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# Identification of Polymorphic SSR Markers and Diversity Analysis in a Set of *Desi* Chickpea Genotypes

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**ABSTRACT: The chickpea (*Cicer arietinum* L.) is a staple legume crop grown in India, North Africa and the Middle East and Ethiopia. To maintain continuous production of chickpea, it is important to develop new varieties tolerant/resistant to different abiotic and biotic stresses. Therefore, it is important to identify diverse genotypes to select as parents before planning hybridization programme. So, it is necessary to analyse diversity among and between genotypes. The molecular characterization of chickpea for genetic diversity may be used for detection of diverse chickpea genotype(s). The persistence of this investigation is to examine the genetic diversity present among 57 chickpea genotypes by using SSR molecular markers. Thirteen of 33 SSR molecular markers were found to be polymorphic and produced an average of seven amplicons per primer pair. The genetic relatedness between cultivars ranged between 0.4334 to 0.8926 and the polymorphic information content arrayed between 0.3820 (STMS-11) to 0.8833 (GAA-44). Hierarchical tree data indicated 6 different clusters in a dendrogram and in bootstrapping. Overall, the study confirmed that SSRs are effective marker methods for revealing genetic diversity in chickpeas, which may be proved helpful for breeding programme such as parent selection as well as cultivar identification.**

**Keywords:** Chickpea, Genetic diversity, SSR, PCR, scoring, Dendogram.

## INTRODUCTION

The chickpea (*Cicer arietinum* L.) is a staple legume crop grown in India, North Africa and the Middle East and Ethiopia. It is a plant from the Fabaceae family that grows during the winter season. It is a self-pollinating diploid (2n=16) crop with a relatively small genome size of 738 Mbp (Varshney *et al*., 2013). In most the world's emerging economies, chickpeas are a significant legume crop. It is also known as "poor man's meat" (Grewal *et al*., 2020), since it is important for supplying protein sources (Sahu *et al*., 2020a; Gupta *et al*., 2021). Nutritionists have also emphasised its significance because of its high nutritional content (Grewal *et al*., 2020; Sahu *et al*., 2020b). On an average, chickpea seeds include 358 calories, 22% protein, 4.5% fat, 63% crude fibre and 2.7% ash. Numerous minerals, including calcium, magnesium, potassium, phosphorus, iron, zinc, and manganese are abundant in it (Ibrikci *et al*., 2003; Asati *et al*., 2022). In more than 50 countries of the world, it is the most widely cultivated (Gaur *et al*., 2019). Nearly 70% of the world's total production of chickpeas is produced by India (Korbu *et al*., 2020). Chickpeas were grown on around 1095 million hectares area worldwide in 2020, with a total yield of 15.1 million tonnes (FAOSTAT, 2023).

Marker-assisted selection (MAS) can significantly increase the precision and efficacy of selection of genotypes in crop breeding (Asati *et al*., 2022; Rathore *et al*., 2022; Tripathi *et al*., 2022; Yadav *et al*., 2023). Through all the pyramiding of genes from several sources and the combination of resistance to diverse stresses, molecular markers might assist indirect selection for traits that are challenging or inconvenient to evaluate directly (Yadav *et al*., 2016; Tripathi *et al*., 2022). The short life cycle of the chickpea makes it a fascinating crop for genetic studies. Numerous examples of microsatellite markers are available for deployment in various crop species for the investigation of molecular diversity and marker trait associations (Adu *et al*., 2019; Mishra *et al*., 2020; Mishra *et al*., 2021). High levels of polymorphism have been reported to be produced using microsatellite markers and because of this characteristic, the markers can be used to study genetic diversity (Bocianowski *et al*., 2021).

In chickpea, numerous molecular markers are reported. Now it is important to analyse the genetic diversity present among the targeted set of chickpea genotypes using these already available markers. So, the present investigation was conducted to analyse microsatellite markers-based diversity among *desi* chickpea genotypes.

## MATERIALS AND METHODS

**Plant materials:** At the Research Farm of the Department of Genetics and Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior Gwalior, Madhya Pradesh, India during Rabi 2021–2022, total 57 chickpea genotypes (Table 1) were grown in a Randomized Block Design in two replications with an R × P distance of 30 × 15 cm. These genotypes were gathered from Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India and RAK College of Agriculture, Sehore, RVSKVV, Gwalior, Madhya Pradesh, India.

