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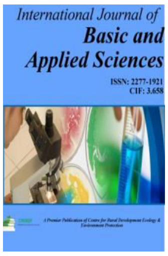

Research Paper

Genetic Basis of Transgressive Segregation and Correlation Between Yield and other Agronomic Traits in Soybean (*Glycine max* L.)

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ARTICLE DETAILS

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ABSTRACT

Soybean [Glycine max (L.) Merrill], is a miracle and premier oilseed crop of the country with its 40 per cent protein and 20 per cent oil. Soybean belongs to family Papilionaceae and believed to have originated in North eastern China and later on distributed in Asia, USA, Brazil, Argentina etc. This crop is aptly called as "Golden Bean" or "Miracle crop" of the 20th century, because of its multiple uses. Transgressive segregation is a phenomenon specific to segregating hybrid generations and refers to the fraction of individuals that exceed parental phenotypic values in either a negative or positive direction. If transgressive segregation is frequent, then an important evolutionary role for hybridization is more easily explained. The present investigation was taken up to make use of line x tester analysis in predicting prepotency of the parents to identify the promising cross combinations and better transgressive segregants in soybean. For the field experiment thirty-two genotypes of soybean comprising of 21 crosses, 7 lines, 3 testers and 1 check were evaluated in F2 and F3 generation using randomized complete block design with two replications for two years at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar. In F_2, The highest frequency of positive transgressive segregants for seed yield per plant was recorded in crosses, PS1042 X PS1347, PS1042 X PS1225 (80.5%), PK1029 X PS1225 (76%), CM60 X PS1225 whereas, in F3 crosses, CM60 X PS1225(73.3%), DT21 X PS1347(65.5%), Doko X PS1225(55.2%) and PK1029 X PS1347(54.5%) showed high frequency of positive transgressive segregants for seed yield. In F_2, Grain yield per plant showed highly significant positive phenotypic and genotypic correlations for number of pods per plant, dry matter weight per plant and harvest index. Whereas, in F_3, seed yield per plant showed highly significant positive phenotypic and genotypic correlations for number of pods per plant, hundred seed weight and harvest index.

1. Introduction

Soybean (*Glycine max* L.) is one of the most important leguminous crops globally, serving as a vital source of protein, oil, and essential nutrients for both human consumption and industrial applications. The improvement of soybean varieties through genetic selection has been a cornerstone of crop breeding programs, aimed at enhancing yield, disease resistance, and abiotic stress tolerance. Among the key genetic phenomena exploited in soybean breeding, transgressive segregation and trait correlation play pivotal roles in determining the potential for developing superior cultivars. Transgressive segregation refers to the occurrence of offspring that exhibit phenotypic traits beyond the range of the parent lines. This phenomenon arises from the recombination of alleles, particularly when multiple genes with additive effects are involved. It is of considerable interest in soybean breeding as it provides the potential to generate varieties with improved traits, such as higher yield, better seed quality, and enhanced resistance to pests and diseases. Additionally, the correlation between traits, whether positive or negative, significantly influences the selection process. For instance, a strong positive correlation between yield and seed size may facilitate simultaneous improvement of both traits, whereas negative correlations might require more complex breeding approaches. This study aims to investigate the extent of transgressive segregation and the relationships among key agronomic traits in soybean. By analyzing these genetic interactions, we seek

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to enhance our understanding of trait inheritance patterns and provide insights for more effective selection strategies in soybean breeding programs.

2. Material and Method

The present investigation was carried out during *Kharif* at, N. E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. Geographically, Pantnagar is situated at the latitude of 29º N, longitude 79.3º E and an altitude of 243.84 meters above the mean sea level. Experimental material in the present investigation comprised 32 genotypes (21 crosses, 7 lines, 3 testers and 1 check) was planted in randomized complete block design with 2 replications during *Kharif*. During next year *i.e.Kharif,* the 32 genotypes consisting of F_3 progenies of 21 crosses along with 7-line, 3 tester and 1 one check were again planted in randomized complete block design with two replications. The experiment material was sown in four-meter row length spaced at 45 cm. Plant to plant distance was maintained at 5 to 7 cm after thinning. The details of number of rows planted and number of plants considered for recording observations on various characters in each generation/genotype are given below. (Table 1)

Table 1. Number of rows planted and number of plants considered for recording observations on various characters in each generation/genotype

Genotype/ Generation	Number of rows planted	Number of plants observed
Parents (Line and Tester) and check	3	5
F2	10	25
F3	15(IPPR)	45(3 plants/ row)

The observations were recorded on 25 randomly selected competitive plants from F_2 and 45 plants in F_3 from each crosses and 5 plants from line, tester and check for plant height, basal node height, basal pod height, number of primary branches per plant, number of nodes per plant, number of pods per plant, number of seeds per pod, dry matter weight per plant, 100 seed weight and seed yield per plant. On the whole plot basis, the observations were recorded for days to 50 per cent flowering and days to maturity.

