



International Journal of Agriculture and Nutrition

ISSN Print: 2664-6064
 ISSN Online: 2664-6072
 NAAS Rating (2026): 4.69
 IJAN 2026; 8(10): 01-06
www.agriculturejournal.net
 Received: 30-07-2026
 Accepted: 26-09-2026
 Published: 06-10-2026

The names and affiliations of all authors are provided below, following the references.

Genetic polymorphism and hybridity testing in elite soybean parental combinations

Namrata Thakare¹, Pravin V Jadhav², Umesh Shinde³, Balaji Jadhav⁴, Mahima Parihar⁵, Chetna Mishra⁶, SS Nichal⁷, Dipika A Padole⁸, SS Mane⁹

DOI: <https://www.doi.org/10.33545/26646064.2026.v8.i10a.761>

ABSTRACT

The present study evaluated parental polymorphism and confirmed hybridity among four soybean cross combinations using simple sequence repeat (SSR) markers. Four elite soybean genotypes, namely AMS MB 5-18, AMS 100-39, NRC-150, and Swarna Vasundhara, were used as parental lines for the development of F_1 populations. A total of 220 SSR markers distributed across 20 linkage groups were screened, of which 145 produced clear amplification and 100 exhibited polymorphisms among the parental genotypes. The identified polymorphic markers showed variation in polymorphism and Polymorphism Information Content (PIC) across the four parental combinations. Two SSR markers, Satt640 and Sat_119, were polymorphic across all four parental combinations and exhibited high PIC values (> 0.85), indicating their potential utility for parental discrimination and background selection. In addition, a null Kunitz trypsin inhibitor (KTI)-specific marker was used to identify F_1 plants carrying the null kti allele derived from NRC-150. Among 36 progenies evaluated from the NRC-150 cross combinations, five plants produced the expected 420 bp amplicon and were identified as putative F_1 hybrids carrying the null KTI allele. The polymorphic SSR markers and KTI-specific marker identified in the present study provide useful molecular resources for parental selection, hybridity confirmation, and marker-assisted breeding aimed at developing food-grade soybean with reduced *anti*-nutritional factors.

Keywords: Soybean, *Glycine max*, SSR markers, Parental polymorphism, Hybridity confirmation, Kunitz trypsin inhibitor, PIC, Marker-assisted breeding

Introduction

Soybean (*Glycine max* L.) often called the “Miracle crop” is an annual dicotyledonous plant belonging to the family Fabaceae (Panzade *et al.*, 2025) [9]. Owing to its exceptionally with high protein content and wide range of application in food, animal feed, and industrial products it's also referred to as functional food and its currently being highlighted for its potential to end malnutrition. (Jadhav *et al.*, 2023) [4] because it comprises protein and oil comprise 60% (40% protein and 20% oil) of the seed with about 30% carbohydrate and other dietary fiber, mineral, vitamins. In 100 g of soybean seeds, the nutritional composition varies among genotypes, with gross energy ranging from 409.82 to 429.98 kcal, crude fat from 17.53 to 23.75 g, calcium from 174.16 to 268.84 mg, iron from 9.84 to 14.30 mg, and phosphorus from 691.73 to 1124 mg (Zewudie *et al.*, 2024) [3]. Soybean is one of the world's most important oilseed and protein crops, playing a vital role in meeting the nutritional requirements of the rapidly growing global population. As the demand for food, feed, and industrial raw materials continues to increase, enhancing crop productivity has become a major priority for ensuring global food security. Global soybean production is estimated at 425.7 million metric tonnes (MMT) in 2025, whereas India's production is projected at 10.5 MMT, representing a decline from 12.5 MMT recorded in 2024. This reduction highlights the need for the development of high-yielding, climate-resilient soybean cultivars capable of maintaining stable productivity under diverse environmental conditions. To address these challenges, modern plant breeding strategies increasingly focus on improving yield stability and sustainability. Among these approaches, marker-assisted selection (MAS) has emerged as a powerful and efficient tool that utilizes DNA markers linked to desirable traits, enabling precise and rapid selection of superior genotypes and thereby accelerating crop improvement programs (Shinde *et al.*, 2018) [11]. In addition to improving yield and productivity, enhancing the nutritional and processing quality of soybean has become an important objective in modern breeding programs. Despite its high protein content, the utilization of soybean is constrained by the presence of *anti*-nutritional factors, particularly the Kunitz trypsin inhibitor (KTI), which interferes with protein digestion. Kunitz trypsin inhibitor (KTI) is a heat-labile, non-glycosylated, monomeric protein of approximately 21–21.5 kDa, consisting of a single polypeptide chain of 181 amino acid residues and containing two disulfide bonds (Liu, 2024; Luo *et al.*, 2025) [7, 8]. It inhibits the activity of trypsin, a proteolytic enzyme secreted by the pancreas, thereby reducing protein di