**Table 1: List of chickpea genotypes with their parentage/source used in the study.**

| Sr. No. | Genotype | Parentage/ Source of collection | Sr. No. | Genotype | Parentage/ Source of collection |
|---|---|---|---|---|---|
| 1. | ICCV-201102 | COA, JNKVV, Jabalpur | 30. | SAGL-152258 | JG 135 × FG 711 |
| 2. | ICCV-201104 | COA, JNKVV, Jabalpur | 31. | SAGL-152265 | PUSA 1088 × VIJAY |
| 3. | ICCV-201105 | COA, JNKVV, Jabalpur | 32. | SAGL-152273 | KAK 2 × IPC 9494 |
| 4. | ICCV-201109 | COA, JNKVV, Jabalpur | 33. | SAGL-152278 | JSC 37 × JSC 36 |
| 5. | ICCV-201111 | COA, JNKVV, Jabalpur | 34. | SAGL-152318 | JSC 19 × JG 16 |
| 6. | ICCV-201112 | COA, JNKVV, Jabalpur | 35. | SAGL-152324 | IPC 4958 × IPC 9494 |
| 7. | ICCV-201113 | COA, JNKVV, Jabalpur | 36. | SAGL-152327 | KAK 2 × JSC 19 |
| 8. | ICCV-201115 | COA, JNKVV, Jabalpur | 37. | SAGL-152330 | ICC 4958 × PHULE G 5 |
| 9. | ICCV-201116 | COA, JNKVV, Jabalpur | 38. | SAGL-152339 | JG16 × KAK 2 |
| 10. | ICCV-201118 | COA, JNKVV, Jabalpur | 39. | SAGL-152344 | IPC9494 × JG16 |
| 11. | ICCV-201205 | COA, JNKVV, Jabalpur | 40. | SAGL-152347 | KAK 2 × JSC 19 |
| 12. | ICCV-201206 | COA, JNKVV, Jabalpur | 41. | SAGL-162299 | RAK, Sehore, RVSKVV, Gwalior |
| 13. | ICCV-201209 | COA, JNKVV, Jabalpur | 42. | SAGL-152349 | KAK 2 × PHULE G5 |
| 14. | ICCV-201210 | COA, JNKVV, Jabalpur | 43. | SAGL-152403 | RAK, Sehore RVSKVV, Gwalior |
| 15. | ICCV-201211 | COA, JNKVV, Jabalpur | 44. | SAGL-152404 | RAK, Sehore RVSKVV, Gwalior |
| 16. | ICCV-201212 | COA, JNKVV, Jabalpur | 45. | SAGL-152405 | RAK, Sehore RVSKVV, Gwalior |
| 17. | ICCV-201214 | COA, JNKVV, Jabalpur | 46. | SAGL-162370 | PG 9425-9 × BG 2064 |
| 18. | ICCV-201217 | COA, JNKVV, Jabalpur | 47. | SAGL-162376 | JSC 52 × RSG 888 |
| 19. | SAGL-152210 | IPC 9494 × ICC 506 | 48. | SAGL 22-101 | KAK-2 × BG-362 |
| 20. | SAGL-152216 | JG 16 × VIJAY | 49. | SAGL 22-102 | JG-6 × RVSSG-2 |
| 21. | SAGL-152223 | RAK, Sehore, RVSKVV, Gwalior | 50. | SAGL 22-103 | JG-130 × FG-703 |
| 22. | SAGL-152231 | KAK2 × JG130 | 51. | SAGL 22-104 | JSC-33 × JG-11 |
| 23. | SAGL-152234 | JSC 19 × ICC 4958 | 52. | SAGL 22-105 | JAKI-9218 × BGD-112 |
| 24. | SAGL-152236 | KAK-2 × BG 362 | 53. | SAGL 22-106 | RVG-204 X JSC-37 |
| 25. | SAGL-152237 | BG 2064 × KAK -2 | 54. | GCP-101 | RAK, Sehore, RVSKVV, Gwalior |
| 26. | SAGL-152238 | PG -9425-9 × IPC 9494 | 55. | RVSSG-64 | RAK, Sehore, RVSKVV, Gwalior |
| 27. | SAGL-152250 | KAK 2 × BG 2064 | 56. | JG-36 | COA, JNKVV, Jabalpur |
| 28. | SAGL-152252 | ICC 4958 × BG 1108 | 57. | JG-14 | COA, JNKVV, Jabalpur |
| 29. | SAGL-152254 | BG 362 × ICC 506 | | | |

**DNA extraction:** Molecular Analysis work was performed at Plant Molecular Biology Laboratory, Department of Plant Molecular Biology & Biotechnology, College of Agriculture, Rajmata Vijayaraje Scindia Agricultural University Gwalior, Madhya Pradesh, India. High quality genomic DNA was extracted from 8-10 days old young and fresh leaves by employing CTAB method as proposed by Doyle and Doyle (1987) with some modifications as suggested by Tiwari *et al*. (2017). Extracted DNA was quantified through electrophoresis on 0.8% agarose gel and compared after loading a known quantity DNA marker (λ DNA) on the same gel as a standard. Apart from it a Spectrophotometer was also used for quantification of DNA.

