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Breeding Novel Rice Hybrids for Aerobic Ecology: A Way Out from Global Warming and Water Crisis

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Abstract: The development of novel rice hybrids is a prospectus area of research for enhancing grain yield to meet the growing population demands. An experiment was conducted in 2016–2017 to develop novel rice hybrids for aerobic ecology with lesser yield penalties than irrigated ecosystems, with the added advantage of reduced methane emissions and water budget as witnessed in irrigated systems. Based on the restorer-maintainer reaction and spikelet fertility (%), ten restorer lines were selected to cross with three CMS (Cytoplasmic male sterile) lines in the Line by Tester fashion in Yasangi (summer) season 2016–2017. They resulted in 30 experimental hybrids besides 13 parental lines (10 restorer lines and 3 B—lines of akin CMS lines) and checks (GK 5022, CR Dhan 201) assessed during the Vankalam (rainy) season 2017 at three different places/locations viz., Rajendranagar, Warangal, and Kampasagar. The outcome of the experiment was that two experimental hybrids viz., APMS-6A × HRSV-7 and IR-79156A × ATR-372, were categorized as stable hybrids with desirable *sca* (Specific combining ability) effects, heterosis (ranging from 7% to 13%) over best check GK 5022, along with an in-essence performance for yield and other yield attributing characters.

Keywords: aerobic rice; hybrids; heterosis; stability; water crisis

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1. Introduction

For over 50 percent of the global population, rice is a significant food crop, and a main food source [1]. Globally, rice is grown as lowland rice at 56.9 percent, rainfed at 30.9 percent, aerobic or non-surface at 9.4 percent, and deepwater at 2.8 percent [2]. India is the world's largest rice-growing nation (nearly 42.5 million ha) and has the second-largest volume alongside China. Asia has 17 million hectares of rice-irrigated areas with substantial water constraints, and 22 million hectares will encompass monetary water shortages by 2025 [3]. Therefore, rice production needs to use water more efficiently.By the end of the 21st Century, it is predicted that the climate of the earth will warm on average by 2–4 °C (IPCC 2007) because of human and natural sources. CO_2, CH_4, and N_2O, like GHG emitted off farming systems, are presumed to be one of the prime causes of planetary soaring heat [4].

Aerobic rice means planting high-yield varieties of rice in non-inundated, non-puddled conditions, which are highly responsive to the supply of nutrients, and can also be irrigated or rainfed and can tolerate (intermittently) flooding [4]. It is the characteristic feature of the aerobic mode of development wherein the crop is directly seeded in free drainage; unpuddled soils are preserved without a standing water layer on the ground, and roots expand in the aerobic climate [5]. It ispossible to safeguard water and to increase water efficiency if rice is produced under aerobic conditions. However, the production of suitable cultivars is a crucial element in the effectiveness of the aerobic method [6]. Water input using the aerobic rice method is projected to be very low (470–650 mm), with higher water efficiency (64–88 percent) and gross returns (28–44 percent) compared with lower labor usage (55 percent less) in comparison to lowland rice [7].

Aerobic rice, with its mixture of the drought resistance of upland rice and the yield capacity oflowland rice, is specifically produced. Therefore, regarding its yield capacity, aerobic rice may be credited as 'improved upland rice' and 'improved lowland rice' in terms of its drought resistance. In India, a study began in 2005 to grow rice varieties appropriate for aerobic conditions, normally restricted to screening existing varieties [8]. To recognize acceptable aerobic rice lines meant for diverse water shortage locations throughout the globe, the coordinated project for rice improvement implementedits initiative forthe methodical assessment of aerobic rice genotypes across India. India officially introduced the first variety suitable to aerobic conditions, MAS 946-1, for production in 2007 [9]. Under aerobic conditions, Apo, IR55419-04, IR7437-46-1-1, Pusa RH10, Pusa 834, and ProAgro-6111 yielded more than 4 t/ha [10]. To date, about 20 aerobic rice varieties/hybrids have been released into the aerobic rice ecosystem in India.

The adoption of aerobic rice is fast and has been reported to be grown in Latin America, Asia, and Africa. In 2006, approximately 35 million acres of aerobic rice were grown, of which 22.4 million acres were cultivated in Asia and 6.3 million acres were cumulatively cultivated in Africa and Latin America [2]. The above figures indicate that this technology must be given due importance to address water scarcity problems worldwide. The success of this production system requires the development of hybrids with several specific features. Hence, the study was carried out to develop high-yielding rice hybrids suitable for the aerobic system.

2. Material and Methods

2.1. Planting Materials

The genotypic materials consisted of 30 experimental hybrids (H01 to H30) of rice obtained by crossing three cytoplasmic male sterility (CMS)-based lines from a Wild-Abortive source with 10 restorers in Line × Tester fashion at ICAR-IIRR, Hyderabad (Table 1a).

Table 1. (**a**) List of male sterile lines, effective restorers used for crosses development, and checks used in the study. (**b**) Detailed description of assessment of eleven traits under study.