2.1 Analysis of Transgressive segregation

Percentage of transgressive segregation in the F_2 and F_3 generations for all the characters observed for each cross was obtained by defining extreme progeny types as transgressive segregants *i.e.*, the plants that exceeded their parental limits in either direction. Analysis and comparison were done based on their individual plant data. The percent value of Transgressive segregants was calculated as per following formula

2.2 Transgressive segregants (%)= $\frac{\text{Number of F2 and F3 progeny,exceed the parental limit}}{\text{Total number of F progeny}}$ x 100

2.3 Analysis of Correlation coefficient

The correlations between all the characters under study at genotypic, phenotypic and environmental levels were estimated according to the method given by Searle (1961) using the following formula:

1. Phenotypic correlation between characters X and Y

$$r_{xy}(p) = \frac{Cov.XY(p)}{\sqrt{Var.X(p) \times Var.Y(p)}}$$

2. Genotypic correlation between characters X and Y

$$r_{xy}(g) = \frac{Cov.XY(g)}{\sqrt{Var.X(g) \times Var.Y(g)}}$$

3. Environmental correlation between character X and Y

$$r_{xy}(e) = \frac{Cov.XY(e)}{\sqrt{Var.X(e) \times Var.Y(e)}}$$

Where, Cov. XY (p), Cov.XY (g), Cov. XY(e) denotes phenotypic, genotypic and environmental covariance between characters X and Y, respectively. Var X (p), Var. X(g), Var.(e) denote phenotypic, genotypic and environmental variance for character X and Var.Y(p), Var. Y (g) and Var.Y(e) denote phenotypic, genotypic and environmental variance for character Y, respectively.

$$t_{cal} = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

Test statistics, (n-2) df. Where, n = number of genotypes.

3. Result and Discussion

Transgressive segregation is a phenomenon specific to segregating hybrid generations and refers to the fraction of individuals that exceed parental phenotypic values in either a negative or positive direction. Best cross combination showing highest frequency of transgressive segregation in desired direction is presented in Table 2. In F_2, both positive and negative transgressive segregants for days to 50 per cent flowering were observed in all crosses except DOKO X

PS1225. Maximum frequency of transgressive segregation with early flowering was exhibited in crosses, CM60 X JS335 and DOKO X PS1225 followed by DS74 X PS1347 and Bhatt x JS335, whereas, in F_3 crosses, DOKO X JS335, DT21 X JS335, DOKO X PS1347, DS74X JS335 and PK1029 X PS1347 exhibited early flowering transgressive segregants. Mansur *et al.* (1996), Jadhav *et al.* (2002) and Sarutayophat, T (2012) reported transgressive segregation for days to 50 per cent flowering. For days to maturity, most of the crosses exhibited negative transgressive segregants in F_2 and F_3. Maximum number of transgressive segregants for early maturity was obtained in the crosses, Bhatt x JS335, PK1029 X PS1225, CM60 X PS1347 and DS74 X PS1225 in F2. Whereas, in F_3 crosses, CM60 X PS1225, DS74 X PS1225, DOKO X PS1347, PK1029 X PS1347 exhibited genes for early maturity. Mansur *et al.* (1996), Massey *et al.* (2008) found transgressive segregation for days to days to maturity in soybean.

Consistent appearance of highest percentage of transgressive segregants for increased plant height in positive direction was observed in cross, Bhatt x PS1347 (96%) followed by Bhatt x PS1225, DS74 X PS1225 and DOKO X PS1347(88%), PK1029 X JS335 (76.5%), PK1029 X PS1225 and PK1029 X PS1347(76%), Bhatt x JS335 (68%), DS74 X PS1347 (64.75%) and CM60 X PS1225(64%) in F_2, while cross, PS1042 X PS1347 followed by PK1029 X PS1225, DOKO X JS335 and DOKO X PS1347 in F_3 indicated the accumulation of such genes contributed by both the parents, as a consequence of recombination, which led to the increased plant height. However, in cross, PS1042 X JS335 (4%) highest percentage of negative transgressive segregants for plant height showed the accumulation of such genes contributed by both the parents, as a consequence of recombination, which led to the decrease plant height. Deokar *et al* .(2019) found transgressive segregation for plant height in soybean. Singh and Singh (1978) reported transgressive segregation for plant height in wide cross between mung bean and urd bean in F_3 and F_4 generations. Deokar *et al*(2019) reported transgressive segregation for plant height in soybean. Dubey *et al* (2015) reported higher number of significantly superior transgressive segregants for plant height in the F_2 generation of E-153 x Pant L-23433 and F_3 generation of EC-151015 x Pant L-40640.

In F_2, the highest percentage of transgressive segregants for less basal node height in negative direction was observed in crosses, PK1029 X PS1347, PS1042 X PS1225, DS74X JS335 (36%) and DS74 X PS1347, while in F_3, PK1029 X PS1225, Bhatt x PS1225 and Bhatt x PS1347 indicated the accumulation of such genes contributed by both the parents, as a consequence of recombination, which led to the decreased basal node height. Consistent appearance of highest percentage of transgressive segregants for less basal pod height in negative direction was observed in cross, DOKO X PS1225 followed by DS74 X PS1225 and PS1042 X PS1225 (32%), Bhatt x JS335 (28.5%) and PS1042 X JS335 in F_2. Whereas, in F_3crosses, PK1029 X PS1347, PS1042 X JS335, PK1029 X PS1225 and PS1042 X PS1225 showed less basal pod height. For number of primary branches per plant high percentage of positive transgressive segregants was noticed in cross, DS74 X PS1225 followed by DOKO X PS1225 (76.6%), DS74 X PS1347 (76%), Bhatt x PS1225(64.9%) Bhatt x JS335 (64.5%), CM60 X PS1225 (64%) and CM60 X JS335 (56.5%). While in F_3crosses, DT21 X PS1225, DT21 X PS1347, CM60 X JS335, DS74 X PS1347 showed high percentage of positive transgressive segregants. Massey, P. (2005) reported that wild species of *Cajanus* possess very few primary branches as compared to cultivated forms. Bahl (1980) reported a large number of primary branches per plant in chickpea from the cross involving Indian (desi) x Kabuli types. Singh and Singh (1998) reported variation for primary branches in the F_3 and F_4 generations in a wide cross of mungbean cv. Pant Moong-2 and blackgram cv. AMP 36.

