Research Article

Analysis of Combining Ability for Early Maturity and Yield in Rice (Genus: *Oryza*) at the Kenyan Coast

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The main challenges facing rain-fed rice farming in Kilifi County at the Kenyan coast are inadequate and erratic rainfall, inadequate skills, and poorly developed infrastructure. Of great importance is erratic rainfall that tends to depress towards the end of long rain season, leading to crop failure. Combining ability analysis is one of the most valuable tools used to ascertain gene action effects and help in selecting desirable parents for making crosses and coming up with high yielding and early maturing lines. Combining ability for early maturity and yield has not been studied at the Kenyan coast. This study aimed at determining and identifying good, general, and specific combiners for selecting better parents and better cross combinations in rice crops for developing high yield and short duration lines in rain-fed rice farming. Seven lines were subjected to half-diallel mating design at the Kenya Agricultural and Livestock Research Organization (KALRO), Mtwapa, and at Bahari in Kilifi town. Evaluation for general combining ability (GCA) and specific combining ability (SCA) analysis was done. Combining ability variance and GCA and SCA effects were determined. Based on GCA effects, best parent for early maturity was *Dourado Precoco*, while for yield, Supaa, Komboka, and NERICA 10. SCA estimates indicated that best crosses for yield were D/S, D/N1, and K/N10, while the best performing cross for early maturity was D/N1.

1. Introduction

In Kenya, cultivation of rice is done in two ecosystems that are categorized based on water regimes basis: irrigated and rain-fed. The irrigated ecosystem produces 80% of cultivated rice, and only 20% comes from rain-fed ecosystem. Irrigated rice is grown in Kirinyaga, Kwale, Kilifi, and Tana River counties, while rain-fed farming is mainly practised in Busia, Kakamega, and Kisumu Counties [1]. Rice consumption in Kenya has been increasing at an annual rate of 12% compared to 1% for maize and 4% for wheat. This has been attributed to changes in eating habits especially in urban populations. In 2017, rice consumption in the country was approximated at 700,000 metric tons seven times more than annual production range of 100,000 metric tons. The

deficit was met through imports of about 600,000 metric tonnes in 2017 [2].

There is potential to develop about 540,000 ha of irrigated land and 1.0 million ha in rain-fed ecology for rice production in Kenya [1]. Irrigated rice productivity in Kenya is estimated at about 4–6 t ha⁻¹, and rain-fed productivity is about 1 t ha⁻¹ which are below optimum production potential of about 10 t ha⁻¹ and 7 t ha⁻¹ for irrigated and rain-fed rice, respectively [1].

Combining ability analysis using Griffing [3] is most widely used as a biometric tool for identifying parental lines in terms of their ability to combine in hybrid combination. The resulting total genetic variation is partitioned into the variance effects of general combining ability (GCA) as a measure of additive gene action and specific combining ability (SCA), as a measure of additive gene action. The aim

of this study was to detect the magnitude of both general and specific combining abilities for grain yield, maturity, and some agronomic characters in seven rice crosses using half-diallel crosses.

2. Materials and Methods

Seven rice lines (Supaa, Komboka, *Dourado Precoce*, NERICA 1, NERICA 2, NERICA 4, and NERICA 10) were planted following half-diallel mating design during the long rain season of 2017 at KALRO, Mtwapa. Crosses were done in all possible combinations between each two of the seven parents without reciprocals to produce 21 F_1 hybrids. The general combining ability (GCA) and specific combining ability (SCA) for yield and maturity among the seven lines and crosses were estimated. The F_1 crosses were advanced to F_2 . In 2018 long rain season, the F_2 crosses together with the parent lines were evaluated at KALRO, Mtwapa, and Bahari in Kilifi. Seeds of the twenty-one F_2 hybrids and the seven parents were sown in a randomized complete block design (RCBD) with three replications. Each genotype was planted in a plot of 1.4 m by 1 m replicate with 20 cm $\times$ 20 cm spacing within the row and 20 cm between the rows. Two seedlings were sown per hill that was later thinned to one.

