Identification of transgressive segregants for yield and yield attributing traits in F_2 population obtained from the cross between Naveen x IR 64 Drt1.

Comment [I1]:

ABSTRACT

Not all crosses display it, and only a small proportion of progeny in any particular cross may be transgressive, but it occurs frequently enough that plant breeding works as a matter of routine. The traditional thinking in plant breeding holds that transgressive segregants are the most rare individuals in the population. However, depending on the level or clarity with which the phenotypic is investigated, it is reasonable to believe that this phenomenon may be more widespread in plant breeding populations than is now recognized. In the present study the F_2 segregants that surpassed both the parentals and had higher values than the increasing parent, were observed in the cross (Naveen x IR64 Drt 1) for all the characters viz plant height, number of panicles, panicle length, number of primary branches, number of filled grains, total number of spikelets and 1000 grain weight except for the character number of secondary branches. The maximum number of transgressives were observed for the character panicle length for the cross Naveen x IR 64 Drt1.

INTRODUCTION

Rice, along with wheat and maize, is one of the world's most extensively produced cereals. Over 400 million small farmers and 15% of the world's arable land are involved in producing global rice. Among them Asia alone produces 90% of the world's rice, rest 10% of rice produced is traded globally. Since the end of the 1980s, the tremendous expansion of rice production that had been observed for nearly 50 years has slowed down significantly. Today, consumption is steadily rising, and rice growth is confronted with significant new obstacles. Everyyear,therice dependent populationincreasesbynearly50million. And thus to fulfill the basic demand of food by this rising population, there is the utmost necessity to increasein the production of rice even on by small marginal lands, by fewer people using less water and fewer chemical inputs.The identification of developmental process of transgressive segregants can aid in the breeding programs for crop improvement and pave paths for meeting with the demands of the rising population(16). The importance of transgressive segregation in crop improvement is not only described, as it provides opportunity for the development of new hybrids species that have superior genetic combination of the parents that are more fit and stable, and having performance better than both the parent, but the transgressive segregants can be further used to create ideal plant species that are more adaptable and resistant to various environmental stresses, so ultimately the occurrenceof transgressive

Comment [I2]: in abstract please include what kind of design did you use segregants not only facilitates in the crop improvement, also these events create genotypes which are more fit than the existing. These extreme phenotypes can be introduced to wide range of environmental conditions where the parental lines cannot to survive (5,18).

Transgressuvesegregants are the extreme phenotypes observed in the segregating populations, which are heritably stable unlike the extreme heterotic phenotypes. The trangressive hybrids which are known to have new multiple genes combination, that surpasses both the parents with more positive or negative effects for yield and yield attributing traits. It is frequently seen in the progeny of both interspecific and intraspecific crossings. Rick and Smith (1953) proposed three potential explanations for the occurrence of interspecific transgression, including de novo mutation caused by hybridization, complementary action of genes from the two parental species, and unmasking of recessive genes typically held heterozygous in the wild species (8,10). The occurrence of the transgressive segregants via de novo mutation are proven in the study of Drosophila strains wherethe activation of dormant transposable elements caused the mutation to occur and thus the occurrence of transgressive hybrids (2). Other experiments conducted on a wide range of plant species have shown evidence for the acceptances of both of the latter two possibilities. The phenotypes of hybrid transgressives are superior to those of the parents as a result of transgressive segregation. Transgressive segregants in hybrid progenies have been documented by many plant breeders, who also proposed that transgressive segregation might be exploited as a useful tool in plant breeding. The traditional concept of hybridization is to mix the favourable traits already present in two parents to create a new derivative (14). Transgressive segregation could be a more creative method to plant breeding. As a result, transgression segregation is used in transgressive breeding to improve yield or its contributing characteristics. When a vast number of physiological components are anticipated to be involved, the recently suggested Omnigenic Theory opens an alternative way to explain the most crucial interactions underpinning transgressive phenotypes (1; 7). This hypothesis characterises quantitative features in terms of both additive and non-additive contributions from a small number of large-effect core loci and hundreds of minute-effect peripheral loci spread across the genome. We further hypothesised that the superiority or inferiority of transgressive segregants is owing to ideal or non-ideal coupling-uncoupling of different compatible and incompatible biochemical, developmental, and physiological properties encoded by the core and peripheral loci from each parent. These pathways result in physiological gain or drag, determining whether specific individuals have positive or negative net gains (3; 10).

Comment [I3]: pl correct the spelling

The present study was taken up for the identification of transgressive segregants based on the number of segregants having mean values for different yield attributing characters more than the increasing parent or lower than the decreasing parent by the critical differences at 5 percent level and 95% confidence level..

MATERIALS AND METHOD

The study was conducted on the F_2 generation in the rice research field, under the department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Jharkhand. The segreganting material used for the study was obtained from the cross between Naveen x IR 64 Drt1 from which the F_2 population was developed using the hybrid generation, for which the F_1 plants obtained after the cross were selfed in the rabi season of 2020-2021. The F_2 seeds thus obtained from the previous season along with the parents were space planted and were raised in the year 2022-2023 with the spacing of 20 cm x 20cm. The segregating population and the parents was phenotypically evaluated for yielding traits like plant height, number of panicles, length of panicle, number of primary and secondary branches, number of filled grains, total number of grains and test (1000 grain) weight. The data were recorded on 607 randomly selected segregants and 10 plants each for each of the parents.

