

Assessment of Genetic Diversity of Different Landraces of Tarter Buckwheat through SSR and ISSR Markers

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Screening of genetic variation through molecular markers in a species provides the basis for tailoring desirable genotypes. Tarter buckwheat, a plant of higher altitude origin, is usually grown at the height greater than 550 meter. It appears to be a suitable component of food products from the nutritional aspect and from the point of view of its antioxidant activity. Microsatellite markers are reliable tool for evaluating the diversity at molecular level. This study aimed to evaluate the genetic diversity and population structure among and within population of Tarter buckwheat (*Fagopyrum tataricum*) collected from 15 different landraces.

In the present study, Inter simple sequence repeat (ISSR) and Simple sequence repeat (SSR) markers were used to study genetic diversity of Tarter buckwheat (*Fagopyrum tataricum*). Genomic DNA was extracted

from young leaves by the use of CTAB method. Thirteen primers of ISSR and seven primers of SSR produced clear and scorable bands. On the basis of these reproducible bands data analysis were performed with software POPGENE 32. The amplified PCR products have shown the 98.1% polymorphism with ISSR markers and 88.89 % with SSR markers. The percentage polymorphism obtained on combining both the markers was 98.4%. Cluster analyses were performed on the basis of Nei's genetic distance to deduce the relationships among 15 genetically diverse landraces.

The result revealed that there is a fair amount of genetic diversity among the diverse geographical regions. Our study demonstrated the usefulness of the two markers (SSR and ISSR) for designing crop improvement programmes for management of germplasm and evolving conservation strategies.