Data were recorded on 20 individual plants chosen at random from each plot excluding border rows, and the last row on the plot was considered the border row. The following characteristics: days to maturity (50% flowering), plant height (cm), panicle length (cm), 1000 grain weight (g), and biomass (g) were measured. Other characteristics included grain yield ($t\ ha^{-1}$), brown rice length (mm), brown rice width (mm), number of tillers, number of unproductive tillers, number of fertile spikelet's per panicle, and number of unfertile spikelets per panicle following SES [4] protocols were also measured.

Analysis of variance was done on the combined data from the two sites. General combining ability and specific combining ability estimates were obtained by employing Griffing's [3] model 1(fixed model) method 2, expressed as

$$X_{ij} = u + g_i + g_j + s_{ij}, \quad (1)$$

where, u is the overall mean of all entries in the diallel design, g_i is the general combining ability of the i th parent, g_j is the general combining ability of the j th parent, and s_{ij} is the specific combining ability between the i th and j th parent.

3. Results and Discussion

3.1. Analysis of Variance. Analysis of variance (Table 1) showed that variation among genotypes for yield, days to 50% flowering, plant height, number of tillers, unproductive tillers, unfertile spikelets, grain length, grain width, 1000 grain weight, and biomass were highly significant at $P \leq 0.001$. Fertile spikelet's, panicle weight, and panicle length were slightly significant at $P \leq 0.05$.

Parent mean squares showed significant variation at $P \leq 0.05$ for 1000 grain weight, grain width, panicle weight, panicle length, biomass, and fertile spikelets. Days to 50% flowering and unfertile spikelet's had the highest significance

at $P \leq 0.001$. Crosses mean squares showed significant difference at $P \leq 0.05$ for all traits except 1000 grain weight. This suggests that parents and crosses were significantly different in mean performance.

Analysis of GCA variance showed significance for days to 50% flowering, biomass, plant height, tillers, fertile spikelets, grain length, unfertile spikelets, and yield. Grain width, unproductive tillers, panicle weight, and panicle length were insignificant. SCA variation reached significance for days to 50% flowering, 1000 grain weight, biomass, and unproductive tillers. Panicle weight, panicle length, unfertile spikelets, yield, grain width, grain length, fertile spikelets, and total tillers were insignificant.

3.2. Mean Performance of Genotypes. Genotypic performance (Table 2) showed that, among parents, Supaa and Komboka flowered late and hence are late maturing. Komboka and Supaa were the highest yielding parents, while NERICA 4 was the least yielding parent. Performance based on other traits showed Komboka was the best performer in terms of total number of fertile tillers and the highest fertile spikelets. Moreover, the best parent in panicle weight, grain width, and 1000 grain weight was *Dourado Precoce*. Lastly, the biomass yield was highest in Komboka and Supaa.

Genotypic performance among crosses showed that N1/N2, N1/N4, and N10/S crosses took fewer days to 50% flowering, while plants from S/K cross took longer. The highest yielding plants were S/K, N4/D, and N2/N10 crosses, while plants from N10/K, N2/D, and N4/S crosses were the least yielding crosses. Performance for other traits under study showed that plants from N2/S and N10/D crosses had the lowest unproductive tillers, while plants from N4/D and N1/N2 crosses had the greatest panicle weight. Furthermore, N4/D and N1/N2 crosses had the most fertile spikelets and the least unfertile spikelets. Rice grains from N4/D and N1/S had the largest width, while those of N4/D were the longest. In terms of 1000 grain weight, N2/D, N10/D, and N1/D crosses were the best performers, while N1/K and N2/K crosses produced the highest biomass yield. This result revealed the positive contribution of the genes to days to 50% flowering and grain and biomass yield. In particular, N4/D and N2/N10 yielded all other crosses and their parents. Plants from N10/S, N2/K, and D/S crosses also outperformed one of their parents as they matured earlier than one of their parents.

3.3. General Combining Ability (GCA) Effects. High positive GCA effects values would be of great interest in all characters except plant height, days to 50% flowering, unfertile spikelets, and unproductive tillers for which negative values become more useful from the breeder's point of view. Most parents showed positive GCA effects for days to 50% flowering except *Dourado Precoce* that showed significant negative GCA effects emerging as the best combiner (Table 3). Supaa was the poorest combiner in terms of days to 50% flowering because of the positive significant GCA effects. Significant GCA effects for grain yield were recorded for Supaa, Komboka, and NERICA 1. Komboka and Supaa

TABLE 1: A combined analysis of variance mean squares for parents and crosses at KALRO, Mtwapa, and Bahari during the long rain season of 2018.