(a)

S. No.	Parental Lines	Source
CMS Lines		
L01	IR-79156B	IRRI, Philippines
L02	APMS-6B	RARS, Maruteru (ANGRAU)
L03	IR-68897B	IRRI, Philippines
Restorer lines		
T01	ATR-177	IIRR, Hyderabad
T02	ATR-186	IIRR, Hyderabad
T03	ATR-216	IIRR, Hyderabad
T04	ATR-372	IIRR, Hyderabad
T05	ATR-374	IIRR, Hyderabad
T06	ATR-375	IIRR, Hyderabad
T07	KS-22	IIRR, Hyderabad
T08	KS-24	IIRR, Hyderabad
T09	AR-19–18	IIRR, Hyderabad
T10	HRSV-7	IIRR, Hyderabad
Checks		
1	CR Dhan-201	NRRI, Cuttak (varietal check)
2	GK 5022	Early duration, hybrid check

Table 1. *Cont.*

(b)		
Measurement	**Unit**	**Description**
Days to 50% flowering	DFF (Number)	The total number of days taken from the date of sowing to extrusion of the panicle tip above the sheath of the flag leaf in 50% of plants in a plot.
Plant height	PH (cm)	It was measured at maturity from the base of the plant to the tip of the main panicle and expressed in cm.
Panicle length	PL (Number)	It was measured as the length of the panicle from the base to the tip in cm.
Number of productive tillers per plant	PT (Number)	The number of tillers in a plant that bears panicles was recorded as the number of productive tillers per plant at maturity.
Number of filled grains per panicle	FG (Number)	The number of filled grains per panicle was counted and recorded.
Spikelet fertility	SF (%)	The spikelet fertility percent was calculated as the ratio of filled grains per panicle to the total number of grains in a panicle and was expressed as a percentage.
1000 grain weight	TGW (g)	Thousand-filled grains were randomly counted, and the weight was recorded in grams with the help of electronic balance.
Biomass	BM (g)	Biomass (above ground), which refers to the total yield of plant material without economic yield, was recorded in grams.
Grain yield per plant	GY (g)	At maturity, single plants were harvested, threshed, cleaned, and dried to 12% moisture content, and the weight was recorded in grams.
Productivity per day	PDP (kg/ha)	It is the ratio of grain yield in kilograms of a parent /hybrid per hectare to the number of days to its maturity and expressed in kilograms per hectare.
Harvest index	HI (%)	Harvest index measured crop yield as the ratio of economical yield, i.e., grain yield per plant, to biological yield (grain plus biomass yield per plant).

Experimental Locations

The multi-location evaluation of developed experimental hybrids, parental lines, and check varieties was carried out using the aerobic method in three locations: E1—ICAR-IIRR, Hyderabad (17°19′ N, 78°29′ E and 542.7 m above the MSL); E2—Agricultural Research Station, Warangal (18.0122° N, 79.5990° E); and E3—Agricultural Research Station, Kampasagar (17°09′60.00″ N, 79°29′59.99″ E).

2.2. Layout and Experimental Design

The study was carried out using the above material replicated three timesin a completely randomized block design. The crop was raised as dry direct, seeded aerobic rice. Two to three dry seeds were dibbled per hill in dry soil and then irrigated. Five rows of three-meter length for each entry and spaced 20 × 15 cm apart were planted. Thinning was carried out to ensure one seedling per hill after one week of sowing. The soil moisture status was maintained below saturation level and, throughout the crop period, it was maintained as an irrigated dry crop. The necessary cultivation practices of aerobic rice were followed to raise a good crop. Surface irrigation can be applied as soon as it has been planted in a dry state in fine tilth conditions of the soil. Surface irrigation was applied on a five-day cycle for up to 50 days after sowing. During the critical phases, such as active tillering, panicle initiation, flowering, and grain filling, watering was provided once every three days. Water was suspended fifteen days before harvesting the crop to ease uniform grain ripening. In rice under aerobic cultivation, weeds are the key issue, which decreases crop yield. Weed management was also successfully carried out using both chemical and manual means.

2.3. Data Collection

Observations were noted for grain yield and associated traits on five plants arbitrarily chosen from each entry for every replicate by following the Standard Evaluation System (IRRI, 2013). The data for eleven traits were collected as mentioned in Table 1b.

2.4. Data Visualization and Analysis

Bean plots are generated with the beanplot package version beanplot_1.2 [11], which is more informative than a boxplot to understand the data. Visualization via Beanplots, which plots graphs of univariate comparison, serves as an alternative to existing boxplots, violin plots, or strip charts. Boxplots were designed for normal data or at least unimodal data. Abeanplot instead shows the real density curve, which is more informative. The shape represents the density, and short horizontal lines represent individual data points. Thus, it combines the best features of boxplots, density plots, and rug plots into one and is highly readable. The longer thick lines represent the mean for each bean. The longer thin lines represent the data, with a sort of "stacking", where wider lines mean more duplicate values.

Furthermore, the data (mean values) pertaining to all the traits were subjugated to statistical and biometrical analysis for combining ability [12]. In combining the ability of ANOVA, based on the significance of genotypes across locations, further combining ability analysis was carried out. The estimates of general and specific combining ability and variances were obtained by using the covariance of half-sibs and full-sibs [12]. Variance due to general combining ability ($\sigma^2 gca$) and specific combining ability ($\sigma^2 sca$) was estimated as:

$$\sigma^2 gca = \text{Covariance of half-sibs}$$

$$\sigma^2 sca = \text{Covariance of full-sibs} - 2\ \text{Covariance of half-sibs}$$

The type of gene action is determined based on the ratio of $\sigma^2 gca$ to $\sigma^2 sca$, which is less than one, indicating non-additive gene action. Further, determining *gca* and *sca* effects helps identify good general and specific combiners. The *gca* (gi) and *sca* effects (Sij) were tested against zero for significance by calculating the t-value using the following formula.

$$\text{t-cal} = \frac{\text{gi} - 0}{\text{SE(gi)}};\ \text{t-cal} = \frac{\text{gj} - 0}{\text{SE(gj)}};$$

$$\text{t-cal} = \frac{\text{Sij} - 0}{\text{SE(Sij)}}$$

Here, the t-cal value is compared with the table value at the error degree of freedom.

