SSR Based Genetic Diversity in Magic Lines of Soybean (Glycine max (L.) Merrill)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Soybean MAGIC lines are recently developed by tailor made source of germplasm that have undergone heavy genetic recombination. The present study was carried out in Kharif 2018 to Rabi 2019 - 20 to assess its extent of genetic diversity at molecular level in 95 soybean MAGIC lines along with six checks by using 30 SSR markers from which 27 were found polymorphic. A total of 106 alleles were generated with an average of 3.53 and a range of two to six alleles per locus. The value of observed heterozygosity was varying from 0.00 to 0.099 indicating a higher frequency of homozygotes among the accessions. Maximum PIC was 0.955 for Staga001 followed by 0.948 (Satt168, Satt453, Satt534), 0.947 (Satt565) and 0.945 (Satt371). The range of Jaccard's similarity coefficient was varying from 0.089 to 1, most of the values were between 0.2 to 0.3 with an average of 0.3 indicating considerable diversity exists among the genotypes. A total of six main clusters were formed by UPGMA clustering method. Cluster II was the largest comprising 48 genotypes which were grouped into four sub-clusters. Clustering based on SSR markers revealed a very precise grouping of the genotypes based on their relatedness than their phenotypic data alone.

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Hence it can be successfully deployed for selecting desirable genotypes which can be utilized in future breeding programs for exploiting heterosis or in the introgression of genes for biotic and abiotic stress tolerance in soybean crop.

**Keywords:** Soybean; SSR markers; magic lines; genetic diversity.

### 1. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is globally cultivated leading oilseed crop otherwise known as golden bean for its various nutritional qualities. The enormous economic value of soybean was realized in the first two decades of the twentieth century, therefore the crop is well known as the miracle bean of the twentieth century [1]. In India, it was introduced in 1000 AD through silk route whereas major commercial cultivation was initiated during 1960s, mostly after the launch of AICRP on soybean in 1967 [2]. Although soybean is classified as an oilseed (18–23% oil on a moisture-free basis), its seed also contains about 38–44% protein [3]. It is a rich source of poly unsaturated fatty acids, vitamin B, fibre, iron, calcium, zinc and isoflavones which substantially increases its nutritional quality. It accounts for the production of two-thirds of the world’s protein concentrates for livestock feeding [4].

Worldwide the crop is cultivated in an area of 124.92 m ha with production of 348.71 mt and productivity of 2791 kg ha$^{-1}$. Globally India stands in fourth position with the cultivable area of 11.40 mha and fifth in the production of 13.78 mt and having a productivity of 1209 kg ha$^{-1}$ [5], which is very low in order to cater the demand of the growing population.

Due to the repetitive use of the same parents during the breeding program, the genetic base of Indian soybean cultivars has become extremely narrow. Diversity among germplasm is the most important thing to be considered before proceeding for any successful and efficient breeding program [6]. The study of diversity is important to reveal the exact allelic diversity among the germplasm at the molecular level.

Among the molecular markers particularly, SSRs are most widely used in the estimation of genetic diversity as it is more reliable, locus-specific, reproducibility, high polymorphism rate, co-dominant and less influenced by environmental fluctuations [10]. Molecular characterization of germplasm accessions reveals underlying allelic diversity and the genetic base of germplasm collection [11]. Soybean being a narrow genetic base crop, analysis of crop diversity using DNA marker is very important to reveal the exact allelic diversity among the germplasm at the molecular level.

### 2. MATERIALS AND METHODS

Five hundred soybean MAGIC lines (F5 generation) obtained from AICRP-Soybean, IISR, Indore was initially evaluated for genetic diversity during *Kharif* 2018 and *Kharif* 2019. The 95 MAGIC lines along with six checks viz., JS 335, Basara, NRC 86, EC333901, EC546882 and EC572109 were exhibiting high genetic diversity. Basara is a high yielding pod-shattering tolerant local check variety which was developed by ARS, Adilabad and remaining five checks are founder parents of the studied MAGIC lines. Hence this material is further subjected to Molecular characterization during *Rabi* 2019-20 at Institute of Biotechnology (IBT), College of Agriculture, PJTSAU, Rajendranagar, Hyderabad to assess lines with high molecular diversity for attempting further crossing programme.