S.O. V	d.f.	Mean squares												
		1000 gwt (g)	Grl (mm)	Grw (mm)	Pht (cm)	Pwt (g)	Pnl (cm)	Ut	Yield (t·ha ⁻¹)	50% f	Biomass (g)	Ti	fs	Ufs
Replication	2	19.185	0.028	0.059	8.52	0.065	22.78	0.108	0.2182*	8.41*	7257	1.1502*	33.7	22.78
Genotype	8	65.685***	0.801***	0.846*	735.54***	1.499***	575.54***	0.461*	2.1934***	163.26***	20158	6.303	1984.6	575.54
Site	1	3.63*	0.001	0.048	158.16*	1.749	62.3*	0.185	2.7419***	574.23	2896**	10.81***	4587.8***	62.3***
Genotype site	8	3.963	0.040	0.015	38.16	0.455	31.61*	0.294*	0.3257	44.88*	5238*	1.39***	751.5***	31.61*
Parents	6	34.614*	0.515	0.0804*	230.729	0.4222*	2.353*	0.0721	1.55492*	203.837***	13862.9*	4.232*	1598.62*	384.27***
Crosses	20	36.854	0.708*	0.0915	332.62***	4.028*	5.454*	0.515*	5.8932*	222.433*	2.684*	12.689*	2204.25*	669.21*
GCA	8	147013	406.42***	2840***	0.8391	404.07***	4.358	295505	2710.1*	0.5758*	0.0928	6.3234*	213.04*	0.5004*
SCA	20	48.54*	335.4*	4101*	12.06*	556.2*	49.18*	1.204*	2998	39.13	0.8188	6.268	1371.1*	7.379*
Residual	34	9.068	0.0906	0.025	18.38	0.156	10.19	0.1385	0.1718	21.87	2924	0.7346	260.8	10.19

ANOVA tested at $P = 0.05$. *** Significant at $P \leq 0.001$ and * significant at $P \leq 0.05$. S.O.V: source of variation, 1000 gwt: 1000 grain weight, 50% f: days to 50% flowering, Grl: grain length, Grw: grain width, Pht: plant height, Pwt: panicle weight, Pnl: panicle length, Ti: total tillers, Fs: fertile spikelets, Ufs: unfertile spikelets, Ut: unproductive tillers, p: probability, g: grams, cm: centimetres, yield in t·ha⁻¹: tonnes per hectare, mm: millimetres, and M.s: mean squares.

TABLE 2: Mean performance of genotypes for parents and crosses at KALRO, Mtwapa, and Bahari during the long rain season of 2018.

