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Transgressive segregants observed for yield and It's component traits in rice (*Oryza sativa* L.)

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Abstract

Transgressive segregation is the creation of hybrid progeny phenotypes that are away from the phenotypes of parents. These extreme phenotypes caused by transgressive segregation are heritably stable unlike heterosis. The genotypic variation present in the F₂ population gives an opportunity for individual selection of plants, which may result in development of a new variety or cultivar. The F₂ plants that exceeded the parental values were observed in all the traits viz., plant height (PH), number of panicles per plant (NPP), panicle length (PL), number of grains per panicle (NGP), spikelet fertility (SF%), grain yield per plant (GY), TGW (thousand grain weight), grain length (GL) and grain width (GW). More number of favourable "transgressive segregants" were observed for PL and TGW traits. There is more chance to pool the favourable alleles into a single line in the next generations through careful selection.

Keywords: Rice, transgressive segregants, yield traits, extreme phenotypes, grain size

Introduction

Rice (*Oryza sativa* L.) is food for more than half of the global population and it is an excellent model crop plant because of its small genome size (*Indica*- 390 Mb and *Japonica*- 430 Mb), availability of more number of transcriptomic and proteomic resources, reference genome. India grows rice in an area of 43.5 million hectares, production of over 171.02 million tons with productivity of 3.93 tons/ha in 2018-19 (USDA, 2019) [17]. Andhra Pradesh (A.P) is growing rice in 2.15 million ha area with 3741 kg ha⁻¹ productivity and 8.05 million tonnes production (<https://www.indiaagrinstat.com/>). The rice yields have been rapidly increased after the Green Revolution in the 1960's and success of hybrid rice technology in the 1970's, but the current day yield levels has almost reached plateau. As per the predictions, 50% more yield is to be produced to feed the anticipated nine billion human population by 2050. The rice production has to be increased by the year 2050 by 2% to ensure the food security in the world, (Carriger and Vallee, 2007) [3].

The yield of rice is a complex trait which is determined mainly by three component traits,

1. Number of panicles per plant (NPP),
2. Grain number per panicle (NGP),
3. Grain size or grain weight.

The weight of grain (TGW) is largely determined by the degree of grain filling and grain size. The grain size depends on its three grain dimensions (grain length, grain width, and grain thickness). The yield and it's related characters are quantitatively inherited which are controlled by many genes (Thoday, 1961) [15] having small effects often regarded as QTL's (Quantitative Trait Locus) (Geldermann, 1975) [5]. Progressive enhancement of crop breeding could be achieved by developing high yielding, superior rice varieties by bringing favourable alleles together.

Transgressive segregation is the formation of extreme phenotypes, or transgressive phenotypes, observed in segregating hybrid populations compared to phenotypes observed in the parental lines. The phenotypic variation range of a particular trait depends on the genetic complexity of that particular trait (Huang and Han 2014) [8].

Transgressive segregation is frequently associated with recombination, rearrangement of chromosomal segments, transposable elements, methylation of DNA and changes in gene expression. The extreme phenotypes that are produced due to transgressive segregation can be fixed or heritable to the next generations after selection in the F₂ generation. Such lines with extreme phenotypes can have important roles in evolution process (Rieseberg *et al.* 2002; Dittrich-Reed and Fitzpatrick 2013) [13, 4]. When seen from a breeding prospect, it has strongly contributed to the crop and animal improvement (Vega and Frey 1980; Tanksley and Mccouch 1997) [16, 14]. It gives an opportunity for the new hybrid progeny to evolve and more fit than their parents.

In view of the above facts and importance of transgressive segregants, the present research was conducted to identify the transgressive segregants in F₂ population of a cross between Samba Mashuri (BPT5204) which is a high yielding, semi-dwarf, medium duration and fine grain variety with Pardhiva (NLR33892) which is having high grain number, long panicle, blast and blight resistance, long duration variety with photoperiod sensitivity.

Materials and Methods

Two parents, Samba Mashuri (BPT5204) and Pardhiva (NLR33892), the F₂ generation derived from the cross between the two parents Samba Mashuri (BPT5204) with Pardhiva (NLR33892) were used as the study material in the present investigation. The F₂ generation along with parents was grown in *kharif* 2018 and the following data was recorded from 686 F₂ lines and two parents. The phenotypic data of yield and yield related traits was recorded.

The plant height was measured in centimetres (cm) from soil level to the tip of the panicle of the tallest tiller of the plant at maturity. Number of panicles per plant in each of the plant were counted. Panicle length was measured in centimeters (cm) from basal node of the panicle on main axis to the tip of panicle in each plant. Total number of grains including chaffy and filled grains per panicle was counted from a single

panicle in each plant. Total number of filled grains per panicle was counted manually. The spikelet fertility is a derived trait and relies on ratio of filled grains to the total number of grains per panicle and is expressed in percentage. For grain yield the total grains from matured panicles in a plant were harvested separately, threshed, cleaned and grain was dried to 12% moisture level and weighed. The grain yield per plant was recorded in grams.

