

Mixed mating patterns and pollen introgression in *Melia volkensii* clonal seed orchard; implication for genetic improvement and germplasm production

T3.34 Tree improvement delivery system: breeding, selection, and seed and seedling production

Stephen Omondi, Japhet Rotich¹, Steve Runo¹, So Hanaoka², James K. Ndufa³

¹ Kenyatta University P.O. Box 43844-00100 Nairobi, Kenya

² Shizuoka University 1623-1, Nishifujidaira, Tenryu-ku, Hamamatsu city, Shizuoka, 431-3352, Japan

³ Kenya Forestry Research Institute P.O Box 20412 Nairobi

Abstract

Melia volkensii is a monoecious, insect-pollinated tree species endemic to semi-arid region of east Africa valued for high quality termite resistant timber, however, limited knowledge of its mating patterns is hampering advancement of its genetic improvement in Kenya. We evaluated mating systems, gene flow patterns and level of pollen introgression within *M. volkensii* clonal seed orchard using 12 microsatellite markers. Four hundred and eighty open pollinated progenies from ten clones and 200 potential pollen donors were studied. One hundred individuals representing the total number of clones within the orchard and 128 individuals from the orchard background population were used as the potential source of pollen. We conducted pedigree reconstruction to assign each seed's male parents, followed by determining the extent of pollen contamination, selfing rate, and, parental gametic contribution. High values of multi-locus ($t_m = 0.933$; 0.016) and single locus ($t_s = 0.919$; 0.013) estimates of outcrossing rate indicates presence of mixed mating pattern with predominant outcrossing breeding system. The difference between t_m - t_s (0.014; 0.027) was low indicating absence of bi-parental inbreeding. Likewise, estimated correlation of paternity ($r_p = 0.029$) was low indicating that many of the progenies did not share the same paternal genitors. The fixation index for maternal genotypes (F_m) within progenies was non-significantly low showing lack of inbreeding. The estimation of the probable number of pollinators ($1/r_p$) indicated that about 69 pollen donors contributed in the fertilization of the progenies. The paternity analysis implicitly assigned 389 out of 471 progenies (82.6%) were assigned to 69 (69%) of the seed orchard clones. The unassigned 82 progenies (17%) did not match any of the 100 seed orchard clones and were considered to be derived from donors outside the orchard. Our findings indicate existence of adequate gene flow within the orchard probably due to predominant out crossing breeding nature and reproductive synchrony among genotypes. The seed orchard design and flowering synchrony with the background population could have contributed to the pollen introgression in the orchard. Review of the current isolation distance between the orchard and the background population should be considered to ensure integrity of the seed source.