Genotype	50% f	Yield	Pht (cm)	Ti	Ut	Pnl (cm)	Pwt (g)	Fs	Ufs	Grl (mm)	Grw (mm)	1000 gwt (g)	Biomass
<i>D. precoce</i>	73.3ab	3.35b	83.8b	5b	0.54ab	23.43bc	4.28c	127.1bc	17.3ab	10.05c	3.005c	35.2d	356b
D/K	77.7ab	2.08ab	78.2ab	7.01c	0.42ab	24.01bc	2.32ab	134.8bc	50.3c	9.35b	2.663ab	31.7bc	404bc
D/S	71.8ab	2.09ab	76.4ab	6.46bc	0.93b	22.25a	2.47ab	116.4ab	44.2bc	9.99c	2.895bc	32.7c	334ab
Komboka	85.8c	4.0c	75ab	8.28d	0.28a	24.26c	3.56bc	115.20bc	30.9b	8.94a	2.487a	24.2a	419bc
NERICA 1	74.2ab	2.61ab	69a	5.29b	0.7ab	23.53bc	3.83bc	138.1bc	12.5a	9.44b	2.784b	31.2bc	351ab
N1/D	77.2ab	2.95ab	73.3ab	5.03ab	0.78ab	22.8bc	3.65bc	151.5c	29ab	9.81bc	3.319 d	33.8c	320ab
N1/K	78.3ab	2.21ab	72.3ab	6.53bc	1.07b	23.55bc	2.57ab	138.3bc	50.1c	9.37b	2.716b	30.2bc	453c
N1/N10	72.8ab	2.91ab	71.4ab	5.93bc	0.6ab	23.76bc	3.85bc	147.6bc	17.4ab	9.21ab	2.64ab	31.8bc	343ab
N1/N2	68.3a	3.43b	73.8ab	5.55b	0.53ab	23.62bc	4.18c	154c	16.1ab	9.16ab	2.741b	32bc	301ab
N1/N4	70a	2.69ab	73ab	5.95bc	0.83ab	22.81b	3.72bc	125.9ab	21.3ab	9.45b	2.814bc	35.2cd	330ab
N1/S	73.7ab	2.59ab	75.2ab	5.01ab	0.46ab	23.6bc	3.49bc	139.6ab	53.2c	9.39b	3.021c	35.2cd	362b
NERICA 10	78ab	3.38b	74.3ab	5.88bc	0.58ab	24.26bc	3.89c	160.7c	22.3ab	8.97a	2.681b	27.8ab	295ab
N10/D	70.5ab	2.87ab	81.6b	4.75ab	0.68ab	22.89b	3.63bc	119.8bc	17.5ab	9.83bc	2.946bc	33.5c	288ab
N10/K	73.2ab	1.72a	72.1ab	6.92c	1b	23.88bc	2.67ab	148.2bc	65.1cd	9.46b	2.77bc	28.8b	387bc
N10/S	69.5a	2.1ab	73.2ab	6.56bc	1.0b	22.86b	2.58ab	130.8bc	50.3bc	9.82bc	2.754bc	29.2b	427bc
NERICA 2	73.7ab	3.13b	73ab	5.66b	0.64ab	21.66ab	3.61bc	140.4bc	19.1ab	9.52bc	2.741bc	28.3ab	301ab
N2/D	71ab	1.98a	73.6ab	5.88bc	0.65ab	24.32bc	3.52bc	146.9bc	57.1c	9.55bc	2.741bc	33.8c	342ab
N2/K	73ab	2.04ab	74.1ab	8.07d	2.03c	23.98bc	2.18a	144.2bc	81.9d	9.48bc	2.599ab	29.5b	436bc
N2/N10	72.7ab	3.54b	66.5a	5.52b	0.58ab	23.06b	3.55bc	131.5b	14.3a	9.31ab	2.686b	29.2b	323ab
N2/N4	71.5ab	2.71ab	72.4ab	5.68b	0.74ab	23.85bc	3.66bc	137.3bc	21ab	9.6ab	2.717bc	31.5bc	320ab
N2/S	78.8ab	2.52ab	73.4ab	4.27a	0.49ab	20.73a	2.52ab	128.2b	40.8b	9.09ab	2.689b	28.3ab	381b
NERICA 4	73.7ab	2.82ab	72ab	4.92ab	0.5ab	23.71bc	3.78bc	133bc	17.8ab	9.48bc	2.69b	29.7b	327ab
N4/D	71.3ab	3.19ab	78.4b	5.15ab	0.47ab	24.58c	4.3c	151.9bc	13.2a	9.92c	2.887c	33.8c	287a
N4/K	79.3bc	2.64ab	84b	6.43bc	0.57ab	23.65bc	3.24b	148.7bc	59.4c	9.59bc	2.689b	31.3bc	435bc
N4/N10	69a	3.31b	72.5ab	6.04b	0.65ab	23.74bc	3.95bc	142.3c	22.9ab	9.6bc	2.65ab	33bc	309ab
N4/S	70a	1.87ab	84.7b	6.81bc	0.87ab	22.69bc	3.08ab	136.2b	48.8bc	9.48b	2.646ab	27.8ab	372ab
Supaa	95.2d	4.55c	93.2c	5.94b	0.33a	23.1b	3.08ab	109.5a	19.7ab	9.87bc	2.928c	30.7bc	490c
S/K	80.5bc	4.09c	80.6ab	6.68bc	0.43a	24.11bc	2.64ab	139.3b	37.7b	9.41b	2.597ab	34c	329ab

Mean values in the table denoted by different letters are significantly different at $P = 0.05$. Two-way ANOVA, 50% f: days to 50% flowering, 100 gwt: 1000 grain weight, Grl: grain length, Grw: grain width, Pht: plant height, Pwt: panicle weight, Pnl: panicle length, Rt: reproductive tillers, Ti: total tillers, Fs: fertile spikelets, Ufs: unfertile spikelets, Ut: unproductive tillers, Mean separation Tukeys.

were found to be best combiner parents for yield, while NERICA 1 was the poorest parent combiner with significant negative GCA effects.

