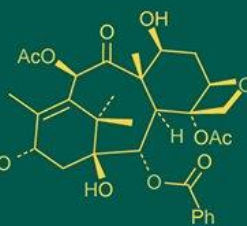
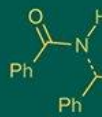


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Bharatkumar VG
M.Sc. Scholar, Department of
Agril. Botany, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

VP Chimote
Professor, Department of Agril.
Botany, State Level Biotechnology
Centre, Mahatma Phule Krishi
Vidyapeeth, Rahuri, Maharashtra,
India

CJ Nair R
M.Sc. Scholar, Department of
Agril. Botany, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

Rasal PP
M.Sc. Scholar, Department of
Agril. Botany, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

Vaishnavi K
M.Sc. Scholar, Department of
Molecular Biology and
Biotechnology, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

Patwe MP
M.Sc. Scholar, Department of
Agril. Botany, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

Niranjan
M.Sc. Scholar, Department of
Agril. Botany, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

Rakesh KR
M.Sc. Scholar, Department of
Agril. Botany, Dr. Balasaheb
Sawant Konkan Krishi Vidyapeeth,
Dapoli, Raigad, Maharashtra,
India

Manoj KM
M.Sc. Scholar, Department of Agril
Botany, Mahatma Phule Krishi
Vidyapeeth, Rahuri, Maharashtra,
India

Corresponding Author:
Bharatkumar VG
M.Sc. Scholar, Department of
Agril. Botany, Mahatma Phule
Krishi Vidyapeeth, Rahuri,
Maharashtra, India

Transgressive segregation studies in F₃ population of soybean (*Glycine max* (L.) Merrill)

Bharatkumar VG, VP Chimote, CJ Nair R, Rasal PP, Vaishnavi K, Patwe MP, Niranjan, Rakesh KR and Manoj KM

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Abstract

Soybean (*Glycine max* (L.) Merrill), often described as a “miracle crop” on account of its high protein and oil-rich seeds, is the world's most extensively grown legume and a crop of major importance to India's agricultural economy, contributing substantially to edible oil production, livestock and aquaculture feed and plant-based protein for human nutrition. Genetic improvement of soybean for yield and adaptability depends heavily on the extent of exploitable variability generated in segregating generations following hybridization. Transgressive segregation, the phenomenon whereby progeny display phenotypic values that fall outside the range of either parent, arises when complementary favourable alleles contributed by genetically diverse parents are brought together through recombination and represents one of the most effective natural mechanisms for generating novel, agronomically superior gene combinations. Such extreme segregants are of considerable interest to plant breeders because they may combine high yield potential with improved physiological efficiency, better adaptability and other desirable agronomic attributes not present in either parental line. The present study was undertaken to identify transgressive segregants for physiological and yield-contributing traits in two F₃ populations of soybean derived from the crosses JS 2212 × NRC 142 and JS 2216 × NRC 142. Field trials were conducted during Kharif 2025 at MPKV, Rahuri, for the evaluation of thirteen agronomic and physiological traits, including the Normalized Difference Vegetation Index (NDVI), canopy temperature and chlorophyll content, recorded on 500 plants of each cross. Statistical analysis revealed significant transgressive segregation across several traits, most notably pods plant⁻¹, seeds pod⁻¹, clusters plant⁻¹, pods cluster⁻¹ and yield plant⁻¹. Fifteen promising transgressive segregants were identified in each cross, exhibiting superior performance beyond both parents with yield improvements over the better parent ranging from 27.80 to 39.21 percent in Cross I and 21.53 to 40.86 percent in Cross II. These results emphasize the effectiveness of transgressive segregation for selecting superior recombinants with enhanced yield and physiological performance.

