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SINGLE-TRAIT AND MULTI-TRAIT GWAS REVEAL LOCI ASSOCIATED WITH OIL PRODUCTION IN ACROCOMIA ACULEATA

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RESUMO

Facing the need to implement renewable energy sources to reduce environmental impacts, the macaúba oil palm (*Acrocomia aculeata* (Jacq.) Lodd. Mart) has stood out as a promising alternative for biofuels production, due to its high fruit production and sizable oil content in the mesocarp. Also, the processing of other parts of the fruit provides products to the cosmetics, food, and charcoal industry, along with the discernable value in the commercial market. Despite the economic importance, macaúba is a non-domesticated neotropical palm, incipient in large-scale cultivation, besides genetic architecture studies on the species, are scarce. Elucidating its genetic information can contribute to accelerating its domestication process. Furthermore, the quantification of simultaneous loci contributions for multiple traits, a phenomenon due to pleiotropy or linkage genes, can be facilitated by using multivariate models in genome-wide association studies (GWAS). Therefore, we conducted single-trait and multi-trait GWAS models to identify SNP markers located in gene regions related to different phenotypic traits involved in fruit production and fruit pulp oil content. For this, 201 palms were randomly selected from a natural population; the fruits were collected within two years of production. Phenotypic measurements of 13 traits involved with fruit production, processing, and pulp oil content were obtained. Genomic libraries were prepared following genotyping-by-sequencing protocol using two restriction enzymes (ddGBS) for SNP markers detection. The SNP calling was performed using three different strategies since macaúba does not have a reference genome: using i) de novo sequencing, ii) the *Elaeis guineensis* Jacq. reference genome and ii) the macaúba transcriptome sequences. Single-trait and multi-trait GWAS models were fitted on the three genotypic datasets to detect candidate and/or pleiotropic genes involved with the traits. For this proposal, we used the BLINK model from the GAPIT to fit single-trait analysis and the mixed linear model from the GEMMA to fit multi-trait analysis, both packages from R software. All phenotypic traits studied showed statistically significant differences and heritability values ranged from 63 to 95%. Traits that showed genotypic correlations above 0.8 were inserted into the multi-trait GWAS model. A total of 47 candidate genes in regions

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involved with different cellular pathways were detected in the single-trait GWAS, while the multi-trait GWAS detected 3 candidate genes that may be inserted in genes in pleiotropy or in linkage. Univariate and multivariate GWAS models can maximize the amount of information derived from the evaluation of multiple traits once they allow the detection of pleiotropic or linked genes. The results achieved in this study revealed different gene regions associated with adaptive traits involved with fruit and oil production, allowing new genetic studies in macaúba for its domestication and pre-breeding.

PALAVRAS-CHAVE: Neotropical oil palm, oil content, associative mapping, pleiotropic or linked genes

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