**SSR markers analysis:** The genetic profile of 57 chickpea genotypes was analysed based on difference in allele size produced using 33 SSR markers (Table 2). The polymerase chain reaction was performed in 10 µl reaction mixture comprising of 1X PCR buffer, 0.1 µl *Taq* DNA polymerase, 1 µl dNTP (1 mM), 0.5 µl of primers (10 pM) and 20 ng/µl of genomic DNA in a thermocycler (Bio-Rad, USA). The PCR protocol comprised of initial denaturation step of 94°C for 3 min followed by 35 cycles of 94°C for 1 min, annealing cycles (from 52°C to 57°C) varied for different markers system for 30 sec, elongation at 72 °C for 1 min with final extension at 72 °C for 7 min. PCR amplified products of SSR markers along with standard markers (100 bp) were separated through electrophoresis on 3% agarose gel respectively at 75 V for two hrs. The agarose gels were stained with Ethidium Bromide (1µg/ml). After electrophoresis the agarose gels were visualized under UV light and photographed under Bio-Rad Gel documentation system.

**Table 2: List of sequences of SSR markers used in present investigation.**

| Sr. No. | Marker | Forward sequence 5'-3' | Reverse sequence 5'-3' |
|---|---|---|---|
| 1. | TA-1 | TGAAATATGGAATGATTACTGAGTGAC | TATTGAAATAGGTCAGGCTTATAAAAA |
| 2. | TA-2 | AAATGGAAGAAGAATAAAAACGAAAC | TTCCATTCTTTATTATCCATATCACTACA |
| 3. | TA-3 | AATCTCAAAATTCCCCAAAT | ATCGAGGAGAGAAGAACCAT |
| 4. | TA-18 | AAAATAATCTCCACTTCACAAATTTTC | ATAAGTGCGTTATTAGTTTGGTCTTGT |
| 5. | TA-27 | ACAATTCCACTTAATCTTTGC | AATTTAGCCTACAGACACACACA |
| 6. | TA-28 | TAATTGATCATACTCTCACTATCTGCC | TGGGAATGAATATTTTTGAAGTAAA |
| 7. | TA-64 | ATATATCGTAACTCATTAATCATCCGC | AAATTGTTGTCATCAAATGGAAAATA |
| 8. | TA-71 | CGATTTAACACAAAACACAAA | CCTATCCATTGTCATCTCGT |
| 9. | TA-135 | TGGTTGGAAATTGATGTTTT | GTGGTGTGAGCATAATTCAA |
| 10. | TA-180 | CATCGTGAATATTGAAGGGT | CGGTAAATAAGTTTCCCTCC |
| 11. | TA-194 | TTTTTGGCTTATTAGACTGACTT | TTGCCATAAAATACAAAATCC |
| 12. | TAA-60 | TCATGCTTGTTGGTTAGCTAGAAA | CAAAGACATAATCGAGTTAAAGAAAA |
| 13. | TR-1 | CGTATGATTTTGCCGTCTAT | ACCTCAAGTTCTCCGAAGT |
| 14. | TS-45 | TGACACAAAATTGTCTCTTGT | TGTTCTTAACGTAACTAACCTAA |
| 15. | TS-82 | TCAAGATTGATATTGATTAGATAAAAGC | CTTTATTTACAACTTGCACAACACTAA |
| 16. | STMS-2 | ATTTTACTTTACTACTTTTTTCCTTTC | AATAAATGGAGTGTAAATTTCATGTA |
| 17. | STMS-11 | GTATCTACTTGTAATATTCTCTTCTCT | ATATCATAAACCCCCCAC |
| 18. | STMS-13 | TATGTTAAAAGAGAAAGAAGAAGTGAT | TTTTATTAGTTGTCGAAATGTATATCA |
| 19. | STMS-20 | CTTNTCGTCATCATCGTTTTG | CACCCTACTTTTTTCCACCAC |
| 20. | STMS-24 | AAAGACAGGTTTTAATCCAAAA | CTAATCTTTCTTCTTCTTTTGTCAT |
| 21. | GA-4 | TTGCGTGTCAATCTCATTGG | TCAACACCCCTAACTCGGAC |
| 22. | GA-11 | GTTGAGCAACAAAGCCACAA | TTCTTGTCTGGTTGTGTGAGC |
| 23. | GAA-40 | TTGACGCAGAGAACTCTCAA | ATTGGTGTGATGGGTGGATT |
| 24. | GAA-42 | CGCTTCAGTGTAGATATTATTCAAACA | TCTCTCTTTCTCTTCAACACGC |
| 25. | GAA-44 | AGCAAGCCCATGATTTTCTC | ATGACATTCCAATCGGCTTC |
| 26. | GAA-45 | TTGGGATCCATTTCATCCAT | GCCTGGAAGTCACACACTTG |
| 27. | GAA-46 | TCTCCTGTGAATGAACCGAA | CTGAGCAACAAAATCAGCCA |
| 28. | TA-22 | TCTCCAACCCTTTAGATTGA | TCGTGTTTACTGAATGTGGA |
| 29. | TA-46 | TTTATTGCAATAAAACTCATTTCTTATC | TTCTTTTTGTGTGAAAAAAAAATATAGTGA |
| 30. | NCPGR-1 | TTACAGCTTGTGCTCAG | AGTCAGATTCTTATCCGA |
| 31. | TAA-58 | CATTGCTTAAGAACCAAAATGG | CAATTTTACATCGACGTGTC |
| 32. | TaaSH | GGTAGACGCAAAAGAGTGTGGG | GCCACATTGACCAGGAATG |
| 33. | TR-9 | GCCCACTGAAAAATAAAAAG | ATTTGAACCTCAAGTTCTCG |

