estimate the leaf area (LA) as reported by [17]:

$$LA = L \times W \times K$$

Where: LA: Leaf Area, L: Leaf Length, W: Leaf Width and K: Constant = 0.75.

Leaf Area Index (LAI) was calculated as defined, LAI as the total one sided area of leaf per unit surface area covered by the plant [18].

$$LAI = \frac{LA}{\text{Area covered by the plant}}$$

Where: LAI = Leaf Area Index, LA = Leaf area.

2.5. Data Analyses

The Statistical Analysis Software (SAS) version 9.2 was used for the analysis of variance (ANOVA). Differences were declared statistically significant at $P \leq 0.05$. The genetic parameters were estimated using mean squares of genotypes and error mean squares to identify the variations among the crosses and the parental lines.

The variation between families was divided into component differences between males and females, as well as that caused by male × female interaction. In this design, male and female expectations were equivalent to the general combining ability (GCA), while male and female interaction (male × female interaction) was equivalent to the specific combining ability (SCA). To investigate the differences between males and females, F-tests were used. The GCA and the SCA effects for the parents and their hybrids were calculated based on the statistical model by [15].

$$\text{GCA effect (male)} = \frac{M_{sm} - M_{sm \times f}}{Fr - Cov(Hs)} = \frac{1}{4} \sigma^2 A \quad (1)$$

$$\text{GCA effect (female)} = \frac{M_{sf} - M_{sm \times f}}{Mr - Cov(Hs)} = \frac{1}{4} \sigma^2 A \quad (2)$$

$$\text{SCA effect (m} \times \text{f)} = \frac{M_{sm \times f} - M_{se}}{r - Cov(Fs) - 2Cov(Hs)} = \frac{1}{4} \sigma^2 D \quad (3)$$

The relative importance of GCA and SCA effects was determined by applying the equation proposed by [19].

$$\frac{2\sigma^2_{GCA}}{2\sigma^2_{GCA} + 2\sigma^2_{SCA}}$$

Where $2\sigma^2_{GCA}$ is the variance component from the mean square of the GCA effect depicting a fixed effect, and σ^2_{SCA} is the quadratic form of SCA effects since the total genetic variation among single-cross progeny is equal to twice the GCA component plus the SCA component [6, 19, 20].

The closer this ratio is to unity, the greater the predictability of a specific hybrid's performance based on GCA alone [19, 20]. A ratio closer to one reveals GCA action while a ratio of less than one predicts SCA action [6].

Broad-sense (H^2) and narrow-sense (h^2) heritability were calculated using the equation outlined below:

$$H^2 = \frac{V_A + V_D}{V_A + V_D + V_E}$$

$$h^2 = \frac{V_A}{V_A + V_D + V_E}$$

Where: V_A : Additive variance, V_D : Dominance variance, V_E : Environmental variance.

The Pearson correlation analysis was computed using the SAS version 9.2 to determine the relationships among the morphological traits studied during this experiment.

Cluster analysis of the morphological traits was done using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) algorithm and Hierarchical clustering was applied for calculating genetic relationships and dendrogram was constructed based on similarity groups using Ward's method.

3. Results

3.1. Analysis of Variance

The analysis of variance (ANOVA) results revealed significant differences among the rice genotypes evaluated in this study for most of the traits under consideration, indicating the presence of genotype variation (Table 1). The general combining ability (GCA) exhibited high significance ($P \leq 0.01$) with the number of days to 50% flowering (DTFL), leaf area, leaf area index, plant height, number of effective tillers, plant height, panicle weight, number of grains per panicle, grain yield, 1000 grain weight and number of vegetative tillers. Specific combining ability (SCA) showed significant effects with the number of days to 50% flowering as well as with the 1000 grain weight (Table 1).

3.2. Estimation of Genetic Parameters

The estimates of genetic parameters for all studied traits are shown in Table 2. The results demonstrated that the additive variance (σ^2_A) which is due to the relative importance of the GCA for the number of days to 50% flowering, plant height, leaf area, number of effective tillers, panicle length, panicle weight, number of grains per panicle and grain yield were greater than the dominance variance (σ^2_D) which is due to the relative importance of the SCA for those traits under study.

3.3. Heritability

In terms of heritability estimation, the results showed that heritability values were high for the majority of the characteristics studied (Table 2). The broad-sense heritability (H^2) depicted higher results for days to 50% flowering at 0.97, while the lowest was reported on leaf area at 0.67. Plant height, number of effective tillers, panicle length, panicle weight, number of grains per panicle and grain yield had 0.77, 0.81, 0.83, 0.83, 0.81, and 0.90 respectively. On the other hand, narrow-sense heritability (h^2) depicted the highest value of 0.81 for panicle length, with the lowest recorded on leaf area and number of grains per panicle both at 0.58. Other traits recorded values as shown in Table 2.

3.4. Mean Performance

The mean performance for yield and its related traits revealed differences between the parental genotypes and their 59 F_1 crosses, as shown in Table 3 and Table 4 respectively. For days to 50% flowering, the lowest mean values are preferable. Two parental genotypes, FARO 58 and NERICA 3 recorded the desirable lowest mean values of 60.83 and 63.50 respectively for the number of days to 50% flowering, while on the other hand, the crosses with the lowest mean values were obtained from UPN 349 \times NERICA 2, UPN 345 \times NERICA 4 and UPN 236 \times NERICA 3, which recorded 57.5, 58.5 and 58.5 days, respectively. The parental lines with the highest mean values were recorded on FARO 52 (83), UPIA 2 (83), UPN 276 (82), and UPIA 1 (82), while the crosses that recorded highest mean values for 50% flowering were UPN 236 \times FARO 44 (76), UPN 257 \times FARO 44 (75), UPN 276 \times FARO 44, and UPN 347 \times NERICA 4 (74.5).

The results on plant height depicted the parental lines NERICA 2 and UPN 345 as having the lowest mean values at 106.33cm and 113.67cm respectively, while the crosses with the lowest mean values were recorded from UNPN 234 \times FARO 44, UPN 257 \times FARO 44, and UPN 236 \times NERICA 1 with values 115cm, 117.50cm, and 117.67cm respectively. On the other hand, UPIA 1 showed the highest mean value for plant height at 132.17cm, followed by FARO 59 with 131.17cm.