Data were further analyzed to determine heterosis, heterobeltiosis, and standard heterosis over varietal check CR Dhan 201, and hybrid check GK 5022 was determined as per the standard procedure outlined [13] and was expressed in percentage. Heterosis was expressed as a percent rise or drop noticed in the F_1 over the mid-parent, as per the below-mentioned formula.

$$\text{Heterosis (\%) } (\text{h}_1) = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

Here,
$\overline{F}_1$= Mean of F_1
$\overline{MP}$ = Mean of parents

Heterobeltiosis was expressed as a percent rise or drop noticed in F_1 over the better parent as per the below-mentioned formula [13].

$$\text{Heterobeltiosis (\%) } (\text{h}_2) = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Here,

$\overline{BP}$ = Mean of better parent (for the traits, for instance, DFF, earliness is preferable, so early parents are considered better).

Standard heterosis was expressed as a percent rise or drop noticed in F_1 over standard check.

$$\text{Standard heterosis}(\%)(\mathrm{h}_3) = [((\overline{F}_1) - \text{Mean of check})/\text{Mean of check}] \times 100$$

Following that, data was subjected to stability analysis [14] where three stability parameters viz., (i) the overall mean of every genotype over a spread of environments, (ii) the regression of individual genotypes over the environmental index, and (iii) a function of squared deviation from the regression, were determined.

The stability model outlined [14] as follows:

$Y_{ij} = \mu + b_i I_j + \delta_{ij}$

Here, (i = 1, 2, 3, 4, . . ., g and j = 1, 2, 3, 4, . . ., e)

Y_{ij} = Mean value of ith variety or genotype in jth location or environment or season

μ = Mean value of all the genotypes across all the locations or environments or season

b_i = The coefficient of regression pertaining to ith variety or genotype on the environmental index that measures the actual response of this individual genotype to the spread of environments

I_j = Environmental index, which is defined as the deviation of the mean of total varieties/genotypes at a given place or location from the overall mean

δ_{ij} = Deviation of ith genotype at the jth environment from regression

A stable genotype, as per Eberhart and Russel (1966) [14], exhibits (i) high mean yield, (ii) a regression coefficient (b_i = 1) equal to unity, and (iii) mean square deviation from regression (S^2di) near to zero. While comprehending the results of the current study, S^2di was considered toward the measure of stability, as suggested [15]. Then, the kind of stability (measuring the response or sensitivity to environmental fluctuations) was determined based on the regression coefficient (b_i) and mean values [16]. If 'b_i' equals unity with a high mean, the genotype is supposed to have good stability (the performance remains unchanged with vagaries in the environment). If 'b_i' is greater than unity, it is expected to possess less than average stability (sensitive to environmental fluctuations but adaptable to favorable environments), and if 'b_i' is less than unity, it is believed to have greater than average stability (widely adaptable yet under poor environmental situations). The estimates of stability parameters, i.e., mean (μ), regression coefficient (b_i), and mean square deviation from regression (S^2di), were considered while assessing the stability of genotypes.

3. Results and Discussion

The mean values for eleven characters under study estimated from the three locations were subjected to statistical analysis, location-wise and pooled. The mean values of parents, hybrids, and standard checks for the pooled data across locations (3) are illustrated using beanplots (Figure 1). The mean value of parents was lower than crosses plus checks for all the characters except TGW. The difference between the means of the parents and crosses plus checks was very narrow for PH and SF. Depending upon the density of the data points, the shape of the bean plots changed for different characters under study.

The results from mean performance revealed that, among the lines, L02 was identified as good (considerably superior or on par with their respective mean) toward PL, PT, FG, BM, PPD, GY, and HI. L03 was considered good for DFF, PH, and TGW, while L01 was good for TGW. Testers T01, T02, and T07 recorded good GY, PT, TGW, and PPD. The testers, T03, exhibited earliness, and T10 recorded a short stature.

Substantially, depending on the inclusive performance, the following hybrids, H04, H18, and H20, performed in a superior way to the hybrid check, GK 5022, in response to GY, plus additional yield ascribing traits such as PL, PT, FG, SF, TGW, and PPD. The tables pertaining to the above results are furnished as Supplementary Data for reference (Table S1).