**Band scoring and data analysis:** The genetic profiles of genotypes were assessed based on allele size variations. Power Marker v3.25 software (Liu and Muse 2005) was used to examine the major allele frequency, number of alleles per locus, polymorphism information content (PIC) and gene diversity. The dendrogram based on unweighted pair group method for arithmetic average (UPGMA) was also constructed using Marker v3.25 software. Based on the banding pattern data was recorded with allele pattern A/A and B/B homozygous condition and A/B for heterozygous condition and in case of no amplification (-/-) was used.

## RESULTS AND DISCUSSION

Genetic diversity analysis of plant genetic resources has played a major role in effective conservation, management, and exploitation. For this purpose, a systematic categorization of targeted plant material and knowledge of the genetic relationships in the germplasm are required (Pramanik *et al.*, 2021; Kumar *et al*., 2022a; Kumar *et al.,* 2022b; Makwana *et al.,* 2023; Yadav *et al.,* 2022; Tomar *et al.,* 2022). Different genetic diversity parameters like numbers of alleles per locus, major allele frequency, genetic diversity and PIC values are indicators of the efficiency of SSR markers used in molecular diversity analysis, geographical relationship, phylogenetic analysis, and genetic differentiation pattern of the studied genotypes. Numbers of alleles per locus is important parameters to determine PIC value of a particular marker (Mandloi *et al*., 2022).

SSR markers are regarded as the preferred molecular markers among the available markers created and employed in breeding efforts. SSR markers are particularly desirable for characterization of germplasm because of their widespread use, high density in many genomes, and other benefits (Tiwari *et al.,* 2019). They have been widely utilised to identify variation in chickpea germplasm lines. During the current investigation, initially at screening stage, total 33 SSR markers were tested for their polymorphic nature with DNA template of *Desi* chickpea genotypes. Out of 33 SSR markers, 13 including GAA-44, STMS-11, STMS-24, GA-4, NCPGR-1, TA-71, TA-135, TA-180, STMS-2, TR-9, TA-18, GAA-40 and TS-45 markers were found reproducible and polymorphic in all 57 lines of *desi* chickpea (Table3). Ninety-one alleles were detected as polymorphic and homozygous. Therefore, 91 alleles were considered effective alleles for 13 markers varied from three to 14 alleles per marker. The aim of the present experiment was to analyse the genetic dissimilarity among 57 lines of *desi* chickpea through SSR markers. The allele size range varied from 150 to 300bp. Similar results are reported by Yadav *et al*. (2016) while using SSR markers for genetic diversity analysis among chickpea cultivars. The genetic divergence among SSR markers ranged from 0.4334 to 0.8926 with an average value of 0.7376. The highest gene diversity was found in GAA-44 (0.8926)

followed by TR-9 (0.8870), NCPGR-1 (0.8655), TA-18 (0.8495), TS-45 (0.8433) and GA-40 (0.7639) (Fig.1). The results are in agreement with findings of earlier studies including Bakshi *et al.* (2016); Aggarwal *et al.* (2018); Amina *et al.* (2020). The polymorphic information content value of the entire polymorphic marker during the present investigation ranged between 0.3820 (STMS-11) to 0.8833 (GAA-44) with a mean value of 0.6955 (Fig. 2). The highest PIC value was recorded with the primer GAA-44 however, lowest value with STMS-11. In accordance with the present findings, Safera *et al.* (2011); Naghvi *et al.* (2012); Ghaffari *et al.* (2014); Samyuktha *et al.* (2018); Seyedimoradi *et al.* (2019); Sachdeva *et al.* (2019); Shanmugam and Kalaimagal (2019) reported almost similar ranges of PIC values in their studies on use of SSR markers for genetic diversity analysis in chickpea genotypes.

**Table 3: Major allele frequency, polymorphic information content, number of alleles per locus, and Gene Diversity of polymorphic SSR markers.**

