

Original Research Article

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## Transgressive Segregation for Yield and its Component Traits in Rice (*Oryza sativa* L.)

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### ABSTRACT

Transgressive segregation produces hybrid progeny phenotypes that exceed the parental phenotypes. Unlike heterosis, extreme phenotypes caused by transgressive segregation are heritably stable. Maximum genetic variation in F<sub>2</sub> generation provides the first opportunity for selection of individual plants, any one of which may end up into a new cultivar. F<sub>2</sub> plants that surpassed the parental limits were observed in both the crosses for all the traits viz., plant height, number of panicles per plant, panicle length, number of grains per panicle, spikelet fertility, biomass per plant, grain yield per plant, harvest index and 1000 grain weight. High frequency of favourable transgressive segregants were observed for plant height and number of grains per panicle in the cross between BPT5204 and NLR33892, whereas BPT5204 x NLR33892 cross recorded higher number of desirable transgressive segregants spikelet fertility. Polygenic inheritance and high frequencies of favourable transgressive segregants for yield and its component traits indicates there is a lot of scope to bring in beneficial alleles into a single genotype through careful selection in later generations.

#### Keywords

Rice (*Oryza sativa* L.), Transgressive segregants

#### Article Info

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### Introduction

Rice (*Oryza sativa* L.) is the primary staple food in many countries and is one of the most important cereal crops grown all over the world. Globally, rice was occupying an area of an area of 162.97 million hectares with a production of 495.03 million tonnes and productivity of 4530 kg ha<sup>-1</sup> in 2017-18 (World Agricultural Production, USDA, May 2019). During 2017-18, in India rice

cultivation was done in an area of 42.95 million hectares with a production and productivity of 112.91 million tonnes and 2585 kg ha<sup>-1</sup>, respectively. In Andhra Pradesh, it is grown in an area of 2.15 million hectares with a production of 8.05 million tonnes and productivity of 3741 kg ha<sup>-1</sup> (<https://www.indiaagristat.com/>). Current global yield increase rates (1.0% per year) of rice are insufficient to meet food demand for the estimated nine billion people in 2050

(Khush, 2005; Ray *et al.*, 2013). Major constraints for productivity and sustainability of rice in the country are the inefficient use of inputs such as fertilizer, water and labour coupled with new emerging challenges from climate change, rising fuel prices, increasing cost of cultivation, and socioeconomic changes such as migration of labour, urbanization, least affected towards agricultural work by youth, and concern from environmental pollution. The only way to sustain rice production for meeting the increasing population demand is to increase the productivity per unit of area of rice with enhanced resource use efficiency.

The rice yield is a complex trait and is mainly determined by three key component traits *viz.*, grain number per panicle, number of panicles per plant (productive tillers) and grain weight or grain size. Number of panicles is in turn dependent on the tillering ability including primary, secondary, and tertiary tillers per plant. Likewise, number of grains per panicle can also be relying on two subcomponents: number of spikelets per panicle and seed setting rate of the spikelets. Grain weight is largely determined by grain size, which is specified by its three grain dimensions (grain length, grain width, and grain thickness), and the degree of grain filling. These yield and its component traits are quantitatively inherited (Allard, 1960; Hallauer and Miranda, 1988) and controlled by many genes (Thoday, 1961) with small effects often regarded as Quantitative Trait Locus (QTL) (Geldermann, 1975).

Transgressive segregation is often observed for quantitative traits in the offspring of both intraspecific and interspecific hybrids. Transgressive segregation produces hybrid progeny phenotypes that are better than the parental phenotypes with respect to one or more characters. Transgressive segregation is often associated with recombinations,

chromosome rearrangements, transposable element mobilization, DNA methylation and changes to gene expression. Success in obtaining the desired transgressive segregants depends on obtaining genetic recombination between both linked and unlinked alleles (Briggs and Allard, 1953). F<sub>2</sub> generation represents maximum genetic variation and provides the first opportunity for selection of individual plants, any one of which may end up into a new cultivar. Unlike F<sub>1</sub> hybrid rice cultivation where farmers buy new seeds every cropping season, transgressive lines would be an inbred. The selection of these phenotypes in segregating hybrid populations may be a major source of novel adaptations in hybrids. Careful selection and identification of these phenotypes are of great contributions to increasing rice production.

Keeping in view of the importance of transgressive segregants, the present investigation was made to identify transgressive segregants for yield and yield attributes in F<sub>2</sub> population of two crosses derived by crossing a popular semi-dwarf, high-yielding and fine grain variety with good cooking quality variety, Samba Mashuri (BPT5204) with Prabhat (MTU3626) having high grain weight and Pardhiva (NLR33892) with long panicle and high grain number per panicle.