Corresponding Author:
Namrata Thakare
 Dr. Panjabrao Deshmukh
 Krishi Vidyapeeth, Akola,
 Maharashtra, India

gestibility in monogastric animals such as poultry and swine, as well as in young ruminants. Therefore, the development of soybean cultivars lacking KTI has become a major breeding objective. Besides the *anti*-nutritional effects of Kunitz trypsin inhibitor (KTI), the characteristic beany flavor is another major constraint affecting the acceptability of soybean-based food products. This undesirable flavor results from the oxidation of polyunsaturated fatty acids by lipoxygenase (LOX) enzymes, leading to the formation of volatile compounds such as *n*-hexanal (Wang *et al.*, 2021). Assessment of genetic variation among parental lines is a prerequisite for successful soybean breeding and hybrid development. Several molecular marker systems, including restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), inter-simple sequence repeats (ISSR), and simple sequence repeats (SSR), have been employed for assessing genetic diversity and parental polymorphism in soybean. Among these, SSR markers are particularly useful for soybean genetic diversity analysis because of their polymorphism, reproducibility, and genome-wide distribution (Zatybekov *et al.*, 2023; Singh *et al.*, 2024) [16]. Consequently, SSR markers are valuable tools for parental polymorphism analysis, hybrid verification, and marker-assisted soybean breeding.

Materials and Methods

The parental polymorphism survey evaluated four soybean (*Glycine max* (L.) Merr.) genotypes. Two elite genotypes AMS MB 5-18 and AMS 100-39 characterized by high yield, and resistance to charcoal rot (*Macrophomina phaseolina*), and elevated seed protein content in AMS 100-39 were procured from Dr. Panjabrao Deshmukh Krishi Vidyapeeth (Dr. PDKV), Akola, and served as the recurrent parents. Two donor parents were utilized: NRC-150, possessing the null alleles for Kunitz trypsin inhibitor (*kti*) and lipoxygenase-2 (*lox2*), sourced from the ICAR–Indian Institute of Soybean Research (ICAR-IISR), Indore; and ‘Swarna Vasundhara’, a bold-seeded vegetable-type genotype, acquired from ICAR-RCER, Ranchi.

Hybridization program

The recurrent parents (AMS MB 5-18 and AMS 100-39) were hybridized with the Donor parents (NRC-150 and Swarna Vasundhara) to develop the F_1 populations. Hybridization program was carried out on staggered sowing plot in Kharif 2025 season.

DNA extraction

The chosen genotypes’ young leaves were harvested for the extraction of genomic DNA using the CTAB (Cetyltrimethyl ammonium bromide) technique. The DNA extraction solution (2% CTAB, 100 mM Tris-HCl, 50 mM ethylene diamine tetra acetate (EDTA), and 100 mM NaCl) was applied to crush 15 to 20-day-old soybean leaves. A nanodrop spectrophotometer was used to measure optical density for the quantity and purity of the DNA at 260 and 280 nm and agarose gel electrophoresis was also used to assess the quality of DNA. The

dilution of genomic DNA was prepared at 40ng/μL for further experiment.

