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Genetic analysis of reciprocal differences for yield and yield attributing traits in segregating populations of rice (*Oryza sativa* L.)

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Abstract

Reciprocal differences prevail in nature mainly due to unequal contribution of cytoplasmic determinants from male and female gametes to the zygote, but the influence of female parent often extends beyond simple genetic transmission. In this report, we estimate the cytoplasmic and maternal effects in rice and their adequacy in describing the observed reciprocal differences based on study of the parents, F₂s, F₃s and reciprocal cross progenies. Our study revealed that significant differences were observed for majority of yield & yield attributing traits between mean performance of straight & reciprocal F₂ & F₃ populations derived by crossing BPT-5204 & HPR-14 indicating the presence of reciprocal differences. High PCV, GCV coupled with high heritability & GAM observed for number of tillers, number of productive tillers, biomass & harvest index. High heritability & high GAM was observed for plant height in straight & reciprocal F₂ & F₃ populations. The variability by Shapiro-Wilk 'W' normality test revealed normal distribution for total grains, fertile grains per panicle & grain weight per panicle in F₂ population, whereas number of productive tillers, flag leaf length, total grains per panicles, fertile grains per panicle, grain weight per panicle, test weight, harvest index & grain length in both straight and reciprocal F₃ population. Multi trait selection index was performed to evaluate F₃ families for quantitative traits & selected top 20 F₃ families in both straight & reciprocal crosses. Best F₃ families showed grain yield of 41% to 52% gain over the better parent BPT-5204 in straight & 37% to 61% gain in reciprocal crosses indicating the effect of cytoplasmic differences among the parents in the derived crosses. Further, these top performing superior F₃ families can be utilized for developing breeding lines for improvement of the traits.

Keywords: Straight cross, reciprocal cross, cytoplasmic effect, normality test, F₃ families

Introduction

Maximum human food is derived from cereal crop plants and major share is from wheat and rice, are supplying more than 65% human food requirement throughout globe. Global demand for these staple crops is on the rise and making these crops ideal targets for improving nutrition through biofortification. Among these, rice is a staple food crop that is consumed by more than 65% of global population (Kalyan *et al.*, 2017) ^[10]; it occupies a position of overwhelming importance in Asian agriculture and constitutes the bulk of the Asian diet too. It is largely grown in Asia (90% area) under diverse conditions of soil, climate, hydrology and topography (Mahapatra and Behera, 2011) ^[16]. For many people in the poor countries, rice is a main source of energy and plays an important role in providing livelihood. To feed the growing population and to achieve food security in the country, current production levels need to be increased minimum by two million tonnes every year (Singh *et al.*, 2018) ^[28]; hence it is critical to produce high yielding cultivars with high quality of rice.

To meet the increasing demand, rice production must be increased with less land, less water using less pesticide in a sustainable way (Anandan *et al.*, 2009) ^[2]. The presence of adequate genetic variability is pre requisite factor for rice improvement. Among the different options, exploiting the variability present in segregating populations is essential for improvement through selection and identification of maternal effect in reciprocal crosses helps to identify some traits which are controlled by cytoplasmic genes and useful for development of new high yielding cultivars. Reciprocal crosses play an important role in the selection of any breeding programme for population improvement and development of new hybrids in the crop. Reciprocal differences prevail in nature mainly due to unequal contribution of cytoplasmic determinants from male and female gametes to the zygote (Valluri *et al.*, 2016) ^[32]. Both the parents contribute genes to their offspring, but the influence of female parent often extends beyond simple genetic transmission (Munganyinka *et al.*, 2015) ^[19].

The reciprocal effect for a trait is based on the assumption that the F₂ plants from direct crosses and reciprocal crosses have same mean value for the trait under study. If the difference exists between F₂ and its reciprocal F₂ population, likely to indicate the maternal effects and this contributes accordingly for the design and interpretation of genetic studies (Mosjidis and Yermanos, 1984) [18]. Using reciprocal crosses, maternal effects have been reported for many characters in rice, including filled-grains and grain weight (Toa *et al.* 2011) [30], grain quality trait (Asfaliza *et al.* 2012) [4], milling quality traits (Shi & Zhu, 1995) [26], protein content (Shi *et al.* 1996) [27], hybrid vigor (Virmani, 1994) [35] and crossability (IRRI, 1993). Diversity of the germplasm has been disclosed to be related to the manifestation of cytoplasmic differences in the expression of various characters (Kalsy & Sharma, 1972) [9]. The significant genetic differences among the straight & reciprocal crosses for the sheath rot disease (Mahadevaiah & Shailaja, 2015) [14, 15]. In this context, the study was conducted to evaluate the straight & reciprocal F₂ & F₃ populations for their yield & yield attributing traits; to identify best performing RILs based on multitrait evaluation and existence of any reciprocal difference among segregating populations.