Keywords: Soybean, *Glycine max* L, F₃, Transgressive segregation, normalized difference vegetation index

Introduction

Soybean (*Glycine max* (L.) Merrill) believed to have originated in ancient China, where it was referred to as “Shu”, is among the earliest leguminous crops to be domesticated by humans. Two species constitute the genus *Glycine*: the cultivated soybean (*Glycine max* (L.) Merrill) and its wild relative, *Glycine soja* (Siebold & Zucc.). The geographic range of *Glycine soja* is largely confined to North East Asia including China, Japan, North Korea and certain regions of Russia. China holds the largest natural range of wild soybeans compared with other regions in East Asia. (Li, 1988 and Kuroda *et al.*, 2008) [6, 4].

With a history of cultivation extending for between 6000-9000 years, soybean has become one of the most extensively cultivated legume crops globally. Liu (1997) [8] described soybean as a “miracle crop” owing to its diverse nutritional and economic significance. On a dry-weight basis, soybean seeds typically comprise approximately 40% protein, 20% oil, 35% carbohydrates and 5% ash. This rich nutritional profile has established soybean as a major plant-based source of protein and edible oil for human consumption, with the crop being recognized as the world's leading source of vegetable oil (Lee *et al.*, 2007) [5]. In addition to its food value, it is extensively utilized in livestock and aquaculture feed formulations and serves as a raw material for a wide range of industrial applications (Kim *et al.*, 2021) [3].

According to Anonymous (2024) ^[1], soybean was cultivated on approximately 12.95 million hectares (Mha) during 2024-25, with a total production of about 15.26 million tonnes (Mt) and a national average yield of 1179 kg ha⁻¹. Among the states, Maharashtra covered 5.11 Mha, producing 5.01 Mt at a yield of 1115 kg ha⁻¹, marginally below the national average. Madhya Pradesh recorded the largest cultivated area (5.20 Mha) with a productivity of 1082 kg ha⁻¹ and a total production of 5.54 Mt, while Rajasthan, despite a considerably smaller area of 1.11 Mha, recorded a productivity of 946 kg ha⁻¹ and a production of 1.05 Mt. These figures highlight substantial variability in soybean productivity across India's agro-ecological zones (Anonymous, 2024) ^[1].

According to Mishra (2010) ^[11], the occurrence of weeds such as broadleaf species, grasses, sedges and perennials can significantly reduce soybean productivity. The introduction of herbicide tolerant transgenic soybean varieties provided a strategy to control these weeds, mitigating the potential adverse effects of herbicide application on soil quality, microflora and the ecological food chain, however GM Soybean cultivation is not allowed in India.

The soybean was originally classified as *Phaseolus max* by Linnaeus (1737) in "General Plantarum", who proposed the genus "*Glycine*" and subsequently referred to the species as *Dolichos soja*. Merrill (1917) ^[10], assigned the currently accepted name *Glycine max* and has a chromosome number of $2n = 2x = 40$.

Transgressive segregation refers to the appearance of progeny with phenotypic values that fall beyond the range exhibited by either parent. This phenomenon arises when genetic variation contributed by both parental lines recombines through hybridization, allowing complementary alleles to combine and produce exceptionally high or low phenotypic expressions. Such extreme segregants are of particular value in crop improvement, as they may possess superior yield potential, enhanced stress tolerance, or other agronomically important traits (Rieseberg *et al.*, 2003) ^[14]. The accumulation of favourable alleles from both parents can generate progeny with greater fitness than either parent, and recombination between genetically contrasting parents can therefore give rise to offspring displaying exceptionally favourable trait values (Rieseberg *et al.*, 1999) ^[13].

Materials and Methods

The field experiments related to the present investigation entitled "Transgressive segregation studies in F₃ population of soybean (*Glycine max* (L.) Merrill)" were carried out during Kharif season, 2025 at Agril. Botany Research Farm, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri. The material used in the present investigation consisted of F₃ segregants derived from two crosses of soybean involving two females viz. JS 2212 and JS 2216 and a male NRC 142 observed to be promising were selected for this investigation.