Presence of both positive and negative transgressive segregants for number of nodes per plant was observed in both F_2 and F_3 generations. The maximum frequency of transgressive segregants with higher number of nodes per plant was exhibited in cross, DS74 X PS1225 in F_2, while in F_3 cross, CM60 X JS335 showed higher percentage of transgressive segregants. The maximum frequency of transgressive segregants with higher number of pods per plant was exhibited by in cross, PK1029 X PS1347 (80%) followed by PS1042 X PS1225 and PS1042 X PS1347 (72%), DOKO X PS1347 (69.75%), DOKO X PS1225 indicating the accumulation of favourable genes from the parents as a consequence of recombination, which led to the increased number of pods per plant. Miku and Damaskin (1984), Malik and Singh (1987) reported transgressive segregants for pods per plant in the F_2 population of soybean. Reddy and Singh (1989, 1990) reported transgressive segregation for pods per plant in the F_2 generation of T-44 x PLN-15 in green gram and in BC_1F_2 and BC_2F_2 generations of UPV-82-5 X IW-3390 in black gram. Raina *et al.* (1994) also reported transgressive segregants for pods per plant in wide cross of pigeon pea.

For number of seeds per pod, moderate to high frequency of transgressive segregants in positive direction was recorded in F_2 and F_3 generations for most of the characters. The maximum transgressive segregants was obtained in crosses, DOKO X PS1347, DS74X JS335, DS74 X PS1225 and Bhatt x PS1225 in F_2. While crosses, DOKO X PS1347, DT21 X PS1347, DOKO X JS335, DT21 X JS335 and CM60 X PS1225 exhibited higher percentage of transgressive segregants in F_3. Deokar *et al.* (2019) observed maximum number of transgressive segregations in F_3 generation for seeds per pod in pea. Singh (1990) observed transgression for seeds per pod in F_2 generation of T44 X PLN 15 in mungbean. Zhang *et al.* (1987), Malik and Singh (1987) reported transgressive segregation in soybean. Sarutayophat, T (2012). The highest number of transgressive segregants for dry matter weight per plant in F_2 generation was shown by the crosses, DS74 X PS1347 (68%), Bhatt x JS335 (55%), PK1029 X PS1347 (52%) and in F_3 crosses, CM60 X PS1225, DT21 X PS1225 and PS1042 X PS1225 exhibited maximum frequency of transgressive segregants. Presence of both positive and negative transgressive segregants for hundred seed weight was observed in half of the F_2 crosses, while, half of the crosses exhibited only positive transgressive segregants indicating the possibility of selecting better types which might have resulted due to accumulation of favourable genes from the concerned parents and also because of favourable epistatic effects. The negligible appearance of positive transgressive segregants for this trait in cross, DT21 X PS1225 may be due to the presence of certain inhibitory genes in the parent involved in the cross which did not allow the genes from other parent to express in segregating generation. In F_3, most of crosses showed positive transgressive segregants. The highest percentage of transgressive segregants in F_3 for this character was found in crosses, PS1042 X PS1347 and DS74 X PS1347. Zhang *et al.* (1987) observed transgressive segregants in soybean. Reddy and Singh (1990) reported higher transgressive segregation for hundred seed weight in T-44 x ML-5 cross in the BC_2F_2 generation on mungbean. For harvest index, crosses**,** CM60 X PS1347, DOKO X PS1225, DS74X JS335, PS1042 X JS335 and Bhatt x PS1225 expressed moderate to high number of positive transgressive segregants in F_2generations indicating the presence of complementary effects of favourable alleles for these traits in these crosses. While crosses, PS1042 X JS335, Bhatt x PS1225, PK1029 X PS1225, DT21 X JS335 and PK1029 X JS335 showed high to low transgressive segregants for harvest index in F_3. Lawrence and Frey (1975) reported transgressive segregation for harvest index in BC_1F_2 and BC_4F_2 of interspecific oat crosses. The highest frequency of positive transgressive segregants for seed yield per plant was recorded in cross, PS1042 X PS1347 followed by PS1042 X PS1225 (80.5%), PK1029 X PS1225 (76%), CM60 X PS1225 (68%), DOKO X PS1347 (64.5%) in F_2. Whereas, in F_3 cross, CM60 X PS1225 followed by DT21 X PS1347, DOKO X PS1225 and PK1029 X PS1347 showed highest percentage of transgressive segregants. According to Robinson and Cockerham (1961) and Marani (1968) significant F_2/F_3 deviations in the form of transgressive segregants indicating the presence of epistatic effects even though linkage may present precise estimates of the type of epistasis operating. The overall appearance of transgressive segregants in F_2 cross, PS1042 X PS1347 indicated the involvement of additive and additive x additive epistatic effect along with the dominance effect in the control of seed yield in this cross. Lawrence and Frey (1975), Cox and Frey (1984) and Mishra and Verma (1985) also reported transgressive segregants for higher seed yield in oats. Auckland and Singh (1977) reported high number of transgressive segregants for yield in Kabuli x Desi crosses. Mansur *et al.* (1996) indicated that transgressive behavior is most pronounced for yield and the related traits and the range of the recombinant inbred lines (RILs) of soybean have been shown to be due to genotypic differences. Miku and Damaskin (1984), Kapila and Gupta (1991), Bhatnagar and Karmakar (1995), Massey *et al.* (2008) and Lee *et al.* (2010) reported higher number of transgressive segregants for yield in soybean.