Material and methods

The experiment was conducted during *khariif-2015 & rabi-2016* using augmented design. The experimental material for the present study comprised the straight and reciprocal crosses previously developed by Mahadevaiah and Shailaja

Hittalmani (2015) [14, 15] was obtained from Marker Assisted Selection laboratory, UAS, GKVK, Bengaluru. It composed of 517 straight cross (BPT-5204 × HPR-14) & 533 individual plants of reciprocal cross (HPR-14 × BPT-5204) of F₂ population. The BPT-5204 is a highly popular variety grown in irrigated conditions in South India is known to fetch high price for its excellent cooking and milling quality. The HPR-14 is a local land race, purple pigmented, not popular and not cultivated on commercial scale but having high protein content. Salient features of parents used to derive the material for the study are presented in table 1. Nursery seedlings were transplanted after 21 DAS in main experimental field with spacing of 0.3 m × 0.2 m and maintained with recommended cultural practices. The best two hundred lines based on yield were selected from F₂ population and forwarded to F₃ generation in both straight & reciprocal crosses. In F₂ & F₃ segregating populations, straight & reciprocal crosses along with parents were evaluated for growth & yield attributing traits. Observations were recorded on all F₂ individual plants & F₃ families (five plants per family) from both straight & reciprocal crosses under aerobic conditions. Statistical analysis was done using WINDOSTAT (version 8.0) for genetic variability and 'SPSS 23.0 version' for Shapiro Wilks 'W' normality test. The top performing families in both straight & reciprocal crosses among F₃ families have been quantified by "Duncan's multiple range test (DMRT)" through 'agricolae' package in R version 4.0.2 statistical software.

Table 1: Salient features of parents (BPT-5204 & HPR-14) selected for the present study

Traits	BPT-5204	HPR-14
Plant stature	Medium tall (60-70 cm), Erect and compact	Tall (>90 cm) Medium spreading
Colour of plant, leaf & sheath	Green	Purple
Duration	Late (160 days)	Early (120 days)
Tillering ability	High (20)	Low (10)
No. of panicles	High (15-18) compact	Low (8-10)
Grain yield	4 ton/ ha	2.5 ton/ ha
Grain type	Short fine	Short bold
Total protein content	7-8%	13-14%

Results and Discussion

The inheritance study of quantitative characters in various crosses will help breeders to choose appropriate breeding methods (Singh *et al.*, 2018) [28]. The pattern of inheritance of different yield contributing and quantitative traits in rice has been reported by Kamara *et al.*, 2017 [11]. Diverse plant types are immediately valuable for shaping new varieties and forms the basic wealth on which plant breeders can operate for reconstructing the existing genotypes. To increase the present levels of production in terms of grain yield, quality & other traits there is ample need to identify & utilize genetically divergent parents for inter- and intra-sub specific and reciprocal crosses in rice. Among the many factors for rice production, cytoplasmic gene effect or maternal gene effect is one the most important factors & it can contribute to heritable variation in both quantitative and qualitative traits in plants (Alexander and Wulff, 1985; Singh *et al.*, 2018) [1, 28].

Significant differences were observed between mean performance of straight & reciprocal F₂ & F₃ populations for majority of yield & yield attributing traits. The traits like plant height, flag leaf length, seed fertility percentage, test weight, grain length & L/B ratio of paddy grain were found higher mean value in reciprocal cross compared to straight cross in both F₂ & F₃ populations (Table 2). The mean performances

of these traits were affected by the parents when used as male and female parents and vice versa. This showed that cytoplasm of BPT-5204 & HPR-14 have an undesirable effect & moderately interferes with manifestation of yield & yield attributing traits. A result indicates the presence of reciprocal differences among straight & reciprocal F₂ & F₃ populations. The cytoplasmic influence of same parents (BPT-5204 & HPR-14) for sheath rot disease was reported (Mahadevaiah, 2015) [14, 15]. The similar kind of reciprocal differences for seed size in maize was reported by Roach & Wulff, 1987 [22]; Zhang *et al.*, 2016 [36]. Even the reciprocal difference clearly reported from Valluri *et al.*, 2016 [32] in pearl millet under *in vitro* conditions via. embryogenic callus quantity & regeneration frequency.

Wide range variability was observed for important traits like plant height, number of productive tillers, panicle length, grain length & grain breadth in straight cross compared to reciprocal cross in both F₂ & F₃ populations. The estimates of GCV & PCV was higher for most of the yield & yield attributing traits *viz.*, days to 50% flowering, number of tillers, number of productive tillers, days to maturity, panicle exertion, flag leaf length, grain yield per plant, biomass, harvest index, grain length & grain in straight F₂ population as compared to reciprocal F₂ population. But in F₃ population,

higher GCV & PCV was observed in reciprocal cross compared to straight cross for most of traits like days to 50% flowering, plant height, panicle exertion, chaffy grains per panicle, test weight, grain yield per plant, biomass, grain length & L/B ratio. Very narrow differences were observed between estimates of GCV & PCV in both straight & reciprocal F_2 & F_3 populations indicate minimal role of environment on the performance of the genotypes. The heritability was ranged from 2.90% (grain weight per plant) to 99.60% (total grain per plant) in F_2 population & 1.50% to 99.50% for the same traits in F_3 population. The higher heritability for days to 50% flowering, number of productive tillers, days to maturity, flag leaf length, total grain per plant, fertile grains per plants & seed fertility percentage and lower heritability for grain breadth, grain weight per plant & panicle length (except reciprocal F_2) was observed in both crosses of F_2 & F_3 populations. The lowest genetic advance per cent over mean (GAM) was observed for grain length (F_2 population), grain breadth (F_3 population) & highest for panicle exertion in both crosses of F_2 & F_3 populations (Table 3). Similar results of high heritability for panicle exertion and plant height were reported by *Das et al.* (2001)^[7]; *Kuldeep et al.* (2004)^[13]; *Uttam et al.* (2005)^[32]. Whereas, high GAM was observed for plant height at maturity and moderate to low was observed for other characters which are similar to results reported by *Prajapat et al.* (2011)^[21].

