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Identification and genetic assessment of transgressive segregants for yield and its contributing traits in wheat (*Triticum aestivum* L.)

Parul Gupta
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India
Ravindra Prasad ✉
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India
Mohit Sharma
Division of Genetics, ICAR- Indian Agricultural Research Institute, New Delhi, India

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ABSTRACT

Two crosses *viz*., K 1006 x LOK 1 and PBW 343 x HUW 234 derived from four diverse parents were examined during *Rabi* 2018-19 and 2019-20 at Agricultural Research Farm, Institute of Agricultural Sciences, BHU in order to identify and assess the robust transgressive segregants (TS) in the segregating F_2 and F_3 population for yield/plant and its contributing traits respectively. Findings reveal that individuals transgressed beyond the parents in both the crosses for grain yield/plant (9 to 9.52 %). The maximum frequency of TS are found for AL (74.29%) in the PBW 343 x HUW 234 and it was higher for 1000 grain weight (72%) in the K 1006 x LOK 1 cross. The highest number of simultaneous TS for grain yield/plant was found in the F_2 for the PBW 343 x HUW 234 (89.5%) followed by K 1006 x LOK 1 (79.0%). The frequency of simultaneous transgression for grain yield coupled with SLPS, GPS, 1000 GW in K 1006 x LOK 1 cross along with NET and AL in PBW 343 x HUW 234 cross was found very frequently. Hence, it is presumed that either grain yield is dependent on these traits or there may be linkage drag among the genes for such traits so that responsible gene(s) could be inherited together. The most promising TS tagged in F_2's were plant No. 36 in the K 1006 x LOK 1 and plant No. 30, 68 and 100 in the other cross. Based on high frequency of TS, it is inferred that transgressive breeding could be used as an excellent tool to improve the crop yield and other desirable traits by recovering the transgressive segregants.

Introduction

Among the cereal crops, wheat (*Triticum aestivum* L.) is considered as one of the most economically important crop as it is widely grown and consumed by large people (Prasad, 2022). Poudel *et al.*(2020) also stated that wheat is one of the major as well as the most consumed cereal crops in the world. Production of wheat supports almost 35 percent of the world's population (Mohammadi-joo*et al.,* 2015) and it is known as one of the most economically essential cereal crops in the world as well (Bedada *et al.,* 2022). Published report by Rangare*et al.*(2010) indicates that it is an important cereal crop and accounts about 33 percent of the nation's total food grain production. In India, it is cultivated in an area of 31.6 mha with the production of 108.75 mt of wheat grain with productivity of 34.41 quintal per hectare (Department of Agriculture, Cooperation and Farmers Welfare, 2021). There are three wheat species likeBread wheat (*Triticum aestivum*), Macaroni wheat (*Triticum durum*) and Emmer wheat (*Triticum dicoccum*) is widely cultivated in India, comprises of 86, 12 and 2 percent of the total areas of wheat (Ukani *et al.,*2015). Besides having satisfactory crop yield, wheat is also good source of nutritional profile like of protein, minerals, vitamins and dietary fiber (Kumar *et al.,*2011; Prasad, 2022; Rashmi *et al.,* 2022). Since, human population is continuously increasing as compared to the total population remained at the time of green

Corresponding author E-mail: *rprasadbhugpb@gmail.com*
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revolution so, in parallel because efforts of scientists, farmers, policymaker and use of updated technology crop yield has been enhanced significantly however, still there is need to improve the crop yield of wheat because of huge demand of rapidly growing population. The ultimate goal of any plant breeding program is to develop the potential and reliable genotypes/cultivars perform better across the environments. The selection of the parent for hybridization in order to develop the superior genotypes is depending to great extent on great adaptation, with considerable yield potential. Plant progeny derived from diverse crosses are expected to throw a wide range of heterogeneity, thereby providing better scope for the isolation of high yielding segregants in the segregating generations.Transgressive segregants in F_2 population may be selected because of accumulation of favorable genes for trait of interest from the parents involved in hybridization (Putri *et al*., 2020). The F_2 generation depicts maximum genetic variation and furnished the first opportunity for selection of individual plants, any one of which may end up into a new cultivar (Reddyyamini *et.al.* 2019). Hence, transgressive breeding could be used as a robust approach to improve the yield and its associated traits by recovering/accumulating the linked genes in tothe segregating plants (Singh, 2000). Exploring the information about the transgressive segregants also helps to find out their proportions for desirable genes responsible for yield and its contributing traitsbecause the traits having high heritability would be very usefulfor population improvement for targeted traits and other future breeding programmes. It is therefore, plant breeders/researchers are more concerned with getting the higher frequency of transgressive segregants as it gives a better scope for exercising the selection of superior lines in order to improve the productivity of wheat crops and supplying the demand of rapidly growing population in 21st century.