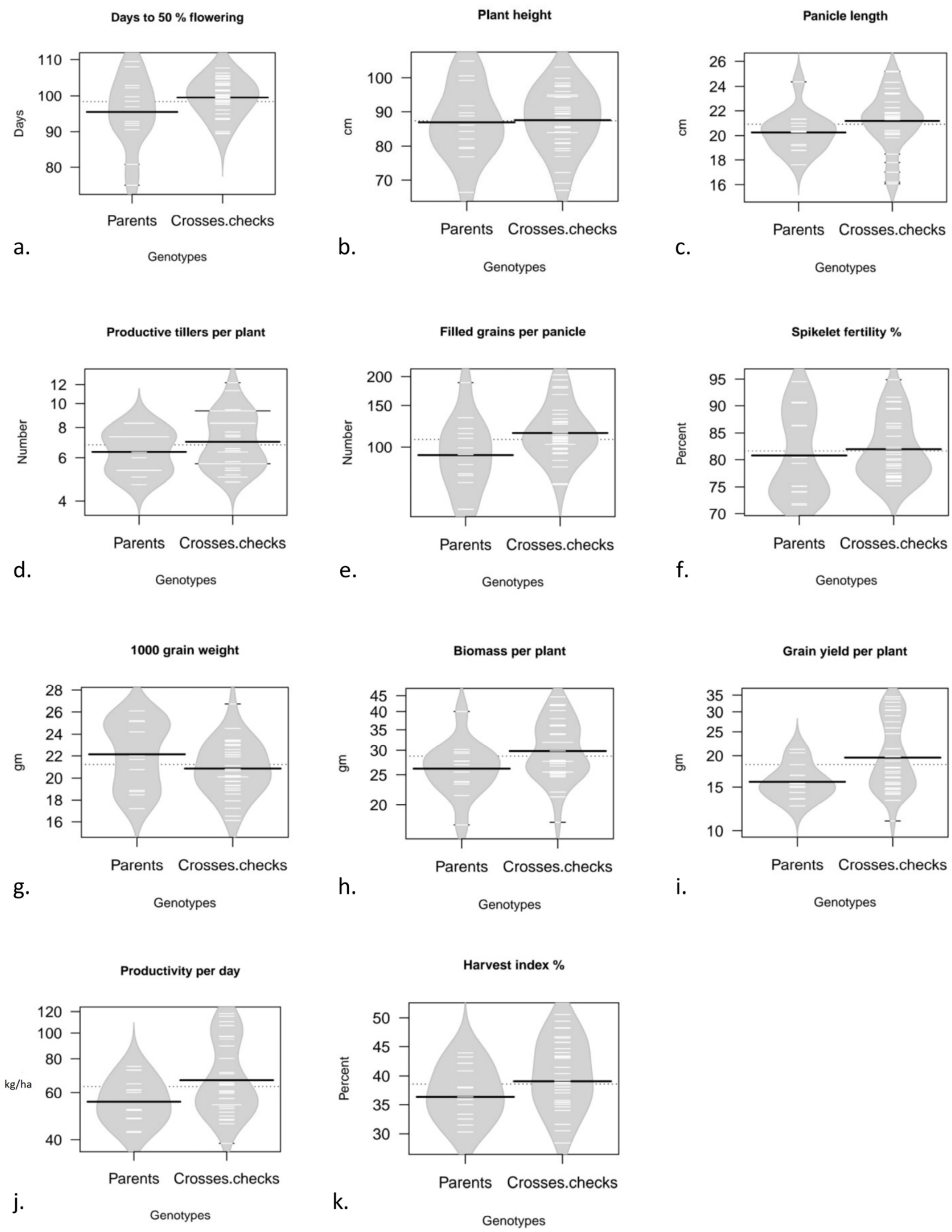

Figure 1. (**a**–**k**) Beanplots for mean data for grain yield and yield attributing traits studied, separately describing the data points distribution for parents and crosses.

The analysis of variance (ANOVA) for grain yield and yield ascribing traits unveiled significant differences among the genotypes (Table 2) toward all the traits studied at every location. The significance of genotypes indicated the existence of commensurable variability amongst the tested genotypes.

Table 2. Analysis of variance for yield and yield components in rice at three locations viz., Rajendranagar (E1), Warangal (E2), and Kampasagar (E3).

Character	Source of Variation and (df)								
	Replication-2			Genotypes-44			Error-88		
	E1	E2	E3	E1	E2	E3	E1	E2	E3
DFF	0.31	3.02	0.71	114.33 **	132.41 **	211.84 **	3.48	3.00	3.75
PH	1.53	1.74	4.18	246.27 **	271.49 **	281.06 **	1.76	2.24	2.83
PL	0.16	0.04	0.06	12.87 **	14.98 **	14.48 **	0.17	0.18	0.13
PT	0.01	0.00	0.00	9.35 **	10.47 **	9.61 **	0.01	0.01	0.01
FG	0.22	2.78	7.47	3824.77 **	3788.74 **	3702.19 **	4.11	3.52	3.85
SF	0.68	1.88	3.82	148.20 **	115.15 **	108.74 **	3.13	3.10	2.80
TGW	0.05	0.03	0.08	20.75 **	20.85 **	20.96 **	0.08	0.06	0.07
BM	0.54	0.04	0.00	129.46 **	129.63 **	122.16 **	0.39	0.37	0.38
GY	0.06	0.01	0.10	127.90 **	131.00 **	113.38 **	0.16	0.17	0.13
PPD	3.50	0.62	4.42	1533.70 **	1451.80 **	1168.95 **	1.39	1.59	1.92
HI	0.07	0.01	0.07	105.19 **	110.60 **	127.48 **	0.29	0.30	0.31

** Significant at 1% level.

Pooled ANOVA toward combining ability over locations unveiled significant differences amongst locations, genotypes (treatments), parents, parents vs. crosses, and crosses for all the traits studied (Table S2).

The significance of parents, crosses, and parents vs. crosses for most traits studied has been previously reported by researchers [17,18]. The splitting up of crosses into components viz., lines, testers, and line × tester, also showed that variances were significant for traits studied. Furthermore, it witnessed significant variances for the line × tester component for all traits studied by rice workers [17,18]. The effect of the interaction of lines × testers × locations recorded substantial differences for the traits DFF, PT, FG, GY, PPD, and HI. Reports in agreement with the above findings presented significant variances of lines × testers × locations for PT, PL, FG, and GY [17,18].