Higher value of broad sense heritability attributed to lesser difference between PCV & GCV values. High heritability values resulted in higher values of expected GAM. High PCV, GCV coupled with high heritability & GAM observed for number of tillers, number of productive tillers, biomass & harvest index. High heritability & high GAM was observed for plant height in straight & reciprocal F_2 & F_3 populations. Similar results were observed by *Thirunganana kumar et al.* (2007)^[31]; *Basavaraja et al.* (2013)^[6]; *Arvind et al.* (2015)^[3] and *Irappa et al.* (2018)^[8]. The results indicated the major genes with additive gene action governing these traits, which offers scope for further improvement through selection which were agreement with *Sala* (2013)^[25]; *Verma et al.* (2000)^[34]; *Ashwini Samak et al.* (2011)^[5]; *Roy* (2000)^[24]. The success in any crop improvement program depends by the ability of the breeder to define & assemble the required genetic variability & select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental components of phenotypic variation (*Mather*, 1949)^[17]. Therefore, it is necessary to have information on both PCV, GCV to estimate heritability, which helps the breeder to predict the expected grains through selection.

Shapiro Wilk 'W' test is the preferred test of normality due to its high statistical power as compared to a wide range of alternative tests. Results showed that non-normal distribution for all the growth and yield attributing traits except total grains per panicle, fertile grains per panicle and grain weight per panicle in both straight & reciprocal F_2 population. In F_3 population, number of tillers, number of productive tillers, flag leaf length, total grains per panicles, fertile grains per panicle, grain weight per panicle, test weight, harvest index, grain length and L/B ratio showed normal distribution in both straight & reciprocal crosses (Table 4). Majority of the traits

showed skewed distribution in straight & reciprocal F_2 populations. Traits like days to 50% flowering, number of tillers, number of productive tillers, days to maturity, grain yield per plant, biomass per plant and grain breadth showed positively skewed, whereas plant height, particle exertion, seed fertility percentage, panicle length (except straight F_3 population) and harvest index (except reciprocal F_3 population) showed negatively skewed distribution in both crosses of F_2 & F_3 populations (Table 4). The skewed distribution of a trait in general suggests that trait is under the control of non-additive gene action, especially epistasis & is influenced by environmental variables (*Pooni et al.*, 1977; *Kimbeng & Bingham*, 1998; *Roy*, 2000)^[20, 12, 24]. Positive skewness is caused complementary gene interactions, while negative skewness is caused by duplicate gene interactions predominantly in the same directions (*Snape & Rizzs*, 1975)^[29]. The genes controlling the traits with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effect on the expression of trait. Most of the growth & yield attributing traits showed platykurtic distribution in both straight & reciprocal F_2 & F_3 population. Traits like panicle length, seed fertility percentage, L/B ratio (except reciprocal F_2 's) & chaffy grains per panicle (except straight F_3 population) in both crosses of F_2 & F_3 populations showed leptokurtic distribution suggesting that few genes governing these traits (Table 4). Kurtosis indicates the relative number of genes controlling the trait under investigation (*Robson*, 1956)^[23].

Positively skewed leptokurtic distribution was observed for chaffy grain per panicle, L/B ratio (straight F_2 's), and panicle length in straight & reciprocal F_3 population indicated that traits were influenced by fewer genes with complimentary gene action. Positively skewed mesokurtic distribution flag leaf length (straight & reciprocal F_2 's), grain breadth (reciprocal F_2 's) and total grains per panicle (reciprocal F_3 population) indicated that traits were governed by moderate number of genes with complimentary gene action. Negatively skewed mesokurtic distribution for panicle length (straight F_2 's), plant height & harvest index (reciprocal F_2 's), panicle exertion & test weight (straight F_3 's), grain length and L/B ratio (reciprocal F_3 's) indicated that traits were governed by large number of genes with additive gene action.

Multi trait selection index was performed using Duncon's Multiple Range Test (DMRT) through "agricolae" package in "R" version 4.0.2 software to evaluate F_3 families for quantitative traits. Individual trait was ranked separately followed by sums of ranks of all the traits & finally arranged by ascending order of rank for all the traits along with parents. The top performing 20 F_3 families in both straight & reciprocal crosses derived from BPT-5204 & HPR-14 was presented in Table 5 & 6. Best F_3 families showed grain yield of 41% to 52% gain over the better parent BPT-5204 in straight and 37% to 61% gain in reciprocal crosses indicating the effect of cytoplasmic differences among the parents in the derived crosses (Table 7 & Fig.1). The significant cytoplasmic effect of reciprocal cross for grain yield was reported in rice (*Singh et al.* 2018)^[8]. Further, these top performing superior F_3 families can be utilized for developing breeding lines for improvement of the traits.