Material and Methods

The experiment was carried out in the *Rabi* season 2018-19 and 2019-20 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India. F_1 population (seeds) of the two crosses *viz*., K 1006 x LOK 1 and PBW 343 x HUW 234 was obtained from my supervisor and the experimental materials (F_2 generation) of these two crosses along with parents were sownin *Rabi* 2018-19 in un-replicated plots having enough distance. The F_2 plants were grown in 20 rows of 2m length and parents in 4 rows of 2m length. Data were recorded on 100 randomly selected individual plants in cross K 1006 x LOK 1 and 105 plants in PBW 343 x HUW 234 cross and 10 plants in each parent for 15 quantitative traits viz., DF, DM, GFD, NET, SPL, AUSDC (Rosyara *et al*., 2007), AL, PL, MTI (I) at flowering and MTI (II) grain filling stage followed by Blum and Ebercon (1981), PLH, SPLS, GPS, TW and GYPP in each cross.

In second season (*Rabi* 2019-20), 19 transgressive segregants tagged in F_2population (based on yield performance) and four parents were grown with aim to test their performance in F_3 generation in Randomized complete block design (RCBD) in three replications. The recommended agronomic practices were followed to raise the good crops. The parental lines and the F_2 and F_3 plants were sown in the line spaced 22.5 cm apart with plant to plant distance of 10 cm. The mean value of ten randomly selected plants of each F_3 families (transgressive segregants) were compared with performance of F_2 generation for GYPP by using F-test for degree of two variances and two sample t-test for equal mean at (n_1+n_2-2) degree of freedom followed by Dhole and Reddy (2011) using Microsoft excel office.

Results and Discussion

In findings, desirable transgressive segregants found in the studied crosses (K 1006 x LOK 1 and PBW 343 x HUW 234) for all the fifteen traits. The frequency of transgressive segregants was differed from cross to cross presented in table 1a, 1b and figure 1 respectively. For grain yield per plant, 9 to 9.52% individuals transgressed beyond the increasing parents in both the crosses, Dahat *et al*. (2017) reported 51 to 55 percent proportion of variation in transgressive segregants. Similarly, range of transgressive segregants (in %) were 23 to 39.05for DF, 42 to 54.29 for DM, 28 to 48.57 for GFD, 19.05 to 20 for NETs, 51.43 to 62, for AUSDC, 39-42 for MTI (I) at flowering stage, 45.71 - 72.0 for MTI (II) at grain filling stage, 14 -

Table 1a:Frequency of transgressive segregants for 15 traits in F_2 Population of K 1006 × LOK 1 crosses

Trait/ cross	F_2 Generation		Parents		Transgressive Segregants	
	Highest value	Lowest value	Higher value	Lower value	Higher than highest parent	Lower than lowest parent
DF	88	70	83 (K 1006)	78.4 (LOK 1)	23 (23%)	42 (42%)
DM	121	106	116.3 (K 1006)	115.4 (LOK 1)	42 (42%)	54 (54%)
GFD	48	23	37 (LOK 1)	33.3 (K 1006)	28 (28%)	40 (40%)
NETs	14	2	10.7 (K 1006)	9.8 (LOK 1)	20 (20%)	61 (61%)
AUSDC	506	370.5	415.1 (K 1006)	412.15 (LOK 1)	62 (62%)	29 (29%)
MTI-I (flowering)	65.83	33.33	52.94 (LOK 1)	46.57 (K 1006)	42 (42%)	28 (28%)
MTI-II (grain filling)	65.06	36.91	48.63(K 1006)	48.568 (LOK 1)	72 (72%)	28 (28%)
SPL	12.3	4.4	10.16 (K 1006)	8.73 (LOK 1)	14 (14%)	52 (52%)
AL	8.8	1.8	7.25 (LOK 1)	4.15 (K 1006)	4 (4%)	9 (9%)
PL	22.5	8.8	16.1(LOK 1)	15.85 (K 1006)	38 (38%)	57 (57%)
PLH	101	46.2	87.51 (K 1006)	75.17 (LOK 1)	16(16%)	19 (19%)
SLPS	27	11	24.07 (K 1006)	18.876 (LOK 1)	16 (16%)	55 (55%)
GPS	78	35	72.6 (K 1006)	57.5 (LOK 1)	14 (14%)	55 (55%)
1000 GW	50.12	24.72	36.039 (LOK 1)	35.19 (K 1006)	72 (72%)	22 (22%)
GYPP	30.81	4.454	27.336 (K 1006)	20.308 (LOK 1)	9 (9%)	65 (65%)