These results expose the omnipresence of sizable variability within the plant material studied, and there is a reliable prospect for the identification of pragmatic hybrid combinations as well as parental lines.

The general combining ability (*GCA*) is linked with additive gene action, whereas the specific combining ability is traceable to dominance and epistasis. Pooled analysis unveiled greater *SCA* variances than *GCA* variances for all the traits, implying the preponderance of non-additive gene action, which was previously envisaged as ideal for exploiting full potential through heterosis breeding.

A comparative study of the measure of variance components due to *GCA* and *SCA* grounded the gene action nature in regulating the trait expression. The *GCA* to *SCA* variance ratio was less than unity, indicating the preponderant role of non-additive gene action for all traits studied, exhibiting a non-additive type of gene action (Table 3). In support of present results, previous rice researchers documented findings envisaging the role of non-additive types of gene action for traits, namely DFF [19–23], PH [18,20,24–27], PT [20,28,29], PL [17,18,26,27,30], FG [18,20,24,25,27,29], SF [18,25,27,30], BM [22,31,32], HI [31–33], TGW [18,27,34–36], and GY [18,20,23,27,30,35–38], as in the current experiment.

The contributory role of lines was recorded as high for four traits viz., PH, FG, PPD, and HI, while it was high for characters, i.e., DFF, PL, SF, TGW, BM, and GY (Table 4). The line × tester interaction component contribution was higher for PT and modest for SF, with the characters being significant in deciding the hybrid potency, especially under aerobic conditions.

Table 3. Estimates of general and specific combining ability variances and proportionate gene action in rice for eleven characters.

Character	Location	$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca/\sigma^2 sca$	Gene Action
DFF	Rajendranagar	2.02	18.03	0.11	Non-additive
	Warangal	2.33	18.92	0.12	Non-additive
	Kampasagar	4.52	30.32	0.15	Non-additive
	Pooled	2.60	20.86	0.12	Non-additive
PH	Rajendranagar	17.69	43.15	0.41	Non-additive
	Warangal	18.73	47.75	0.39	Non-additive
	Kampasagar	17.19	46.83	0.37	Non-additive
	Pooled	17.78	45.96	0.39	Non-additive
PL	Rajendranagar	0.57	5.47	0.10	Non-additive
	Warangal	0.70	6.36	0.11	Non-additive
	Kampasagar	0.71	6.43	0.11	Non-additive
	Pooled	0.66	6.10	0.11	Non-additive
PT	Rajendranagar	1.69	1.89	0.90	Non-additive
	Warangal	2.07	2.37	0.87	Non-additive
	Kampasagar	1.96	2.21	0.89	Non-additive
	Pooled	1.90	2.14	0.89	Non-additive
FG	Rajendranagar	262.92	621.79	0.42	Non-additive
	Warangal	262.34	604.36	0.43	Non-additive
	Kampasagar	246.11	601.61	0.41	Non-additive
	Pooled	257.04	608.69	0.42	Non-additive
SF	Rajendranagar	9.62	19.14	0.50	Non-additive
	Warangal	14.76	14.82	0.99	Non-additive
	Kampasagar	12.71	19.63	0.65	Non-additive
	Pooled	12.30	17.93	0.69	Non-additive
TGW	Rajendranagar	0.77	4.55	0.17	Non-additive
	Warangal	0.96	5.44	0.18	Non-additive
	Kampasagar	0.71	5.47	0.13	Non-additive
	Pooled	0.79	5.01	0.16	Non-additive
BM	Rajendranagar	8.85	39.04	0.23	Non-additive
	Warangal	8.50	39.06	0.22	Non-additive
	Kampasagar	7.98	36.59	0.22	Non-additive
	Pooled	8.42	38.22	0.22	Non-additive
GY	Rajendranagar	12.25	36.44	0.34	Non-additive
	Warangal	13.26	37.13	0.36	Non-additive
	Kampasagar	10.76	31.37	0.34	Non-additive
	Pooled	12.05	34.84	0.35	Non-additive
PDP	Rajendranagar	144.64	437.87	0.33	Non-additive
	Warangal	139.36	405.95	0.34	Non-additive
	Kampasagar	104.81	307.45	0.34	Non-additive
	Pooled	128.66	379.45	0.34	Non-additive
HI	Rajendranagar	6.01	30.00	0.20	Non-additive
	Warangal	6.85	29.63	0.23	Non-additive
	Kampasagar	11.65	35.89	0.32	Non-additive
	Pooled	7.28	27.08	0.27	Non-additive

Table 4. Proportional contribution of lines, testers, and their interactions to total variance.

S. No.	Character	Contribution		
		Line (%)	Tester (%)	Lines × Tester (%)
1	DFF	38.29%	59.48%	2.24%
2	PH	58.14%	35.18%	6.68%
3	PL	28.32%	67.40%	4.28%
4	PT	30.07%	33.55%	36.37%
5	FG	62.79%	31.78%	5.42%
6	SF	19.47%	42.96%	37.57%
7	TGW	42.21%	54.77%	3.02%

Table 4. *Cont.*

S. No.	Character	Contribution Line (%)	Tester (%)	Lines × Tester (%)
8	BM	38.75%	53.00%	8.25%
9	GY	42.26%	44.78%	12.97%
10	PDP	44.44%	43.93%	11.63%
11	HI	46.65%	45.90%	7.44%

L02 was a good general combiner for PL, PT, FG, BM, PPD, HI, and GY, among lines. Out of ten testers, five were identified as excellent general combiners for GY as well as yield-attributing traits, including T02 for GY, PPD and HI; T04 for GY, DFF, PL, PT, FG, SF, BM, PPD, and HI; T06 for GY, PH, FG, and BM; T08 for GY, PL, PT, FG, SF, BM, PPD, and HI and T10 for GY, DFF, PH, SF, TGW, BM, and PPD (Tables S3 and S4).