Table 2: Estimates of traits mean performance of F₂ and F₃ generations in straight and reciprocal crosses of rice

Traits	F ₂			F ₃			Parents	
	SC	RC	Two sample t test P value/ t statistics (assuming unequal variance)	SC	RC	Two sample t test P value/ t statistics (assuming equal variance)	BPT 5204	HPR 14
DF	96.59	94.61	2.97**	96.56	97.49	-1.05	104.06	101.94
PH	88.15	90.82	-2.97**	91.76	96.35	-3.72***	97.75	107.41
NT	15.01	14	3.07**	15.47	15.12	0.94	14.22	10.24
NPT	12.62	10.95	4.95***	12.76	12.04	2.09*	12.06	7.88
DM	127.1	125.51	2.38*	127.12	128.67	-1.76	133.44	131.71
PL	20.2	19.99	-0.41	20.19	19.67	1.36	19.97	22.32
PE	0.14	0.65	-2.13*	0.41	0.95	-1.56	1.88	5.19
FLL	26.55	27.29	-2.39*	27.39	28.36	-2.17*	21.08	32.64
TGPP	142.61	137.74	2.21*	144.84	141.94	1.12	149.89	167.12
FGPP	117.44	113.54	1.85	119.22	118.51	0.35	122.61	133.76
CGPP	25.17	24.2	0.77	25.63	23.33	2.18*	27.28	33.35
SFP	81.86	82.4	-0.63	82.03	83.59	-2.25*	79.17	79.04
GWPP	2.26	2.24	0.58	2.39	2.3	1.85	1.87	2.72
TW	1.81	1.86	-3.26**	1.92	1.96	-2.06	1.42	1.97
GYPP	15.14	14.19	1.63	16.49	17.07	-0.87	23.3	17.5
BM	27.41	24.09	4.34***	29.16	28.95	0.24	45.69	29.76
HI	0.53	0.56	-1.8	0.56	0.59	-2.23*	0.51	0.59
GL	7.14	7.34	-8.46***	7.13	7.33	-4.59***	7.03	6.78
GB	2.35	2.33	1.32	2.31	2.35	-1.96	2.11	2.45
LBR	3.06	3.19	-6.16***	3.13	3.15	-0.83	3.36	2.8

* Significant at 5% ** Significant at 1% *** Significant at 0.1%

SC: Straight Cross (BPT 5204 × HPR-14); RC: Reciprocal Cross (HPR-14 × BPT 5204)

DF=50% flowering

FLL= Flag leaf length (cm)

GYPP= Grain yield per plant (g)

PH= Plant height (cm)

TGPP= Total grains per panicle

BM= Biomass (g)

NT: Number of tillers

FGPP= Fertile grains per panicle

HI: harvest index (%)

NPT= Number of productive tillers

CGPP: Chaffy grains per panicle

GL= Grain length (cm)

DM= Days to maturity

SFP: Seed fertility percentage

GB= Grain breadth (cm)

PL= Panicle length(cm)

GWPP= Grain weight per panicle (g)

LBR: L/B ratio of paddy grain

PE= Panicle exertion (cm)

TW= Test weight (g)

Table 3: Estimates of components of quantitative traits' variability in straight and reciprocal crosses in F₂ & F₃ populations of rice