Regarding the leaf area, genotype UPN 349 and UPN 234 recorded the highest mean values among the parental lines at 51.40cm² and 51.37cm² respectively, while among the F_1 hybrids, FARO 58 \times UPN 349 depicted a mean value of 75.74cm² and UPN 349 \times NERICA 3 exhibited a mean value

of 66.63cm² under leaf area. Furthermore, the data on panicle weight for the parental lines depicted NERICA 1 as having the highest mean value at 6.45g, followed by UPN 345 at 5.31g. For the crosses, UPN 276 × FARO 58 and UPN 349 × NERICA 4 recorded the highest mean values of 6.15g and 5.81g, respectively. The results indicated that the panicle weight has a direct positive effect with the grain yield, as the higher the panicle weight, the higher the mean values for grain yield. On the other hand, highest mean values for number of grains per panicle of the parental lines was recorded by UPN 345 and UPN 234 as 153.67g and 148.50g respectively.

The crosses UPN 228 × NERICA 1 and UPN 347 × FARO 52 depicted the highest mean values for number of grains per panicle of 169.0 g and 159.50 g respectively (Table 4). For grain yield per plot, among the parental lines, the genotypes UPN 266 and UPIA 2 recorded the highest mean values of 1962.15 g and 1367.72 g, respectively. The highest mean values for crosses under grain yield per plot were observed under the cross combinations UPN 236 × FARO 52 and UPN 228 × NERICA 1 with values of 1435.14 g and 1261.82 g. In addition, the result for 1000-grain weight among the parental lines indicated that lines UPN 347 (33.20 g) and UPIA 2 (30.50 g) recorded the highest mean values, while for the cross combinations, UPN 349 × NERICA 3 and UPN 268 × NERICA 4 exhibited the highest mean values of 35.50 g and 32.85 g, respectively.

3.5. General Combining Ability (GCA) Effects

The inbred lines tested in this study displayed significant ($p \leq 0.01$) negative and positive GCA effects for GY and key secondary traits under study (Table 5 and Table 6). FARO 44 and FARO 52 displayed positive and significant GCA effects when used as males under days to 50% flowering. FARO 59, UPN 266, UPN 349 and NERICA 4 showed positive but non-significant GCA effects when used as males under DTFL. The other inbred lines, FARO58, NERICA 2, NERICA 3, UPN 228, UPN 236, UPN 266, UPN 268, UPN 345 and NERICA 1 evaluated under DTFL showed negative and nonsignificant GCA effects. However, when used as female parents (Table 6), FARO 52 and FARO 44 showed positive significant GCA effects, while FARO 58, NERICA 2, NERICA 3, UPN 228, UPN 236, UPN 268, UPN 345, and NERICA 1 showed negative GCA effects. The other parental lines showed positive GCA effects as shown in Table 6.

Under grain yield, FARO 52 displayed a positive significant GCA effect when used as male parent. On the other hand, NERICA 2 showed a negative but significant GCA effect when evaluated under the same trait. The other inbred lines showed non-significant GCA effects with FARO 58, UPN 349, UPN 228, FARO 44 and NERICA 4 showing positive GCA effects, while FARO 59, NERICA 3, UPN 236, UPN 266, UPN 268, UPN 345 and NERICA 1 showing negative GCA effects when used as male parents for GY. On the other hand, the parental genotypes when used as females depicted UPN 228, UPN 268, UPN 276, and UPN 349 as

having positive GCA effects, while the other lines showed negative GCA effects under grain yield per plot.

For panicle length, NERICA 1 and UPN 266 displayed positive significant GCA effect as opposed to FARO 59 and UPN 345 that had negative significant effects. The other inbred lines showed non-significant effects when used as male parents. When the parents are used as female parents, UPN 266 recorded positive significance GCA effect for panicle length, while FARO 58, NERICA 3, UPN 234, and UPN 276 depicted positive effects of general combining ability. The other lines indicated negative effects under that same yield component trait. FARO 44 and NERICA 1 showed negative significant GCA effects for plant height while the other lines did not show any level of significance. Meanwhile, when the genotypes were used as the female parents, FARO 59, NERICA 3, UPN 228, UPN 236, UPN 257, and UPN 345 showed a negative general combining ability effects, while the other lines depicted positive GCA effects for plant height. A positive significant GCA effect was observed on FARO 52 for the number of grains per panicle, while most of the lines used as parents did not show much significant differences. As female parent, FARO 59, NERICA 3, UPN 234, UPN 236, UPN 266, UPN 268, and UPN 345 depicted negative effect for general combining ability for the number of grains per panicle.

Positive significant difference was observed in NERICA 1 for the number of effective tillers while only FARO 44 showed a positive significance for number of vegetative tillers. There was no observed significant difference for leaf area for the parental lines used as males, while when used as female, UPN 236 recorded negative significance GCA effect, with FARO 58, FARO 59, UPN 228, UPN 234, UPN 268, and UPN 349 recording positive general combining ability effects for leaf area.

As regard to panicle weight, UPN 236, UPN 268, UPN 345, FARO 44, and NERICA 1 (Table 5) showed negative non-significant GCA effects when used as male parents, while FARO 59, NERICA 3, UPN 236, UPN 266, UPN 268, and UPN 345 observed negative GCA effects when used as female parents (Table 6).

3.6. Specific Combining Ability (SCA) Effects of F1 Hybrids for Rice Grain Yield and Yield Related Traits

The specific combining ability of the crosses are presented in Table 7. Based on the estimates of SCA effects under number of days to 50% flowering, the cross combinations UPN 236 × FARO 44, UPN 266 × NERICA 1, and UPN 347 × NERICA 4 recorded the highest positive significant SCA effects, while the combinations of UPN 345 × FARO 59 and UPN 349 × FARO 52 depicted the highest positive but non-significance SCA effects. For leaf area, FARO 58 × UPN 349 registered the highest positive GCA effect while majority of the cross combinations recorded negative specific combining ability effects.

For panicle length, both positive and negative SCA effects were recorded, with majority of the hybrid crosses having negative effects as compared to the positive values. A high

positive significant SCA effect was depicted by UPN 228 × NERICA for grain yield, while other combinations depicted non-significant positive and negative SCA effects. UPN 349 × NERICA 3 exhibited positive significant SCA effect for 1000-grain weight.

3.7. Pearson Correlation Analysis Among the Traits

The correlation coefficients were calculated among the quantitative traits, and the results revealed that some of the characters developed positive correlations with one another, while others developed negative correlations with one another (Table 8).

Panicle weight (PW) had a high significant positive correlation with the grain yield (0.39489). Number of grains per panicle (NGPP) also displayed a highly significant and positive correlation with the grain yield (0.64909). The number of days to 50% flowering (DTFL) showed significant and positive correlation with the grain yield. The total number of effective tillers (ET) showed significant negative correlation with the grain yield (-0.3676). 1000 GWT showed a positive correlation with the grain yield as well (0.05009). Similarly, the other traits also displayed positive and negative significant correlations among themselves. The correlation analysis on the number of days to 50% flowering (DTFL) depicted a high significant negative correlation with the number of effective tillers (-0.355).