Table 2: Best cross combination showing highest frequency of transgressive segregation in desired direction

S. No.	Character	F_2	F_3
1	Days to 50% flowering	CM60 X JS335 and Doko X PS1225 DS74 X PS1347 (32%) and Bhatt x JS335 (20%).	Doko X JS335 (40%) DT21 X JS335 (37.78%), Doko X PS1347 (35.56), DS74X JS335 (33%)
2	Days to maturity	Bhatt x JS335 (16%), PK1029 X PS1225 (20%), CM60 X PS1347 (23.45%), DS74 X PS1225 (36.45%)	PK1029 X PS1347 (12.76%). Doko X PS1347 (12.5%) DS74 X PS1225 (12.3%), and CM60 X PS1225 (9%),
3	Plant height (cm)	Bhatt x PS1347 (96%), Bhatt x PS1225, DS74 X PS1225 and Doko X PS1347 (88%), PK1029 X JS335 (76.5%),	PS1042 X PS1347 (93.5%) , PK1029 X PS1225 (82%), Doko X JS335 (77.78), Doko X PS1347 (71%), Doko X PS1225
4	Basal node heigh (cm)	PK1029 X PS1347 (40%), PS1042 X PS1225 (40.5%), DS74X JS335 (36%), DS74 X PS1347 (28%).	PK1029 X PS1225 (47%), Bhatt x PS1225 (33.33%) and Bhatt x PS1347 (31%).
5	Basal pod height (cm)	Doko X PS1225, DS74 X PS1225 and PS1042 X PS1225 (32%), Bhatt x JS335 (28.5%) and PS1042 X JS335 (28%).	PK1029 X PS1347 (77.5%), PS1042 X JS335 (55%) and PS1042 X PS1225 (44.47%).
6	Number of primary branches per plant	DS74 X PS1225and Doko X PS1225 (76.6%), DS74 X PS1347 (76%), Bhatt x PS1225 (64.9%) Bhatt x JS335 (64.5%), CM60 X PS1225 (64%)	DT21 X PS1225 (88%), DT21 X PS1347 (84.5%), CM60 X JS335 (77.7%), DS74 X PS1347 (71.15%).
7	Number of nodes /plants	DS74 X PS1225 (90.5%)	CM60 X JS335 (82.22%)
8	Number of pods per plant	PK1029 X PS1347 (80%) PS1042 X PS1225 and PS1042 X PS1347 (72%), Doko X PS1347 (69.75%), Doko X PS1225 (68.5%)	DT21 X JS335 (95.56%), DT21 X PS1225 (93.5%), Doko X JS335 (86.55%) and PK1029 X JS335 (60.5%)
9	Number of seeds per pod	Doko X PS1347 (72%), DS74X JS335 (56.8%), DS74 X PS1225 (56%) and Bhatt x PS1225 (48%).	Doko X PS1347 (93.25%), DT21 X PS1347 (84.5%), Doko X JS335 (82.4%), DT21 X JS335 (77%) and CM60 X PS1225 (71%).
10	Dry matter weight/plant (g)	CM60 X PS1225, DT21 X PS1225, PS1042 X JS335 and PS1042 X PS1347, DS74 X PS1347 (68%), Bhatt x JS335 (55%), PK1029 X PS1347 (52%)	CM60 X PS1225 (30%), DT21 X PS1225 (25%) and PS1042 X PS1225 (24.5%),
11	Hundred seed weight (g)	PK1029 X PS1347(96%), DS74 X PS1225 and Doko X PS1225	PS1042 X PS1347 (56.50%) and DS74 X PS1347 (34.50%).
12	Harvest index (%)	Bhatt x PS1225 (88 %), PS1042 X JS335 (80.5%), DS74X JS335 (72%), Doko X PS1225	PS1042 X JS335 (77.70 %), Bhatt x PS1225 (72.32%) and PK1029 X PS1225 (70.25%)

		(65%)	
13	Grain yield per plant (g)	PS1042 X PS1347 (88%), PS1042 X PS1225 (80.5%), PK1029 X PS1225 (76%), CM60 X PS1225 (68%),	CM60 X PS1225 (73.30%), DT21 X PS1347 (65.50%), Doko X PS1225 (55.20%) and PK1029 X PS1347 (54.50%).

Table 3: Common crosses showing Transgressive Segregation in F_2 and F_3 Generations

Trait Analyzed	Cross (Parent 1 × Parent 2)	F_2 Range	F_3 Range	Findings
Plant height (cm)	Doko X PS1347 (88%),	(88%)	(71%)	The reduction of transgressive segregants in F_3 compared to F_2 is mainly due to the reduction in genetic variability, increased homozygosity, genetic stabilization, and selection pressures during selfing and breeding processes.
Basal pod height (cm)	PS1042 X PS1225	(32%)	(55%)	Reflects a combination of genetic fixation, recombination, homozygosity, and possibly selection. It might also indicate that the F_2 generation was not yet fully segregated for certain loci, and the F_3 generation allowed for the expression of those hidden combinations.
Number of seeds per pod	Doko X PS1347	(72%)	(93.25%)	Is shows genetic fixation, recombination, homozygosity, and possibly selection.
Dry matter weight/plant (g)	CM60 X PS1225,	(68%)	(30%)	The results show decreased genetic variability, increased homozygosity, genetic stabilization, and selection pressures during selfing and breeding processes.
Harvest index (%)	Bhatt x PS1225	(88 %)	(72.32%)	The reduction of transgressive segregants in F_3 compared to F_2 is mainly due to the reduction in genetic variability, increased homozygosity, genetic stabilization, and selection pressures during selfing and breeding processes.
Grain yield per plant (g)	CM60 X PS1225	(68%)	(73.30%)	Reflects a combination of genetic fixation, recombination, homozygosity, and possibly selection. It might also indicate that the F_2 generation was not yet fully segregated for certain loci, and the F_3 generation allowed for the expression of those hidden combinations.