| Marker | Major Allele Frequency | Number of Genotype | Number of Allele | Gene Diversity | PIC value |
|---|---|---|---|---|---|
| GAA-44 | 0.1930 | 14.0000 | 14.0000 | 0.8926 | 0.8833 |
| STMS-11 | 0.7193 | 3.0000 | 3.0000 | 0.4334 | 0.3820 |
| STMS-24 | 0.4211 | 6.0000 | 6.0000 | 0.6931 | 0.6429 |
| GA-4 | 0.3684 | 4.0000 | 4.0000 | 0.6716 | 0.6021 |
| NCPGR-1 | 0.2632 | 12.0000 | 12.0000 | 0.8655 | 0.8529 |
| TA-71 | 0.3860 | 4.0000 | 4.0000 | 0.6808 | 0.6159 |
| TA-135 | 0.3684 | 4.0000 | 4.0000 | 0.6845 | 0.6196 |
| TA-180 | 0.4035 | 4.0000 | 4.0000 | 0.6630 | 0.5957 |
| STMS-2 | 0.3860 | 3.0000 | 3.0000 | 0.6611 | 0.5870 |
| TR-9 | 0.2105 | 13.0000 | 13.0000 | 0.8870 | 0.8774 |
| TA-18 | 0.2456 | 10.0000 | 10.0000 | 0.8495 | 0.8324 |
| GAA-40 | 0.3158 | 5.0000 | 5.0000 | 0.7639 | 0.7250 |
| TS-45 | 0.2632 | 9.0000 | 9.0000 | 0.8433 | 0.8252 |
| **Mean** | **0.3495** | **7.0000** | **7.0000** | **0.7376** | **0.6955** |