## **Materials and Methods**

The base material for the present investigation includes three high yielding varieties of rice *viz.*, Samba Mashuri (BPT5204), Prabhat (MTU3626) and Pardhiva (NLR33892) which were used as parents to develop F<sub>2</sub> populations. Varietal characteristics of parents were presented in Table 1 and Figure 1. During *kharif*, 2016 Samba Mashuri (BPT5204) was crossed with two male parents Prabhat (High grain weight) and Pardhiva (Large Panicle length and high grain

number) to develop F<sub>1</sub> seeds. F<sub>1</sub> plants of two crosses were selfed to produce F<sub>2</sub> seed in *rabi*, 2016-17. F<sub>2</sub> population of two crosses was evaluated phenotypically for yield and its components traits along with parents during *khariif*, 2017 at wetland farm, S. V. Agricultural College, Tirupati. Mature plants were harvested individually. Data was recorded on yield and yield attributed *viz.*, plant height, number of panicles per plant, panicle length, number of grains per panicle, spikelet fertility, biomass per plant, grain yield per plant, harvest index and 1000 grain weight in 280 randomly selected F<sub>2</sub> plants in each cross and 30 plants in each parent.

In the present study, transgressive segregants were identified by finding the number of plants exceeding mean value of the higher parent or lagging behind the mean value of the lower parent by critical difference at 5 percent level.

## Results and Discussion

Transgressive segregation produces hybrid progeny phenotypes that are superior to the parental phenotypes. Such plants are produced by accumulation of favourable genes from both the parents as a consequence of segregation and recombination. Unlike heterosis, extreme phenotypes caused by transgressive segregation are heritably stable. Kshirsagar *et al.*, 2013 suggested that transgressive segregation can be exploited for development of genotypes with positive characters from both the parents. Transgressive segregants for yield and its component traits in F<sub>2</sub> population of the crosses BPT5204 x MTU3626 and BPT5204 x NLR33892 were presented in Table 2 and 3, respectively. The F<sub>2</sub> mean value was in-between the parents for all the characters except for harvest index in BPT5204 x MTU3626 and for all the traits in BPT5204 x NLR33892 cross. In both the crosses wide

range of phenotypes were observed for all the characters in the F<sub>2</sub>. This clearly suggests that all traits were governed by many genes and alleles governing these traits seem to act in additive manner showing polygenic inheritance. High variability for number of tillers, biological yield and grain yield in F<sub>2</sub> populations of rice was reported by Balat *et al.*, 2018, Kiran *et al.*, 2012 and Ratnakar *et al.*, 2012.

F<sub>2</sub> plants that surpassed the parental limits were observed in both the crosses for all the traits *viz.*, plant height, number of panicles per plant, panicle length, number of grains per panicle, spikelet fertility, biomass per plant, grain yield per plant, harvest index and 1000 grain weight. Reddy, 2008 reported transgressive segregants over both the parents for panicle length, filled grains, spikelet number, spikelet fertility and single plant yield in Basmati370 x Jaya F<sub>2</sub> population. This clearly indicates that the parents had different alleles and genes governing yield and its component traits. Hence, there is a lot of scope to bring in beneficial alleles into a single genotype through rigorous selection in later generations for yield and yield attributes. High frequency of favourable transgressive segregants were observed for plant height and number of grains per panicle in the cross between BPT5204 and NLR33892, whereas BPT5204 x NLR33892 cross recorded higher number of desirable transgressive segregants spikelet fertility. Transgressive segregants with lower value than lowest parent were high in number of panicles per plant, panicle length, spikelet fertility, biomass per plant, grain yield per plant and harvest index for the cross between BPT5204 and MTU3626. In BPT5204 x NLR33892 cross, number of panicles per plant, biomass per plant, grain yield per plant and harvest index recorded higher number of lowest value transgressive segregants.

**Table.1** Salient Features of Parents used in developing F<sub>2</sub> populations

S. No.	Variety	Pedigree	Duration	Thousand Grain Weight (g)	Year of release	Characters
1	SambaMashuri (BPT5204)	(GEB24xTN-1) x Mahsuri	140-145 days	13	1986, Bapatla, A.P., India	Medium slender grains, non-lodging open type canopy with dark green erect short leaves. Fine grain variety with excellent cooking quality. Susceptible to blast and bacterial leaf blight.
2	Prabhat (MTU3626)	IRB x MTU 3	130-135 days	28	1976, RARS, Maruteru	Bold seeded high yielding variety. Non lodging, suitable for direct seeding and suitable for parboiled rice.
3	Pardhiva (NLR33892)	Tikkana x MTU 4870	155-160 days	17	2007 ARS, Nellore	Long duration, highly Photosensitive variety with 28cm panicle length and around 350-400 grains per panicle. Resistant to blast.

**Table.2** Transgressive segregants for yield and its component traits in F<sub>2</sub> population of the cross between BPT 5204 and MTU 3626

Trait	F <sub>2</sub> Generation of BPT 5204 X MTU 3626 cross				Parents		No. of Transgressive Segregants	
	Total No. of Plants Scored	Mean	Highest Plant Value	Lowest Plant Value	BPT5204	MTU3626	Higher than Highest Parent	Lower Than Lowest Parent
Plant height (cm)	280	95	119	71	95.17	88.17	103	73
Number of panicles per plant	280	7.05	23	2	9.53	7.17	25	203
Panicle length (cm)	280	24.11	30	17	24.52	26.53	19	188
Number of grains per panicle	280	243.30	420	93	234.19	194.3	102	86
Spikelet fertility (%)	280	68.48	96.15	4.55	87.99	85.13	9	253
Biomass per plant (g/plant)	280	43.72	130.9	12.3	48.02	35.1	50	142
Seed yield per plant (g/plant)	280	16.48	90.6	1.51	22.4	15.6	18	234
Harvest index (%)	280	39.19	75.97	5.67	46.72	44.51	35	237
1000 grain weight (g)	280	25.89	33	12	13.23	29.2	2	3