3.1 Estimates of inter-character Correlation

The seed yield is a complex and highly variable character and a result of cumulative effect of its component characters and therefore, direct selection for yield may not be very effective. The yield components may not always be independent in their action but may be inter-linked. For selection purpose phenotypic correlation is of little practical value unless genetic and environmental correlations between pairs of characters are in the same direction when estimated separately. Genetic correlation provides a measure of genetic association between characters and is generally used in selection for one character as a mean of improving another one. Genetic correlation may be accounted by linkage or pleiotropy.Thus, the association between two traitsthat can be directly observed is the phenotypic correlation. The genotypic correlation in the true sense may be interpreted as the correlation of breeding value. The environmental correlation includes both environmental and non-additive genetic deviations. Phenotypic, genotypic and environmental correlations between character pairs for all the characters are presented in Tables 4, 5 and 6, respectively. Genotypic correlations, in general, were higher than phenotypic correlations. Directions of phenotypic and genotypic correlations were almost same for all the character combinations. The environment correlations, in general, were lower in magnitude as compared to the phenotypic and genotypic correlations. In F_3, seed yield per plant showed highly significant positive phenotypic and genotypic correlations for number of primary branches per plant ($r_p=0.194^{**}$, $r_g=0.530^{**}$), number of pods per plant ($r_p=0.290^{**}$, $r_g=0.402^{**}$), hundred seed weight $r_p=0.300^{**}$, $r_g=0.539^{**}$) and harvest index ($r_p=0.658^{**}$, $r_g=0.714^{**}$). Whereas, Seed yield showed significant negative values of genotypic correlations with days to maturity ($r_g=-0.355^{**}$). Seed yields also showed significant positive correlation with days to 50% flowering at genotypic levels ($r_g=0.281^{*}$). Similar results were obtained by Showkat and Tyagi,2010, Zafar Iqbal *et al.*, 2010 and Machikowa Laosuwan, 2011 and Deokar *et al.* (2019). Days to fifty per cent flowering showed significant positive correlation with plant height both at phenotypic and genotypic levels, respectively. Whereas, genotypic correlation showed significant negative correlation with basal node height, number of seeds per pod (rp=-0.348**) and seed yield/plant in F_2. In F_3, harvest index showed significant positive correlation at both phenotypic and genotypic levels. While days to maturity, seed yield/plant plant height showed negative non-significant genotypic correlation. Similar results were reported by Chettri *et. al.,* Thorat *et al.,* 2001. Days to maturity had significant positive correlation with plant height at both the levels in F_2. Whereas, in F_3 days to maturity had significant positive correlation with number of nodes per plant and number of seeds per pod both at both the levels. There were negative significant phenotypic and genotypic correlations with harvest index at both the levels. Whereas, it showed negative significant correlations with basal pod height and seed yield/plant at genotypic level. Similar results were reported by Haghi *et al.* (2012) and Karkute *et al.* (2016). Number of primary branches per plant showed significant positive values of phenotypic and genotypic correlations with number of pods per plant and number of seeds per pod. Whereas, it showed non-significant negative value of genotypic correlation with 100 seed weight in F_2.Highly significant and positive value of phenotypic and genotypic correlations was observed only with number of seeds per pods in F_3. Similar results were reported by Rubaihaya, (1973), Rajput *et al.,* (2000), Gaikwad *et al.,* (2007) and Machikowa and Laosuwan, (2011). Number of pods per plant showed significant positive values of phenotypic and genotypic correlations with number of seeds per pod and seed yield per plant. Whereas, it showed non-significant positive value of phenotypic and genotypic correlations with dry matter weight and harvest index in F_2. In F_3, number of pods per plant showed significant negative values of phenotypic and genotypic correlations for dry matter weight per plant. Karnwal and Singh, (2009) Sarutayophat (2012) showed significant association between number of pods per plant and seed yield per plant. Dry matter weight per plant showed **h**ighly significant and positive value of phenotypic and genotypic correlations with seed yield per plant. Negative and highly significant phenotypic and genotypic correlations were observed for harvest index in F_2.Whereas, in F_3 harvest index showed significant and negative value of phenotypic correlation with dry matter weight. The results reported are in agreement with the earlier findings of Kharakwal (2003)and Samiullah Khan and Wani (2006). Seed yield per plant showed highly significant positive phenotypic and genotypic correlations with number of pods per plant, dry matter weight per plant and harvest index. Whereas, seed yield showed non-significant negative values of phenotypic and genotypic correlations with plant height. In F_3, seed yield per plant showed highly significant positive phenotypic and genotypic correlations for number of pods per plant, hundred seed weight and harvest index. Whereas, seed yield showed non-significant negative values of genotypic correlations with days to maturity. Chaudhary and Singh (1974), Myakushko and Dudka (1986), Singh and Yadava (2000), Thorat *et al.* (2001), Chettri*et al.*(2003), Yadav (2005), Bhairav *et al.* (2006), Pandey *et al.* (2008), Karnwal and Singh (2009) and Sarutayophat (2012).