Table 1b: Frequency of transgressive segregants for 15 traits in F_2 Population of PBW 343 × HUW 234 cross

Trait/ cross	F_2 Generation		Parents		Transgressive Segregants	
	Highest value	Lowest value	Higher value	Lower value	Higher than highest parent	Lower than lowest parent
DF	96	75	88.4 (PBW 343)	81.9 (HUW 234)	41 (39.05%)	33 (31.43%)
DM	125	109	118.7 (PBW 343)	115.5 (HUW234)	57 (54.29%)	17 (16.19%)
GFD	45	17	33.6 (HUW234)	30.3 (PBW 343)	51(48.57%)	41 (39.05%)
NETs	16	4	10.8 (PBW 343)	10.5 (HUW234)	20 (19.05%)	85 (80.95%)
AUSDC	534.5	301	417.1 (HUW234)	414.7 (PBW 343)	54 (51.43%)	50 (47.62%)
MTI I (flowering)	66.58	22.71	50.88 (HUW234)	49.4 (PBW 343)	41(39.05%)	58 (55.24%)
MTI II (grain filling)	63.36	40.71	51.46(PBW 343)	50.02 (HUW234)	48 (45.71%)	50 (47.62%)
SPL	13	4.4	10.34 (PBW 343)	9.57(HUW234)	21 (20%)	71 (67.62%)
AL	9.8	2.2	4.81 (PBW 343)	4.75 (HUW234)	78 (74.29%)	23 (21.90%)
PL	27.6	4.1	14.83 (HUW234)	11.09 (PBW 343)	40 (38.09%)	26 (24.76%)
PLH	113	67.4	91.41(PBW 343)	90.57 (HUW234)	53(50.48%)	49 (46.67%)
SLPS	28	14	23.91(PBW343)	20.81(HUW 234)	33(31.43%)	64(60.95%)
GPS	86	42	72.1 (PBW 343)	62.8 (HUW234)	27 (25.71%)	51 (48.57%)
1000 GW	56.86	29.8	35.75 (PBW 343)	30.42 (HUW234)	72 (68.57%)	3 (2.86%)
GYPP	35.49	6.72	27.84 (PBW 343)	20.06 (HUW234)	10 (9.52%)	63 (60%)

20 for SPL, 4-74.29 for AL, 38-38.09 for PL, 16 - 50 for PLH, 16 - 31.43 for SPLS,14 - 25.71 for GPS, 68.57-72 for 1000 grain weight in both the crosses respectively. Promising transgressive segregants for the traits like spike length, SLPS, GPS, 1000 GW and grain yield per plant which is supported with findings of Mitra and Mehra (2005). Similarly,for PLH, DM, DF, 1000 GW, GPS, SLPS, SPL, productive tiller per plant and effective tillers supported byothers. Publication of Ahmed *et al.* (2022) suggested that identified transgressive segregants have wider range of variations for desirable traits and very useful for crop improvement.The highest proportion of transgressive segregants are remarked for AL (74.29%) followed by 1000 grain weight (68.57 %), AUSDC (51.43%), GFD (48.57 %), PLH (46.67 %), MTI (I) at grain filling stage (45.71 %) in F_2 generation of the PBW 343 x HUW 234.Therefore, it is presumed that, HUW 234(higher parent) contributed desirable allele for AUSDC, GFD, and PLH traits while PBW 343 (higher parent) contributed desirable allele for the trait like AL, 1000 grain weight and MTI (II) at grain filling stage. Similarly, maximum frequency of transgressive segregants identifiedfor 1000 grain weight (72 %), MTI (II) at grain filling stage (72 %), AUSDC (62 %), DM (54 %), days to flowering (42 %) was found in F_2 of cross K 1006 x LOK 1(table 1a). Hence, its appeared that parent K1006 (higher parent) contributed desirable alleles for AUSDC, MTI (II) at grain filling stage while LOK 1contributed desirable alleles for DF, DM, 1000 grain weight. Transgressive segregants having lower value than lower parent was accounted high in GYPP, NET in F_2 of cross K 1006 x LOK 1