A high significant negative correlation was also observed between DTFL and grain yield (-0.3819), leaf area (LA) (-0.3819) and leaf area index (LAI) (-0.3819). However, a significant positive correlation was observed with the number of grains per panicle (NGPP) (0.25671). The number of

effective tillers (ET) depicted highly significant negative correlation with grain yield (-0.3676), number of grains per panicle (-0.463), plant height (-0.3445) and panicle weight (-0.4779). On the other hand, ET had a significant positive correlation with panicle length (0.39813). Plant height depicted a significant positive correlation with LA and LAI (0.30594). Similarly, panicle weight also depicted a highly significant positive correlation with number of grains per panicle (0.62872).

3.8. Cluster Analysis of the Evaluated Rice Parental Lines

Cluster analysis provides useful means for estimating morphological diversity among different groups. It is a useful tool that can be used to the potential of a breeding program. The clusters formed among the rice genotypes evaluated for grain yield and yield components are shown in Figure 1. The clustering resulted into three major cluster groups (Cluster 1, 2 and 3). A total of 18 parental lines were subjected for cluster analysis, of which FARO 59, NERICA 2, and NERICA 3 resulted into cluster 1, while UPN 266 and UPIA were categorized in cluster 2. The other remaining parental lines namely UPN 347, UPIA 2, FARO 52, UPN 228, UPN 345, UPN 276, UPN 234, UPN 268, UPN 349, UPN 236, UPIA 3, UPN 257, and FARO 44 were recorded under cluster group 3 (Figure 1).

The cluster analysis showed the wide diversity of the planting genetic materials that were evaluated in this study, thus crossing of genotypes among the clusters could result to higher segregation. Breeders therefore need to evaluate genotypes in order to group them into their distinct clusters based on each trait under study.

Table 1. Analysis of variance for various grain yield and yield related components for rice crosses.

SV	DF	DTFL	PH (cm)	LA (cm ²)	LAI	VT	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)	GWT (g)
Rep	1	6.48	18.92	797.56*	0.005*	42.12*	15.74	6.33	0.05	1081.28	40474.32	59.65***
Gen	58	47.75***	118.52**	127.1	0.001	7.84	21.59*	4.18**	1.51**	1401.06*	88369.84***	22.79***
Male	13	100.44***	254.24***	210.14*	0.001*	18.10**	34.94**	10.08***	1.22	2029.88**	213291.92***	16.17***
Female	11	58.03***	169.93**	153.7	0.001	6.36	23.44*	4.09*	3.07***	1826.83*	70407.63*	42.57***
Male × Female	34	24.27***	50	86.74	0.001	4.4	15.88	1.95	1.12	1022.88	46416.81	18.92***
Error	57	7.91	67.06	89.8	0.001	7.21	12.15	1.9	0.78	826.31	33948.35	13.81

*, **, *** indicating the levels of significance at 0.05, 0.01 and 0.001 respectively. SV= Source of variation. DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tillers.

Table 2. Prediction of hybrid performance based on variances, relative importance ratio and heritability.

SV	DTFL	PH (cm)	LA (cm ²)	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)
σ_m^2	9.03	24.26	4.05	2.58	1.28	0.06	147.06	23460.67
σ_f^2	5.05	12.60	13.93	1.36	0.26	0.17	85.24	2113.22
$\Sigma (\sigma_m^2 + \sigma_f^2)$	14.08	36.86	17.99	3.94	1.54	0.23	232.30	25573.89
$\sigma_{m \times f}^2$	7.70	22.42	3.09	1.30	0.02	0.14	117.88	8047.00
$\frac{2\sigma_{GCA}^2}{2\sigma_{GCA}^2 + 2\sigma_{SCA}^2}$	0.65	0.62	0.85	0.75	0.98	0.62	0.66	0.76
H^2	0.97	0.77	0.67	0.81	0.83	0.83	0.81	0.90
h^2	0.70	0.77	0.58	0.65	0.81	0.59	0.58	0.70
$\sigma^2 A$	82.16	106.76	79.40	20.57	106.76	1.39	1196.29	19.34
$\sigma^2 D$	30.7	32.13	12.36	5.19	32.13	0.56	471.53	15.13

SV = Source of variation, DTFL= Days to 50% flowering, LA= Leaf Area, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, σ_m^2 = Male variance, σ_f^2 = Female variance, $\sigma_{m \times f}^2$ = Interaction effect of male and female, H^2 = Broad-sense heritability, h^2 = Narrow-sense heritability.

Table 3. Mean performance of parental lines for rice grain yield and yield related traits.

Genotype	DTFL	PH (cm)	LA (cm ²)	LAI	VT	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)	GWT (g)
FARO 58	60.83	-	-	-	12.51	-	-	-	-	-	-
FARO 59	64.00	131.17	49.64	0.12	8.00	7.00	23.67	4.39	100.50	914.05	25.70
NERICA 2	66.50	106.33	48.92	0.12	9.17	8.50	26.83	3.82	140.17	657.34	22.95
NERICA 3	63.50	117.67	46.03	0.12	10.33	7.33	28.00	6.45	127.83	614.37	22.95
UPN 228	79.00	117.83	46.21	0.12	17.50	12.50	22.50	4.48	148.17	823.06	20.00
UPN 234	80.50	125.67	51.37	0.13	12.67	13.00	22.50	4.61	148.50	1178.82	21.50
UPN 236	67.50	117.83	40.20	0.10	11.50	14.50	24.33	3.41	136.67	1211.77	23.50
UPN 257	76.50	119.00	45.48	0.11	10.00	14.67	22.67	3.72	82.00	871.70	27.90
UPN 266	81.00	124.67	51.03	0.13	17.33	19.83	27.00	3.95	126.83	1962.15	22.25
UPN 268	80.00	122.83	49.55	0.12	12.00	15.17	24.00	4.88	124.33	1042.63	22.80
UPN 276	82.00	121.33	51.08	0.13	12.00	13.67	23.83	4.79	142.33	1032.05	29.30
UPN 345	78.00	113.67	45.54	0.11	14.17	11.33	22.83	5.31	153.67	1261.59	22.40
UPN 347	82.00	124.00	39.04	0.10	17.17	14.00	23.50	4.68	117.17	1014.27	33.20
UPN 349	81.00	124.83	51.40	0.13	11.67	13.33	23.67	4.12	131.83	898.18	24.40
UPIA 1	82.00	132.17	46.50	0.12	10.67	14.83	28.17	3.61	133.00	1171.78	26.20
UPIA 2	83.00	128.17	42.20	0.11	17.67	19.17	25.50	3.45	101.33	1367.77	30.50
UPIA 3	69.50	122.83	40.33	0.10	13.50	14.50	23.17	3.99	128.33	1193.65	22.45
FARO 52	83.00	128.50	37.47	0.09	19.67	14.50	26.33	3.33	110.83	1290.04	22.90
FARO 44	81.00	118.33	39.29	0.10	11.50	14.33	25.50	3.51	102.67	996.76	25.15
MEAN	75.83	122.05	45.67	0.11	13.11	13.45	24.39	4.17	122.21	1083.44	24.78
CV (%)	3.00	4.19	14.00	14.00	21.27	23.76	5.67	18.89	21.15	31.14	8.63

DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tiller.