Source of microsatellite sequences

The primer sequence and SSR sites were retrieved from the soybean database. A total of 220 SSR markers from 20 linkage groups (LG) were used, with an average density of one SSR marker per 5 cM, to assess the level of polymorphism between different parental combinations for background selection. Null allele specific marker (F 5’ CTTTGTGCCTTCACCCCT3’ and R 5’ GAATTCATCATCAGAACTCTA 3’) was used for screening of positive F_1 plants (Hybrids).

SSR profiling of parents

The polymerase chain reaction was performed using 325 primers in an Eppendorf thermal cycler. In a 10 μL reaction mixture with 2.0 μL DNA (20 ng/l), 1.0 μL 10X buffer, 1.1 μL MgCl₂, 0.1 μL dNTPs (10 mM), 0.4 μL each of forward and reverse SSR primers, 0.068 μL Taq DNA polymerase (5U/ μL), and 4.932 μL nuclease-free water was subjected to PCR amplification. The template DNAs were amplified in a thermo cycler (Applied Bioscience by Thermo Fischer, Waltham, Massachusetts, United states) using the PCR profile: Initial denaturation at 94 °C for 2 minutes. Followed by 32 cycles of denaturation at 94 °C for 1 min, primer annealing at 49 to 52 °C for 2 minutes, and primer elongation at 72 °C for 3 minutes each are then performed. The amplicons’ final elongation was allowed to run its course at 72 °C for 10 min before being put on hold at 4 °C. After completion of amplification, PCR products were stored at –20 °C and the amplified products were analyzed by electrophoresis using 8 % Polyacrylamide gel and visualized by EtBr.

Analysis of SSR polymorphism and detection of informative markers

To assess four genotypes, genotyping by SSR marker was scored based on the presence or absence of the bands was used. The data was then organized as discrete variables into a binary matrix, where score ‘1’ denoted the existence of the band and ‘0’ denoted its absence. This data matrix was subsequently subjected to analysis. The polymorphism information content (PIC) for each chromosomal SSR was calculated using the formula to assess the markers’ informativeness.

$PIC = 1 - \sum P_i^2$ Where P_i is the frequency of the *i*th plus allele among the group of 4 parental genotypes under investigation, and I is the total number of alleles discovered for the SSR marker. The SSR marker’s discriminating power is estimated by the PIC value. The PIC values are divided into three classes: $PIC > 0.7$ = highly informative, then $0.25 > PIC > 0.7$ = moderate, and $PIC < 0.25$ = low. Markers with PIC value above 0.5 are informative in genetic studies and are extremely useful in determining polymorphism rate of specific locus [21]. The evaluation of genetic markers is based on DNA bands of PCR amplification results. The polymorphism percentage was also calculated between the parents with the formula illustrated below:

$$\text{Polymorphism percentage} = \frac{\text{No. of Polymorphic markers}}{\text{Total no. of markers}} \times 100$$

The polymorphism percentage of markers will be calculated as:

$$\text{Polymorphism percentage of marker} = \frac{\text{No. of Polymorphic amplicons}}{\text{Total no. of amplicons}} \times 100$$

Result and Discussion

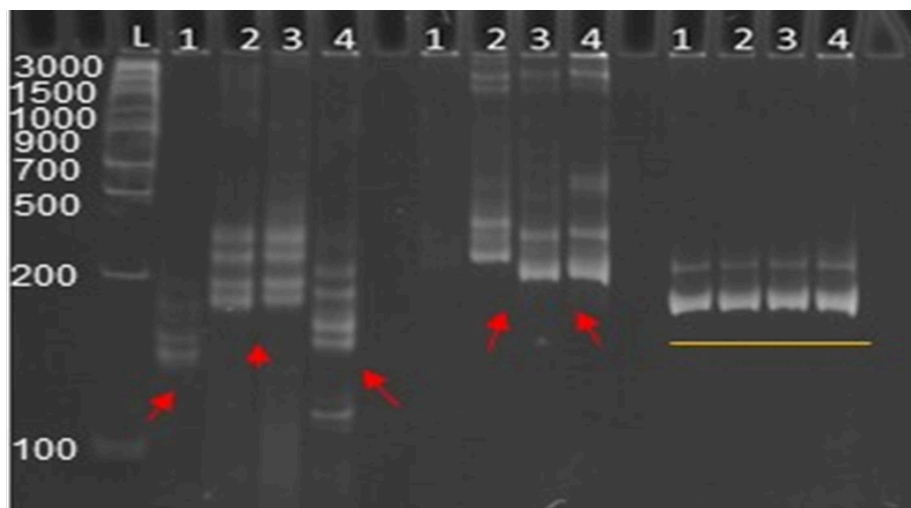
In Kharif 2025 season hybridization program was carried out on four elite soybean genotypes. AMS MB 5-18 and AMS 100-39 as recurrent parents and NRC-150 and Swarna Vasundhara as donor parents. Total 301 crosses of 04 cross combinations were attempted. Out of them 32 were successful to developed pod formations (Table.1)