Table 2: Frequency distribution of transgressive segregants for yield and combination of traits in F_2 generation in K 1006 x LOK 1 and PBW 343 × HUW 234 crosses

SN	Character(s)	Frequency of transgressive segregants	
	Grain yield with other traits	K 1006 x LOK 1	PBW 343 × HUW 234
1	DF	6(6%)	6(5.71%)
2	DM	5(5%)	2(1.90%)
3	GFD	3(3%)	7(6.67%)
4	NETs	4(4%)	9(8.57%)
5	AUSDC	5(5%)	6(5.71%)
6	MSI I (Flowering stage)	3(3%)	2(1.90%)
7	MSI II (Grain filling stage)	5(5%)	5(4.76%)
8	SPL	3(3%)	2(1.90%)
9	AL	-	7(6.67%)
10	PLH	-	2(1.90%)
11	PL	5(5%)	7(6.67%)
12	SLPS	6(6%)	3(2.86%)
13	GPS	3(3%)	2(1.90%)
14	1000 Grain Weight	9(9%)	9(8.57%)
15	GYPP	9(9%)	10(9.52%)
16	DF+DM+GFD+NET	-	2(1.90%)
17	DF+AUSDC+MTI(I)+MTI(II)	-	-
18	DF+SPL+AL+PLH+PL	-	-
19	DF+SLPS+GPS+TW	1(1%)	-
20	DM+AUSDC+MTI(I)+MTI(II)	-	-
21	DM+SPL+AL+PLH+PL	-	-
22	DM+SLPS+GPS+TW	2(2%)	-
23	GFD+MTI(I)+MTI(II)+AUSDC	-	-
24	GFD+SPL+AL+PLH+PL	-	-
25.	GFD+SLPS+GPS+TW	1(1%)	-
26	NET+AUSDC+MTI(I)+MTI(II)	-	-
27	NET+SPL+AL+PLH+PL	-	-
28	NET+SLPS+GPS+TW	1(1%)	1(0.95%)
29	AUSDC+MTI(I)+MTI(II)+SPL	-	-
30	AUSDC+AL+PLH+PL	-	1(0.95%)
31	AUSDC+SLPS+GPS+TW	1(1%)	1(0.95%)
32	MTI(I)+MTI(II)+SPL+AL	-	1(0.95%)
33	MTI(I)+MTI(II)+PLH+PL	-	-
34	MTI(I)+MTI(II)+SLPS+GPS+TW	1(1%)	1(0.95%)
35	SPL+AL+PLH+PL	-	-
36	SPL+SLPS+GPS+TW	2(2%)	2(1.90%)
37	AL+PLH+PL	-	1(0.95%)
38	AL+SLPS+GPS+TW	-	1(0.95%)
39	PLH+PL+SLPS+GPS+TW	-	-
40	PL+SLPS+GPS+TW	1(1%)	2(1.90%)
41	SLPS+GPS+TW	3(3%)	2(1.90%)
	Total transgressive segregants	(79)79%	(94) 89.52%

Table 3: Promising transgressive segregants in F_3 having combination of desirable traits in the cross K 1006 xLOK1

SN	Transgressive Segregants	Grain Yield Per Plant (GYPP) in combination with	Combination of desirable traits with GYPP
1	L2	DF, DM, AUSDC, TW	4
2	L6	DF, GFD, NET, AUSDC, PL, MTI(II), TW	7
3	L25	DM, SPLS, GPS, TW, MTI(I)	5
4	L36	DF, DM, NET, SPL, PL, SPLS, GPS, TW, MTI (I), MTI(II)	10
5	L59	DF, DM, NET, SPLS, GPS, MTI(II), TW	7
6	L88	GFD, SPL, AUSDC, SPLS, MTI(II), TW	6
7	L89	AUSDC, PL, SPLS, TW	4
8	L91	DF, GFD, NET, AUSDC, PL, MTI(II), TW	7
9	L96	DF, DM, SPL, PL, SPLS, MTI(I), TW	7

