

P0527 A Genetic Linkage Map Using an F1 Population in Rubber Tree (*Hevea brasiliensis*) based on microsatellite markers

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The construction of molecular gene linkage map in *Hevea* requires specific methodology because of high heterozygosity. Unlike annual crops, a cross between two heterozygous parents in *Hevea* can yield information up to four alleles, which are segregated further. The mapping population was a full-sib progeny (F1 progeny) derived from a cross between the cultivars PB217 and PR255. A set of 603 microsatellite primer pairs was tested for polymorphism the two parents and six F₁ progenies genotypes. Linkage map was obtained using OneMap (Margarido et al., 2007). LOD Score 4.5 and recombination fraction of 0.40 was considered to determine linkage between markers. In total, 288 marks were genotyped (230 SSR genomic loci and 58 EST-SSR). The map consists of 288 markers, distributed in 23 linkage groups (LG) and 2833.8 cM in length with an average genetic distance of 9.8 cM between adjacent markers. The largest group has 228.7 cM (29 markers) and the smallest has 10.3 cM (4 markers). SSRs provide powerful tool for genetic linkage map construction that can be applied for identification of QTL. Importantly, the marker linked to the QTL can be further applied to MAS in rubber tree breeding program for selecting plant that contains desirable phenotype. The map is not saturated enough and some chromosome regions could not be linked. The chromosome number accepted today, for most *Hevea* species, is 18 (2n=36). The present map will be used for yield rubber QTL mapping and other important economical characteristics.

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