The F₃ populations, along with their respective parents, were sown in a non-replicated trial. The F₃ population of each cross was represented by 76 rows, while the parents were represented by double rows of 5.0 m length, spaced 45 cm apart with a plant-to-plant distance of 15 cm. A basal dose of 40 kg N, 20 kg P₂O₅ and 20 kg K₂O ha⁻¹ was applied at sowing and two irrigations were given, one at sowing and the second at the pod-filling stage. All other cultural

operations, including weeding, hoeing and recommended crop protection measures, were carried out as required.

For each cross, observation on thirteen characters were recorded on 500 randomly selected, tagged plants of each F₃ cross and on 20 parent plants: days to first flower initiation, days to maturity, plant height (cm), number of pods plant⁻¹, number of seeds pod⁻¹, number of clusters plant⁻¹, number of primary branches plant⁻¹, number of pods cluster⁻¹, canopy temperature, normalized difference vegetation index, chlorophyll content, 100-seed weight (g) and yield plant⁻¹ (g), determined by standard field measurement and counting procedures at maturity. The Normalized Difference Vegetation Index (NDVI, 0-1 scale) was recorded at different phenological stages using a GreenSeeker handheld crop sensor under clean, dry-canopy conditions; canopy temperature (°C) was measured with a portable Barnes Model PR-10 infrared thermometer at an angle of less than 45° to avoid interference from the soil surface; and chlorophyll content was assessed non-destructively using a SPAD-502 meter.

Transgressive segregants were estimated by calculating the mean, standard deviation, standard error of mean, variance, standard variate and normal deviation (threshold value) for each character (Panse and Sukhatme, 1967). The limiting value of the standard variate corresponding to the range of parental means at the 5 percent probability level was calculated and segregants showing deviation beyond this threshold in the desirable direction alone were considered transgressive segregants.

Results and Discussion

The F₃ populations of two soybean crosses, JS 2212 × NRC 142 (Cross I) and JS 2216 × NRC 142 (Cross II), were examined for transgressive segregation during Kharif, 2025. For thirteen agronomic and physiological traits, frequency distributions and proportions of desirable transgressive segregants were calculated for both individual trait performance and character combinations (Table 1).

For Cross I (JS 2212 × NRC 142), the mean number of days to first flower initiation in the F₃ generation was 36.80, compared with 37.35 and 37.10 days for parents JS 2212 and NRC 142, respectively; 46 plants (9.20 percentage) flowered earlier than the better parent, within a range of 30-47 days. The mean duration to maturity was 99.18 days, with 75 plants having percentage of 15 maturing earlier than the better parent, NRC 142. Mean plant height in the F₃ generation was 42.62 cm, with 38 plants (7.60%) exceeding the better parent. The mean number of pods plant⁻¹ was 34.51, with 66 plants (13.20%) surpassing the better parent, NRC 142. The mean number of seeds pod⁻¹ was 2.73, with 36 plants (7.20%) exceeding the better parent, JS 2212. A mean of 12.52 clusters plant⁻¹ was recorded, with 58 plants (11.60%) exceeding the better parent, NRC 142, while for primary branches plant⁻¹ (mean 5.51), 45 plants (9.00%) exceeded the better parent, JS 2212. The mean number of pods cluster⁻¹ was 2.85, with 40 plants (8.00%) exceeding the better parent, NRC 142. The mean NDVI score was 0.74, with 42 plants (8.40%) recording higher values than the better parent. Mean canopy temperature was 34.65 °C, with 58 plants (11.60%) recording lower canopy temperatures than the better parent, JS 2212. Mean chlorophyll content was 36.70 mg/g, with 42 plants (8.40%) exceeding the better parent. The mean 100-seed weight was 10.29 g, with 61 plants (12.20%) exceeding the better

parent, NRC 142. In the F₃ generation, mean yield plant⁻¹ was 9.68 g, with 64 plants (12.80%) exceeding the better parent, NRC 142 (Table 1).