while for NET and SPL in of cross PBW 343 x HUW 234 respectively. Appearance or occurrence of such transgressions may be due accumulation of matching alleles comes from the parents and unmasking of recessive harmful alleles as well as inbreeding (Reddyyamini *et al*., 2019). The highest proportion of simultaneous transgressive segregation for GYPP i.e., 94 (89.52 %) was observed in F_2 population for the cross of PBW 343 x HUW 234) and 79 (79%) in the F_2 for the cross K 1006 x LOK 1. In majority of individuals, where better parent yield was transgressed, there was simultaneous transgression for one or more of yield contributing traits like SLPS, GPS, 1000 grain weight (40 out of 79 individuals in F_2 of the crossK 1006 x LOK 1 while SLPS, GPS, 1000 grain weight along with NET and AL (55 individuals out of 94 in F_2 of cross PBW 343 x HUW 234) demonstrating reliance of GYPP on above said characters in both the crosses or there might be linkage drag among genes of attributes. Dependency or linkage drag has extraordinary significance in plant breeding for synchronous improvement because plant yield is the complex trait and also come in the category of dependent variable so, exploring of its contributing key component/traits/dependency in order to enhancing the crop yield/output should be main priority of the plant breeders, such findings are agreed with Al-Bakry*et al.* (2011); Kadam *et al*. (2017) and Dahat*et al*. (2017). Plant No. 36 (F_2) was found to be most potential transgressive segregant having combination of desirable traits for GYPP in addition to higher intensity of expression for DF, DM, NET, MTI (I) at flowering stage MTI (II) at grain filling stage, SPL, PL, SLPS, GPS, 1000 grain weight (table 3). In F_2 population of the cross PBW 343 x HUW 234, plant No.100 , 68 and 30 accounted to be most worth noting transgressive segregant which surpassed the better parent in terms of yield, in addition to DF, DM, GFD, NET, AUSDC, AL, PLH, TW along with PL, SPL, SPLS, GPS MTI(I), MTI (II) respectively(table 4). Further assessment is needed for improvement of the most promising transgressive segregants as it is shown that when optimal intensity of a trait is not available in the parents, transgressive breeding can be used to expand the limit of the character. The achievements of obtaining the desired transgressive segregants rely on obtaining genetic recombination between linked and unlinked alleles.

Table 4:Promising transgressive segregants in F_3having combination of desirable traits in cross PBW 343× HUW 234

SN	Transgressive Segregants	Grain Yield Per Plant (GYPP) in combination with	Combination of desirable traits with GYPP
1	K3	DF, GFD, NET, AL, TW	5
2	K5	NET, AUSDC, PL, MTI(I), MTI(II)	5
3	K9	GFD, NET, AUSDC, PL, TW	5
4	K28	DF, GFD, NET, AL, PL, TW, MTI(II)	7
5	K30	NET, SPL, AL, PL, SPLS, GPS. TW, MTI(I), MTI(II)	9
6	K40	DF, GFD, NET, AUSDC, AL, TW	6
7	K52	DF, GFD, NET, AL, PL, SPLS, TW, MTI(II)	8
8	K60	SPL. AUSDC, PL, SPLS, GPS, TW	6
9	K68	DF, DM, GFD, NET, AUSDC, AL, PLH, TW, MTI(II)	9
10	K100	DF, DM, GFD, NET, AUSDC, AL, PL, PLH, 1000 GW	9

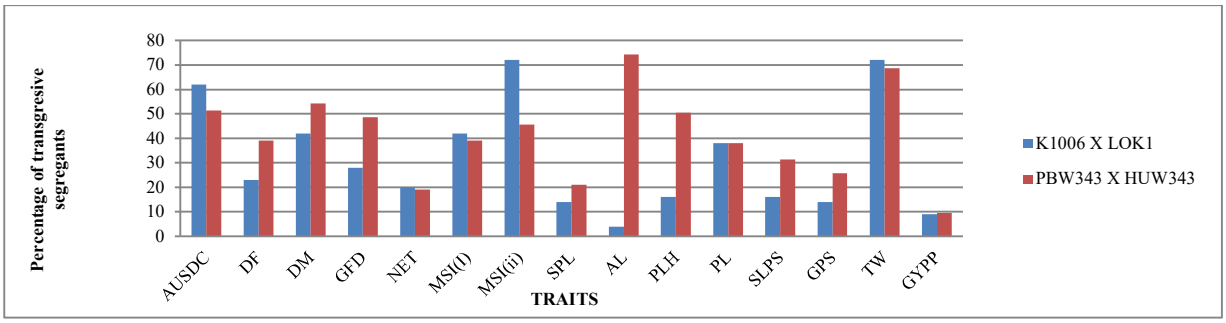

Figure 1:Bar chart representing percentage of transgressive segregants for 15 traits in two crosses (K 1006 x LOK 1 and PBW 343 × HUW 234)