Traits	Generation	Range		Phenotypic coefficient of variation (%)		Genotypic coefficient of variation (%)		Heritability % (broad sense)		Expected genetic advance over mean	
		SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
DF (days)	F ₂	78-136	77-136	14.60	13.46	12.20	10.30	69.90	58.60	21.01	16.24
	F ₃	74.60-122.80	80.40-117.33	10.55	11.81	10.07	10.99	91.10	86.70	19.50	21.07
PH (cm)	F ₂	51-136	50-128	16.32	16.54	8.74	16.26	70.81	72.29	23.82	24.22
	F ₃	55.20-121.00	64.50-127.50	11.68	12.78	4.09	5.19	52.30	56.07	12.59	14.77
NT	F ₂	4-37	3-32	44.55	43.12	36.88	33.45	68.60	60.20	62.91	53.46
	F ₃	7.20-27.20	9.60-24.20	34.95	29.05	27.34	19.24	61.20	43.90	44.04	26.25
NPT	F ₂	2-36	1-29	49.15	46.89	46.13	43.53	88.10	86.20	89.17	83.27
	F ₃	4.40-24.40	6.80-21.40	35.08	25.20	32.05	22.41	83.50	79.10	60.34	41.05
DM (days)	F ₂	108-167	109-167	9.49	8.03	9.31	7.85	96.20	95.60	18.82	15.82
	F ₃	96.20-152.40	93.25-148.60	7.77	5.89	7.62	5.76	96.20	95.80	15.40	11.62
PL (cm)	F ₂	12.60-27	9.5-21	19.66	44.61	10.10	41.92	26.40	88.30	10.69	81.15
	F ₃	16.00-38.60	14.82-22.67	18.22	14.68	9.95	5.79	29.80	15.60	11.20	4.70
PE (cm)	F ₂	-9.6 -10.00	-9.0 -12.0	2812.13	561.54	2751.86	501.27	69.79	65.87	4043.47	99.07
	F ₃	-8.04-6.00	-6.90-10.30	325.66	793.12	265.39	732.85	53.77	57.95	360.73	946.85
FLL (cm)	F ₂	10.00-43.00	14.70-45.0	20.82	19.36	19.52	18.34	87.90	89.70	37.69	35.78
	F ₃	16.40-39.50	17.10-43.04	17.14	17.13	15.89	15.42	86.00	81.12	30.36	28.60
TGPP	F ₂	40-268	30-263	24.49	25.29	24.44	25.24	99.60	99.60	50.25	51.89
	F ₃	57.20-213.00	71.00-219.40	19.59	18.83	19.54	18.78	99.50	99.45	40.15	38.58
FGPP	F ₂	6-236	4-200	30.02	29.30	29.59	28.84	97.20	96.90	60.11	58.47
	F ₃	38.40-192.80	52.60-193.40	22.72	20.18	22.28	19.71	96.20	95.36	45.00	39.64
CGPP	F ₂	0-133	0-145	68.65	82.70	24.13	38.19	39.35	54.82	55.64	93.40
	F ₃	10.50-62.40	6.25-70.20	43.01	55.79	38.05	51.83	78.30	86.30	69.36	99.19
SFP (%)	F ₂	6.90-100	6.06-100	16.17	17.47	15.40	16.64	90.70	90.70	30.21	32.65
	F ₃	60.46-93.63	54.77-94.26	19.06	16.16	18.73	15.67	96.60	94.03	37.93	31.30
GWPP (g)	F ₂	0.20-25	0.20-5.30	155.8	163.74	29.00	27.97	3.50	2.90	11.12	9.84
	F ₃	1.08-3.96	0.96-3.44	164.95	153.36	20.53	31.19	1.50	4.14	5.26	13.07
TW (g)	F ₂	0.39-3.20	0.89-3.08	24.72	23.45	15.39	15.57	38.80	44.00	19.75	21.28
	F ₃	1.42-2.50	1.42-2.94	15.97	22.63	9.45	10.89	35.00	23.17	11.51	10.80
GYPP (g)	F ₂	0.40-60.60	0.20-41.50	65.88	59.62	28.77	22.51	41.91	19.21	56.87	23.59

	F ₃	6.33-35.46	7.94-37.66	37.11	43.16	3.89	6.05	44.15	14.02	33.75	12.46
BM (g)	F ₂	5.17-105.50	3.60-76.60	49.70	46.24	48.34	44.64	94.6	93.2	96.86	88.79
	F ₃	12.15-67.55	14.68-54.36	30.76	36.79	3.08	6.02	52.90	18.40	33.53	13.95
HI (%)	F ₂	0.05-0.99	0.01-0.98	52.43	33.99	32.50	14.06	85.13	67.93	91.95	47.56
	F ₃	0.27-0.88	0.38-0.91	19.93	20.71	3.10	0.78	16.50	13.50	6.78	5.76
GL (cm)	F ₂	5.60-9.0	6.0-8.90	6.49	6.02	1.01	0.53	33.36	27.29	4.46	3.38
	F ₃	5.94-8.46	6.36-8.30	5.54	13.33	5.43	13.30	96.03	99.63	10.95	27.35
GB (cm)	F ₂	1.20-3.10	1.90-3.30	29.92	30.14	9.79	10.69	10.70	12.60	6.60	7.81
	F ₃	1.60-2.92	1.90-2.98	28.11	42.79	8.86	7.73	9.94	3.26	5.75	2.88
L/B ratio	F ₂	2.0-6.0	2.32-4.10	14.29	14.49	11.13	11.12	60.60	58.80	17.85	17.56
	F ₃	2.13-4.30	2.44-3.69	12.95	20.03	10.11	19.21	60.92	92.02	16.25	37.96

Table 4: Test for normality for growth and yield related traits in F₂ and F₃ populations of straight and reciprocal crosses of rice

