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Mating system analysis through microsatellite markers in *Acacia auriculiformis*

Arunachalam Shanthi, Maheswar Hegde, Vijakumar Bachpai and Sivadasan Padmini
Institute of Forest Genetics and Tree Breeding, India

Acacia auriculiformis A. Cunn. ex Benth is an important fast growing exotic tree species in plantation forestry and also useful in pulp and paper industry. The genetic structure of forest trees and the pattern of genetic variation that are maintained in the successive generations are essentially a function of the mating systems. In the Institute of Forest Genetics and Tree Breeding, Coimbatore has been established seedling seed orchards of first and second generation trials. We have attempted a study on mating system of Acacia in two successive generations based on microsatellite markers. Three hundred half-sib progenies in the first and second generation orchards were studied for five different microsatellite loci and were profiled for detecting homozygous/heterozygous alleles. Specific amplicon sizes (150-250 bp) were sequenced, confirmed microsatellites and were submitted to NCBI (Accession No-KG699501.1; KG699563.1; KG699564.1). The microsatellite repeats as di-repeats viz., (CA)7, (TA)8, (CT)7 in three loci, and as tri-repeats such as (CTT)6, (TTC)7 in two loci. The allelic data were analyzed through maximum likelihood estimation of mating systems (MLTR) software. Single and multilocus out-crossing rate was estimated from the analysis. The range of the maternal, paternal genotypes among the individuals in the family was also studied in both generation orchards. The present study indicated high out-crossing rate (tm=0.98; SE=0.05; tm=1.0; SE=0.02) in first and second generation orchards population and it reflects that this species is highly out-crossed.

Shanthia@icfre.org

Analysis of misinsertion and mispair extension by human immunodeficiency virus type 1 reverse transcriptase (HIV-1RT) in development of drug resistance

Bechan Sharma
University of Allahabad, India

The unique properties of human immunodeficiency virus type 1 reverse trancriptase (HIV-1 RT) include its high propensity for misinsertion and misincorporation of deoxyribonucleotide triphosphates (dNTP) in the growing chain's 3' terminus. It was envisaged that the interaction of the side chain of K154 in HIV-1RT with the penultimate nucleotide of template may be crucial in determination of fidelity of proviral cDNA synthesis. This hypothesis was tested by steady-state kinetic studies using wild-type HIV-1 RT and five K154 mutants. These mutants contained replacement of positively charged side chain of Lysine with two amino acids' hydrophobic and two amino acids' negatively charged side chains. In one of the mutants, the positive charge of Lysine was retained but the side chain was extended by one carbon atom while replacing it with Arginine. The results indicated that the mutants with negatively charged side chains displayed significant decrease in enzyme activity whereas other mutants exhibited enzyme activities almost comparable to the wild type. It was observed that excepting the mutants with negatively charged side chains which displayed higher fidelity than wild type, all other mutants showed enhanced levels of misinsertion and mispair extension; K154R being the more prominent. All mutants when tested for their response to an approved antiHIV-RT agent i.e., 3TC, reflected significant resistance to this nucleotide analog when compared to wild type enzyme. The mechanisms of misinsertion, mispair extension as well as drug resistance of these mutants would be explained in the light of three dimensional crystal structures of HIV-1RT.

sharmabi@yahoo.com