Thousand grain weight (g): The 100 grain weight was measured for 100 well developed and filled grains using weighing balance and was multiplied by ten to get thousand grain weight expressed in grams.

Grain length (mm): Ten fully filled rice grains from each individual chosen randomly were lined up length-wise along a 30 cm scale to measure grain length and average value was recorded.

Grain width (mm): Ten grains, were arranged by width-wise along a 30 cm scale to measure grain width and average value was recorded.

The transgressive segregants were identified in the present study by finding the number of plants higher than the mean value of the higher parent or lower than the the mean value of the lower parent.

Results and Discussion

The “transgressive segregants” or extreme phenotypes that are observed in F₂ population of the cross BPT5204 x NLR33892 were given in Table 1. The parents mean values, highest and lowest plant values in F₂ population were there in Table 2. A broad range of phenotypes were observed in the F₂ population. This variation clearly shows that these characters are controlled by poly genes and the genes/alleles controlling these characters are seem to act in an additive manner which is polygenic inheritance. High variability in rice F₂ population was reported by Balat *et al.*, 2018, Kiran *et al.*, 2012 and Ratnakar *et al.*, 2012 [2, 9, 10] for biological yield, number of tillers and grain yield characters.

Table 1: Transgressive segregants observed in F₂ generation of cross between BPT5204 and NLR33892

S. No	Trait	No. of “Transgressive segregants” in F ₂ (Population size = 686)	
		< Lesser parent value	> Higher parent value
1	PH	111 (16.18%)	53 (7.73%)
2	NPP	383 (55.83%)	111 (16.18%)
3	PL	62 (9.04%)	131 (19.10%)
4	NGP	317 (46.21%)	72 (10.50%)
5	SF	357 (52.04%)	110 (16.03%)
6	Yield (g)	256 (37.32%)	148 (21.57%)
7	TGW	119 (17.35%)	195 (28.43%)
8	GL	255 (37.17%)	136 (19.83%)
9	GW	208 (30.32%)	48 (7%)

PH-Plant height (cm); NPP- No. of panicles per plant; PL- Panicle length (cm); NGP-Number of grains per panicle; SF-spikelet fertility (%); Yield- grain yield/plant (g); TGW-Thousand grain weight (g); GL-Grain Length (cm); GW-Grain width (cm).

F₂ plants that crossed the parental values for *viz.*, plant height (PH), NGP, panicle length (PL), NPP, spikelet fertility (SF), grain yield per plant, TGW, grain length (GL) and width (GW) were observed. Transgressive segregants that are over both the parents in the F₂ population of a cross between two parents, Basmati 370 and Jaya for number of filled grains, PL,

SF% and for yield were reported by Reddy, 2008 [11]. It has shown that the parents had different alleles governing yield related traits. Hence the scope or opportunity to bring in favourable alleles into one plant through careful selection in the next generations is more.

Table 2: Parents mean values, highest and lowest plant values for selected traits in F₂ population

Trait	Parents		F ₂ population of BPT 5204 X NLR33892 cross		
	“BPT5204”	“NLR33892”	No. of plants scored	Highest plant value	Lowest plant value
PH	97.5	133.67	686	147	68
NPP	7.53	9.67	686	19	2
PL	25.03	27.13	686	29	18
NGP	234.87	382	686	458	29
SF	97.01	94.20	686	98.2	79.3
Yield	21.9	26.63	686	68.1	4.4
TGW	13.65	17.83	686	21.8	8.9
GL	7.6	7.4	686	8.1	6.1
GW	2.38	2.47	686	2.6	1.9

PH-Plant height (cm); NPP- No. of panicles per plant; PL- Panicle length (cm); NGP-Number of grains per panicle; SF-spikelet fertility (%); Yield- grain yield/plant (g); TGW-Thousand grain weight (g); GL-Grain Length (cm); GW-Grain width (cm).

In this study high number of favourable transgressive segregants (TS's) were observed for PL and for TGW. The transgressive segregants with < lowest parent value were high in NPP, PH, NGP, SF%, GL and yield per plant. Transgressive segregants with > highest parent were high in panicle length and TGW. Occurrence of such extreme phenotypes is possibly due to the complementary alleles accumulation from both the parents in certain F₂ population and unmasking of the recessive deleterious alleles (Rick and Smith 1953).

The individual plants with desirable characters like long PL, more NPP, high NGP, high yield per plant, high TGW and long grain length were selected phenotypically and those selected plants were advanced to F₃ and F₄ generations for further evaluation.

Conclusion

High number of favourable transgressive segregants were observed for yield related traits. There is a chance to bring in all the favourable alleles into a single individual plant through careful selection in the future generations. Maximum genotypic variation present in the F₂ population gives the opportunity for individual plants selection, which may help in the development of a new variety. The single plants with more number of favourable traits can be selected in F₂, which can be used for the development of a new variety which is of great contribution to increase the rice production.

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