Traits	Shapiro Wilk's test for normality															
	F ₂								F ₃							
	SC				RC				SC				RC			
	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis	W	P<W	Skewness	Kurtosis
DF	0.9244	<0.0001	0.83	0.38	0.8826	<0.0001	1.24	1.28	0.9308	<0.0001	0.87	0.34	0.9091	<0.0001	1.01	0.56
PH	0.9702	<0.0001	-0.32	-0.38	0.9706	<0.0001	-0.48	-0.22	0.9556	<0.0001	-0.72	0.29	0.9815	0.0099	-0.43	0.39
NT	0.9596	<0.0001	0.79	0.71	0.9850	<0.0001	0.34	-0.18	0.9782	0.0033	0.46	-0.05	0.9823	0.0128	0.34	-0.35
NPT	0.9540	<0.0001	0.84	0.76	0.9845	<0.0001	0.36	-0.03	0.9840	0.0226	0.39	-0.13	0.9789	0.0042	0.46	-0.05
DM	0.9303	<0.0001	0.79	0.30	0.8894	<0.0001	1.24	1.35	0.9336	<0.0001	0.73	0.56	0.8943	<0.0001	0.43	2.59
PL	0.9904	<0.0001	-0.27	0.69	0.1382	<0.0001	-0.79	2.70	0.6874	<0.0001	4.52	36.67	0.9398	<0.0001	-1.09	3.34
PE	0.9171	<0.0001	-0.70	-0.10	0.9227	<0.0001	-0.77	-0.04	0.8699	<0.0001	-1.02	0.01	0.9000	<0.0001	-0.85	0.52
FLL	0.9827	<0.0001	0.44	0.15	0.9914	<0.0001	0.34	0.15	0.9901	0.1877	0.24	-0.20	0.9728	0.0006	0.33	0.79
TGPP	0.9945	0.0586	0.18	0.29	0.9947	0.0611	0.12	0.55	0.9949	0.7293	0.05	-0.16	0.9884	0.1029	0.21	0.08
FGPP	0.9953	0.1166	0.03	0.46	0.9935	0.0220	-0.25	0.26	0.9936	0.5367	0.18	0.27	0.9942	0.6325	0.16	0.32
CGPP	0.8911	<0.0001	1.62	4.81	0.8568	<0.0001	1.71	4.39	0.9228	<0.0001	1.16	1.77	0.8894	<0.0001	1.52	3.23
SFP	0.8810	<0.0001	-1.67	4.58	0.8741	<0.0001	-1.57	3.59	0.9466	<0.0001	-0.92	0.83	0.9101	<0.0001	-1.31	2.33
GWPP	0.9887	0.0005	-0.07	0.89	0.9870	0.0001	-0.09	1.01	0.9872	0.0672	0.26	-0.24	0.9858	0.0423	0.14	-0.01
TW	0.9635	<0.0001	-0.40	2.64	0.8704	<0.0001	0.37	2.92	0.9955	0.8191	-0.01	-0.09	0.9700	0.0003	0.66	2.12
GYP	0.9233	<0.0001	1.15	1.75	0.9587	<0.0001	0.74	0.39	0.9437	<0.0001	0.63	-0.35	0.9366	<0.0001	0.92	0.60
BM	0.9238	<0.0001	1.26	2.77	0.9426	<0.0001	1.08	2.42	0.9548	<0.0001	0.74	0.26	0.9529	<0.0001	0.82	0.48
HI	0.5719	<0.0001	-0.42	-0.36	0.9769	<0.0001	-0.51	-0.17	0.9879	0.0857	0.10	-0.53	0.9900	0.1802	0.27	-0.29
GL	0.9832	<0.0001	0.21	0.59	0.9823	<0.0001	-0.17	0.41	0.9764	0.0019	0.50	1.15	0.9915	0.2940	-0.04	-0.21
GB	0.9563	<0.0001	0.37	1.35	0.9407	<0.0001	0.66	0.13	0.9768	0.0022	0.31	0.55	0.9256	<0.0001	1.17	2.41
LBR	0.9317	<0.0001	1.35	10.54	0.9894	0.0007	-0.04	-0.59	0.9802	0.0064	-0.13	1.33	0.9864	0.0513	-0.34	-0.15

Table 5: Quantitatively top performing F₃ families derived from straight cross of rice for yield and yield attributing characters

