

## ABSTRACT

Genetic diversity assessment enables plant breeders and genetic researchers to conserve unique plant genomes. Conservation of sole genetic characteristics enables plants to endure environmental fluctuations in variety of environments. Molecular marker is the latest technique adopted in plant genetics to assess genetic diversity between species or within a specie at their genomic level. AFLP (Amplified Fragment Length Polymorphism), RFLP (Restriction Fragment Length Polymorphism), RAPD (Random Amplified Polymorphic DNA) and SSR (Simple Sequence Repeats) are widely being used by plant genetic researchers independently. ISSR (Inter Simple Sequence Repeats) molecular markers to assess genetic diversity proved reliable, efficient, cost-effective and easy to handle in laboratory scale. Here, ISSR markers used to analyze genetic diversity in *Convolvulus arvensis* L. (Bindweed) samples collected from Murree and Lahore areas with phenotypic variant flower colors. Bindweed, a perennial herbaceous vine grew in dry habitats and noxious weed for plant vegetation. Two different flower colors (white and pink) of bindweed in different geographical locations was due to influences of biotic and a-biotic factors. CTAB (Cetyltrimethyl Ammonium Bromide) method used for the extraction of genomic DNA of two variant samples. Then, universal ISSR primers UBC-825 and UBC-835 were used with optimum conditions (annealing temperature ranges 50°C -52°C) in PCR of both genomic DNA samples. UBC-835 produce polymorphic bands for both samples. Five pink flower samples and two white flower samples produce amplification products in ISSR PCR analysis. Size of amplified bands for pink flower and white flower samples ranges from 200bp-500bp with 1kb ladder used in gel electrophoresis. Informativeness of ISSR marker analyzed with 50% polymorphism in samples, 0.1371 PIC value for markers, 0.9158 mean value of allelic frequency and mean value of genetic diversity was 0.1507 in variant samples. For polymorphic bindweed samples, dendrogram was constructed using power marker 3.25 and drawn using Mega. Dendrogram, UPGM tree using Euclidean distance divided the total nineteen samples of bindweed into two groups. Group 1, represented pink flower samples and group 2 represented white flower samples. Evolutionary relationship in variant samples was quietly indicated in group 2. ISSR molecular marker indicated genetic diversity within