Parental polymorphism survey

To estimate the level of polymorphism in different parental combinations and select SSR markers for background selection, 220 SSR markers spanning 20 linkage groups (LG) were employed. The four parental genotypes were screened with 220 SSR markers among 145 SSR marker were able to produced amplicons (Fig.1).

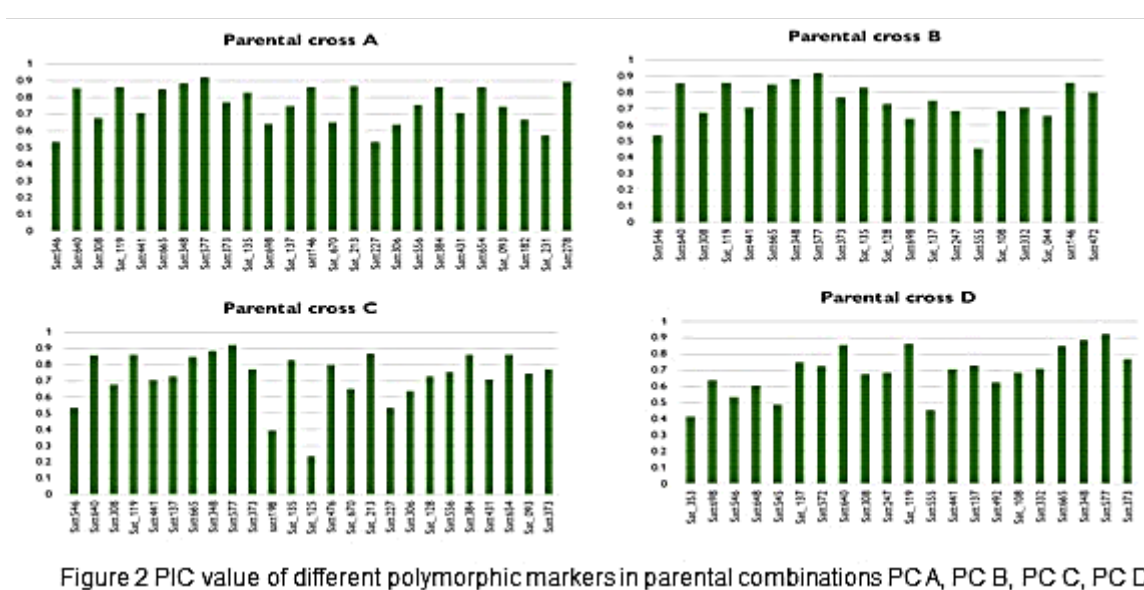
Table 1. Development of F_1 population

Cross combinations	Total No Crosses attempted	No of Pod set	No of Seeds develop	Percentage
AMS MB 5-18 X NRC-150	145	11	20	7.58
AMS MB 5-18 X Swarna Vasundhara	30	6	8	20
AMS 100-39 X NRC-150	96	9	16	9.37
AMS 100-39 X Swarna Vasundhara	36	6	13	16.66
Total	301	32	57	10.63