Table 4. The mean performance of F_1 crosses for rice grain yield and yield related traits.

Genotype	DTFL	PH (cm)	LA (cm ²)	LAI	VT	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)	GWT (g)
FARO 58 × UPN228	63.50	125.67	53.53	0.13	7.50	14.83	24.17	4.61	124.83	884.17	20.25
FARO 58 × UPN 266	66.50	130.17	55.80	0.14	10.50	11.00	26.83	4.01	93.17	703.29	22.45
FARO 58 × UPN 268	60.00	128.67	55.66	0.14	13.67	11.17	24.83	2.74	110.17	713.22	31.60
FARO 58 × UPN 349	64.50	146.83	75.74	0.19	15.00	12.67	26.33	4.16	129.00	1029.05	24.20
FARO 59 × UPN 266	63.00	153.00	61.46	0.15	12.50	11.50	26.83	3.39	86.50	683.66	29.50
FARO 59 × UPN 345	60.50	132.83	50.65	0.13	15.17	12.83	21.17	2.40	54.83	821.47	22.65
NERICA 3 × UPN 236	60.50	129.17	50.18	0.13	17.83	15.33	27.17	3.35	70.00	715.32	25.40
NERICA 4 × UPN 345	65.00	131.33	49.60	0.12	10.83	12.67	23.17	5.20	132.67	955.64	31.85
UPN 228 × FARO 58	66.00	123.00	59.88	0.15	12.33	9.17	22.33	4.23	116.50	1256.94	32.60
UPN 228 × FARO 59	61.50	131.50	55.66	0.14	12.67	13.00	21.67	3.04	115.50	978.91	24.45
UPN 228 × NERICA 1	61.00	130.67	60.98	0.15	12.00	10.83	27.67	4.80	169.00	1261.82	29.20
UPN 228 × NERICA 3	61.00	128.33	43.80	0.11	12.17	11.50	24.83	4.78	107.83	988.63	31.85
UPN 228 × NERICA 4	64.50	136.00	51.13	0.13	11.50	13.67	24.83	3.46	99.50	965.38	27.80
UPN 234 × FARO 58	68.50	134.50	61.06	0.15	12.83	14.50	25.67	4.46	102.00	944.92	20.30
UPN 236 × FARO 44	76.00	115.00	39.48	0.10	15.17	13.67	25.00	3.24	120.00	835.43	26.20
UPN 236 × FARO 52	66.50	131.33	39.21	0.10	14.83	12.50	24.67	3.96	144.50	1435.14	26.65
UPN 236 × FARO 58	62.00	122.50	45.05	0.11	15.00	17.17	25.67	2.60	71.00	762.94	21.45
UPN 236 × NERICA 1	61.00	117.67	42.73	0.11	13.67	22.33	25.50	2.25	59.33	637.75	22.60
UPN 236 × NERICA 3	58.50	125.50	43.78	0.11	11.83	13.17	25.00	3.89	76.50	868.30	26.45
UPN 236 × NERICA 4	66.50	139.17	45.00	0.11	11.17	15.33	23.83	3.62	97.67	924.88	24.05
UPN 257 × FARO 44	75.00	117.50	55.37	0.14	16.50	12.00	25.17	4.31	127.17	1176.42	23.05
UPN 257 × FARO 59	72.50	129.00	45.06	0.11	10.50	9.67	24.50	4.17	107.50	686.23	26.35
UPN 257 × NERICA 1	63.00	124.00	46.68	0.12	11.50	13.50	27.17	4.85	111.00	744.38	24.30
UPN 257 × NERICA 2	67.00	131.17	49.38	0.12	10.33	9.17	25.33	4.17	95.33	715.81	23.60
UPN 257 × NERICA 3	69.00	132.67	44.10	0.11	11.83	10.83	22.67	4.37	127.67	800.88	29.20
UPN 257 × NERICA 4	73.50	129.67	49.29	0.12	13.33	10.67	23.50	5.06	119.50	823.50	27.20
UPN 266 × FARO 58	62.50	134.83	41.28	0.10	10.67	15.83	26.50	4.33	120.17	1012.07	26.80
UPN 266 × FARO 59	69.00	139.50	52.07	0.13	12.50	9.33	24.17	4.22	106.67	539.15	27.80
UPN 266 × NERICA 1	72.00	131.17	42.83	0.11	14.00	13.33	27.50	1.84	35.50	325.02	29.25
UPN 266 × NERICA 2	62.50	125.83	52.39	0.13	12.00	26.50	27.50	2.27	28.50	458.03	28.30
UPN 266 × NERICA 4	70.50	141.50	44.01	0.11	12.33	13.67	26.67	3.65	85.33	863.26	26.00
UPN 268 × FARO 58	64.50	128.33	48.48	0.12	14.00	14.00	24.33	3.03	98.83	854.03	28.45
UPN 268 × NERICA 1	63.00	135.00	49.65	0.12	12.33	14.67	25.67	3.04	86.17	716.72	31.35
UPN 268 × NERICA 3	62.00	132.67	55.06	0.14	15.00	13.00	24.67	3.21	76.67	782.50	22.90
UPN 268 × NERICA 4	60.50	145.50	63.20	0.16	13.50	11.83	24.17	3.38	90.33	734.38	32.85
UPN 276 × FARO 44	75.00	126.50	40.71	0.10	12.50	11.00	25.50	4.37	122.33	1145.14	24.25
UPN 276 × FARO 52	73.50	130.83	37.02	0.09	11.50	13.33	24.83	3.99	118.67	1135.00	24.80
UPN 276 × FARO 58	69.00	138.83	53.09	0.13	11.83	9.17	23.67	6.15	117.67	881.27	26.70