**Table.3** Transgressive segregants for yield and its component traits in F<sub>2</sub> population of the cross between BPT 5204 and NLR33892

Trait	F <sub>2</sub> Generation of BPT 5204 X MTU 3626 cross				Parents		No. of Transgressive Segregants	
	Total No. of Plants Scored	Mean	Highest Plant Value	Lowest Plant Value	BPT5204	NLR33892	Higher than Highest Parent	Lower Than Lowest Parent
Plant height (cm)	280	110.48	140	70	95.17	137.85	2	32
Number of panicles per plant	280	6.17	20	2	9.53	7.53	33	220
Panicle length (cm)	280	25.82	32	18	24.52	29.23	20	75
Number of grains per panicle	280	310.10	582	125	234.19	389.37	27	46
Spikelet fertility (%)	280	85.23	92.44	63.87	87.99	83.79	87	85
Biomass per plant (g/plant)	280	41.84	103.4	17.6	48.02	64.24	24	196
Seed yield per plant (g/plant)	280	15.44	40	4.9	22.4	24.9	20	252
Harvest index (%)	280	36.45	62.01	18.37	46.72	38.65	17	163
1000 grain weight (g)	280	14.77	18	12	13.23	17.23	38	71

**Fig.1** Variation in panicle characters of parents and their F<sub>1</sub>s of BPT5204 x MTU3626 and BPT5204 x NLR33892 crosses



Occurrence of such transgressions is possibly due to accumulation of complementary alleles from both the parents at multiple loci in certain F<sub>2</sub> population (Tanksley, 1993) and unmasking of recessive deleterious alleles due to inbreeding (Rick and Smith 1953).

Polygenic inheritance and high frequencies of favourable transgressive segregants for yield and its component traits indicates there is a lot of scope to bring in beneficial alleles into a single genotype through careful selection in later generations and identification of plants with many desirable traits are of great contributions to increasing rice production.

## References

- Allard RW. 1960. Principles of plant breeding. *John Wiley and sons*, Inc, New York.
- Balat, J.R., Patel, V.P., Visat, M.L. and Bhagora, R.N., Variability analysis in F<sub>2</sub> population of rice (*Oryza sativa* L.) for yield and related traits. *Int. J. Pure App. Biosci.* 6(1): 1021-1027 (2018)
- Briggs, F.N., Allard, R.W. 1953. The current status of the backcross method of plant breeding. *Agron. J.*, vol. 45, pp. 131-138.
- Geldermann H. 1975. Investigations on inheritance of quantitative characters in animals by gene markers. I. Methods. *Theor Appl. Genet.* 46: 319-330.
- Hallauer AR and Miranda JB. 1998. Quantitative genetics in maize breeding. *Iowa state university press*, Ames, Iowa  
<https://www.indiaagriscistat.com/>
- Khush, G.S. 2005. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology.* 59(1):1–6.
- Kiran, K. K., Gururaja Rao, M. R., Rajanna, M. P., Rao, M. A., Mahadevu, P. and Siddegowda, D. K., Variability, Heritability and Genetic Advance Studies in F<sub>2</sub> Populations of Two Crosses of Rice (*Oryza sativa* L.). *Mysore J. Agric. Sci.*, 46 (4): 917-919 (2012)
- Kshirsagar, D.B., Bhalekar, M.N., Patil, R.S., Kute, N.S and Patil, S.B. 2013. Transgressive segregation in F<sub>3</sub> generation of intervarietal crosses of tomato (*Solanum lycopersicon* L.). *Vegetable science.* 40(2): 240-242.
- Ratnakar, M. S., Rajanna, M. P., Ramesh, S., Sheshshayee, M. S. and Mahadevu, P., Genetic variability, correlation and path coefficient studies in F<sub>2</sub> generation of aerobic rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 3 (3): 925-931 (2012).
- Ray, D.K., Mueller, N.D., West, P.C and Foley, J.A. 2013. Yield trends are insufficient to double global crop production by 2050. *PLOS One.* 8(6):e66428.
- Reddy, VLN. 2008. QTL Mapping of Economically Important Traits and DNA based Detection and Quantification of Adulteration of Basmati rice (*Oryza sativa* L.). *Ph. D Thesis.* School of Life Sciences, University of Hyderabad, Hyderabad – 500 046, India
- Rick CM and Smith PG (1953) Novel variation in tomato species hybrids. *Am. Nat.* 88.
- Tanksley, S. D. (1993). Mapping Polygenes. *Annual Review of Genetics*, 27(1), 205–233
- Thoday JM. 1961. Location of polygenes. *Nature* 191: 368-370
- World Agricultural Production, USDA, May 2019

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