**Figure 1.** Representative gel picture of polymorphic and monomorphic amplicons ; where L – Ladder 100bp , 1 Swarna Vasundhara, 2 AMS 100-39, 3 AMS MB 5-18, 4 NRC 150

During present investigation, 100 SSR markers clearly showed polymorphic amplification in parental genotypes and 45 SSR marker were showed monomorphic band. Some SSR markers Sat_119, Satt373 and Satt137 shows highly polymorphic present on the K, L and K linkage group with highest PIC value > 0.75. For parental combinations A (AMS MB 5-18 X NRC 150) 25 polymorphic markers identified. The Polymorphic Information Content (PIC) value ranges from 0.53 to 0.9 with 123 polymorphic allele and average percentage is 79.88 % among the identified polymorphic markers for parental combinations A. Across all polymorphic markers the polymorphism percentage varied from 30 to 100 % and seven markers exhibited 100% polymorphism with PIC value 0.63 to 0.89 in parental combination A.

Likewise, 20 polymorphic markers were found for parental combination B (AMS MB 5-18 X Swarna Vasundhara) with PIC value ranging from 0.53 to 0.93. The polymorphism percentage of marker with 108 polymorphic allele for parental combination B. parental combination C (AMS 100-39 X NRC 150) 22 polymorphic markers were found, PIC value ranging from 0.23 to 0.88 and 135 polymorphic allele with average polymorphic percentage 82.78. Furthermore, 21 polymorphic markers were identified for parental combination D. For this combination, the PIC value ranged from 0.45 to 0.92 with a polymorphic percentage 68.97% and a total 107 polymorphic alleles (Table 2, Fig 2).

**Figure 2** PIC value of different polymorphic markers in parental combinations PCA, PC B, PC C, PC D**Figure 2.** PIC Value wise distribution of SSR markers in 4 cross combinations

The PIC value is greater than 0.50% of SSR markers are more informative which will be selected for further breeding programme. Across highly polymorphic SSR markers, two markers i.e. Satt640 and

Sat_119 were found polymorphic in all parental combinations with high PIC value > 0.85 and there are located on chromosome 6. In parental polymorphism analysis revealed three classes of microsatel

lite repeat motifs, namely di, tri and tetra nucleotide repeats. Among the polymorphic SSR markers tri nucleotide repeats were predomi-

nant, followed by di nucleotide 24 and tetra nucleotide 10 across different parental combinations (Table 3, Fig. 3).

Table 2. List of polymorphic markers to 4 parental combinations.

Sr.No	Linkage group	Chr.no	PC A	PC B	PC C	PC D
1	D1a	1			satt198	Sat_353
2	D1b	2	Satt546, Sat_135, Satt698	Satt546, Sat_135, Satt698	Satt546, Sat_135	Satt698, Satt546
3	N	3			Sat_125	
4	C1	4	Sat_670		Satt476, Sat_670	
5	A1	5	Sat_137	Sat_137		Satt648, Satt545, Sat_137, Satt572
6	C2	6	Satt640, Sat_213, Satt227	Satt640	Sat_213, Satt22, Satt640	Satt640
7	M	7	Satt306, Satt308	Satt308	Satt306, Satt308	Satt308
8	K	9	Sat_119, Satt441	Sat_119, Satt441, Satt247, Satt555, Sat_044	Sat_119, Satt441	Satt247, Sat_119, Satt555, Satt441
9	O	10	Sat_231	Sat_108		Satt492, Sat_108
10	B1	11	Satt665	Satt665, Sat_128, Satt332	Sat_128, Satt665	Satt332, Satt665
11	F	13	Satt348	Satt348, satt146	Satt348	Satt348
12	B2	14	Satt577, Satt556	Satt577	Satt577, Satt556	Satt577
13	E	15	Satt384		Satt384	
14	J	16	Satt431, Satt654, Sat_093		Satt431, Satt654, Sat_093	
15	L	19	Satt182, Satt278, Satt373		Satt373, Satt373	Satt373

Table 3. Features of markers with high pic values of different cross combinations