RESULT AND DISCUSSION

Under the study all the characters namely plant height, number of panicles, number of primary branches, number of secondary branches, number of filled grains, total number of grains and test (1000 grain) weight were observed to portray high variability. in the present study the mean performances of the segregating F_2 generation was observed to be lower than the mean performances of both the parents for the characters like secondary branches and 1000 test weight. and for other characters like plant height, number of panicles, length of panicle, number of primary branches, number of filled grains and total number of grains the mean values were between the parents. all the characters were observed to have wide range of phenotypes for the cross Naveen x IR 64 Drt1(as seen in table 1.), which suggests that all the traits under the study are polygenic in nature and the alleles governing these characters have an additive gene action for their polygenic inheritances. Thus one can say that genetic variability is determined by multiple genes and these genes ultimately contribute additively to the phenotype of the genotypes. The occurance of transgressive segregants in any cross is possible only when one parent is fixed for increasing alleles at a proportion of the genetic loci, and the other parent is fixed for increasing alleles at the remainder or the another proportion of the genetic loci. and so the transgressive segregants or in general an improved progeny can then be selected which will be fixed for a greater number of increasing alleles than the better parent due to the process of recombination.

This simple explanation has its own strength as this explanation fits in many cases with the observed patterns of genetic segregation and genetic improvement. Transgressive variance is a potential source of unique genetic variation in crop improvement. Because polygenic systems control the majority of critical traits in domestic plants, detecting allele dispersion can aid in the selection of favourable new germplasm. It is extremely simple to obtain stable extreme strains for quantitative features regulated by a few genes with additive effects (9,14). It is typical in plant breeding to not screen genetic populations for certain features unless one of the parents has a superior phenotype for that trait. However, it is widely recognised that phenotype alone is not an acceptable predictor of an individual's genuine potential as a genetic donor due to the possibility of positive or negative combintorial effects (4).

In the present study the F_2 segregants that surpassed both the parentals and had higher values than the increasing parent, were observed in the cross (Naveen x IR64 Drt 1) for all the characters viz plant height, number of panicles, panicle length, number of primary branches, number of filled grains, total number of spikelets and 1000 grain weight except for the character number of secondary branches. The highest number of transgressive segregants were observed for panicle length, where the segregants observed supassed both the parents. The presences of transgressive segregants in the present segregating F_2 population in the cross between Naveen x IR 64 Drt 1 suggests that both the parents NaveenandIR 64 Drt differed in the genes and alleles governing the yielding traits, which increased the scope of bringing in the beneficial alleles into one individual genotype which is thus identified through intensive rigorous selection process.

Similarly the extreme phenotypes or the transgressive segregants lower than the lowest parents were observed for all the characters under study, with the characters like number of primary branches, number of filled grains and total number of grains having the highest frequency of lowest value transgressive segregants in the cross between Naveen x IR 64 Drt1. The higher frequency of lower value segregants than the higher value segregants indicates the accumulation of majority of the alleles with complementary gene action from both the parents at multiple and majority of the genetic loci accompanied by the unmasked deleterious recessive alleles due to the phenomenon of inbreeding. These consequences as discussed earlier can be the contribution of genome shock or exon shuffling (11; 1), which could possibly lead to novel gene products with new functions (12). Other works done also suggested that altered DNA methylation site causes random gene silencing or reactivation of silenced genes, which could may be responsible at least in part to the non-additive transcriptome signatures that are often observed in interspecies hybrids which is known as transcriptome shock (6).

Table 1: Morphological characteristic of transgressive segregants of F_2 population for yield and yield attributing traits for the cross Naveen x IR 64 Drt1

Comment [I4]: pl correct the table title

		F_2 GENERATION OF NAVEEN X IR 64 DRT 1 CROSS				PARENTS		NO. OF TRANSGRESSIVE SEGREGANTS	
Sl.no	TRAIT	TOTAL NO. OF PLANTS SCORED	MEAN	HIGHEST PLANT VALUE	LOWEST PLANT VALUE	NAVEEN	IR 64 DRT1	HIGHER THAN HIGEST PARENT	LOWER THAN LOWEST PARENT VALUE
1	PH	607	79.34778	163	46	111.84	123.26	4	599
2	NP	607	6.283361	21	1	13.37	11.6	4	1
3	PL	607	20.30511	46	10	24.60	23.39	27	553
4	PB	607	8.400329	19	4	16.00	15.6	1	606
5	SB	607	14.07084	46	2	54.00	48	0	607
6	FG	607	69.35091	208	10	192.14	180.8	2	605
7	TNG	607	79.46458	229	15	196.20	183.5	4	602
8	TGW	607	7.395748	36.7	0.02	32.16	28.59	9	577

PH- plant height, NP- number of panicles, PL-panicle length, PB- number of primar branches, SB- number of secondary branches, FG-number of filled grains, TNG-total number of grains, TGW-test weight.

CONCLUSION

Breeding is accomplished by crossing parents, who are frequently cultivated varieties, and selecting improved recombinant progeny. Plant breeding would be useless if no children (or descendants) were ever discovered that were better than their parents (or ancestors). Transgressive segregation refers to the property of progeny falling outside the range of the parents. Not all crosses display it, and only a small proportion of progeny in any particular cross may be transgressive, but it occurs frequently enough that plant breeding works as a matter of routine. The traditional thinking in plant breeding holds that transgressive segregants are the most rare individuals in the population. However, depending on the level or clarity with which the phenotypic is investigated, it is reasonable to believe that this phenomena may be more widespread in plant breeding populations than is now recognized.

Comment [I5]: pl improve the conclusion

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