Genotype	DTFL	PH (cm)	LA (cm ²)	LAI	VT	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)	GWT (g)
UPN 276 × FARO 59	66.00	136.67	46.13	0.12	10.33	8.17	24.17	4.59	138.50	714.87	24.25
UPN 276 × NERICA 1	62.00	130.50	57.42	0.14	13.27	17.83	25.83	3.17	79.67	475.02	25.05
UPN 276 × NERICA 3	65.50	136.67	58.81	0.15	11.33	11.33	24.50	4.80	98.50	718.56	21.30
UPN 276 × NERICA 4	68.50	148.17	47.87	0.12	11.83	10.83	26.33	4.40	84.50	787.65	25.90
UPN 345 × FARO 58	59.00	127.33	57.92	0.14	10.00	11.50	23.83	4.01	56.83	764.41	28.40
UPN 345 × FARO 59	70.00	118.33	43.88	0.11	14.00	10.50	22.00	4.22	124.00	991.02	23.75
UPN 345 × NERICA 1	59.00	120.17	34.65	0.09	14.00	18.50	25.17	2.47	58.50	509.02	22.95
UPN 345 × NERICA 2	61.00	120.50	56.15	0.14	11.67	15.50	25.67	4.52	107.50	464.55	26.10
UPN 345 × NERICA 3	60.00	128.83	58.35	0.15	12.83	11.00	23.17	3.65	89.17	724.34	21.35
UPN 345 × NERICA 4	58.50	136.17	53.00	0.13	10.67	14.83	23.33	3.38	123.83	709.52	25.55
UPN 347 × FARO 44	67.50	129.50	49.53	0.12	17.00	17.33	26.67	3.68	88.33	651.29	22.30
UPN 347 × FARO 52	69.00	138.00	46.27	0.12	16.17	12.83	25.50	3.46	159.50	978.08	26.05
UPN 347 × NERICA 2	59.00	122.67	60.35	0.15	11.00	18.33	25.00	5.31	118.83	750.99	25.15
UPN 347 × NERICA 4	74.50	137.83	45.60	0.11	9.50	10.17	23.00	4.13	81.50	670.17	22.60
UPN 349 × FARO 52	71.50	128.67	48.49	0.12	11.33	10.00	24.50	4.36	125.00	1229.04	23.35
UPN 349 × FARO 58	62.50	132.17	53.01	0.13	11.33	15.67	26.00	4.80	117.83	782.19	26.55
UPN 349 × FARO 59	64.00	141.33	50.46	0.13	10.50	12.33	24.50	3.52	106.17	721.28	25.10
UPN 349 × NERICA 1	62.00	131.50	63.18	0.16	15.00	14.67	25.50	3.27	90.50	517.93	25.10
UPN 349 × NERICA 2	57.50	126.83	63.06	0.16	11.17	15.17	25.00	3.90	92.67	432.86	24.10
UPN 349 × NERICA 3	62.00	141.17	66.63	0.17	11.33	9.83	24.00	3.37	94.00	770.64	35.50
UPN 349 × NERICA 4	62.00	138.67	47.18	0.12	11.17	9.00	24.00	5.81	120.17	976.65	25.00
MEAN	65.11	131.51	51.15	0.13	12.54	13.15	24.89	3.89	101.88	815.27	25.93
CV (%)	4.28	6.23	18.44	18.44	21.46	26.46	5.38	22.35	26.91	22.53	14.76

DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tillers.

Table 5. General combining ability (GCA) effects of male parents for yield and yield components of rice.

Genotypes	DTFL	PH (cm)	LA (cm ²)	ET	VT	PL (cm)	PW (g)	NGPP	GY (g/plot)
FARO 58	-0.44	-1.30	0.49	0.03	-0.47	-0.22	0.19	-0.19	91.58
FARO 59	1.47	0.97	-0.76	-1.63	-0.85	-1.30**	0.00	8.74	-23.84
NERICA 2	-3.19	-4.73	1.57	2.36*	-1.22	0.61	0.05	-7.07	-165.50*
NERICA 3	-1.86	1.16	0.70	-1.05	-0.39	-0.63	0.06	-4.73	-5.35
UPN 228	-0.40	-2.29	-0.19	0.52	-2.18	-0.52	0.07	4.04	2.16
UPN 236	-1.57	-0.80	-0.09	0.52	2.07	1.10	-0.03	-6.33	-79.52
UPN 266	0.42	4.97	0.58	-0.68	-0.76	1.38*	0.01	-4.16	-121.30
UPN 268	-1.92	-1.00	-0.02	-0.45	0.35	-0.14	-0.10	0.80	-81.45
UPN 345	-1.40	-1.21	-0.20	-0.02	0.97	-2.02*	-0.10	-9.12	-26.91
UPN 349	0.04	6.82	1.54	-0.05	0.90	0.70	0.03	4.96	73.02
FARO 52	3.88*	0.02	-1.95	-0.74	0.48	-0.09	0.00	18.61*	330.57***
FARO 44	5.42**	-6.70*	-0.74	0.18	1.83*	0.53	-0.03	5.89	113.81
NERICA 1	-1.73	-2.31**	-0.39	2.03*	0.20	1.07*	-0.30	-11.50	-131.89
NERICA 4	1.29	6.41	-0.54	-1.02	-0.91	-0.48	0.15	0.09	24.61

*, **, *** indicating the levels of significance at 0.05, 0.01 and 0.001 respectively. DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tiller.

Table 6. General combining ability (GCA) effects of female parents for grain yield and yield components of rice.

Genotype	DTFL	PH (cm)	LA (cm ²)	LAI	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)	GWT (g)
FARO 58	-0.56	-0.44	4.33	0.011	-0.21	0.11	0.04	4.17	-5.32	-0.35
FARO 59	-1.27	4.22	1.55	0.004	-0.15	-0.23	-0.34	-6.19	-8.59	0.05
NERICA 3	-0.88	-0.41	-0.30	-0.001	0.28	0.22	-0.10	-3.67	-7.16	-0.04
UPN 228	-1.13	-1.09	1.58	0.004	-0.68	-0.32	0.16	9.33	63.82	1.10
UPN 234	1.20	1.23	2.01	0.005	0.22	0.19	0.11	-0.02	-2.52	-0.53
UPN 236	-0.71	-4.06	-5.51*	-0.014*	1.44	-0.04	-0.37	-4.41	-15.31	-0.48
UPN 257	3.461*	-2.27	-2.09	-0.005	-1.19	-0.14	0.46	6.83	-9.95	-0.07
UPN 266	2.01	1.69	-3.07	-0.008	0.99	0.88*	-0.35	-10.28	-19.67	0.64
UPN 268	-1.08	1.33	1.29	0.003	0.02	-0.11	-0.38	-3.15	8.04	0.93
UPN 276	1.85	2.56	-1.64	-0.004	-0.77	0.10	0.47	3.27	12.76	-0.51
UPN 345	-2.09	-4.93	-0.73	-0.002	0.10	-0.59	-0.09	-2.12	-5.77	-0.44
UPN 347	0.48	0.64	-0.42	-0.001	0.49	-0.04	0.16	3.03	-15.15	-0.53
UPN 349	-1.30	1.53	3.01	0.008	-0.54	-0.03	0.22	3.22	4.82	0.25

*, **, *** indicating the levels of significance at 0.05, 0.01 and 0.001 respectively. DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tillers.