3.2 Environmental Correlation

It includes both environmental and non-additive effects. Invariably, environmental correlation values were lower as compared to the genotypic and phenotypic ones. A perusal of environmental correlation in F_2 and F_3 is given in Table Almost all the correlation values between different characters were non-significant. Whereas, highly significant positive correlation was found between days to fifty percent flowering and number of pods per plant (re=0.496**), days to fifty percent flowering and number of seeds per pod (re=0.393**). Highly significant positive correlation was observed between days to maturity and number of nodes per plant (re=0.471**), number of primary branches per plant and number of pods per plant (re=0.353**), number of primary branches per plant and number of seed per pod (re=0.389**), harvest index and seed yield per plant (re=0.361**), whereas, significant positive correlation was found between days to 50 % flowering and days to maturity (re=0.256*), basal pod height and harvest index (re=0.262*) and number of pods per plant and seed yield per plant (re=0.258*). It also showed highly significant negative correlation between number of nodes per plant and hundred seed weight (re=-0.423**) and dry matter weight per plant and harvest index (re=-0.692**). While, significant negative correlation was found between days to maturity and hundred seed weight (re=-0.292*), plant height and basal pod height (re=-0.282*), plant height and number of primary branches (re=-0.293*), plant height and harvest index (re=-0.320*) and number of seed per pod and hundred seed weight (re=-0.287*). In environmental correlation, some of the characters showed highly significant and significant correlation as described above and maximum characters showed non-significant negative and non-significant positive correlation to each other in F_2. In F_3, most of the correlation values between different characters were non-significant. Whereas, highly significant positive correlation was observed between plant height and basal pod height (re=0.32**), basal node height and number of seeds per pod (re=0.37**), basal node height and hundred seed weight (re=0.33**), number of pods per plant and hundred seed weight (re=0.43**) and harvest index and seed yield per plant (re=0.41**). Whereas, significant positive correlation was found between plant height and number of nodes per plant (re=0.26*) and basal node height and number of pods per plant (re=0.27*). It also showed highly significant negative correlation between plant height and basal node height (re=-0.35**), plant height and number of pods per plant (re=-0.44**), number of nodes per plant and number of seeds per pod (re=-0.35**) and dry matter weight per plant and harvest index (re=-0.67**). While significant negative correlation was found between days to 50% flowering and seed yield per plant (re=-0.25*), days to maturity and number of seeds per pod (re=-0.26*) and basal pod height and number of pods per plant (re=-0.270*).

4. Conclusion

Occurrence of transgressive segregants in segregating generation was helpful for the development of homozygous lines by continued selfing in self pollinated crop like soybean. Maximum number of transgressive segregants for higher plant height was obtained in crosses, Bhatt x PS1347 (96%), Bhatt x PS1225, DS74 X PS1225 and Doko X PS1347(88%), PK1029 X JS335 (76.5%), in both F_2 and F_3. The maximum frequency of transgressive segregants with higher number of pods per plant was exhibited by crosses, PK1029 X PS1347 (80%), PS1042 X PS1225 and PS1042 X PS1347. For number of seeds per pod, moderate to high frequency of transgressive segregants in positive direction was recorded in F_2 and F_3 generations for most of the characters. The highest frequency of positive transgressive segregants for seed yield per plant was recorded in crosses, PS1042 X PS1347, PS1042 X PS1225 (80.5%), PK1029 X PS1225 (76%), CM60 X PS1225 (68%), Doko X PS1347 (64.5%). Whereas, in F_3 crosses, CM60 X PS1225, DT21 X PS1347, Doko X PS1225 and PK1029 X PS1347 showed high frequency of positive transgressive segregants for seed yield. Grain yield per plant showed highly significant positive phenotypic and genotypic correlations for number of pods per plant, dry matter weight per plant and harvest index. Whereas, in F_3, seed yield per plant showed highly significant positive phenotypic and genotypic correlations for number of pods per plant, hundred seed weight and harvest index. Present study revealed that in F_2 and F_3, harvest index was the most positive direct contributor towards seed yield followed by dry matter weight, number of pods per plant. Since these characters also exhibited significant and positive correlation with seed yield per plant and hence, improvement in these component characters would result in the improvement of seed yield per plant. Therefore, during selection maximum emphasis should be given to the improvement of these component characters.

References

Aditya. 2003. Studies of residual heterosis and transgressive segregants for yield and its components in soybean (*G. max.* (L.) Merrill). Unpublished M.Sc. Thesis submitted to G.B.P.U.A. & T., Pantnagar. 145 p.

Anonymous (2019-20). Area & Production Estimates of Soybean [Glycine max (L.) Merrill], Crop survey conducted by SOPA. in India in Kharif 2019 -20.

Bhairav, B., Sharma, S.P. and Sharma, V. 2006. Correlation and path coefficient analysis of soybean [*Glycine max* (L.) Merrill]. *Crop Improv.* 33(2): 190-193.

Bhartiya, A. 2004. Residual heterosis and transgressive segregation studies for yield and its components in soybean (*Glycine max* (L.) Merrill). Unpublished M.Sc. Thesis submitted to G.B.P.U.A.T., Pantnagar. 145 p.

Ball M. Y., Ibrahim S. E. (2017). Genotypic correlation and path coefficient Analysis of Soybean [Glycine max (L.) Merr.] For yield and its components. Agri Res &Tech: Open Access J.; 7 (3); 555715. DOI: DOI: 10.19080 / ARTOAJ. 2017. 07. 555715

Chaudhary, D. N. and Singh, B. 1974. Correlation and path coefficient analysis of yield components of soybean. *Indian J. Agric.Sci*., 44: 487-490.

Chettri, M., Mondal, S. and Nath, R. 2001. Studies on correlation and path analysis in soybean [*Glycine max* (L.) Merrill] in the Darjeeling hills. *Journal of Hill Research*., 16(12): 101-103.

Deokar S.D., V. S. Girase, S. G. Patil and V. V. Bhavsar. (2019). Correlation and Path Analysis in Soybean. International Research Journal of Multidiciplinary Studies. Vol 2 ISSN (online): 2454 – 8499.

Deokar S.D., V. S. Girase, S. G. Patil and V. V. Bhavsar. (2019). Assessment and implication of selection indices in F2 Generation of chickpea (cice rarientinum L.), International Journal of Current Microbiology and Applied science. 8(10). 934-939.