A total of 30 Soybean SSR markers distributed across 18 chromosomes were selected for genotyping all the 101 soybean MAGIC lines which are enlisted in Table 1. The assessment of
molecular diversity was carried out from the SSR allelic data.

2.1 Scoring of SSR Markers

Amplified PCR products generated by SSR markers for all the soybean accessions were scored visually for the presence or absence of the corresponding DNA bands. The score ‘1’ and ‘0’ indicates the presence and absence of the bands, respectively. The size of the amplified PCR product was estimated with the help of image lab software of BIORAD XR⁺ Gel documentation system using 50bp DNA ladder as the standard size.

2.2 Marker Polymorphism

The polymorphism information content (PIC) is the value that indicates the polymorphism exists among the genotypes for a marker locus used in the linkage analysis. PIC value for each SSR marker was calculated to measure the informativeness of the markers, according to the following formula [12].

\[ \text{PIC} = 1 - \left( \sum P_i^2 \right) \]

Where,
\[ i = \text{total number of alleles detected for SSR marker} \]
\[ P_i = \text{frequency of the } i^{th} \text{ allele of a particular locus} \]

2.2.1 Observed heterozygosity

Observed heterozygosity indicates the proportion of individual in a population that are heterozygous for a particular locus. It was calculated by the following formula.

\[ H_o = \frac{\sum N_i}{N} \]

Where,
\[ H_o = \text{Observed heterozygosity} \]
\[ N_i = \text{Number of diploid individual with genotype } A_A \text{ (Heterozygotes)} \]
\[ N = \text{Total number of genotypes} \]

2.2.2 Cluster analysis

For assessing the molecular diversity among all the soybean accessions binary data matrix (score ‘1’ and ‘0’) of SSR markers of all the genotype were subjected to cluster analysis using SAHN (Sequential agglomerative hierarchical non-overlapping) clustering technique performed on squared Euclidean distance matrix. Then Jaccard’s coefficient was calculated using SIMQUAL (Similarity for Qualitative Data) program. The similarity coefficients were used to construct dendrogram using UPGMA (Unweighted Pair Group Method with Arithmetic mean) tool of NTSYS-pc (Numerical Taxonomy and Multivariate Analysis System) version 2.11 software [13].

3. RESULTS AND DISCUSSION

3.1 SSR Polymorphism among All the Soybean Accessions

The PCR amplification of the genomic region of 101 soybean accessions was carried out using 30 SSR markers. Twenty seven markers were polymorphic and three markers (Satt400, Satt175 and Satt618) were found to be monomorphic. The per cent polymorphism was observed to be 90 % for all the markers indicating the presence of variable SSR loci in the studied soybean accessions. A total of 106 alleles were generated with an average of 3.53 and a range of two to six alleles per loci. A maximum of six alleles were generated by Staga001 and a minimum of two alleles were detected by four markers namely Satt289, Satt162, Satt538 and Satt481. The amplified PCR product size was ranging from 95 to 350 base pairs. The mean observed heterozygosity (Ho) and the mean polymorphic Information content (PIC) were observed to be 0.03 and 0.79 respectively.

3.2 Observed Heterozygosity (Ho) and Polymorphic Information Content (PIC)

The heterozygosity of a marker is the likelihood of an individual being heterozygous at the marker site and depends on the number of alleles and their frequency in the population [14]. It provides an overall picture of the presence of heterozygote individuals in the population. Soybean being a self-pollinated crop observed heterozygosity is likely to be very less. The range of observed heterozygosity was varying from 0.00 to 0.099 (Table 2). The maximum heterozygosity was shown by the marker staga001 (0.099), followed by Satt126 (0.089), Satt619 (0.079), Satt168 (0.079) and Satt523 (0.059). The complete homozygosity was recorded in seven markers including monomorphic markers viz., Satt162, SOYGPATR, Satt463, Satt143, Satt400, Satt175,
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3.3 Genetic Similarity Coefficient among All the Soybean Cultivars