Table 7. Specific combining ability (SCA) effects of F_1 hybrids for different yield related traits.

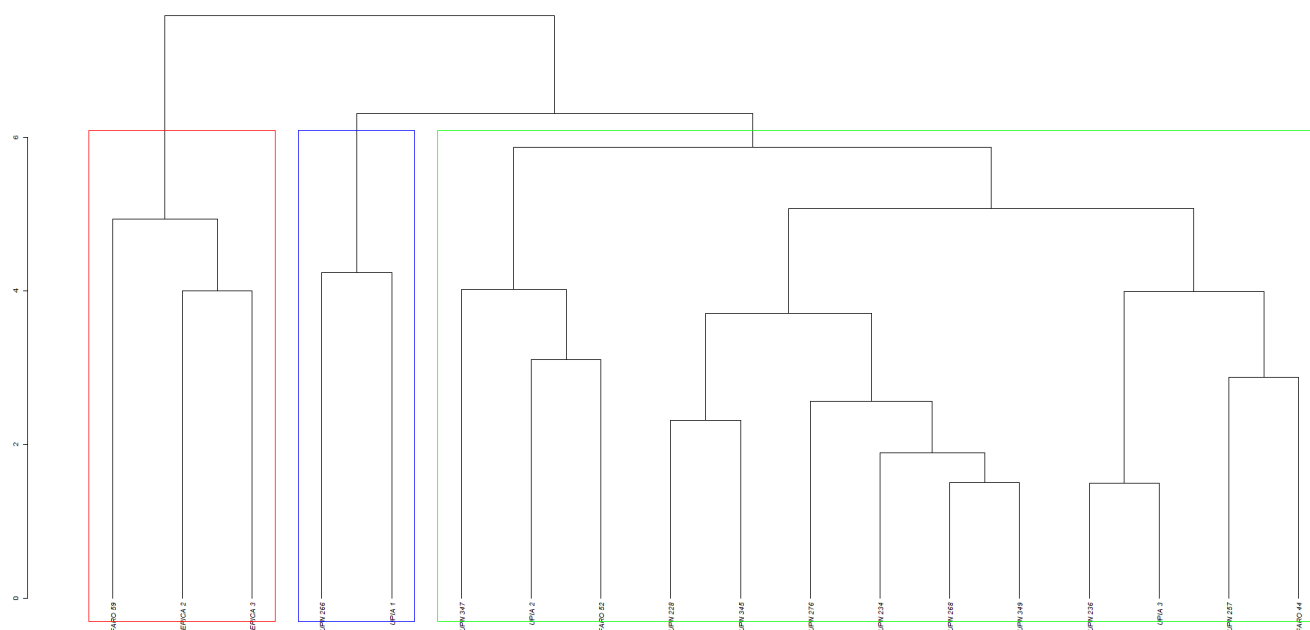
Genotype	DTFL	LA (cm ²)	LAI	ET	PL (cm)	PW (g)	NGPP	GY (g/plot)	GWT (g)
FARO 58 × UPN228	-0.34	-0.14	-0.0004	0.260	-0.010	0.181	3.24	0.74	-1.97
FARO 58 × UPN 266	1.10	-0.05	-0.0001	-0.212	0.009	0.041	-2.09	-18.12	-1.13
FARO 58 × UPN 268	-1.64	-0.02	0.0000	-0.224	-0.003	-0.261	0.64	-27.94	2.33
FARO 58 × UPN 349	0.03	1.17	0.0029	-0.026	0.014	0.074	3.97	25.05	-0.47
FARO 59 × UPN 266	-0.74	0.49	0.0012	-0.133	0.017	-0.022	-1.25	-23.49	1.38
FARO 59 × UPN 345	-1.19	-0.15	-0.0004	-0.012	-0.039	-0.252	-7.31	-9.23	-1.21
NERICA 3 × UPN 236	-1.33	-0.07	-0.0002	0.262	0.021	-0.083	-5.08	-27.28	-0.14
UPN 228 × FARO 58	1.71	0.40	0.0010	-0.585	-0.052	0.021	1.14	71.08	2.16
UPN 228 × FARO 59	-2.50	0.21	0.0005	0.401	-0.042	-0.242	-1.12	17.68	-0.93
UPN 228 × NERICA 1	0.09	0.53	0.0013	-0.363	0.023	0.214	12.81	159.99*	1.61
UPN 228 × NERICA 3	-0.64	-0.65	-0.0016	0.026	0.020	0.199	0.20	14.80	1.88
UPN 228 × NERICA 4	-0.39	-0.13	-0.0003	-0.124	0.021	-0.063	-0.13	-20.55	-0.87
UPN 234 × FARO 58	1.82	0.44	0.0011	0.210	0.018	0.093	-0.03	-9.59	-1.88
UPN 236 × FARO 44	4.15*	-0.38	-0.0009	-0.184	-0.012	-0.043	3.67	-48.65	0.33
UPN 236 × FARO 52	-1.08	-0.32	-0.0008	-0.229	-0.005	0.137	6.34	77.10	0.51
UPN 236 × FARO 58	-1.20	-0.10	-0.0003	0.470	0.023	-0.269	-6.07	-65.15	-1.46
UPN 236 × NERICA 1	-1.01	-0.19	-0.0005	1.037	-0.013	-0.234	-6.16	-32.88	-1.03
UPN 236 × NERICA 3	-2.56	-0.20	-0.0005	-0.054	0.017	0.104	-3.80	1.27	0.43
UPN 236 × NERICA 4	0.62	-0.04	-0.0001	0.330	-0.016	0.009	-0.08	10.01	-0.48
UPN 257 × FARO 44	0.76	0.42	0.0011	-0.011	-0.005	0.019	2.74	61.56	-1.01
UPN 257 × FARO 59	1.71	-0.24	-0.0006	-0.105	0.024	-0.026	-2.37	-54.20	0.24
UPN 257 × NERICA 1	-2.43	-0.16	-0.0004	-0.075	0.031	0.233	3.02	0.38	-0.54
UPN 257 × NERICA 2	1.15	-0.11	-0.0003	-0.910	-0.003	-0.037	-1.54	2.03	-0.81
UPN 257 × NERICA 3	1.60	-0.39	-0.0010	-0.001	-0.038	0.014	5.27	-22.62	1.32
UPN 257 × NERICA 4	2.48	0.02	0.0000	-0.035	-0.021	0.170	2.32	-25.04	0.56
UPN 266 × FARO 58	-2.60	-0.50	-0.0012	0.265	0.021	0.177	6.95	63.82	0.14
UPN 266 × FARO 59	0.42	0.27	0.0007	-0.602	-0.010	0.198	1.86	-53.57	0.52
UPN 266 × NERICA 1	4.50*	-0.34	-0.0009	-0.542	0.014	-0.346	-9.70	-88.40	1.06
UPN 266 × NERICA 2	-0.79	0.14	0.0004	1.760	0.026	-0.326	-12.30	-33.69	0.70
UPN 266 × NERICA 4	1.52	-0.26	-0.0006	0.065	0.032	0.012	-1.02	36.94	-0.17
UPN 268 × FARO 58	0.74	-0.32	-0.0008	0.111	-0.008	-0.157	0.49	2.82	0.65
UPN 268 × NERICA 1	0.61	-0.18	-0.0005	-0.128	-0.007	-0.025	0.18	31.11	1.75
UPN 268 × NERICA 3	0.04	0.09	0.0002	0.125	0.011	-0.073	-3.51	11.16	-1.45
UPN 268 × NERICA 4	-3.02	0.69	0.0017	-0.089	-0.006	-0.053	-1.51	-14.48	2.32
UPN 276 × FARO 44	1.87	-0.55	-0.0014	-0.312	-0.003	0.030	2.99	89.56	-0.39
UPN 276 × FARO 52	1.89	-0.71	-0.0018	0.270	-0.004	-0.076	-0.73	15.06	-0.18
UPN 276 × FARO 58	1.77	0.17	0.0004	-0.614	-0.030	0.440	3.31	10.22	0.54
UPN 276 × FARO 59	-1.45	-0.20	-0.0005	-0.495	0.010	0.081	6.01	-6.52	-0.39
UPN 276 × NERICA 1	-1.98	0.50	0.0013	0.580	-0.008	-0.213	-2.75	-49.80	-0.09
UPN 276 × NERICA 3	0.41	0.52	0.0013	-0.033	0.001	0.121	-0.01	-11.38	-1.51
UPN 276 × NERICA 4	0.31	-0.10	-0.0003	-0.127	0.043	-0.006	-4.29	1.46	0.23
UPN 345 × FARO 58	-2.21	0.42	0.0010	-0.351	-0.008	0.024	-9.28	-22.07	1.15
UPN 345 × FARO 59	3.77	-0.40	-0.0010	-0.232	-0.027	0.129	3.94	90.24	-0.61
UPN 345 × NERICA 1	-1.36	-1.02	-0.0025	0.544	-0.007	-0.251	-6.33	-32.55	-0.91
UPN 345 × NERICA 2	0.91	0.24	0.0006	-0.052	0.016	0.195	3.78	-36.12	0.28
UPN 345 × NERICA 3	-0.61	0.43	0.0011	-0.248	-0.015	-0.036	-0.91	-3.40	-1.52
UPN 345 × NERICA 4	-3.67	0.17	0.0004	0.435	-0.014	-0.130	5.87	-18.10	0.07
UPN 347 × FARO 44	-2.16	-0.06	-0.0002	0.598	0.030	-0.071	-4.68	-63.44	-1.12
UPN 347 × FARO 52	-0.16	-0.19	-0.0005	-0.045	0.016	-0.137	8.59	-27.31	0.30
UPN 347 × NERICA 2	-2.09	0.49	0.0012	0.386	-0.014	0.337	5.19	61.02	-0.04
UPN 347 × NERICA 4	5.15**	-0.33	-0.0008	-0.472	-0.036	0.003	-4.91	-27.95	-1.01
UPN 349 × FARO 52	2.65	-0.27	-0.0007	-0.368	-0.009	0.085	0.71	48.54	-1.02
UPN 349 × FARO 58	-0.42	-0.14	-0.0003	0.510	0.031	0.151	3.35	-19.71	0.19
UPN 349 × FARO 59	-0.69	-0.22	-0.0005	0.211	0.021	-0.134	-1.32	-1.81	-0.36
UPN 349 × NERICA 1	0.10	0.57	0.0014	-0.028	-0.013	-0.121	-0.28	-33.10	-0.36
UPN 349 × NERICA 2	-1.90	0.44	0.0011	0.003	-0.014	-0.047	-0.80	-50.00	-0.74
UPN 349 × NERICA 3	0.18	0.72	0.0018	-0.343	-0.008	-0.186	-1.03	8.33	3.58*
UPN 349 × NERICA 4	-1.89	-0.44	-0.0011	-0.497	-0.012	0.428	3.82	66.13	-0.40