Dubey N., Shrivasthava A. N., Avinashe H. A. and Samidha J. 2015. Genetic diversity, correlation and path analysis for yield and yield contributing characters in soybean (Glycine max L.). Electronic Journal Plant Breeding 6(1): 318-325.

Jadhav, D. J., Deosarkar, D. B. and Jawale, L. N. 2002. Correlation and path coefficient analysis in seed quality characters of soybean. *J. of Maharashtra Agric. Universities.* 26 (3): 325-326.

Massey, P. 2005. Transgressive segregants and residual heterosis in soybean (*Glycine max* (L.) Merrill). Unpublished M.Sc. Thesis submitted to G.B.P.U.A.T., Pantnagar. 106 p.

Massey,P, Singh, B.V., Singh, K., Pushpendra and Gupta, M.K 2008. Transgressive segregation for yield and yield contributing traits in F2 generations in soybean [Glycine max (L.) Merrill]. *Pantnagar-Journal-of-Research* 6(1): 106-109.

Sarutayophat, T 2012. Correlation and path coefficient analysis for yield and its components in vegetable soybean. *Songklanakarin-Journal-of-Science-and-Technology.* 34(3): 273-277.

Haghi Y., Boroomandan P., Mordin M., Hassankhali M., Farhadi P., Farsaei F. and Dabiri S. 2012. Correlation and path analysis for yield, oil and protein content of soybean genotypes under different levels of nitrogen starter and plant density. Biharian Bio., 6 (1): pp. 32-37.

Karkute, S. M., V. S. Girase and A. J. Patil. 2016. Transgressive segregation and in mungbean [Vigna radiate L.) Wilczek]. Journal of Agriculture Research and Technology, 41(1):48 51.

Painkara P., R. Shrivastava., S.K. Nag and I. Kute (2018) Correlation analysis for seed yield and Its Attributing Traits in soybean (glycine max L. Merill). International journal of current Microbiology and applied sciences. 7(4): 2034-2040 How to cite this article:

Table: 4 . Inter-character correlation coefficient between different characters at Genotypic level in F_2 and F_3 generations of Soybean

	Generation	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Basal node height(cm)**	**Basal pod height (cm)**	**Number of Primary branches per plant**	**Number of nodes per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Dry matter weight per plant (g)**	**Hundred seed weight (g)**	**Harvest index (%)**	**Seed Yield/plant (g)**
Days to 50% flowering	F_2	1.000	0.186	0.308*	-0.213	0.033	0.13	0.063	0.117	-0.039	-0.035	-0.219	-0.194	-0.226
	F_3	1.000	0.043	-0.159	-0.198	-0.081	0.144	-0.013	0.088	0.001	-0.188	0.349**	0.124	0.082
Days to maturity	F_2		1.000	0.345**	0.067	0.217	-0.052	0	-0.078	0.029	-0.076	-0.169	0.077	-0.03
	F_3		1.000	-0.129	0.068	-0.228	0.165	0.251*	0.077	0.135	-0.089	-0.034	-0.429**	-0.192
Plant height (cm)	F_2			1.000	-0.109	0.226	-0.052	0.258*	-0.206	-0.255*	-0.05	-0.114	-0.223	-0.265*
	F_3			1.000	-0.105	0.003	-0.169	-0.285*	-0.149	0.031	0.050	-0.250	0.100	-0.034
Basal node height(cm)	F_2				1.000	-0.007	0.099	-0.146	0.231	0.315*	-0.092	0.236	0.085	-0.021
	F_3				1.000	-0.024	-0.267*	-0.059	-0.015	0.167	-0.009	-0.043	0.018	-0.048
Basal pod height (cm)	F_2					1.000	-0.219	-0.122	-0.142	-0.188	0.237	-0.324*	-0.169	-0.02
	F_3					1.000	0.172	0.065	-0.265*	-0.251*	0.229	0.023	0.152	0.030
Number of Primary branches per plant	F_2						1.000	0.072	0.392**	0.382**	0.126	-0.132	-0.137	-0.035
	F_3						1.000	0.158	-0.107	0.158*	0.026	0.144	-0.105	0.019
Number of nodes per plant	F_2							1.000	0.226	-0.234	0.053	0.141*	-0.188	-0.125
	F_3							1.000	-0.086	-0.033	0.310*	0.149	-0.328**	-0.021
Number of pods per plant	F_2								1.000	0.424**	0.214	-0.122	0.084	0.323*
	F_3								1.000	-0.081	-0.296*	-0.031	0.090	0.092
Number of seeds per pod	F_2									1.000	0.098	-0.086	0.082*	0.152
	F_3									1.000	-0.057	0.396**	0.123	0.290*
Dry matter weight per plant	F_2										1.000	-0.175	-0.549**	0.391**
	F_3										1.000	-0.031	-0.282*	0.145
Hundred seed weight (g)	F_2											1.000	0.325**	0.202
	F_3											1.000	0.187**	0.300**
Harvest index (%)	F_2												1.000	0.530**
	F_3												1.000	0.658**
Seed yield/plant	F_2													1.000
	F_3													1.000

Table: 5 . Inter-character correlation coefficient between different characters at Genotypic level in F_2 and F_3 generations of Soybean

