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

Carneiro, F.A.\(^a\), Régo, E.C.S.\(^a\), Aquino, S.O.\(^a\), Costa, T.S.\(^a\), Lima, E.A.\(^a\), Rocha, O.C.\(^a\), Rodrigues, G.C.\(^a\), Carvalho, M.A.P.\(^a\), Vega, A.D.\(^a\), Guerra, A.P.\(^a\), Bartholo, G.F.\(^a\), Silveira-Junior, O.B.\(^a\), Maracana, P.M.\(^a\), Grattaglia, D.\(^a\), Andrade, A.C.\(^a\)

\(^a\) Graduate Course on Plant Biotechnology – University of Lavras (UFLA), Brazil; \(^b\) Brazilian Agricultural Research Corporation (Embrapa), Brazil; \(^c\) CIRAD LMR AGAP, France; \(^d\) Laboratory of Molecular Genetics, INOVACAPÉ (UFLA), Brazil. e-mail: alan.andrade@embrapa.br

Recent technological advancements and cost decreases in 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 (vs. \& 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* cordon 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 (Ψpm) 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.

Acknowledgments: Consórcio Pesquisa Café, CAPES, INCT-Café (Papernig/CNPq).