The best combiner for plant height was NERICA 1. For number of tillers, Supaa and Komboka showed significant positive GCA indicating they were the best combiners for a number of tillers. NERICA 2 was the poorest combiner with negative GCA effects. For unfertile spikelets, NERICA 10 had the most significant positive effects, thus emerging as the poorest combiner. Significant negative GCA was shown by NERICA 1 and *Dourado Precoce* which emerged as the best combiners. *Dourado Precoce*, Supaa, and NERICA 2 were the best combiners for grain length, while NERICA 10 was the poorest combiner. For biomass, Supaa and Komboka had the most significant positive GCA and were the best combiners, while NERICA 10 posed significant negative GCA effect and was the poorest combiner.

3.4. Specific Combining Ability (SCA) Effects. A significant deviation from zero in SCA of across would indicate high or low specific combining ability (SCA) depending on weather the sign is positive or negative. Significant negative SCA is desirable for all traits under study except plant height, days

to 50% flowering, unfertile spikelets, and unproductive tillers. The positive SCA effects for days to 50% flowering were significant for S/K, N1/S, and K/N10 crosses, thus emerging as the poorest performing crosses based on SCA effects (Table 4), while cross D/N1 with significant positive SCA effects was the best performer. The best yielding crosses were D/S and N10/S crosses with high significant negative SCA effects, while N1/N2 was the poorest combiner with significant positive SCA effects.

Plants from K/N10 and D/S crosses were the best crosses in terms of plant height as they had positive significant SCA effects. N10/K and K/N2 crosses performed better in relation to unproductive tillers, while N1/N2 cross performed poorly as it had significant negative SCA effects. Performance based on panicle length indicated that K/N4 and D/N10 were the best crosses, while K/N2 was the poorest cross. Panicles from K/N2 cross were the best in terms of SCA effects, as K/N2, N1/N2, and N10/S crosses were best for unfertile spikelets. For 1000 grain weight, N10/N2 cross was the best, as K/S, N1/S, and D/S crosses emerged as the best crosses in terms of biomass. Results from this study reveal that SCA effects and cross performance might closely relate. A cross with high SCA effects may not be the one with the highest genotypic performance and vice versa. The best way is to explore where

TABLE 3: General combining ability effects for parents at KALRO, Mtwapa, and Bahari during the long rain season of 2018.

Parents	Yield (t·ha ⁻¹)	50% <i>f</i>	Pht (cm)	Ut	Pnl (cm)	Pwt (g)	Fs	Ufs	Grl (mm)	Grw (mm)	1000 gwt (g)	Ti	Biomass (g)
<i>Dourado</i>	0.59	-0.67*	10.58	-0.15	0.08	0.93	-12.8	-16.65*	0.55*	0.234	3.97	-0.86	-2
<i>Precoce</i>													
Komboka	1.24*	11.83	-0.72*	-0.41	0.91	0.21	41.4*	-3.05	-0.56	-0.28	-7.03	2.43*	46*
Supaa	1.79*	21.17*	17.48*	-0.36	-0.25	-0.3	-30.4	14.25	0.37*	0.161	-0.53	0.83*	132*
NERICA 1	-0.15*	0.17*	-6.62*	0.01	0.18	0.48	-1.08	-21.45*	-0.06	0.017	-0.03	-0.56	-7
NERICA 2	-0.05	0.33	-2.72	-0.05	-1.69	0.26	0.5	-14.85	0.02*	0.043	-2.93	-0.20*	-57
NERICA 4	0.052	0.33	-3.72	-0.19	0.36	0.43	11.1435	-16.15	-0.02	0.094	-1.53	-0.94	-31
NERICA 10	0.62	4	-1.42	-0.11	0.91	0.54	20.8	11.65*	-0.53*	0.103	-3.43	0.025	-63*

Significance tested at $P = 0.05$, *significant at $P \leq 0.05$. 1000 gwt: 1000 grain weight, 50% *f*: days to 50% flowering, Grl: grain length, Grw: grain width, Pht: plant height, Pwt: panicle weight, Pnl: panicle length, Ti: total tillers, Fs: fertile spikelets, Ufs: unfertile spikelets, Ut: unproductive tillers, g: grams, cm: centimetres, t·ha⁻¹: tonnes per hectare, and mm: millimetres.

