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Low genetic diversity in cultivated population of *Terminalia arjuna* revealed through RAPD profiling

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Sustainable genetic diversity is an important issue for forest restoration more willingly than low genetic diversity is suitable for commercial forestry for their economic importance and value. Viable diversity upholds in platelets generated through clonal propagation and horticulture is slightly difficult and this may be created genetic drift. Low genetic diversity among five cultivated populations of *Terminalia arjuna* was revealed using DNA fingerprints generated by ten commercially available random (RAPD) primers i.e. RPI01 to RPI10. Out of ten primers, eight primers generated total 79 bands with 69 polymorphic bands and 87.34 percentage of polymorphism, while primer RPI02 and RPI08 did not show amplification. Applied all 8 primes having a good polymorphic informativeness among the populations (mean PIC=0.355±0.032 and Ho=0.463±0.018). Higher genetic variation, gene diversity (H), Shannon's Information index (I) and Percentage of polymorphic bands (PPB) among populations (H=0.290±0.162, I=0.440±0.221 and PPB=87.34%) was observed compared to within populations (maximum H=0.165±0.212, I=0.239±0.304 and PPB=39.24%, minimum H=0.026±0.104, I=0.038±0.150, PPB=06.33%). Low average gene diversity (π=0.075±0.062) within population, higher pair wise Fst (ranged from 0.498 to 0.844) among the population and Analysis of Molecular Variance (AMOVA) shown adequate genetic variation among population (Percentage of variation Pv=75.57) but serious low genetic variation within populations (Pv=24.43, ΦST=0.756). Among the populations of *T. arjuna* the higher relative differentiation (GST=0.7843) with restricted gene flow GST (Nm)=0.1375 was observed. Unbiased measures of genetic distance and phylogram revealed that all locations have their once genetic identity and they arranged in their respective clusters. Lowest distance was showed by accession collected from JNKVV and TFRI Jabalpur.

Keywords: *Terminalia arjuna*, genetic and molecular diversity, population genetics, relative differentiation and gene flow, AMOVA, polymorphic information content (PIC), heterozygosity.

Biography

Pramod Sairkar has submitted his Ph.D. thesis at the Rani Durgavati University, Jabalpur in Biotechnology. He is working as Technical Assistant in Centre of Excellence in Biotechnology, the M.P. Council of Science and Technology, Bhopal, Madhya Pradesh, India a government organization with 12 years of research experience. He has published more than 13 research papers in national/international journals and 15 abstracts. He has submitted 18 unique DNA sequences of plants in NCBI Databank. Under his regulation, creation and authentication of DNA barcode for identification of medicinal plants is in progress. In regular practice, has a good command on analysis of sequences, gene prediction and annotation, molecular diversity assessment using DNA sequence and dominant markers mostly by frequent population genetic softwares like DnaSP, Arlequin, Popgene, MEGA, GeneAlEx, PICcalc etc.. He is actively involved in the organization of more than 50 institutional training programs on various subjects like molecular biology, microbiology, DNA fingerprinting, molecular diversity, HPTLC and plant tissue culture.

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