The estimation of genetic similarity between the individuals is an important and decisive point for clustering and analysing the extent of diversity present among the genotypes within a population [19]. Jaccard’s similarity coefficient is most widely used to compute the genetic relationship among the cultivars so as to group them into various clusters. Among all the soybean accessions a total of 5050 pairs of Jaccard’s similarity coefficients were computed. The range of similarity coefficient was observed varying from 0.089 to 1. However, most of the values were between 0.2 to 0.3 with an average of 0.3 indicating considerable diversity exists among the genotypes. The distribution pattern of all the similarity coefficient indicating a very low level of genetic similarity among the soybean accessions which may have resulted due to the genetic recombination and gene reshuffling during the development of MAGIC lines. The results revealed a low value of average similarity coefficient which is in agreement with the result obtained by [20,21] and [22].

3.4 Cluster Analysis

Cluster analysis is a very useful technique in computing the genetic relationships among the populations of diverse origins in a simplified manner. It is also effective in indicating accessions with useful traits belonging to different clusters for hybridization. In the present study, the molecular diversity was computed by UPGMA (Unweighted Pair Group Method with Arithmetic mean) and SAHN (Sequential, Agglomerative, Hierarchical and Nested) clustering algorithm of NTSYS-pc version 2.02 software [13]. The dendrogram was constructed using Jaccard’s similarity coefficients among all the pairs of genotypes based on SSR marker data. The average of all the pairs of similarity coefficient among the genotypes was found to be 0.3 at which the cut-off line was drawn to calculate the number of clusters. The dendrogram (Fig. 2) reveals a significant amount of diversity among the accessions that grouped them into six main clusters and is presented in Table 3.

Cluster I was formed at 0.34 Jaccard’s similarity coefficient which comprised of 12 genotypes. A total of four checks (EC333901, EC546882, Basara and EC572109) along with eight MAGIC lines were grouped into it indicating that these checks have distinct genotypic composition than rest of the accessions. Cluster II was found to be the largest comprised of 48 genotypes which formed at 0.3 similarity coefficient. The cluster II was grouped into two sub-clusters viz., IIA and IIB which were further grouped into IIA1, IIA2, and IIB1, IIB2 respectively. These four sub-clusters were formed at 0.35, 0.37, 0.40 and 0.35 similarity coefficient respectively. The sub-cluster IIA1 had a total of 21 MAGIC lines belongs to the series 7 (7-126, 7-144, 7-141), 8 (8-06, 8-29, 8-41, 8-13, 8-42, 8-98, 8-11), 9 (9-114, 9-115, 9-149, 9-144, 9-145) and 10 (10-03, 10-20, 10-01, 10-06, 10-02, 10-10) including the check JS 335. The grouping suggests some amount of similarities among the MAGIC lines with JS 335 which may have resulted during the MAGIC pedigree development. The sub-cluster IIA2 had a total of 11 MAGIC lines belongs to the series 9. The sub-cluster IIB1 was formed at similarity coefficient 0.4, comprised of six MAGIC lines belongs to the series 8 (8-106, 8-107, 8-118, 8-120, 8-125, 8-137). Similarly, nine accessions (8-53, 9-125, 8-67, 8-92, 8-86, 8-99, 8-95, 8-68, 8-69) were grouped together in cluster IIB2. Cluster III had nine accessions which were formed at similarity coefficient 0.35. The cluster IV (16
accessions) was formed at the similarity coefficient 0.34 which was further grouped into IVa (6 genotypes) and IVb (10 genotypes) with similarity coefficient 0.35 and 0.39 respectively. Cluster V was found to be a solitary cluster formed at similarity coefficient of 0.26. It contained a single genotype namely, 7-124 indicating its distinctness from the rest of the accessions. Cluster VI was formed at similarity coefficient 0.32 and was grouped into two sub-clusters namely, VIa and VIb formed at similarity coefficient 0.34 and 0.37 respectively. The genotypes belong to cluster VIa was NRC-86, 6-32, 6-43, 8-134. Similarly, a total of 11 MAGIC lines of series 6 (6-46, 6-68, 6-48, 6-62, 6-97, 6-100, 6-120, 6-124) and 7 (7-36, 7-03, 7-04) were included in the cluster VIb indicating a considerable amount of similarity exist among these genotypes.