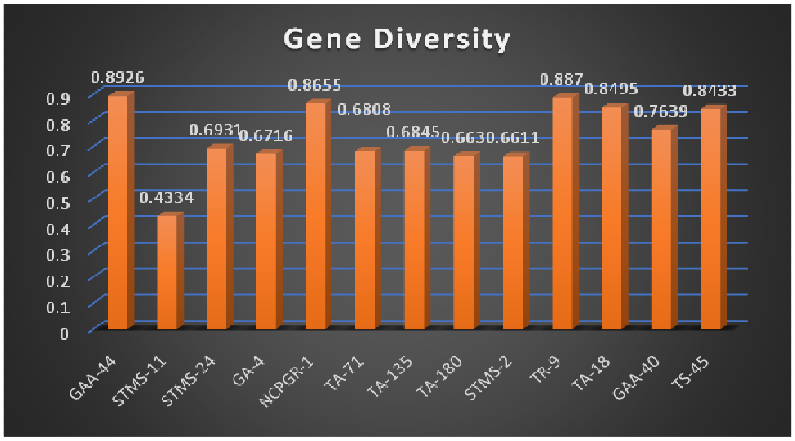


**Fig. 1.** Graphical representation of gene diversity.

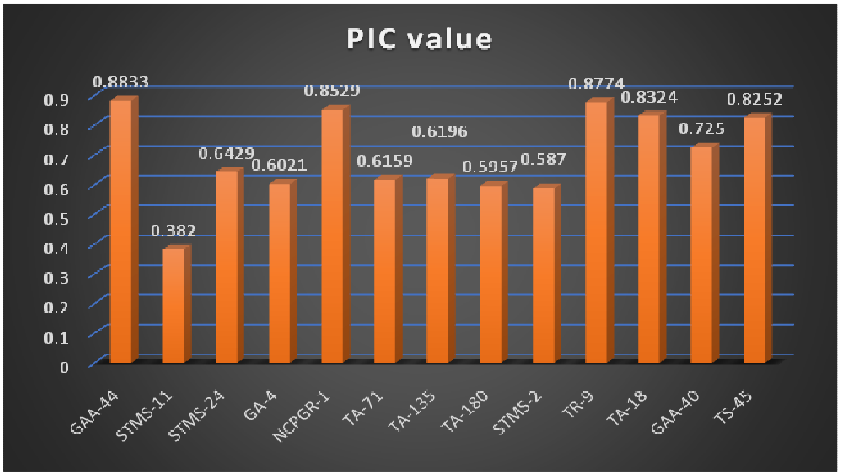


**Fig. 2.** Graphical representation of Polymorphic Information Content (PIC) Value.

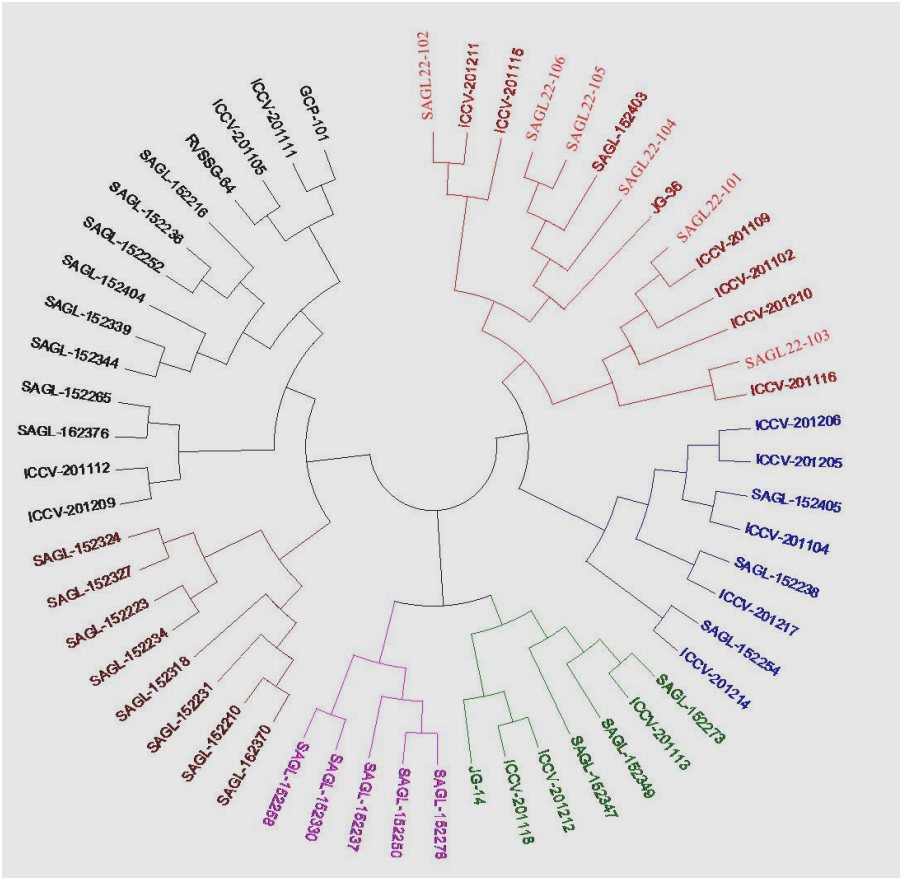


**Fig. 3.** Dendrogram formed based on UPGMA (Unweighted Pair Group Method with Arithmetic Mean).

Molecular markers based genetic dissimilarity among a set of chickpea genotypes helped to construct an UPGMA tree (Fig. 3). The studied chickpea genotypes were grouped into 6 clusters according to genetic distance among and between them. Cluster 1: Included 14 genotypes *i.e.*, SAGL 22-102, ICCV-201211, ICCV-201115, SAGL 22-106, SAGL 22-105, SAGL-152403, SAGL 22-104, JG-36, SAGL 22-101, ICCV-201109, ICCV-201102, ICCV-201210, SAGL 22-103 and ICCV-201116. Cluster 2 contained 8 genotypes including ICCV-201206, ICCV-201205, SAGL-152405, ICCV-201104, SAGL-152238, ICCV-201217, SAGL-152254 and ICCV-201214 while cluster 3 contains 7 genotypes *viz.,* SAGL-152273, ICCV - 201113, SAGL-152349, SAGL-152347, ICCV-201212, ICCV-201118 and JG-14. Cluster 4 had 5 genotypes *i.e.*, SAGL-152278, SAGL-152250, SAGL-152237, SAGL-152330 and SAGL-152258. Cluster 5 included 8 genotypes *namely* SAGL-162370, SAGL-152210, SAGL-152231, SAGL-152318, SAGL-152234, SAGL-152223, SAGL-152327 and SAGL-152324. Whilst cluster 6 contains 14 genotypes including ICCV-201209, ICCV-201112, SAGL-162376, SAGL-152265, SAGL-152344, SAGL-152339, SAGL-152404, SAGL-152252, SAGL-152236, SAGL-152216, RVSSG-64, ICCV-201105, ICCV-201111 and GCP-101. Grouping of some of the SAGL genotypes collected from the same centre (RAK College, Sehore) confirms their close relationship with each other. Similar results were found by Rizvi *et al.* (2014); Datta *et al.* (2015). Similarly, most of the ICCV genotypes showed resemblance and grouped together. Similar results have been reported by various research groups (Solanki *et al.,* 2022).

## CONCLUSIONS

High genetic diversity within a chickpea population provides an opportunity to the breeders to plant hybridization strategies for improvement of chickpea. Thirteen SSR primers were found to be polymorphic out of the 32 SSR markers used in the current study. Through the crossing of genetically diverse genotypes, traits with a wide range of allele sizes, a large number of genotype-specific alleles per locus, high polymorphic information content, and expected heterozygosity made it possible to improve yield and specific traits like heat, cold, and drought.

**Conflict of Interest.** None.

## REFERENCES

Adu, G. B., Awuku, F. J., Amegbor, I. K., Haruna, A., Manigben, K. A. and Aboyadana, P. A. (2019). Genetic characterization and population structure of maize populations using SSR markers. *Annals of Agricultural Sciences, 64,* 47–54.

Agrawal, T., Kumar, A., Kumar, S., Kumar, A., Kumar, R. R., Kumar, S. and Singh, P. K. (2018). Correlation and path coefficient analysis for grain yield and yield components in chickpea (*Cicer arietinum* L.) under normal and late sown conditions of Bihar, India.

*International Journal of Current Microbiology and Applied Sciences*, *7,* 2319-7706.

Amina, B., Rida, M. M., Abdelkader, A. A., Sripada, U. and Semir, G. S. (2020). Genetic diversity analysis in chickpea (*Cicer arietinum* L.) genotypes grown in Northwestern Algeria using microsatellite markers (SSR). *Indian Journal of Agricultural Research*, *54*, 129-138.

Asati, R., Tripathi, M. K., Tiwari, S., Yadav, R. K. and Tripathi, N. (2022). Molecular breeding and drought tolerance in chickpea. *Life, 12*, 1846.