Sr.no.	Primer	Parental Combination	Motif	Product size	Primer Sequence
1	satt198	C	(AAT)11	232	GGCGGTTTGTTTTATCTATTCA
2	Sat_353	D	(TA)22	262	GCGGGTAATGCTAGGTTTGGAAAATGATT
3	Satt546	A,B,C,D	(TTA)20	240	TTTGGATCGCATAACACTTTA
4	Sat_135	A,B,C	(TA)29	200	GCCTCCGCCTCCGAAATACACTTA
5	Satt698	A,B,D	(TTA)17	283	GCGCAATCGCTTCTTTAGAT
6	Sat_125	C	(AT)37	138	GGGATGCTGTTATCAAAATCA
7	Satt476	C	(ATA)20	212	TTGTTAGAATGGGACTACTTCACTA
8	Sat_670	C	(ATT)18	235	TTCTGCATAAGAGATTTTCAGTTTA
9	Sat_137	A,B,D	(AT)16	263	GGTGC GGTTCCACAGTTTTTT
10	Satt545	D	(TTA)24	201	CAATTGCCCTAGTTTGTAGAT
11	Satt572	D	(CAT)4(TAT)17	168	GCGGGCTA ACTTATGTTACTAAACAAT
12	Satt640	A,B,D	(TATT)24	231	GGTTCCCCGGTGGCTACACAAC
13	Sat_213	A,C	(AT)17	193	GCGATCCCTAATTGTTATCTAATAA
14	Satt227	A,C	(GTT)5	144	CACCCTGGCACATAGA
15	Satt640	A,B,C,D	(TATT)24	231	GGTTCCCCGGTGGCTACACAAC
16	Satt306	A,C	(AAT)4	229	GCGTCTCTTTCGATTGTTCTATTAG
17	Satt308	A,B,C,D	(TTA)20	170	GCGCAGCTTTATACAAAATCAACAA
18	Sat_119	A,B,C,D	(TA)24	150	GTTAGGTGTCCCAAGCAACTTA
19	Satt441	A,B,C,D	(ATT)32	282	AAACCCACCCCTCAAAAATAAAAA
20	Satt247	B,D	(ATT)21	218	GCGGATCAATAATAAACAAAGTGACAA
21	Satt555	B,D	(AAT)6tgac (TAT)14	267	TTACCGCATGTTCTTGACTA
22	Sat_044	B	(AT)20	165	TTACCACTAAGAATTAGGTCTAA
23	Sat_108	B,D	(CT)21(AT)16	158	AAAAATCTATTCACCTTTGAGTCTA
24	Satt665	A,B,C,D	(ATT)18	262	GCGCATGACTTAATTTACACCCTTTATTTATTT
25	Sat_128	B,C	(AT)30	218	GGGAGAAAATTTTAATGCCAGTAGTTA

(continued on next page)

Sr.no.	Primer	Parental Combination	Motif	Product size	Primer Sequence	
26	Satt332	B,D	(TTA)8c(TATA)13	245	GCGGTCCTTATATATGGAAGATCA	GCGCATCCAGGGCTTGC
27	Satt348	A,B,C,D	(ATA)20	217	GCGCTTAGTAATGGTTCCCACAGATAA	GCGGTGATATCTAGCA
38	satt146	B	(TAA)16	287	GTGGTGGTGGTGAAGAACTATTAGAA	AAGGGATCCCTCAAC
29	Satt577	A,B,C,D	(ATT)12	118	GGCCTGACCCAAAATAAGGGAAGTG	CAAGCTTAAGTCTTGGT
30	Satt384	A,C	(ATA)16	148	ATTTCCCTTTCACCCACCTCTGTTT	TGGGGGTCAATTCTAA
31	Satt431	A,C	(AAT)21	230	GCGCACGAAAGTTTTTCTGTAACA	GCGTGGCACCCCTGAT
32	Satt654	A,C	(ATA)5 (AAT)4	154	GCTGGGACTCCTCATGTC	AGACGCGCACACAA
33	Sat_093	A,C	(TA)23	203	TATTCATAAGCTTTAATTACACTATAAGAA	CAAGGACTAAATAAGAT
34	Satt472	B	(TTA)37	279	GCGTTCATAAATTCATTCATAGTTTCAAT	GCGAATACATAAAACT
35	Satt182	A	(TAT)17	218	TCTCAGCCTGCAAAGAAAA	GGTCCACATGAATC
36	Satt278	A	(TAA)26	246	GCGGATTCCGTTATCGCCAGTAAT	GCGCTGGTGCATTGAG
37	Satt373	A,C,D	(TAT)21	248	GGCCAGATACCCAAGTTGTACTTGT	TCCGCGAGATAAATTC