| S. No. | Markers      | Markers sequence             |
|-------|--------------|------------------------------|
| 1     | Staga001 Forward | GCGGAGGGAGTTTGCGAGATTA       |
|       | Staga001 Reverse  | GCGGCAAGGGCAACTGAAAAAT     |
| 2     | Satt720 Forward  | GGCATATACGAAAAATTTTGTCAAGTTACA |
|       | Satt720 Reverse   | GCGTCATGAGTGGTTGTCTATACTTCTAT |
| 3     | Satt656 Forward   | GCGTACTAATATGGCAATTATTTGTG     |
|       | Satt656 Reverse    | GCGTGTTTACGATTTGGATAATAGAAT |
| 4     | Satt666 Forward   | TGCTGTTGACCTCTACTTTTTATTAG       |
|       | Satt666 Reverse    | TCATGCACTCAATTTCTTTATCATAT |
| 5     | Satt686 Forward   | AGGGAAATAAATGAAAACTAAGA |
|       | Satt686 Reverse    | GCGCATCAGATAGAGCAGAGAAATAGAAT |
| 6     | Satt631 Forward   | GGTAGATCCAGAGGTTGCTGACAG |
|       | Satt631 Reverse    | GGCATCCTACTGCACCTGTATTTT |
| 7     | Satt126 Forward   | GCTTGGTAGCTGTAGAGA |
|       | Satt126 Reverse    | ATAAAAACAAATTTCTGATAT      |
| 8     | Satt129 Forward   | TTCAGTACAAGTGCCGGAATAATAATAA |
|       | Satt129 Reverse    | TTCAGTACAAGTGCCGGAATAATAATAA |
| 9     | Satt168 Forward   | CGCTTGCCAAAAATTTAGTA |
|       | Satt168 Reverse    | CACTTCTTCAAATTTCTATAT |
| 10    | Satt289 Forward   | GCGCCAGGTGTATAAAGT |
|       | Satt289 Reverse    | CGCCCCATCAGCTAGCCTTTT |
| 11    | Satt286 Forward   | GCGCGTAAATTTATGCCGGAAGA |
|       | Satt286 Reverse    | GCGTTGGCTAGAGATTTTCTCA |
| 12    | Satt371 Forward   | TGCAAATACCTGGCATTCTCA |
|       | Satt371 Reverse    | GAGATCAGGAAATTTATGTGAAC |
| 13    | Satt453 Forward   | GCGGAAAAAAACAAATTAACAAAC |
|       | Satt453 Reverse    | TAGTTGGGAGGAGGAGTTACC |
| 14    | Satt534 Forward   | CTCCTCTTTGCCCAAACAAATA |
|       | Satt534 Reverse    | GGGGGAATCTAGGCAGCAAG |
| 15    | Satt565 Forward   | GCGCCCGGAAACTTTGATAAATCTTAA |
|       | Satt565 Reverse    | GCGCTCTTTATGTTTTCATATATAA |
| 16    | Satt162 Forward   | GGGGAAGAAGGTTATGTGCTACTCAA |
|       | Satt162 Reverse    | GGTTAAATTTTTATTTCTCTAATAAGT |
| 17    | Satt619 Forward   | GCGAGAAGTCTAGCGCTTTCTGATT |
|       | Satt619 Reverse    | GCGGTAGCGATAATAGACGACCT |
| 18    | SOYGPATR Forward  | GGAAGAAGTATTTGCTGT |
|       | SOYGPATR Reverse   | AGAGAGAGATGACAGAGATTA |
| 19    | Satt523 Forward   | GCGATTTCCTTCTGTTTAAGAATTCTTCTG |
|       | Satt523 Reverse    | GCGCTTTTTTCGGCTTATTTTTAACT |
| 20    | Satt389 Forward   | GCGGCTGGTGATGTTGGAATACAA |
|       | Satt389 Reverse    | GGCAGGAAAAAAAGCTTTATT |
| 21    | Satt600 Forward   | GCGCAGGAAAAAAACGCTTTTATT |
|       | Satt600 Reverse    | GCGGAAATCCTACTGGTTAAT |
| 22    | Satt598 Forward   | CGATTGGAATATATATTACCTCGCTATA |
| S. No. | Markers     | Markers sequence                      |
|-------|-------------|---------------------------------------|
| 12    | Satt598     | CACAATACCTGTGGCTGTTATACTAT            |
| 13    | Satt538     | GCAGGCTTATCTTAAGACAAAT                |
| 24    | Satt481     | GGGTAAACGTCCACACATCTATT              |
| 25    | Satt463     | GACGTTTTAAACGGAAGAAAAT               |
| 26    | Satt143     | GTGCCAATAATTGAGAACAGGA               |
| 27    | Satt400     | TGGTACATCAAACGTTA                    |
| 28    | Satt175     | GACCTCGTCTCTTGTATTTCG                |
| 29    | Satt618     | GCGGTGATATTACCCCAAAAAAAATGA          |
| 30    | Satt184     | GCCACCTGTTACTCAT                     |

