

Investigation of Morphological and Molecular Marker Segregation of an F₂ Population of Coconut (*Cocos nucifera* L.) and Deriving Marker-Trait Associations

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Investigations based on segregating populations such as F₂ are essential for genome mapping and QTL analysis of crops. Deriving an F₂ population of coconut is difficult due to the long generation interval. The objectives of the current study were to investigate two F₂ populations of coconut for morphological and molecular segregation and to derive marker-trait associations. The study was done using 80 individuals of 2 five-year old F₂ populations derived from crosses; Red dwarf × Brown dwarf (RDBD) and Green dwarf × Yellow dwarf (GDYD) planted at Middeniya Research Station, Coconut Research Institute. The populations were phenotyped considering 16 quantitative and qualitative parameters, followed by genotyping based on 6 SSR marker loci. Descriptive statistics were generated for morphological data and genotypic data were analyzed by Powermarker software. Marker-trait associations were derived by single marker analysis. High values of standard deviation, variance and range of quantitative traits and the presence of different categories of qualitative traits indicated high levels of phenotypic segregation within the populations. Of the 6 SSR loci, only 5 were polymorphic and revealed 20 alleles in 2 populations reporting 2-6 alleles per marker. Mean values of gene diversity, heterozygosity and polymorphic information content for RDBD were 0.64, 0.62 and 0.57, while the same for GDYD were 0.60, 0.60 and 0.54, respectively. Significant associations (P<0.05) were identified for; leaflet number at *CnCirB12*; petiole width at *CnCirB12* and *CnCirE10*; number of leaflets at *CnCirB12*; petiole length at *CnCirC3*, *CnCirE10*; leaflet length at *CnCirE10* and pollination behaviour at *CnCirG11* marker loci. Accordingly, the two populations were identified to be highly segregating, facilitating their use in QTL analysis. The revealed marker-trait associations can be used for parental selection in coconut breeding. Detailed genotyping and phenotyping is recommended for comprehensive QTL analyses.

Keywords: Coconut, F₂ population, Morphological analysis, QTL analysis, SSR markers

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