HIGH DENSITY GENETIC MAPPING OF DWARFISM TRAITS IN A TALL X DWARF COCONUT (*COCOS NUCIFERA* L.) F_2 POPULATION UNCOVERS A MAJOR QTL FOR EARLY FLOWERING CO-LOCALIZED WITH THE FLOWERING TIME GENE FT

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Abstract:
The coconut palm (*Cocos nucifera* L.) is a worldwide important tropical tree crop providing vital resources for millions of farmers and industries with a diverse use of its oil and fruit products. The only species belonging to the genus *Cocos*, the coconut palm is a diploid (2n = 32) monoecious, perennial monocotyledon of the family Arecaceae (Palmae), with a relatively large genome size (1C = 2.74 Gb). With its most likely center of origin in Southeastern Asia, it is currently cultivated in more than 92 tropical countries covering more than 12 million hectares worldwide. Early flowering of the dwarf varieties is a feature of great agronomic relevance that results not only in precocity of nut harvest, but also increased production, while facilitating coconut tree deployment and harvest operation. In the present study, we used a unique segregating F2 population generated by open pollination of the F1 hybrid between Brazilian Green Dwarf from Jiqui (BGDJ) and West African Giant (WAG) to dissect the quantitative variation underlying the genetic divergence between tall and dwarf coconut types. This work aims to advance in coconut tree improvement generation using F2 generation plants derived from intervarietal crossing and using genomic data of SNPs molecular markers generated from the DArTseq technique in the coconut, with the objectives of to use plants of the F2 generation to build a genetic map and map identify QTLs for early flowering in coconut palms. Genotyping by sequencing using DArTseq generated 86,719 raw SNP calls based on the standard parameters used in DArTsoft. After applying a call rate threshold of 95% and a test for adherence to a null hypothesis of 1:2:1 segregation ratio ($p>0.05$), 3,714 SNPs. All 3,714 SNPs were mapped with LOD 15 and maximum recombination fraction of 0.4, in 16 linkage groups matching the expected 16 Coconut chromosomes. An average of 184.5 SNPs were mapped to each chromosome, varying from a maximum of 329 SNPs on chromosome 1 to a minimum of 101 SNPs on chromosome 15. The QTL analysis detected peaks (LOD >11) identifying possible loci related to early flowering control. A block of 57 SNPs located at the tip of chromosome 3 presented a set responsible for 55.30% of the explained variation and a significance threshold of 99%. The present study provides relevant information about the characteristics involving dwarf plants in coconut trees. Despite the lack of knowledge about the genes involved in precocity, QTLs can strongly help in the elucidation of what is behind precocity in dwarf plants. Knowledge of the chromosomal region responsible for the phenotype is essential for future research into responsible genes. There is also the possibility of building a marker chip capable of identifying the presence of precocity in coconut plants still in the early stages of life, allowing the producer to select only precocious plants, reducing the time of plant selection and reducing expenses with plants. erroneously installed in the coconut grove, a common error since the selection generally uses morphological markers that do not have high precision.
Palavras-chave: Coconut; genetic mapping; SNP; DArTseq; QTL

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