Characters		**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Basal node height(cm)**	**Basal pod height (cm)**	**Number of Primary branches per plant**	**Number of nodes per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Dry matter weight per plant (g)**	**Hundred seed weight (g)**	**Harvest index (%)**	**Grain Yield/plant (g)**
Days to 50% flowering	F_2	1.000	0.152	0.409**	-0.364**	0.036	0.116	0.059	0.021	-0.348**	-0.085	-0.207	-0.287*	-0.331**
	F_3	1.000	0.30*	-0.41**	-0.382**	-0.132	0.174	-0.085	0.108	0.010	-0.150	0.60**	0.197	0.281*
Days to maturity	F_2		1.000	0.518**	0.178	0.415**	-0.47**	-0.201	-0.21	-0.66**	-0.33**	-0.072	0.272*	-0.046
	F_3		1.000	-0.156	0.178	-0.295*	0.126	0.324*	0.110	0.389**	-0.006	0.029	-0.635**	-0.355**
Plant height (cm)	F_2			1.000	-0.08	0.298*	0.073	0.222	-0.23	-0.457**	-0.129	-0.078	-0.197	-0.283*
	F_3			1.000	0.342**	-0.220	-0.236	-0.562**	-0.114	0.116	-0.154	-0.270*	0.244	-0.120
Basal node height(cm)	F_2				1.000	0.03	0.295*	-0.134	0.427**	0.931**	-0.142	0.355**	0.124	-0.077
	F_3				1.000	0.108	-0.412**	-0.024	-0.120	-0.067	-0.160	-0.697**	0.036	-0.006
Basal pod height (cm)	F_2					1.000	-0.42**	-0.12	-0.175	-0.228	0.310*	-0.46**	-0.243	-0.034
	F_3					1.000	0.366**	0.054	-0.278*	-0.407**	0.477**	0.173	0.197	0.103
Number of Primary branches per plant	F_2						1.000	0.147	0.487**	0.373**	0.08	-0.33**	-0.162	0.664*
	F_3						1.000	0.189	-0.131	0.330**	0.050	0.266*	-0.103	0.530*
Number of nodes per plant	F_2							1.000	0.234	-0.433**	0.013	0.289*	-0.194	-0.145
	F_3							1.000	-0.090	0.044	0.563**	0.281*	-0.364**	0.001
Number of pods per plant	F_2								1.000	0.588**	0.208	-0.148	0.115	0.335**
	F_3								1.000	-0.085	-0.451**	-0.168	0.093	0.121
Number of seeds per pod	F_2									1.000	1.000	1.000	0.252**	0.339
	F_3									1.000	1.000	1.000	0.179**	0.402 **
Dry matter weight per plant (g)	F_2												-0.497**	0.477**
	F_3												-0.092	0.715
Hundred seed weight (g)	F_2												0.440**	0.273*
	F_3												0.372**	0.539**
Harvest index (%)	F_2												1.000	0.508**
Grain yield/plant	F_3												1.000	0.714**
	F_2													1.000
														1.000

Table 6 . Inter-character correlation coefficient between different characters at environmental level in F_2 and F_3 generations of Soybean

Characters	**Generation**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Basal node height (cm)**	**Basal pod height (cm)**	**Number of Primary branches per plant**	**Number of nodes per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Dry matter weight per plant (g)**	**Hundred seed weight (g)**	**Harvest index (%)**	**Seed yield/ plant (g)**
Days to 50% flowering	F_2	1.000	0.256*	-0.02	0.003	0.026	0.164	0.088	0.496**	0.393**	0.099	-0.245	0.036	0.127
	F_3	1.000	-0.243	0.019	-0.093	-0.017	0.117	0.180	0.113	-0.008	-0.213	0.163	0.024	-0.25*
Days to maturity	F_2		1.000	0.218	-0.007	-0.054	0.198	0.382**	0.109	0.469**	0.228	-0.292*	-0.124	-0.016
	F_3		1.000	-0.106	-0.023	-0.081	0.228	0.031	-0.058	-0.26*	-0.180	-0.107	0.096	0.238
Plant height (cm)	F_2			1.000	-0.192	-0.282*	-0.293*	0.471**	-0.083	0.068	0.244	-0.235	-0.320*	-0.18
	F_3			1.000	-0.35**	0.32**	-0.108	0.26*	-0.44**	-0.054	0.183	-0.235	-0.122	0.105
Basal node height(cm)	F_2				1.000	-0.135	-0.061	-0.233	-0.166	-0.222	-0.017	0.079	0.032	0.095
	F_3				1.000	-0.187	-0.167	-0.193	0.27*	0.37**	0.071	0.33**	-0.001	-0.12
Basal pod height (cm)	F_2					1.000	0.214	-0.146	0.124	-0.199	-0.151	0.262*	0.181	0.085
	F_3					1.000	-0.245	0.138	-0.270*	0.069	-0.069	-0.198	-0.010	-0.23
Number of Primary branches per plant	F_2						1.000	-0.061	0.353**	0.389**	0.214	0.1	-0.118	-0.099
	F_3						1.000	0.090	-0.051	-0.103	0.004	0.018	-0.120	0.084
Number of nodes per plant	F_2							1.000	0.175	0.143	0.243	-0.423**	-0.186	-0.007
	F_3							1.000	-0.038	-0.35**	-0.103	-0.118	-0.114	-0.17
Number of pods per plant	F_2								1.000	0.216	0.247	-0.039	-0.028	0.258*
	F_3								1.000	-0.115	-0.137	0.43**	0.091	-0.14
Number of seeds per pod	F_2									1.000	0.128	-0.287*	-0.15	-0.177
	F_3									1.000	0.163	0.207	-0.006	0.035
Dry matter weight per plant (g)	F_2										1.000	-0.135	-0.692**	0.069
	F_3										1.000	0.055	-0.67**	0.140
Hundred seed weight (g)	F_2											1.000	0.062	-0.014
	F_3											1.000	-0.094	-0.04
Harvest index (%)	F_2												1.000	0.631**
	F_3												1.000	0.41**
Seed yield/plant	F_2													1.000
	F_3													1.000