Table 2. Molecular profile of 101 soybean accessions generated by 30 SSR markers

| S. No. | Markers | Allelic size (bp) | Chromosome number | Linkage group | Number of alleles | Observed heterozygosity | PIC |
|--------|---------|------------------|------------------|---------------|------------------|-------------------------|-----|
| 1      | Staga001 | 200-300          | 6                | C2            | 6                | 0.0396                  | 0.955 |
| 2      | Satt720  | 270-305          | 15               | E             | 3                | 0.0396                  | 0.859 |
| 3      | Satt656  | 120-155          | 13               | F             | 3                | 0.0396                  | 0.852 |
| 4      | Satt666  | 200-265          | 12               | H             | 5                | 0.0198                  | 0.929 |
| 5      | Satt686  | 290-350          | 16               | J             | 4                | 0.0594                  | 0.914 |
| 6      | Satt631  | 110-160          | 3                | N             | 4                | 0.0297                  | 0.895 |
| 7      | Satt129  | 110-140          | 14               | B2            | 3                | 0.0891                  | 0.846 |
| 8      | Satt129  | 110-140          | 1                | D1a           | 3                | 0.0198                  | 0.835 |
| 9      | Satt168  | 140-200          | 14               | B2            | 5                | 0.0792                  | 0.948 |
| 10     | Satt289  | 200-240          | 6                | C2            | 2                | 0.0198                  | 0.608 |
| 11     | Satt286  | 200-250          | 6                | C2            | 4                | 0.0198                  | 0.917 |
| 12     | Satt371  | 240-300          | 6                | C2            | 5                | 0.0099                  | 0.945 |
| 13     | Satt453  | 210-270          | 11               | B1            | 5                | 0.0297                  | 0.948 |
| 14     | Satt534  | 145-210          | 14               | B2            | 5                | 0.0495                  | 0.948 |
| 15     | Satt565  | 160-225          | 4                | C1            | 5                | 0.0297                  | 0.947 |
| 16     | Satt162  | 260-300          | 20               | I             | 2                | 0                       | 0.768 |
| 17     | Satt619  | 110-140          | 5                | A1            | 4                | 0.0792                  | 0.928 |
| 18     | SOYGPA   | 95-125           | 4                | C1            | 5                | 0                       | 0.943 |
| 19     | Satt523  | 150-190          | 19               | L             | 4                | 0.0594                  | 0.922 |
| 20     | Satt389  | 200-250          | 17               | D2            | 3                | 0.0495                  | 0.824 |
| 21     | Satt600  | 150-240          | 2                | D1b           | 5                | 0.099                   | 0.926 |
| 22     | Satt598  | 150-190          | 15               | E             | 4                | 0.0297                  | 0.921 |
| 23     | Satt538  | 100-110          | 8                | A2            | 2                | 0.0999                  | 0.613 |
| 24     | Satt481  | 145-155          | 19               | L             | 2                | 0.0099                  | 0.743 |
| 25     | Satt463  | 150-190          | 7                | M             | 4                | 0                       | 0.928 |
| 26     | Satt143  | 190-220          | 19               | L             | 3                | 0                       | 0.878 |
| 27     | Satt400  | 205              | 18               | G             | 1                | 0                       | 0     |
| 28     | Satt175  | 160              | 7                | M             | 1                | 0                       | 0     |
| 29     | Satt618  | 260              | 7                | M             | 1                | 0                       | 0     |
| 30     | Satt184  | 140-175          | 1                | D1a           | 3                | 0.0099                  | 0.921 |
Fig. 1. Polymorphic Information content (PIC) of all the 30 SSR markers