In a few cases, it was noticed that the lines and testers with good performance were not necessarily the best general combiners, and the opposite is also true. Thus, the choice of parents must be predicated on both (by itself) the expression and parent's *gca* effects. Line L02 was confirmed as a good combiner for GY and its ascribing traits. L02 has been previously reported as a good general combiner for GY [39]. Amongst testers, T02, T04, T06, T08, and T10 were good combiners considering high *gca* effects and for most of the yield ascribing traits. Hence, the above testers and lines are well-thought-out, potent donors for improving GY and linked components in upcoming rice breeding programs.

Among the crosses studied, 12 hybrids (H01, H03, H04, H07, H09, H15, H16, H18, H20, H21, H22, and H29) exhibited considerably positive *sca* effects for GY. H27 (for DFF); H07, H10, H21, and H30 (for PH); H01, H08, H15, H27, and H28 (for PL); H04, H15, H18, and H20 (for PT); H04 and H20 (for FG); H04 (for SF); H07 and H11 (for TGW); H14 and H15 (for BM); H04, H18, and H20 (for PPD); and H18, H20, H22, and H24 (for HI) were identified as the best specific combiners based on considerable *sca* effects (the above details in tables are furnished as Supplementary Data for reference). However, H04, H18, and H20 (for GY) expression were exceedingly excellent for grain yield and its components regarding the good *sca* effects of crosses and good *gca* of parents. Here, it is clear that the significance of *sca* effects alone has no effect as long as its mean value is in a desirable direction. Sometimes, the higher *sca* effect may not be a choice among its counterparts after looking at the mean values. Hence, mean values have greater priority.

Thus, three outstanding specific combiners were detected amongst crosses, assumed from *sca* effects and commensurable mean expression in descending order (Tables S3 and S4). H20 for GY, PT, FG, BM, PPD, and HI; H18 for GY, PH, PT, BM, PPD, and HI; and H04 for GY, DFF, PL, PT, FG, BM, GY, PPD, and HI.

Heterosis toward grain yield/plant is predominantly because of concurrent exemplification of heterosis for the yield component character. Average heterosis or heterosis (h1), heterobeltiosis (h2), and standard heterosis (h3) arethe superior expressions as preferable over the mid parent, better parent, and the standard checks viz., GK 5022 (commercial hybrid) and CR–Dhan 201 (variety), projected for thirty hybrids for eleven traits (viz., DFF, PH, PL, PT, FG, SF, TGW, BM, GY, PPD, and HI for three locations and pooled data is a computed trait. The negative heterosis for DFF denotes earliness, and the negative heterosis for PH denotes short stature, which is preferable. In contrast, positive heterosis values were considered preferable for other traits.

The percentage of heterosis was calculated for pooled data pertaining to top specific-combiners for yield and yield-ascribing traits (Tables 5, S5 and S6).

Table 5. Percent heterosis, heterobeltiosis, and standard heterosis recorded for best specific combiners.

S. No.	Crosses	Heterosis	Heterobeltiosis	Standard Heterosis	
				CR Dhan 201	GK 5022
	DFF				
H27	IR-68897A × KS-22	−2.25 **	−12.50 **	−0.25	−6.83 **
	PH				
H30	IR-68897A × HRSV-7	−8.00 **	−15.41 **	−31.36 **	−18.27 **
H21	IR-68897A × ATR-177	−8.39 **	−18.05 **	−29.32 **	−15.83 **
H10	IR-79156A × HRSV-7	−7.47 **	−8.96 **	−26.14 **	−12.05 **
H07	IR-79156A × KS-22	−8.77 **	−16.22 **	−21.36 **	−6.36 **
	PL				
H27	IR-68897A × KS-22	24.66 **	18.41 **	13.37 **	16.71 **
H08	IR-79156A × KS-24	25.88 **	21.46 **	13.18 **	16.51 **
H28	IR-68897A × KS-24	22.01 **	17.41 **	9.40 **	12.62 **
H15	APMS-6A × ATR-374	17.28 **	17.00 **	7.14 **	10.29 **
H01	IR-79156A × ATR-177	27.17 **	21.68 **	5.42 **	8.52 **
	PT				
H18	APMS-6A × KS-24	98.20 **	66.68 **	115.66 **	86.39 **
H15	APMS-6A × ATR-374	78.91 **	54.53 **	99.94 **	72.81 **
H04	IR-79156A × ATR-372	61.87 **	49.10 **	66.63 **	44.02 **
H20	APMS-6A × HRSV-7	27.29 **	27.29 **	64.69 **	42.34 **
	FG				
H20	APMS-6A × HRSV-7	90.74 **	78.31 **	54.55 **	107.59 **
H04	IR-79156A × ATR-372	84.54 **	45.49 **	46.96 **	97.40 **
	SF				
H04	IR-79156A × ATR-372	11.21 **	1.17	6.15 **	−3.52 **
	TGW				
H11	APMS-6A × ATR-177	26.25 **	6.30 **	38.48 **	13.91 **
H07	IR-79156A × KS-22	12.30 **	−2.68 *	27.07 **	4.52 **
	BM				
H15	APMS-6A × ATR-374	51.41 **	50.56 **	80.91 **	23.15 **
H14	APMS-6A × ATR-372	53.78 **	43.80 **	70.84 **	16.30 **
	GY				
H20	APMS-6A × HRSV-7	94.17 **	62.44 **	109.43 **	12.86 **
H18	APMS-6A × KS-24	99.93 **	59.17 **	105.21 **	10.59 **
H04	IR-79156A × ATR-372	131.13 **	119.25 **	99.21 **	7.36 **
	PPD				
H20	APMS-6A × HRSV-7	90.08 **	62.54 **	95.44 **	10.69 **
H04	IR-79156A × ATR-372	131.21 **	122.76 **	91.11 **	8.24 **
H18	APMS-6A × KS-24	91.29 **	51.66 **	82.36 **	3.28 **
	HI				
H20	APMS-6A × HRSV-7	28.79 **	20.01 **	29.91 **	10.54 **
H22	IR-68897A × ATR-186	25.23 **	20.99 **	26.98 **	8.05 **
H24	IR-68897A × ATR-372	30.56 **	26.77 **	24.04 **	5.54 **
H18	APMS-6A × KS-24	27.70 **	14.38 **	23.81 **	5.35 **