For Cross II (JS 2216 × NRC 142), the mean number of days to first flower initiation was 37.12, with 64 plants (12.80%) flowering earlier than the better parent, JS 2216. Mean maturity duration was 98.89 days, with 34 plants (6.80%) maturing earlier than the better parent. Mean plant height was 37.25 cm, with 40 plants (8.00%) exceeding the better parent, NRC 142. The mean number of pods plant⁻¹ was 31.94, with 24 plants (4.80%) exceeding the better parent, NRC 142, while the mean number of seeds pod⁻¹ (2.64) showed 14 plants (2.80%) exceeding the better parent. A mean of 11.62 clusters plant⁻¹ was recorded, with 30 plants (6.00%) exceeding the better parent, JS 2216, and for primary branches plant⁻¹ (mean 5.38), 27 plants (5.40%) exceeded the better parent. The mean number of pods cluster⁻¹ was 2.80, with 32 plants (6.40%) exceeding the better parent, NRC 142. Mean NDVI was 0.74, with 24 plants (4.80%) exceeding the better parent. Mean canopy temperature was 33.21 °C, with 21 plants (4.20%) recording lower values than the better parent, NRC 142. Mean chlorophyll content was 38.08 mg/g, with 22 plants (4.40%) exceeding the better parent. The mean 100-seed weight was 11.31 g, with 35 plants (7.00%) exceeding the better parent, and mean yield plant⁻¹ was 9.89 g, with 27 plants (5.40%) exceeding the better parent, NRC 142 (Table 1).

Similar results were obtained by Massey *et al.*, (2008) [9] for days to maturity, plant height, number of pods per plant, number of seeds per plant, 100-seed weight and seed yield. Karkute *et al.*, (2016) [12] reported transgressive segregants for clusters per plant. Analogous results were recorded by Sinhasan (2023) [16] for days to flower initiation, days to maturity, number of pods per plant, number of seeds per pod, 100-seed weight, canopy temperature, chlorophyll content and yield per plant in the crosses viz., KDS 992 × TGX 709-50E and EC 107407 × TGX 709-50E where KDS 992 was a high yielding elite variety. Concordant findings were recorded by Shinde *et al.*, (2025) [15] for plant height, number of primary branches per plant, number of clusters per plant and chlorophyll content from the cross: JS 20-98 × NRC 142, where JS 20-98 was an early maturing and

tolerant to abiotic stresses whereas NRC 142 had null *kti* and *lox2*. Similar results were reported by Nair *et al.*, (2025) [12] in soybean, where significant transgressive segregation was observed for several agronomic and physiological traits in F₂ populations derived from KDS 1201 × TGX 709-50E and JS 20-98 × TGX 709-50E under restricted irrigation, transgressive segregants were identified for days to flowering, days to maturity, plant height, number of pods per plant, seeds per pod, clusters per plant, primary branches per plant, chlorophyll content, canopy temperature, 100-seed weight and yield per plant.

In Cross I (JS 2212 × NRC 142), the transgressive segregants identified as plant numbers # 403, # 385, # 91, # 202, # 229, # 246, # 50, # 155, # 149, # 399, # 72, # 79, # 434, # 290 and # 458 were found to be the most promising transgressive segregants. In addition to enhanced grain yield, these segregants demonstrated superior performance for several important agronomic traits, including days to maturity, plant height (cm), number of pods per plant, seeds per pod, primary branches per plant, 100-seed weight (g), normalized difference vegetation index score, clusters per plant, canopy temperature and chlorophyll content (Table 2). Furthermore, these segregants recorded higher values for the majority of traits compared to the inferior parent.

Similarly, in Cross II (JS 2216 × NRC 142), plant numbers #49, # 400, # 411, # 336, # 325, # 148, # 329, # 137, # 379, # 185, # 183, # 58, # 219, # 294 and # 313 were identified as the most promising transgressive segregants. Alongside improved yield performance, these segregants also showed higher expressions of days to first flower initiation, plant height (cm), number of pods per plant, seeds per pod, primary branches per plant, 100-seed weight (g), normalized difference vegetation index score, clusters per plant, canopy temperature and chlorophyll content (Table 3). These segregants also surpassed the inferior parents for most evaluated traits.