Fig. 2. Dendrogram of 101 soybean accessions by UPGMA clustering method using Jaccard's similarity coefficient

Table 3. Clusters formed by 101 soybean genotypes using UPGMA and SAHN clustering

| Cluster | Genotypes included                                                                 | Total |
|---------|------------------------------------------------------------------------------------|-------|
| Cluster I | EC333901, EC546882, Basara, 10-33, 10-34, EC572109, 7-112, 9-12, 9-14, 9-24, 10-31, 10-32 | 12    |
| Cluster IIa | JS 335, 7-126, 7-144, 8-06, 8-29, 8-41, 8-13, 8-98, 7-141, 8-11, 9-114, 9-115, 8-42, 9-149, 9-144, 9-145, 10-03, 10-20, 10-01, 10-06, 10-02, 10-10 | 22    |
| Cluster IIa | 9-94, 9-97, 9-91, 9-116, 9-120, 9-122, 9-132, 9-135, 9-143, 9-141, 9-131 | 11    |
| Cluster IIb | 8-106, 8-107, 8-118, 8-120, 8-125, 8-137 | 6     |
| Cluster IIb | 8-53, 9-125, 8-67, 8-92, 8-86, 8-99, 8-95, 8-68, 8-69 | 9     |
| Cluster III | 7-51, 7-53, 7-78, 7-80, 7-82, 7-85, 7-94, 7-92, 7-122 | 9     |
| Cluster IVa | 10-38, 8-39, 6-05, 6-23, 6-31, 6-30 | 6     |
| Cluster IVa | 10-35, 10-41, 10-42, 10-50, 10-51, 10-54, 10-48, 10-36, 10-52, 10-53 | 10    |
| Cluster V  | 7-124 | 1     |
| Cluster VIa | NRC 86, 6-32, 6-43, 8-134 | 4     |
| Cluster VIa | 6-46, 6-68, 6-48, 7-03, 6-62, 6-97, 6-100, 7-04, 6-120, 6-124, 7-36 | 11    |
4. CONCLUSION

Soybean MAGIC lines belong to the same series were usually grouped together indicating a better similarity among these genotypes. Three founder parents (EC333901, EC546882, EC572109) and the check Basara, were clustered separately from majority of the accessions indicating that the studied MAGIC lines have undergone several new recombinations which were found to be genetically varied with their founder parents and are also have an average similarity coefficient of 0.3. Hence, the selected MAGIC lines are highly variable and diverse which can be utilized in crop improvement program.