TABLE 4: Specific combining ability effects for crosses at KALRO, Mtwapa, and Bahari during the long rain season of 2018.

Cross	Yield (t·ha ⁻¹)	50% <i>f</i>	Pht (cm)	Ti	Ut	Pnl (cm)	Pwt (g)	Fs	Ufs	Grl (mm)	Grw (mm)	1000 gwt (g)	Biomass (g)
D/N1	-0.37	3*	-7.7	0.84	0.29	-1.87	-1.46	-25.17	35.42	-0.16	0.3	-0.87	-30.7
K/N1	-1.76	-8.4	3.1	2.34	0.84	-1.12	-1.82	-42.2	43.02	-0.6	0.21	6.53	39.34
D/N10	-1.22	-7.5	-4.7	-0.03	0.31	-2.51*	2.24	-29.1	14.22	0.32	0.03	2.23	23.34
K/N10	-3.02	-17.3*	-5.8*	-1.14	0.89*	-2.35	1.78	-54.8	11.9	1.067	0.37	8.53	29.34
N1/ N10	-0.44	-6.1	0	0.86	0.71	-1.74	-0.87	-12.3	18.92	0.31	0.05	4.53	53.34
D/N2	-1.86	-2.7	-11.4	1.32	0.22	1.52	-1.37	18.27	57.02	-0.5	-0.23	2.03	41.34
K/N2	-2.45	-13.2	8.9	-0.44	1.86*	0.35*	-1.99*	-38.6	31.9*	0.53	0.14	8.73	72.34*
N1/N2	0.12*	-6.3	3.6	0.06	-0.06*	0.72	-0.26	14.37	20.82	-0.29	-0.01	4.23	5.335
N10/ N2	-0.33	-5.7	-9	0.08	0.11	-0.57	-0.95	30.73	9.22*	0.33	0.03	4.83*	83.34*
D/N4	-0.34	-2.4	-5.6	1.33	0.18	-0.27	-0.76	30.5	14.96	-0.09	0.03	0.63	-39.7
K/N4	-1.54	-6.9	8.8	-0.67	0.54	-2.03*	-1.1	16.47	47.06	0.68	0.28	9.13	45.34
N1/N4	2.46	-4.6	3.8	1.84	0.38	-2.14	-0.89	-7.1	27.3	0.04	0.11	6.03	8.34
N10/ N4	-0.27	-9.4	-2	1.34	0.32	-1.94	-0.72	-13.3	19.12	0.66	0.04	7.23	43.335
N2/N4	-0.6	-2.6	0.8	1.2	0.35	0.77	-0.73	2.77	20.42	0.11	0.05	5.23	48.34
D/S	-3.17*	-1.9	-28.8*	1.62	0.81	1.99	-1.89	18.67	43.56	-0.418	-0.26	-1.47	-156*
K/S	-1.82	-26.9*	-15.8	-7.54	0.57	-0.96	-1	-12.43	23.42	0.11	-0.04	10.83	-224*
N1/S	-1.93	-22.4*	-22.2	-0.12	0.18	-0.74	-0.42	30.87	57.32*	-0.4	0.07	5.03	-123*
N10/S	-3.19*	-30.4	-22.2	-0.84	0.84	-2.21	-1.39	-0.53	44.6	0.49	-0.09	2.43	-1.67
N2/S	-2.54	-16.8	-21	-1.23	0.27	-2.14	-1.17	17.17	38.2	-0.788	-0.21	1.03	-53.7
N4/S	-2.88	-5.6	-8.7	2.05	0.79	-1.88	0.78	32.57	47.62	-0.35	-0.2	-0.87	-88.7

Significance tested at $P = 0.05$, *significant at $P \leq 0.05$. S. O. V.: source of variation, 1000 gwt: 1000 grain weight, 50% *f*: days to 50% flowering, Grl: grain length, Grw: grain width, Pht: plant height, Pwt: panicle weight, Pnl: panicle length, Ti: total tillers, Fs: fertile spikelets, Ufs: unfertile spikelets, Ut: unproductive tillers, g: grams, cm: centimetres, t·ha⁻¹: tonnes per hectare, and mm: millimetres.

there is high magnitude of SCA effect in addition to high GCA effects from both or at least one of the parents. Similar findings were reported by Dorosti and Monojjen [5], Kumar et al. [6], and Thakare et al. [7]. It is not a must that parents involved in making of crosses are of high GCA effects to get desirable SCA effects. Reason being that there are positive interactions between cytoplasmic genes and nuclear genes becoming more important than interactions between nuclear genes alone.