* Significant at 5% level; ** Significant at 1% level.

As per the pooled analysis, average heterosis and heterobeltiosis estimates ranged from −42.29 (H11) to 131.13 (H04) percent and from −48.44 (H11) to 119.25 (H04) percent, respectively. Of the 30 hybrids studied, 18 excelled with considerable positive average heterosis and 16 exhibited considerable positive heterobeltiosis. Concerning heterosis, over best standard check GK 5022, the range was from −64.17 (H11) to 12.86 percent (H20) and positive significant standard heterosis was exhibited by four hybrids that included H20 (12.86), H18 (10.59), H04 (7.36), and H14 (3.20)

Heterosis and heterobeltiosis of the positive kind have been documented by previous workers in rice [18,27,40–43]. At the same time, few rice workers have proclaimed positive heterobeltiosis and standard heterosis values for this character [18,27,40,42,43]. However, mean performance is also an important consideration coupled with *gca*, *sca* effects, and heterosis percentage [44].

Further, top-ranking crosses were presented based on the high mean and their *sca* effects, parent's *gca* effects, and standard heterosis for yield and its attributes (presented as Supplementary Data). The hybrid, H20, which showcased extremely significant heterosis (positive) for grain yield compared to the checks, also proved its performance for PL, PT, FG, BM, PPD, and HI. Similar observations were noticed with H18 and H04 pertaining to GY and yield-ascribing traits. It was noticed in the cross combinations that involved lines IR-68897A and APMS-6A reported their superiority for GY [39].

The stability ANOVA unveiled that genotypes and environments were significant for most traits except HI, signifying diversity amongst genotypes and environments (Table S7). G $\times$ E interaction was considerable for the traits excluding PL, PT, TGW, and HI against pooled error, implying overwhelming behavioral differences of genotypes in erratic environments. G $\times$ E interaction for PL, PT, TGW, and HI were detected to be insignificant. Henceforth, stability assessment was not pursued for those traits.

Dissecting the sum of squares into varieties, environments + (genotypes $\times$ environment), and pooled error unveiled that mean squares owing to genotypes were highly considerable for all the traits examined, implying the manifestation of genetic variability in the studied experimental genotypic material [18,45]. Mean squares owing to environments + (genotypes $\times$ environments) were considerable for the entire range of traits except for TGW and HI. The above findings conformed to those of a few previous rice workers [18,45].

The sum of squares owing to environment + (genotype $\times$ environment) was further dissected into the environment (linear), genotype $\times$ environment (linear), and pooled deviation. Considerable variation owing to the environment (linear) was noticed for traits excluding HI, clarifying the linear contribution of environmental effects and additive environmental variance on these traits. Results in favor of the above findings have been documented by earlier researchers [18,45]. The linear component of G $\times$ E was considerable for traits excluding PL, PT, TGW, and HI, implying that genotypes considerably differ in their linear response to environments. The mean sum of squares for pooled deviation was considerable for DFF, PT, TGW, GY, PPD, and HI, implying the non-linear response and non-predictable nature of genotypes considerably differing in terms of stability. Thus, it unveils the significance of both linear and non-linear components in weighing the interaction of the genotypes with environments in the current study. The above findings conformed to those of a few previous rice workers [18,45–47].

As further stability analysis was not carried out for the following traits, viz., PL, PT, TGW, and HI, the adjudication of the promising experimental hybrids was made only considering their pooled mean expression.

Environmental indices of eleven characters viz., DFF, PH, PL, PT, FG, SF, TGW, BM, GY, PPD, and HI, are presented in Table 6. The environmental index reveals how favorable one environment is at a peculiar location. It has been confirmed that the estimates of the environmental index can bestow the rationale for identifying the favorable environments for the expression of the maximum potential of the genotype [15].

Table 6. Environmental indices for yield and yield components in rice.