Table 5: Mean performance of transgressive segregants for GYPP in F_2 and F_3 families for the cross K 1006 x LOK 1 and PBW 343 × HUW 234

Crosses	Identified transgressive segregants Plant No.	GYPP (g) in F_2 generation	GYPP (g) in F_3 generation
K 1006 × LOK 1	Line 2	29.52	27.12
	Line 6	28.65	26.44
	Line 25	29.26	27.79
	Line 36	30.60	28.16
	Line 59	30.80	27.92
	Line 88	30.81	31.06
	Line 89	28.65	25.98
	Line 91	30.61	29.86
	Line 96	29.16	26.69
	Mean	29.78	27.89
PBW 343 × HUW 234			
	Line 3	29.52	27.75
	Line 5	28.81	26.81
	Line 9	29.08	27.66
	Line 28	29.82	27.66
	Line 30	35.49	32.62
	Line 40	30.84	29.85
	Line 52	30.49	28.00
	Line 60	30.11	28.47
	Line 68	30.75	28.62
	Line 100	30.96	28.11
	Mean	30.59	28.56

Abbreviations:DF=Days to 50% flowering (days), DM= Days to maturity (days), GFD=Grain Filling Duration (days), NET= Net Effective Tiller (numbers), SPL=Spike length (cm), AUSDC= Area Under SPAD Decline Curve (SPAD value), AL=Awn Length (cm), PL= Peduncle Length (cm), MTI (I) and (II) = Membrane thermo stability index at flowering and grain filling (%), PLH= Plant height (cm), SPLS= No. of spikelets per spike (number), GPS= No. of grains per spike (numbers), TW= 1000 Grain Weight (gm), GYPP= Grain Yield/Plant (gm)

Further evaluation of identified F_2 transgressive segregants was carried out through progeny testing of segregants in F_3 generation for GYPP and there was significant difference between F_2 mean of nine transgressive segregants (29.789 g) and mean of their F_3 population (27.894 g) found for GYPP (table 5) in cross K 1006 × LOK 1. Similarly, significant difference between F_2 mean of ten transgressive segregants (30.592 g) and mean of their F_3 population (28.56 g) was found for GYPP (table 5) in the cross PBW 343 × HUW 234. Such finding may be because of moderate heritability and non-additive gene action in early segregation generation for GYPP which is agreed by Dhole and Reddy (2011). Since, yield is as complex trait and polygenic in nature hence, presence of high frequency of transgressive segregants for grain yield and its components indicates the ample scope for crop improvement in future breeding programme by exploiting such useful findings.

Conclusion

Besides development of high yielding genotypes of crop plants along with genetic improvement for resistance to biotic and abiotic factors. Still there is need to enhance the crop yield production for supplying the demand growing population. In order to this, the assessment of the performance of promising transgressive segregants for yield and its contributing traits in two crosses of wheat is performed. Our finding indicates that parents could have multiple alleles regulating the corresponding traits, showed the potential for the incorporation of beneficial alleles into a solitary genotype by intensive selection. Further evaluation of the most superior transgressive segregants for yield and it contributing traits can be done to achieve the desired plant type by selection in succeeding generations. As per observing the high estimates of transgressive segregants in two crosses of wheat in present study, it is concluded that transgressive breeding can proficiently be utilized to broaden the limits, if desired characters which may not be well expressed/available in parents too.

Since, plant breeding is a key approach to combining the desirable gene(s) into single genotype/line, so making the crosses by using diverse parents and selecting the superior recombinants/segregants for trait of interest in F_2 and advance generations is one of the crucial

approach to develop the genotypes better for yield and other desirable traits in order to produce the enough food for human being in 21st century.

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Conflict of interest
The authors declare that they have no conflict of interest.

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