*, **, *** indicating the levels of significance at 0.05, 0.01 and 0.001 respectively. DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tillers.

Table 8. Pearson correlation analysis among the traits.

	DTFL	ET	GWT (g)	GY (g/plot)	LA (cm ²)	LAI	NGPP	PH (cm)	PL (cm)
ET	-0.355**								
GWT	-0.127ns	-0.1870ns							
GY	0.28476*	-0.3676**	0.05009ns						
LA	-0.3819**	-0.0845ns	0.13697ns	-0.1184ns					
LAI	-0.3819**	-0.0845ns	0.13697ns	-0.1184ns	1***				
NGPP	0.25671*	-0.463***	0.0663ns	0.64909***	0.03848ns	0.03848ns			
PH	-0.0043ns	-0.3445**	0.2254ns	-0.0073ns	0.30594*	0.30594*	0.05619ns		
PL	-0.0306ns	0.39813**	-0.0190ns	-0.2201ns	0.02003ns	0.02003ns	-0.1820ns	0.04604ns	
PW	0.19946ns	-0.4779**	-0.0332ns	0.39489**	0.10226ns	0.10226ns	0.62872***	0.10248ns	-0.1336

*, **, ***, indicating the levels of significance at 0.05, 0.01 and 0.001 and respectively, ns indicates non-significance. DTFL= Days to 50% flowering, LA= Leaf Area, LAI= Leaf Area Index, PH= Plant Height, ET= Effective Tillers, PL= Panicle Length, PW= Panicle Weight, NGPP= Number of Grains Per Panicle, GY= Grain Yield, GWT= 1000 Grain Weight, VT= Vegetative Tillers.

**Figure 1.** Dendrogram of the parental rice inbred lines generated from Euclidean genetic distance- based GCA effect of grain yield and other yield related traits using Agglomerative clustering method.