Bakshi, A., Kumar, V., Sagar, S., Chaudhary, S., Kumar, R. and Kumar, M. (2016). Molecular characterization of chickpea (*Cicer arietinum* L.) genotypes using sequence tagged microsatellite site (STMS) markers. *Journal of Natural and Applied Sciences*, *8*, 1068 – 1074.

Bocianowski, J., Nowosad, K., Wróbel, B. and Szulc, P. (2021). Identification of associations between SSR markers and quantitative traits of maize (*Zea mays* L.). *Agronomy*, *11,* 182.

Datta, S., Kashyap, M. and Gupta P. (2015). Development of EST derived microsatellite markers in chickpea and their validation in diversity analysis. *Indian Journal of Biotechnology*, *14*, 55-58.

Doyle, J. J. and Doyle, J. L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, *19*, 11-15.

FAOSTAT (2023). Available online at: http://www.fao.org/faostat/ (accessed 15th February 2023).

Gaur, P. M., Samineni, S., Thudi, M., Tripathi, S., Sajja, S. B. and Jayalakshmi, V. (2019). Integrated breeding approaches for improving drought and heat adaptation in chickpea (*Cicer arietinum* L.). *Plant Breeding, 138*, 389–400.

Ghaffari, P., Talebi, R. and Keshavarzi, F. (2014). Genetic diversity and geographical differentiation of Iranian landrace, cultivars, and exotic chickpea lines as revealed by morphological and microsatellite markers. *Physiology and Molecular Biology of Plants, 20,* 225-33

Grewal, S. K., Sharma, K. P., Bharadwaj, R. D., Hegde, V., Tripathi, S., Singh, S., Jain, P. K., Agrawal, P. K. and Mondal, B. (2020). Understanding genotypic variation and identification of promising genotypes for iron and zinc content in chickpea (*Cicer arietinum* L.). *Journal of Food Composition and Analysis, 88*, 103458.

Gupta, N., Tiwari, S., Tripathi, M. K. and Bhagyawant, S. S. (2021). Antinutritional and protein-based profiling of diverse desi and wild chickpea accessions. *Current Journal of Applied Science and Technology, 40*, 7-18

Ibrikci, H., Knewtson, S. and Grusak, M. A. (2003). Chickpea leaves as a vegetable green for humans: evaluation of mineral composition. *Journal of the Science of Food and Agriculture, 83,* 945–950.

Korbu, L., Tafes, B., Kassa, G., Mola, T. and Fikre, A. (2020). Unlocking the genetic potential of chickpea through improved crop management practices in Ethiopia. A review. *Agronomy for Sustainable Development*, *40*, 13.

Kumar, B., Choudhary, M., Kumar, P., Kumar, K., Kumar, S., Singh, B. K., Lahkar, C., Meenakshi, Kumar, P., Dar, Z. A., Devlash, R., Hooda, K. S., Guleria, S. K. and Rakshit, S. (2022a). Population structure analysis and association mapping for Turcicum leaf blight resistance in tropical maize using SSR markers. *Genes, 13*, 618.

Kumar, A., Longmei, N., Kumar, P. and Kaushik, P. (2022b), Molecular marker analysis of genetic diversity in maize: A Review. *OBM Genetics, 6,* 150.

Liu, K. and Muse, S. V. (2005). Power marker integrated analysis environment for genetic marker data. *Bioinformatics*, *21*, 2128-2129.

Makwana, K., Tiwari, S., Tripathi, M. K. and Patel, V. (2023). Selection of Blast Resistant Lines from Diverse Germplasm Set of Foxtail Millet. *Biological Forum – An International Journal, 15*(1), 1-6.

Mandloi, S., Tripathi, M. K., Tiwari, S. and Tripathi, N. (2022). Genetic diversity analysis among late leaf spot and rust resistant and susceptible germplasm in groundnut (*Arachis hypogea* L.). *Israel Journal of Plant Sciences.*

Mishra, N., Tripathi, M. K., Tiwari, S., Tripathi, N. and Trivedi, H. K. (2020). Morphological and molecular screening of soybean genotypes against yellow mosaic virus disease. *Legume Research.*

Mishra, N., Tripathi, M. K., Tiwari, S., Tripathi, N., Gupta, N., Sharma, A. and Solanki, R. S. (2021). Evaluation of diversity among soybean genotypes *via* yield attributing traits and SSR molecular markers. *Current Journal of Applied Science and Technology, 40*, 9-24.

Naghvi, M. R., Monfared, S. R. and Humberto, G. (2012). Genetic diversity in Iranian chickpea (*Cicer arietinum* L.) landraces as revealed by microsatellite markers. *Czech Journal of Genetics and Plant Breeding*, *48*, 131-138.

