

## Assessment of population structure in cornelian cherry (*Cornus mas* L.) genotypes using bioinformatics STRUCTURE 2.3.4 software

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**Abstract:** Molecular markers play an important role in genome studies and population structure of different plants. In this study, the population structure of Arasbaran cornelian cherry genotypes was evaluated using the ISSR molecular marker and bioinformatics STRUCTURE 2.3.4 software. The number of amplified bands by each primer was different, so that the UBC807 amplified 15 bands, and UBC817 amplified 8 bands. The highest polymorphism (77.77%) belonged to the P811 and the lowest (50%) was related to A11 and UBC834. Because of the evaluating of population structure, identify distinct sub-populations, genetic erosion, and admixture individuals, Model-based clustering method was performed in STRUCTURE 2.3.4 software, assuming the ancestry and allele frequency models to be "admixture" and "continuous" respectively. These proceed by assuming that observations from each cluster are random draws from some parametric model. Inference for the parameters corresponding to each cluster is then done jointly with inference for the cluster membership of each individual, using standard statistical methods. The actual number of sub-populations is determined by Evanno *et al.*, method (2005) assuming  $K = 1$  to  $K = 10$  ( $K$  represents the number of sub- population). Therefore, maximum  $\Delta k$  value was obtained at  $K = 7$  and the sub-populations were partitioned into different color sections in population structure diagram.

**Keywords:** *Cornelian cherry*; *Arasbaran*; *ISSR*; *bioinformatics*; *STRUCTURE 2.3.4*.

### References

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