The identified transgressive segregants of both crosses should be advanced and evaluated across multiple locations in subsequent generations; if their superiority is confirmed, they may be considered for release as new varieties or used as valuable parental lines in future breeding programmes.

Table 1: Threshold value, frequency and range of values of transgressive segregants for 13 characters in F₃ generation of two crosses

Sr. No.	Character	F3±S.E.	S.D.	Threshold value	N.D. value	Frequency total	T.S. No.	T.S. Percentage	Range
Cross I: JS 2212 × NRC 142									
1	Days to 1st flowering (No.)	36.80±0.16	3.64	32.30	-1.23	500	46	9.20	30-47
2	Days to maturity (No.)	99.18±0.17	3.80	95.89	-0.87	500	75	15.00	90-108
3	Plant height (cm)	42.62±0.43	9.69	57.77	1.56	500	38	7.60	26.3-60.4
4	No. of pods plant ⁻¹	34.51±0.30	6.73	39.66	0.77	500	66	13.20	19-65
5	No. of seeds pod ⁻¹	2.73±0.01	0.26	3.19	1.82	500	36	7.20	2.1-3.3
6	No. of clusters plant ⁻¹	12.52±0.15	3.35	16.98	1.33	500	58	11.60	7-23
7	No. of primary branches plant ⁻¹	5.51±0.04	0.85	6.98	1.72	500	45	9.00	3-7
8	No. of pods cluster ⁻¹	2.85±0.02	0.54	3.83	1.82	500	40	8.00	2-4
9	NDVI (0-1 scale)	0.74±0.00	0.05	0.82	1.51	500	42	8.40	0.59-0.85
10	Canopy temperature (°C)	34.65±0.21	4.61	28.38	-1.36	500	58	11.60	22.9-45.7
11	Chlorophyll content (mg/g)	36.70±0.21	4.64	43.84	1.54	500	42	8.40	26.3-46.1
12	100 seed weight (g)	10.29±0.07	1.57	12.90	1.66	500	61	12.20	8.04-15.25
13	Yield plant ⁻¹ (g)	9.68±0.12	2.70	12.70	1.12	500	64	12.80	6.01-19.29
Cross II: JS 2216 × NRC 142									
1	Days to 1st flowering (No.)	37.12±0.15	3.31	32.84	-1.29	500	64	12.80	30-43
2	Days to maturity (No.)	98.89±0.24	5.43	91.70	-1.32	500	34	6.80	86-110
3	Plant height (cm)	37.25±0.33	7.36	48.29	1.50	500	40	8.00	24.9-63.4
4	No. of pods plant ⁻¹	31.94±0.35	7.86	45.05	1.67	500	24	4.80	18-64
5	No. of seeds pod ⁻¹	2.64±0.01	0.24	3.17	1.22	500	14	2.80	1.9-3.3

6	No. of clusters plant ⁻¹	11.62±0.11	2.46	15.46	1.56	500	30	6.00	6-21
7	No. of primary branches plant ⁻¹	5.38±0.04	0.82	6.99	1.98	500	27	5.40	3-7
8	No. of pods cluster ⁻¹	2.80±0.02	0.54	3.99	2.21	500	32	6.40	2-4
9	NDVI (0-1 scale)	0.74±0.00	0.04	0.82	1.82	500	24	4.80	0.57-0.86
10	Canopy temperature (°C)	33.21±0.17	3.81	27.78	-1.42	500	21	4.20	26.1-42.7
11	Chlorophyll content (mg/g)	38.08±0.17	3.71	43.99	1.59	500	22	4.40	27.2-45.2
12	100 seed weight (g)	11.31±0.09	1.92	14.16	1.49	500	35	7.00	8.28-17.75
13	Yield plant ⁻¹ (g)	9.89±0.15	3.41	14.03	1.30	500	27	5.40	5.80-22.89

SE: Standard error, SD: Standard deviation, ND: Normal deviation, T.S.: Transgressive segregants