Character	Locations		
	Rajendranagar	**Warangal**	**Kampasagar**
DFF	−5.281	−0.400	5.681
PH	−4.040	0.138	3.901
PL	−0.561	0.669	−0.107
PT	−0.286	0.602	−0.316
FG	−3.126	−0.978	4.104
SF	−1.221	0.218	1.003
TGW	−0.19	0.094	0.096
BM	−0.839	−0.309	1.148
GY	−0.873	−0.105	0.978
PPD	−0.320	−0.159	0.479
HI	−0.408	0.170	0.239

Environmental indices unveiled that Kampasagar was the most favorable location for FG, SF, TGW, BM, GY, PPD, and HI, while Warangal was the best location for PL and PT. Rajendranagar was the best location for DFF, PH, and PT.

Pooled ANOVA delineated the existence of considerable G × E interaction for GY. Linear and non-linear components pertaining to G × E interaction were considerable, which unveiled that only part of the performance could be predicted. A stable genotype, as per Eberhart and Russel (1966) [14], exhibits (i) high mean yield, (ii) a regression coefficient (b_i = 1) equal to unity, and (iii) mean square deviation from regression (S^2di) near to zero. While comprehending the results of the current study, S^2di was considered toward the measure of stability, as suggested in [15]. The estimates of stability parameters, i.e., mean (μ), the regression coefficient (b_i), and mean square deviation from regression (S^2di), were considered while assessing the stability of genotypes. The data related to stability parameters are furnished in Supplementary Data for reference.

Among the genotypes, two lines, eight testers, twenty-one hybrids, and one check showcased inconsiderable deviations from the regression (S^2di) values. Among the parents, one tester, T02 (20.54), exhibited average stability (mean significantly greater than varietal check, CR-Dhan 201) while another tester, T05 (13.49), was found to be adaptable to favorable environments (more than the average stability). None of the parents were found to be considerably superior over hybrid check GK 5022.

Two hybrids, H04 (32.78 g) and H20 (34.46 g), exemplified considerably higher GY over hybrid check GK 5022 (30.54 g) and recorded unit b_i values with non-significant deviation from regression. Hence, they were identified as highly adaptable hybrids and were thought to express well in various environments. H04 was also found to be stable for DFF, FG, and BM in addition to GY. Similarly, H20 was found to be highly adaptable for FG in addition to GY. Earlier rice researchers have also documented stable high-yielding GY hybrids based on stability parameters [14,46–49].

Stable parents and crosses for grain yield and its component traits are listed (Tables 7 and S8). Accordingly, parents, as well as crosses, are classified as stable and suitable to favorable environments and poor environments, respectively, based on the prescribed three features, i.e., mean (μ), the regression coefficient (b_i), and a mean square deviation from regression (S^2di).

Table 7. Stable parents and crosses for grain yield and its component traits.

Characters		**X > X, b_i = 1, S^2di = 0** **Average Stability**	**b_i > 1, S^2di = 0** **Suitable for Favorable Environments**	**b_i < 1, S^2di = 0** **Specifically Adapted to Poor Environments**
DFF	**P**	L03 and T03	T01 and T02	-
	C	H04, H05, H10, H27 and H30	H17 and H18	-
PH	**P**	L01, L03, T06 and T10	T04	-
	C	H07, H10, H13, H21, H22 and H30	H14 and H15	
FG	**P**	T04 and T09	L02 and T03	-
	C	H03, H04, H14, H16, H17, H18 and H20	H05, H10, H19 and H21	
SF	**P**	-	-	-
	C	-	H05, H20, H23, H27 and H30	
BM	**P**	T09	-	-
	C	H04, H15, H16 and H18	H14 and H03	
GY	**P**	T02	T05	-
	C	H04 and H20	-	-
PPD	**P**	L02 and T02	-	-
	C	-	H03	H04, H15, H16 and H20

P—Parents (Lines & testers); C—Crosses.

Previous workers reported stable hybrids for various characters, viz., DFF, PH, and FG [18,45,46] and SF [18,45].

4. Conclusions

The outcome of the present experiment was to identify novel rice hybrids for aerobic ecology with lower yield penalties and the added advantage of reduced water budget (almost half of irrigated rice paddies) and reduced methane emissions from irrigated paddies, which are believed to contribute to global warming. From the current study, the two best hybrids were identified, namely H20 (APMS-6A × HRSV-7) and H04 (IR-79156A × ATR-372). They were categorized as stable hybrids due to their (i) high mean yield, (ii) regression coefficients (b_i = 1) equal to unity, and (iii) mean square deviations from regression (S^2di) near zero. Furthermore, in terms of their desirable *sca* effects, heterosis over best check GK 5022, and grain yield expression, as well as other important characters, they excelled. The best cross, H20, besides being identified as a stable hybrid, recorded the highest mean GY (34.46g) with considerably positive *sca* effects (10.27 **); parents L02 (3.39 **) and T10 (0.30 **) recorded considerably positive *gca* effects; and registered standard heterosis (12.86%) for GY over the best check in addition toexpressing heterosis for PT, FG, PPD, and HI.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy13092353/s1, Table S1: Mean performance of parents, crosses and standard checks for various characters; Table S2: Pooled analysis of variance for combining ability for yield and yield components in rice; Table S3: Estimates of general and specific combining ability effects for various characters; Table S4: Estimates of general and specific combining ability effects pooled over three locations for grain yield and yield attributing traits against mean grain yield of good general and specific combiners; Table S5: Estimates of heterosis, heterobeltiosis and standard heterosis (over CR Dhan 201 and GK 5022) for various characters; Table S6: Top ranking crosses based on the high mean and their sca effects, gca effects of parents, standard heterosis for yield, and its components in hybrid rice; Table S7: Analysis of variance for yield and yield components for stability in rice; Table S8: Mean performance and stability parameters for various characters.

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