3.5. GCA and SCA Variance Components Ratios. The current investigation found out that the GCA variance-to-SCA variance ratio was less than one for all traits under study except for biomass, which had more than one GCA

variance-to-SCA variance ratio (Table 5). More than one GCA variance-to-SCA variance ratio indicates additive gene action for biomass, while less than one GCA variance-to-SCA variance ratio indicates that additive gene action prevailed for all other traits. Preponderance of additive gene action over nonadditive gene action is ideal for exploitation in breeding. This study revealed non-additive gene action for days to 50% flowering. Similar findings were reported by Upadhyay and Jaiswal [8] and Kumar et al. [9], though Contrary findings were reported by Patil et al. [10] and Salgotra et al. [11] who reported additive gene action for days to 50% flowering. This study also revealed nonadditive gene action for yield which was similar to Bhadrui et al. [12] but differed with reports by Upadhyay and Jaiswal [8], Gnanasekaran [13], and

TABLE 5: Ratios of GCA variance to SCA variance for grain yield and agronomic traits at Bahari and KALRO Mtwapa during 2018 long rain season.

Characters	σ^2 gca	σ^2 sca	$2\sigma^2$ GCA/($2\sigma^2$ GCA + σ^2 SCA)	Gene action
Yield	0.518	1.964	0.2637	Nonadditive
Days to 50% flowering	67.946	74.144	0.9164	Nonadditive
Plant height	76.91	110.873	0.6936	Nonadditive
Number of tillers	1.411	4.23	0.8335	Nonadditive
Unproductive tillers	0.024	0.172	0.0132	Nonadditive
Panicle length	0.785	1.818	0.431	Nonadditive
Panicle weight	0.141	1.343	0.104	Nonadditive
Fertile spikelets	532.872	734.75	0.7252	Nonadditive
Unfertile spikelets	128.089	223.07	0.574	Nonadditive
Grain length	0.172	0.236	0.7288	Nonadditive
Grain width	0.027	0.031	0.87	Nonadditive
1000 grain weight	11.538	12.285	0.939	Nonadditive
Biomass	4620.952	8.949	916.258	Additive

Kumar et al. [9] that showed additive gene action for yield.

This study further revealed nonadditive gene action for plant height and unfertile spikelets. Nonadditive gene action was also reported in plant height by Patil et al. [10] and Dorosti and Monajjem [5]. Nonadditive gene action in unfertile spikelets was reported by Hassan et al. [14] and Nagaraju et al. [15]. The findings in this study agree with their reports. However, contradiction of this finding's additive gene action in plant height was reported by Updhyay and Jaiswal [8], Gnanasekaran et al. [13], and Kumar et al. [9] which reported additive gene action for unfertile spikelets. Biomass inheritance was attributed to additive gene action, though not much has been reported on nature of gene action in biomass. Discrepancies in these reports are attributed to differences in materials used. Thus, findings from one population cannot be extrapolated to another population. Gene action must be estimated for every population.

4. Conclusion

In conclusion, from GCA effects, best parents' combiners were *Dourado Precoce* for days to 50% flowering, while Supaa and Komboka were best parents for yield. Based on SCA effects, the best performing crosses in terms of yield were D/S and N10/S, the in terms of days to 50% flowering was D/N1. Based on GCA variances, the findings were that additive gene action effects were found in biomass, while nonadditive gene action was obtained in all the other traits under study.

From the findings in this study, we recommend as follows.

Best parents' combiners were *Dourado Precoce* for days to 50% flowering, and Supaa and Komboka for yield can be utilized in hybrid and hybridization studies to generate better genotypes. Promising crosses were D/N1 for days to 50% flowering, and D/S and N10/S for yield can be further developed and extensively tested for stability and superiority before eventual release to farmers.

Data Availability

Raw data are available from the corresponding author upon request.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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