Rank	F ₃ Family	DF	PH	NPT	DM	PL	PE	FLL	FGPP	SFP	GWPP	TW	GYP	BM	HI	GL	GB	LBR
1	15	122.80	70.60	20.80	149.60	19.84	-4.60	23.30	134.40	79.89	3.02	2.22	32.68	46.37	0.70	7.18	1.60	4.30
2	21	86.40	91.10	21.60	117.20	21.80	0.72	31.80	117.40	87.55	2.40	1.94	29.17	50.10	0.58	7.34	2.18	3.39
3	22	120.00	101.60	19.40	150.40	20.20	0.50	20.46	118.80	87.83	1.66	1.64	31.69	53.34	0.60	6.90	2.02	3.43
4	38	99.80	91.60	17.60	130.80	19.50	2.08	33.80	171.20	83.49	2.62	1.86	27.54	40.26	0.68	6.54	2.40	2.75
5	41	91.20	93.30	18.20	122.00	19.90	0.82	31.66	143.20	84.55	3.16	1.98	27.07	36.74	0.74	7.14	2.32	3.09
6	55	85.40	95.80	17.60	116.00	20.06	1.22	30.10	147.60	84.28	3.20	2.26	28.57	35.62	0.80	7.04	2.46	2.89
7	79	105.60	104.40	21.20	134.40	20.90	2.20	22.70	148.20	82.65	3.10	2.04	28.31	54.87	0.52	6.88	2.10	3.29
8	81	88.60	105.00	16.20	119.80	21.96	1.98	32.40	162.60	89.79	3.14	1.88	27.11	38.88	0.70	7.28	2.26	3.24
9	109	108.80	84.00	18.00	139.20	19.00	-5.68	30.00	143.60	74.25	2.52	2.12	32.84	40.82	0.81	6.40	2.32	2.76
10	118	96.20	93.50	12.00	126.80	18.90	0.02	23.10	125.40	86.43	2.46	2.20	32.86	48.29	0.68	7.40	2.56	2.92
11	153	88.60	104.60	16.20	119.00	21.16	0.66	34.70	143.80	86.39	2.86	2.08	27.00	60.36	0.45	7.48	2.40	3.16
12	171	104.00	106.50	11.00	135.00	22.00	3.07	31.67	151.33	86.75	3.40	2.50	34.21	46.22	0.74	7.13	2.80	2.56
13	182	100.25	105.00	19.75	131.00	20.88	2.13	28.38	148.50	83.82	3.13	1.93	35.05	46.69	0.75	7.63	2.73	2.81
14	193	98.60	102.30	16.00	129.20	22.90	2.76	21.10	192.80	91.60	3.06	1.74	29.75	38.40	0.77	6.78	2.58	2.71
15	207	98.60	102.20	17.40	130.40	21.90	4.34	33.36	120.20	84.48	2.28	2.14	28.48	40.10	0.71	7.28	2.56	2.86
16	293	93.00	97.10	17.80	124.00	20.30	2.24	26.40	147.80	82.19	3.32	2.00	27.69	36.38	0.76	6.98	2.12	3.31
17	295	104.60	112.00	24.40	135.40	20.36	3.90	26.98	108.80	82.66	2.06	1.78	35.46	55.08	0.64	6.96	2.18	3.21
18	318	103.60	110.00	17.60	133.80	21.50	3.44	36.30	162.40	87.52	3.02	1.92	27.33	42.20	0.65	6.72	2.60	2.61
19	324	103.00	112.00	15.40	133.20	21.90	4.60	37.10	192.40	93.63	3.96	2.10	34.92	67.55	0.52	6.90	2.80	2.47
20	387	96.33	112.33	16.67	127.00	24.17	2.67	39.50	160.67	83.40	3.50	1.87	31.78	38.07	0.84	7.00	2.17	3.24
Parents	BPT-5204	104.06	97.75	12.06	133.44	19.97	1.88	21.08	122.61	79.17	1.87	1.42	23.30	37.23	0.46	7.03	2.11	3.36
	HPR-14	101.94	107.41	7.88	131.71	22.32	5.19	32.64	133.76	79.04	2.72	1.97	17.50	33.73	0.59	6.78	2.45	2.80

Table 6: Quantitatively top performing F₃ families derived from reciprocal cross of rice for yield and yield attributing characters

Rank	F ₃ Family	DF	PH	NPT	DM	PL	PE	FLL	FGPP	SFP	GWPP	TW	GYPP	BM	HI	GL	GB	L/B
1	60	99.80	105.80	13.20	130.20	20.64	3.84	32.40	161.60	87.19	2.98	1.88	32.32	51.80	0.62	7.30	2.34	3.14
2	87	86.33	98.00	11.33	117.67	21.67	0.57	29.00	119.67	87.00	2.83	2.50	24.77	27.33	0.91	7.43	2.30	3.23
3	113	114.00	105.75	16.00	145.50	20.38	2.68	26.25	122.00	80.88	2.20	1.79	26.01	40.66	0.64	7.40	2.25	3.31
4	122	98.20	110.40	14.60	128.80	18.90	0.72	24.00	149.80	87.52	3.44	2.58	32.17	42.83	0.75	7.54	2.22	3.41
5	170	95.40	90.20	15.80	126.80	20.00	1.36	28.16	115.80	88.53	2.32	2.08	29.42	43.73	0.67	7.32	2.26	3.26
6	208	105.80	98.60	14.00	136.40	20.48	2.04	30.94	184.40	89.68	3.38	2.00	32.01	44.48	0.72	7.60	2.38	3.19
7	248	90.20	108.60	15.60	121.80	20.68	-0.58	32.30	155.00	91.30	3.28	2.30	32.52	52.62	0.62	7.50	2.38	3.18
8	249	102.60	111.60	15.00	134.80	22.14	3.74	38.26	193.40	88.26	3.16	1.74	28.06	50.97	0.55	7.00	2.26	3.12
9	255	94.20	109.80	18.00	125.40	20.50	0.70	29.20	141.60	80.46	3.04	1.78	37.66	47.61	0.79	6.90	2.50	2.79
10	256	97.00	103.20	13.40	128.20	21.40	1.54	29.88	160.80	85.99	3.28	1.90	27.49	41.03	0.67	7.44	2.32	3.21
11	290	101.40	91.40	15.20	132.60	20.50	1.48	21.72	134.80	85.34	2.18	1.68	26.54	39.06	0.68	7.22	2.22	3.27
12	291	90.80	96.80	16.20	122.40	20.95	1.40	31.84	121.40	87.57	2.60	2.14	29.17	42.25	0.69	7.72	2.44	3.20
13	311	91.40	110.40	15.20	123.80	21.04	3.80	31.96	124.80	85.06	2.34	1.92	25.47	49.00	0.52	7.38	2.30	3.23
14	320	90.60	99.00	21.40	123.00	21.90	2.88	34.10	135.80	89.48	3.02	1.94	31.68	50.79	0.62	6.38	2.36	2.72
15	322	94.40	76.40	18.60	126.00	19.36	-3.80	21.12	104.40	87.98	1.90	1.80	24.42	36.95	0.66	8.04	2.32	3.49
16	383	89.40	93.00	16.00	121.60	19.20	3.12	27.50	129.60	88.94	2.66	2.06	28.58	40.38	0.71	7.32	2.28	3.24
17	398	96.00	63.00	13.75	127.75	20.00	-2.38	30.75	125.25	78.70	2.53	1.90	26.29	34.24	0.77	7.88	2.20	3.60
18	423	102.60	100.80	13.60	135.60	20.34	3.56	24.90	140.60	84.62	2.62	1.60	24.42	34.01	0.72	7.04	2.28	3.11
19	434	94.00	101.40	14.40	125.00	20.20	1.42	31.80	132.80	87.96	3.02	2.10	28.51	54.36	0.52	7.76	2.40	3.29
20	481	93.40	97.10	15.60	124.20	19.70	1.12	30.80	120.00	89.75	2.42	2.06	30.77	44.61	0.69	7.18	2.38	3.03
Parents	BPT-5204	104.06	97.75	12.06	133.44	19.97	1.88	21.08	122.61	79.17	1.87	1.42	23.30	37.23	0.46	7.03	2.11	3.36
	HPR-14	101.94	107.41	7.88	131.71	22.32	5.19	32.64	133.76	79.04	2.72	1.97	17.50	33.73	0.59	6.78	2.45	2.80