Confirmation of hybrid by using null KTI specific primer

The F_1 progenies developed in Kharif 2025 seasons were checked with the help of Null KTI specific marker specified for the null KTI allele from donor NRC150 with 420bp amplicons. Out of 36 plants

derived from NRC150 cross combinations 5 plants found to be hybrid with presence of null KTI allele at 420bp (Fig.3).

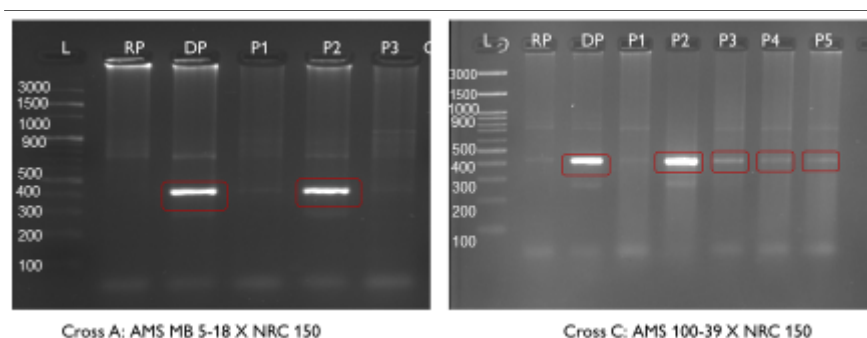


Figure 3. Hybridity confirmation in F_1 progenies

Conclusion

The present study identified informative SSR markers for assessing genetic polymorphism among four soybean parental genotypes used in the development of food-grade soybean breeding populations. Among the 220 SSR markers screened, 145 produced clear amplification and 100 were polymorphic, providing a useful set of markers for distinguishing the parental genotypes and supporting background selection. Satt640 and Sat_119 showed polymorphism across all four parental combinations with high PIC values, indicating their potential utility for parental discrimination. In addition, screening with a null KTI-specific marker identified five putative F_1 hybrids carrying the null *kTi* allele among the 36 progenies evaluated from NRC-150-derived crosses. These marker resources can support subsequent generation advancement, selection and molecular characterization of segregating populations aimed at developing soybean lines with reduced KTI content and improved food quality. Further evaluation of the identified progenies through segregation analysis and phenotypic and/or biochemical characterization will be required to confirm the stability and breeding value of the selected material.

Acknowledgement

This work was supported by the State Government of Maharashtra under the project "Establishment of Centre of Excellence for Enhancing Crop Productivity under Climate Resilience of Vidarbha Region" (Sanction No. BBA/2023/880; dated 27.06.2023). The authors are grateful to Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, for providing parental seed materials and field/laboratory facilities at the Biotechnology Centre, Post Graduate Institute. We also sincerely thank Dr. Vineet Kumar, Principal Scientist, ICAR-IISR,

Indore, Madhya Pradesh, for kindly supplying the donor seed material.