Pramanik, A., Tiwari, S., Tripathi, M. K., Mandloi, S. and Tomar, R. S. (2021). Identification of groundnut germplasm lines for foliar disease resistance and high oleic traits using SNP and gene-based markers and their morphological characterization. *Legume Research.*

Rathore, M. S., Tiwari, S., Tripathi, M. K., Gupta, N., Yadav, S., Singh, S. and Tomar, R. S. (2022). Genetic diversity analysis of groundnut germplasm lines in respect to early and late leaf spot diseases and biochemical traits. *Legume Research.*

Rizvi, H., Kalyanbabu, B. and Agrawal, P. K. (2014). Molecular analysis of kabuli and desi type of Indian chickpea cultivars using STMS markers. *Journal of Plant Biochemistry and Biotechnology*, *23,* 52-60.

Sachdeva, S., Bharadaj, C., Singh, S., Roorkiwal, M., Sharma, V., Singh, A. and Varshney, R. (2019). Yield plasticity and molecular diversity analysis in chickpea (*Cicer arietinum* L). *Indian Journal of Agriculture Sciences*, *89*, 834–841.

Safera, T., Abebiel, B., Gaur, P. M., Assefa, K. and Varshney, R. K. (2011). Characterization and genetic diversity analysis of selected chickpea cultivars of nine countries using SSR markers. *Crop Pasture Science*, *62*, 177-187.

Sahu, V. K., Tiwari, S., Tripathi, M. K., Gupta, N., Tomar, R. S. and Yasin, M. (2020a). Morpho-physiological and biochemical traits analysis for Fusarium wilt disease using gene-based markers in desi and Kabuli genotypes of chickpea (*Cicer arietinum* L.). *Indian Journal of Genetics, 80,* 16.

Sahu, V. K., Tiwari, S., Gupta, N., Tripathi, M. K. and Yasin, M. (2020b). Evaluation of physiological and biochemical contents in desi and Kabuli chickpea. *Legume Research.*

Samyuktha, S. M., Kannan, J. R. and Bapu, G. S. (2018). Molecular genetic diversity and population structure analysis in chickpea (*Cicer arietinum* L.) germplasm using SSR markers. *International Journal of Current Microbiology and Applied Sciences*, *7*, 639-651.

Seyedimoradi, H., Talebi, R., Kanouni, H., Naji, A. M. and Karami, E. (2019). Agro-morphological description, genetic diversity and population structure of chickpea using genomic-SSR and ESR-SSR molecular markers. *Journal of Plant Biochemistry and Biotechnology*, *28*, 483-95.

Shanmugam, M. and Kalaimagal, T. (2019). Genetic variability, correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.) for yield and its component traits. *International Journal of Current Microbiology and Applied Sciences*, *8*, 1801-1808.

Solanki, R. S., Babbar, A. and Tripathi, N. (2022). Genetic diversity analysis in *kabuli* chickpea (*Cicer arietinum* L.) genotypes based on quantitative traits and molecular markers. *Bangladesh Journal of Botany*, *51*, 581-587.

Tiwari, S., Tomar, R. S, Tripathi, M. K. and Ahuja, A. (2017). Modified protocol for plant genomic DNA isolation. *Indian Research Journal of Genetics and Biotechnology*, *9*, 478–485.

Tiwari, S., Tripathi, N., Tsuji, K. and Tantwai, K. (2019). Genetic diversity and population structure of Indian soybean (*Glycine max* (L.) Merr.) as revealed by microsatellite markers. *Physiology and Molecular Biology of Plants, 25*, 953-964.

Tomar, Y. S., Tiwari, S., Tripathi, M. K. and Gupta, N. (2022). Influence of Myo-inositol Phosphate Synthase Gene In phytic Acid contents and Superoxide Dismutase Activity (SOD) of Groundnut (*Arachis hypogaea* L.). *Biological Forum – An International Journal, 14*(2), 1402-1406

Tripathi, N., Tripathi, M. K., Tiwari, S. and Payasi, D. K. (2022). Molecular breeding to oovercome biotic stresses in soybean: update. *Plants, 11*, 1967.

Varshney, R. K., Song, C., Saxena, R. K., Azam, S., Yu, S. and Sharpe, A. G. (2013). Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nature Biotechnology*, *31,* 240–246.

Yadav, P. K., Singh, A. K., Tripathi, M. K., Tiwari, S. and Rathore, J. (2022). Morpho-physiological characterization of maize (*Zea mays* L.) genotypes against drought. *Biological Forum An International Journal, 14*(2), 0975- 1130.

Yadav, S., and Sharma, K. D. (2016). Molecular and morphophysiological analysis of drought stress in plants. *Plant Growth*, *10,* 5772/65246.

Yadav, S., Shah, V. and Mod, B. (2019). Genetic diversity analysis between different varieties of chickpea (*Cicer arietinum* L.) using SSR markers. *International Journal of Applied Sciences and Biotechnology, 7*, 236-242.

Yadav, S., Tiwari, S., Tripathi, M. K., Tripathi, N., Gupta, N. and Tiwari, S. (2023). Evaluation of high oleic acid content in a set of 96 genotypes of *Arachis hypogaea* L. *Scientist*, *2*, 132-143.

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