FURTHER RESEARCH

Rational use of both the morphological and molecular clustering pattern may be useful for selecting desirable genotypes which can be utilized in future breeding programs for exploiting heterosis or in the introgression of genes for biotic and abiotic stress tolerance.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Bidush Ranjan Swar, Swarna latha V, Rajendar Reddy M, Vanisri S. Assessment of genetic variability parameters in magic population of Soybean [Glycine max (L.) Merrill]. The Bioscan. 2020;15(2):271-274.
2. Tiwari SP. Raising the yield ceiling in soybean-An Indian overview. Soybean Research. 2014;12(2):1-43.
3. Rizzo G, Baroni L. Soy, soy foods and their role in vegetarian diets. Nutrients. 2018;10:1-51.
4. Agarwal DK, Billore SD, Sharma AN, Dupare BU, Srivastava SK. Soybean: Introduction, improvement and utilization in India—Problems and prospects. Agricultural Research. 2013;2(4):293-300.
5. Anonymous. 2018. Available:https://www.fao.org/faostat/en/#data/QC
6. Darvasi A, Soller M. Advanced intercross lines, an experimental population for fine genetic mapping. Genetics. 1995;141(3):1199-1207.
7. Swarna Latha V, Eswari KB, Sudheer Kumar S. Genetic diversity analysis in Greene gram (Vigna radiata (L.) Wilczek.). Progressive Research. 2016;11(V):3051-3053.
8. Bandillo N, Raghavan C, Muyco PA, Sevilla MAL, Lobina IT, Dilla-Ermita CJ, Tung CW, McCouch S, Thomson M, Mauleon R, Singh RK. Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding. Rice. 2013;6(1):1-15.
9. Mackay IJ, Bansept-Basler P, Barber T, Bentley AR, Cockram J, Gosman N, Greenland AJ, Horsnell R, Howells R, O’Sullivan DM, Rose GA. An eight-parent multiparent advanced generation inter-cross population for winter-sown wheat: creation, properties, and validation. Genes, Genomes, Genetics. 2014;4(9):1603-1610.
10. Gupta S, Manjaya J. Genetic diversity and population structure of Indian soybean [Glycine max (L.) Merr.] revealed by simple sequence repeat markers. Journal of Crop Science and Biotechnology. 2017;20(3):221-230.
11. Kumawat G, Singh G, Gireesh C, Shivakumar M, Arya M, Agarwal DK, Husain SM. Molecular characterization and genetic diversity analysis of soybean (Glycine max (L.) Merr.) germplasm accessions in India. Physiology and Molecular Biology of Plants. 2015;21(1):101-106.
12. 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;32:314-331.
13. Rohlf FJ. NTSYS-PC.Numerical taxonomy and multivariate analysis system. New York. 1993;1:3-4.
14. Serrote CML, Reiniger LRS, Silva KB, Santos Rabaialli SM, Stefanel CM. Determining the polymorphism information content of a molecular marker. Gene. 2020;726:1-18.
15. Mulato BM, Möller M, Zucchi MI, Quecini V, Pinheiro JB. Genetic diversity in
soybean germplasm identified by SSR and EST-SSR markers. Pesquisa Agropecuária Brasileira. 2010;45(3):276-283.

16. Bisen A, Khare D, Nair P, Tripathi N. SSR analysis of 38 genotypes of soybean (Glycine Max (L.) Merr.) genetic diversity in India. Physiology and Molecular Biology of Plants. 2014;21(1):109-115.

17. Fu YB, Peterson GW, Morrison MJ. Genetic diversity of Canadian soybean cultivars and exotic germplasm revealed by simple sequence repeat markers. Crop Science. 2007;47(5):1947-1954.

18. Hu Z, Kan G, Zhang G, Zhang D, Hao D, Yu D. Genetic diversity analysis using simple sequence repeat markers in soybean. Plant Genetic Resources. 2014;12(1):S87-S90.

19. Kosman E, Leonard KJ. Similarity coefficients for molecular markers in studies of genetic relationships between individuals for haploid, diploid, and polyploid species. Molecular Ecology. 2005;14(2):415-424.

20. Xie H, Guan R, Chang R, Qiu L. Genetic diversity of Chinese summer soybean germplasm revealed by SSR markers. Chinese Science Bulletin. 2005;50(6):526-535.

21. Mimura M, Coyne CJ, Bambuck MW, Lumpkin TA. SSR diversity of vegetable soybean [Glycine max (L.) Merr.]. Genetic Resources and Crop Evolution. 2007;54(3):497-508.

22. Chauhan DK, Bhat JA, Thakur AK, Kumari S, Hussain Z, Satyawathi CT. Molecular characterization and genetic diversity assessment in soybean [Glycine max (L.) Merr.] varieties using SSR markers. Indian Journal of Biotechnology. 2015;14:504-51.