

Genome Wide Association study for drought tolerance and other agronomic traits of a *Coffea canephora* population

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Recent technological advancements and cost decreases on DNA-sequencing technologies allowed the completion of a reference sequence of the *C. canephora* genome. In due time, perhaps with some delay, in view of the economic and social importance of coffee worldwide as well as its perennial aspect (*vis à vis* annual crops), to provide the research power to face the challenges lying ahead, imposed by the real/potential climate changes impacts. Studies on a genome-wide scale are now being performed allowing researchers to narrow down some key molecular players that will certainly be applicable to fast and cost-effective molecular breeding programs. This work describes a Genome Wide Association Study (GWAS) for drought tolerance and other important agronomic traits such as yield of a *C. canephora* conilon population, cultivated in Planaltina-DF (1175m altitude) at the experimental field of Embrapa Cerrados. Phenotyping started in 2012, evaluating characteristics such as vigor, secondary branching, leaf-rust susceptibility, precocity and fruit load. Furthermore, the yield of each plant was measured for three consecutive years (2012-2014) and the predawn-leaf water potential (Ψ_{am}) of 400 plants was also evaluated under field conditions (drought season of 2012/2013). Genotyping was performed using the nextRAD technique provided by SNPSaurus (<http://snpsaurus.com/>), yielding 11.230 SNPs with a call rate above 80%. Population structure was determined using the admixture model of the software STRUCTURE. Marker-trait associations (MTAs) studies were conducted employing mixed linear model (MLM) analysis with optimum compression and kinship matrix (TASSEL). Significant MTAs were found and will be presented.

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