Table 2: Promising transgressive segregants having combinations of desirable attributes in Cross I (JS 2212 × NRC 142)

Plant No.	DFF (No.)	DM (No.)	PH (cm)	PPP (No.)	SPP (No.)	CPP (No.)	PBPP (No.)	PPC (No.)	NDVI (0-1)	CT (°C)	CC (SPAD)	100 SW (g)	YPP (g)	% Yield increase over better parent
Cross I: JS 2212 × NRC 142														
403	32*	93*	30.8	38*	3.1*	11	7*	4*	0.82*	23.3*	44.8*	13.07*	15.40*	39.21
385	30*	90*	32.9	38*	3.1*	10	6*	4*	0.82*	23.7*	46.1*	12.97*	15.28*	38.14
91	42	102*	55.2*	49*	2.7*	16*	6*	3*	0.72	33.3	38.5*	11.50*	15.21*	37.56
202	41	101*	34.5	38*	2.9*	13*	5	3*	0.80*	37.1	43.7*	13.66*	15.05*	36.11
229	31*	91*	60.3*	37*	3.1*	10	6*	4*	0.83*	23.1*	46.1*	13.07*	14.99*	35.55
246	44	105	30.9	46*	2.9*	15*	6*	3*	0.72	33.9	36.5*	11.22*	14.97*	35.33
50	40	100*	55.1*	38*	2.9*	21*	5	2	0.80*	33.5	36.4*	13.50*	14.88*	34.51
155	32*	93*	60.3*	37*	3.1*	12*	7*	3*	0.84*	23.8*	44.9*	12.97*	14.88*	34.51
149	44	105	55.3*	47*	2.8*	16*	6*	3*	0.74*	39.6	35.2	11.25*	14.81*	33.86
399	31*	92*	60.3*	35*	3.2*	9	7*	4*	0.81*	24.1*	44.1*	13.05*	14.62*	32.15
72	46	107	34.2	46*	2.8*	15*	4	3*	0.76*	39.3	40.2*	11.25*	14.49*	31.01
79	44	105	27.8	38*	2.5	13*	6*	3*	0.72	39.8	36.6*	15.25*	14.49*	30.99
434	36*	95*	52.6*	39*	2.6	19*	6*	2	0.73*	40.8	40.1*	14.25*	14.45*	30.65
290	40	101*	52.3*	37*	2.8*	13*	6*	3*	0.77*	33.5	37.4*	13.74*	14.23*	28.70
458	31*	91*	60.4*	33*	3.3*	8	6*	4*	0.83*	23.1*	46.1*	12.98*	14.14*	27.80
JS 2212	37.35	104.00	41.71	27.15	2.67	10.90	5.15	2.65	0.70	32.27	36.29	9.41	6.75	-
NRC 142	37.10	103.00	41.94	32.95	2.59	11.70	5.10	2.75	0.72	32.52	36.17	10.18	9.08	-

*Expression of character higher than the increasing parent

- DFF = Days to first flower initiation
- DM = Days to maturity
- PH = Plant height
- PPP = Pods plant⁻¹
- SPP = Seeds pod⁻¹
- CC = Chlorophyll content (SPAD index)
- CPP = Clusters plant⁻¹
- PBPP = Primary branches plant⁻¹
- PPC = Pods cluster⁻¹
- NDVI = Normalized Difference Vegetation Index (0-1 scale)
- CT = Canopy temperature (°C)
- 100 SW = 100 seed weight
- YPP = Yield plant⁻¹

Table 3: Promising transgressive segregants having combinations of desirable attributes in Cross II (JS 2216 × NRC 142)