4. Discussion

4.1. Analysis of Variance

These results observed from the analysis of variance were in agreement with that reported significant GCA and SCA effects among the rice genotypes for all the grain yield and yield related components that were under study [6, 21]. The significant general and specific combining ability indicated the importance of both additive and non-additive gene actions respectively in the expression of these characters [21]. These results reflected the interactions between the female and male lines and produced significantly different specific combining ability effects, which could be attributed to the genetic variability of the parental inbred lines used to develop the hybrids. The role of additive and non-additive gene effects in controlling the aforementioned traits were also reported [22, 23].

4.2. Estimation of Genetic Parameters and Heritability

The results obtained suggested that most of the traits studied are governed by the additive gene action. The results conform with the findings on the mode of gene action for the stated traits [24]. The current study also discovered that the GCA variance-to-SCA variance ratio was less than one for all traits studied (Table 2). In the study conducted and reported that a GCA variance to SCA variance ratio of less than one indicates that additive gene action prevailed for all the traits and that predominance of additive gene action over non-additive gene action is ideal for breeding [25].

The analysis on variances showed that additive variance accounted for a significant portion of total genotypic variance [24]. Previous research indicated that characteristics with high heritability and high genetic advance are controlled by additive gene action and can be improved through simple selection methods, and that, they could be improved by crossing superior genotypes of segregating populations developed through combination in breeding programme [23].

The findings also suggest a high proportion of heritable variation, which is exploited by breeders, and that selection for these traits can be accomplished directly based on their phenotypic performance similar to this study. As reported by this study, a similar report showed a parent-progeny regression predicts heritability and gives a measure of general combining ability (GCA) of parents for a trait. Therefore, to facilitate selection in population improvement, the yield components of genotypes should have sufficient genetic variation and be highly heritable [26].

4.3. Mean Performance

The crosses with the lowest mean values for days to 50% flowering were obtained from UPN 349 \times NERICA 2, UPN 345 \times NERICA 4 and UPN 236 \times NERICA 3, which recorded 57.5, 58.5 and 58.5 days, respectively while the F_1 hybrids with the lowest mean values were recorded from UNPN 234 \times FARO 44, UPN 257 \times FARO 44, and UPN 236 \times NERICA 1 with values 115cm, 117.50cm, and 117.67cm respectively. The research conducted and reported that the lowest mean values are preferable for traits such as days to 50% flowering and plant height, thus conforming with the results of this study [23].

For grain yield per plot, among the parental lines, the genotypes UPN 266 and UPIA 2 recorded the highest mean values of 1962.15 g and 1367.72 g, respectively. The highest mean values for crosses under grain yield per plot were observed under the cross combinations UPN 236 \times FARO 52 and UPN 228 \times NERICA 1 with values of 1435.14 g and 1261.82 g. In addition, the result for 1000-grain weight among the parental lines indicated that lines UPN 347 (33.20 g) and UPIA 2 (30.50 g) recorded the highest mean values, while for the cross combinations, UPN 349 \times NERICA 3 and UPN 268 \times NERICA 4 exhibited the highest mean values of 35.50 g and 32.85 g, respectively.

From the results, it is depicted that the grain yield and the studied yield components are positively correlated and can be used for grain improvement in hybridization programs. This corresponds with the findings of [23].

4.4. General Combining Ability Effects

Previous studies showed that it is possible to use parents with a high positive or negative GCA in breeding programmes, depending on the breeding target [22]. Estimates of general combining ability effects are regarded as a crucial indicator of the ability of parental lines to generate superior breeding populations. The average performance of a parent in a series of crosses is represented by the general combining ability of the parental genotypes as shown (Table 6) and reports also showed that negative GCA effect estimates could be preferable for some agronomic traits like earliness and medium dwarf plant height [23]. According to this experiments, none of the parents possessed favorable genes for all of the traits studied. As a result, multiple crossings among these parents would be desirable in order to obtain superior recombinants with desirable traits as well as

grain yield.

Furthermore, these parents could be useful as donors in hybridization or multiple cross programmes to obtain high yielding hybrid varieties. Therefore, concurrent improvement in yield, yield component, and other related traits is possible and critical for increasing rice yield potential. Previous reports showed that grain yield and yield component traits as well, the additive genetic effects are naturally fixable, thus implying that all the examined traits in this experiment are favorable to improve and develop through background selection in early generations [23].

Reports also showed that high positive GCA effects values are of significant interest in all agronomic characters like the grain yield as observed in FARO52 (330.57) and UPN228 (216.0) [25].

4.5. Specific Combining Ability Effects

A significant deviation from zero in SCA of across would indicate high or low SCA depending on whether the sign is positive or negative [25]. The SCA effects could represent gene actions of dominance and epistasis and can be used as an index to determine the effectiveness of a specific cross combination in hybrid exploitation as shown (Table 7). Therefore, the findings of this study on specific combining ability are in agreement [27, 28]. It was observed that it may not be necessary for the parents involved in the creation of crosses to have high GCA effects in order to obtain desirable SCA effects, this could be due to the fact that positive interactions between cytoplasmic genes and nuclear genes are becoming more important than interactions between nuclear genes alone [25].

4.6. Pearson Correlation Analysis Among Traits

Grain yield is the end result of various components that are not directly controlled by any single gene. Therefore, understanding the mechanism of correlation provides the foundation for developing appropriate selection criteria for breeding programmes based on yield components in order to achieve reasonable improvement of yield and yield components [29]. The correlation analysis results are in consonance with previous reports. [4, 30]. These reports showed that grain yield was significantly positive correlated to number of grain per panicle (NGPP), thus indicates that increase in yield the NGPP will increase too. The significant correlations between grain yield and other agronomic traits either in positive or negative direction are strong indication that these traits are major factors in relation to grain yield, thus suggesting that selection directed towards these characters will be effective in ensuring high grain yield in rice [31].

5. Conclusion

Specific Combining ability (SCA) variance was generally reported to be greater than general combining ability (GCA) variance. Furthermore, for grain yield and the majority of studied traits, non-additive genetic variance was found to be

greater in magnitude than the corresponding additive variance in this study. The study further reveals that characters with high heritability are controlled by additive gene action and can be improved through simple selection methods, and that they can be improved by crossing superior genotypes of segregating populations developed through combination breeding. The crosses with the lowest mean values for days to 50% flowering were obtained from UPN 349 × NERICA 2, UPN 345 × NERICA 4 and UPN 236 × NERICA 3, which recorded 57.5, 58.5 and 58.5 days, respectively, thus indicating that they are early maturing. The results indicated that the number of grain per panicle (NGPP) has a direct positive effect with the grain yield, as the higher the NGPP, the higher the mean values for grain yield. It is possible to use parents with a high positive or negative GCA in breeding programmes, depending on the breeding target. Estimates of general combining ability effects are regarded as a crucial indicator of the ability of parental lines to generate superior breeding populations.

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