DF=50% flowering

PH= Plant height (cm)

NPT= Number of productive tillers

DM= Days to maturity

PL= Panicle length(cm)

PE= Panicle exertion (cm)

FLL= Flag leaf length (cm)

FGPP= Fertile grains per panicle

SFP: Seed fertility percentage

GWPP= Grain weight per panicle (g)

TW= Test weight (g)

GYPP= Grain yield per plant (g)

BM= Biomass (g)

HI: harvest index (%)

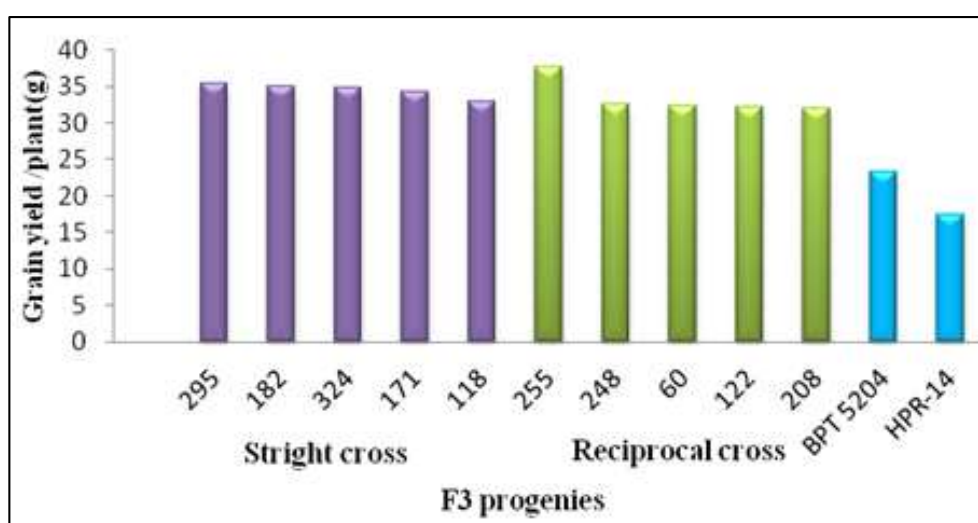
GL= Grain length (cm)

GB= Grain breadth (cm)

LBR: L/B ratio of paddy grain

Table 7: Best F₃ families derived from straight and reciprocal cross for grain yield

Sl. No.	Straight cross			Reciprocal cross		
	F ₃ family identity	Grain yield per plant (g)	% gain over BPT-5204	F ₃ family identity	Grain yield per plant (g)	% gain over BPT-5204
1	295	35.46	52.18	255	37.66	61.63
2	182	35.05	50.43	248	32.52	39.57
3	324	34.92	49.87	60	32.32	38.71
4	171	34.21	46.82	122	32.17	38.07
5	118	32.86	41.03	208	32.01	37.38
Parents	BPT 5204	23.30		BPT 5204	23.30	
	HPR-14	17.50		HPR-14	17.50	

**Fig 1:** Grain yield performance of best F₃ families derived from stright & reciprocal crosses**Conclusion**

In the present study, significant differences were observed for majority of yield & yield attributing traits between mean performance of straight & reciprocal F₂ & F₃ populations

derived by crossing BPT-5204 & HPR-14 indicating the presence of reciprocal differences. The performance of F₃ families for yield & yield attributing traits indicated that the majority of the traits not exhibited differences among the

straight & reciprocal crosses but performance of reciprocal cross for grain yield found to be higher, indicating the influence of cytoplasmic differences on the expression of the trait. Best F₃ families showed 37% to 61% gain in grain yield per plant. The F₃ family 295 & 255 were identified as superior for grain yield per plant in straight & reciprocal crosses, respectively. The best performing F₃ families for various traits can serve as potential genotypes for various economical traits as per the need & can be utilized in the future crop improvement programme.

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