Plant No.	DFF (No.)	DM (No.)	PH (cm)	PPP (No.)	SPP (No.)	CPP (No.)	PBPP (No.)	PPC (No.)	NDVI (0-1)	CT (°C)	CC (SPAD)	100 SW (g)	YPP (g)	% Yield increase over better parent
Cross II: JS 2216 × NRC 142														
49	43	98*	29.2	64*	3.2*	16*	6*	4*	0.72	33.3*	44.3*	9.65	19.76*	40.86
400	31*	103	30.6	64*	2.2	16*	5	4*	0.74*	37.6	33.5	14.03*	19.75*	40.80
411	42	91*	43.7*	42*	3.2*	21*	7*	2	0.69	32.3*	41.3*	14.66*	19.70*	40.44
336	31*	92*	41.3*	40*	3.1*	10	7*	4*	0.85*	33.3*	44.5*	15.75*	19.53*	39.20
325	38	106	45.7*	45*	3.2*	15*	5	3*	0.73	40.4	42.8*	13.25*	19.08*	35.99
148	31*	100	35.2	34*	3.1*	17*	7*	2	0.82*	29.9*	44.2*	17.75*	18.71*	33.35
329	35*	102	45.6*	48*	3.2*	16*	6*	3*	0.78*	37.9	40.8*	11.88*	18.25*	30.06
137	39	105	32.7	55*	2.9*	17*	6*	4*	0.75*	39.4	37.5*	11.24*	17.93*	27.78
379	31*	92*	44.2*	47*	2.5	16*	6*	3*	0.84*	41.3	31.6	15.25*	17.92*	27.72
185	31*	102	30.9	52*	2.9*	13*	6*	4*	0.75*	33.2*	39.3*	11.82*	17.82*	27.05
183	40	99*	36.7	49*	2.6	14*	6*	4*	0.79*	33.7	40.9*	13.68*	17.43*	24.22
58	39	96*	29.8	60*	2.6	15*	6*	4*	0.71	33.6	37.8*	11.15	17.39*	23.98
219	37*	107	30.5	48*	2.6	13*	6*	4*	0.73	30.2*	42.3*	13.75*	17.16*	22.31
294	42	102	28.9	43*	2.9*	14*	6*	3*	0.69	35.9	37.2*	13.75*	17.15*	22.21
313	38	95*	38.2*	44*	2.8*	14*	6*	3*	0.72	33.7	38.7*	13.84*	17.05*	21.53
JS 2216	37.35	99.05	35.73	29.05	2.61	11.25	5.30	2.60	0.71	33.73	36.00	10.44	7.91	-
NRC 142	37.55	99.90	36.96	30.50	2.62	11.15	5.20	2.70	0.73	33.53	36.45	11.22	8.90	-

*Expression of character higher than the increasing parent

- DFF = Days to first flower initiation
- DM = Days to maturity
- PH = Plant height
- PPP = Pods plant⁻¹
- SPP = Seeds pod⁻¹
- CC = Chlorophyll content (SPAD index)
- CPP = Clusters plant⁻¹
- PBPP = Primary branches plant⁻¹
- PPC = Pods cluster⁻¹
- NDVI = Normalized Difference Vegetation Index (0-1 scale)
- CT = Canopy temperature (°C)
- 100 SW = 100 seed weight
- YPP = Yield plant⁻¹

Conclusion

Transgressive segregation in the F₃ generation of two soybean crosses led to the identification of valuable recombinants with superior agronomic and physiological performance. In Cross I (JS 2212 × NRC 142), promising segregants recorded yield increases of 27.80 to 39.21 percent over the better parent, while in Cross II (JS 2216 × NRC 142), yield increases ranged from 21.53 to 40.86 percent, with Cross II showing the greater maximum improvement. In both crosses, yield-related traits, particularly pods plant⁻¹, seeds pod⁻¹, clusters plant⁻¹, pods cluster⁻¹ and yield plant⁻¹, were consistently transgressed, alongside frequent transgression for plant height, NDVI, canopy temperature, chlorophyll content and 100-seed weight. These results confirm that favourable alleles from both parents can accumulate through transgressive segregation to produce hybrids with superior trait combinations. The most promising segregants identified in this study, particularly plant No. 403 in Cross I and plant No. 49 in Cross II, merit further evaluation in advanced generations and multi-location trials to confirm their stability and suitability for release as new cultivars or as parental lines in future breeding programmes.

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