Data availability

Data will be made available on request

References

- Botstein D, White RL, Skolnick M, Davis RW. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *American Journal of Human Genetics*. 1980;32(3):314.
- Cregan PB, Mudge J, Fickus EW, Marek LF, Danesh D, Denny R, Young ND. Targeted isolation of simple sequence repeat markers through the use of bacterial artificial chromosomes. *Theoretical and Applied Genetics*. 1999;98(6):919-928.
- Getaneh Zewudie K, Gemedie HF. Assessment of nutritional, antinutritional, antioxidant and functional properties of different soybean varieties: Implications for soy milk development. *Cogent Food & Agriculture*. 2024;10(1):2380496.
- Jadhav PV, Shinde AN, Thakur PP, Shinde UD, Mahobia A. Genome-wide microsatellite survey and introgression of null KTI allele in charcoal rot resistant soybean. *Journal of Human Nutrition and Food Science*. 2023;11(4):1172.
- Karp A, Seberg OLE, Buiatti M. Molecular techniques in the assessment of botanical diversity. *Annals of Botany*. 1996;78(2):143-149.
- Koide T, Ikenaka T. Studies on soybean trypsin inhibitors. 1. Fragmentation of soybean trypsin inhibitor (Kunitz) by limited proteolysis and by chemical cleavage. *European Journal of Biochemistry*. 1973;32(3):401-407.

7. Liu K. Enzymatic and algebraic methodology to determine the contents of kunitz and Bowman-Birk inhibitors and their contributions to total trypsin or chymotrypsin inhibition in soybeans. *Journal of Agricultural and Food Chemistry*. 2024;72(20):11782.
8. Luo Z, Zhu Y, Xiang H, Wang Z, Jiang Z, Zhao X, Guo Z. Advancements in inactivation of soybean trypsin inhibitors. *Foods*. 2025;14(6):975.
9. Panzade SA, Chimote VP, Shinde CS, Aher AR. Identification of Soybean (*Glycine max* L.) Segregants for Kunitz Trypsin Inhibitor and Lipxygenase Free Gene Using Linked Molecular Markers. *Plant Cell Biotechnol. Mol. Biol.* 2025;26:33-34.
10. Saini M, Yadav RR, Kumar R, Chandra S, Rathod NKK, Taku M, Talukdar A. Mapping of quantitative trait loci and mining of candidate genes for seed viability in soybean [*Glycine max* (L.) Merr.]. *Frontiers in Plant Science*. 2025;15:1372037.
11. Shinde UD, Agrawal T, Pradhan A, Kadu T, Kotasthane AS, Verulkar SB. Development of blast resistant Dubraj by introgression of resistant genes through marker assisted selection. *International Journal of Current Microbiology and Applied Sciences*. 2018;7(6):3113-3118.
12. Shen Y, Jia QL, Liu MZ, Li ZW, Wang LL, Zhao CZ, Li ZX, Zhang M. Genome-wide characterization and phylogenetic and expression analyses of the Caleosin gene family in soybean, common bean, and barrel medic. *Archives of Biological Sciences*. 2016;68(3):575-585.
13. Wang J, Kuang H, Zhang Z, Yang Y, Yan L, Zhang M, Song S, Guan Y. Generation of seed lipoxygenase-free soybean using CRISPR-Cas9. *Crop Journal*. 2020;8:432-439.
14. Williams JGK, Kubelik AR, Livak KJ, Rafalski JA, Tingey SV. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*. 1990;18:6531-6535.
15. Welsh J, McClelland M. Fingerprinting genomes using PCR with arbitrary primers. *Nucleic Acids Research*. 1990;18:7213-7218.
16. Zatybekov A, Yermagambetova M, Genievskaya Y, Didorenko S, Abugaliyeva S. Genetic diversity analysis of soybean collection using simple sequence repeat markers. *Plants*. 2023;12(19):3445.

How to cite this article: Thakare N, Jadhav PV, Shinde U, Jadhav B, Parihar M, Mishra C, et al. Genetic polymorphism and hybridity testing in elite soybean parental combinations. *International Journal of Agriculture and Nutrition*. 2026;8(10):01-06. doi: <https://www.doi.org/10.33545/26646064.2026.v8.i10a.761>

Authors

Namrata Thakare

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

Pravin V Jadhav

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

Umesh Shinde

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

Balaji Jadhav

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

Mahima Parihar

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

Chetna Mishra

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

SS Nichal

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

Dipika A Padole

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

SS Mane

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India