

*Fernanda de Araújo Carneiro*¹; *Pierre Marraccini*²; *Marcio Balestre*³; *Dario Grattapaglia*⁴;
*Alan Carvalho Andrade*⁵

Coffee is one of the most heavily globally traded commodities and its production is based on *Coffea arabica* and *Coffea canephora* and Brazil being the world's largest coffee producer. It is believed that all this production will be affected due to climatic changes, with low flower viability, fruit development, yield and beverage quality. An alternative to assist in obtaining coffee plants more adapted to future climatic conditions would be genomic selection (GS). The implementation of these programs requires a lot of genetic markers, which are more readily discovered now after the reference genome of *C. canephora* became available. Another important factor is the high genetic variability of *C. canephora*, due to its level of allogamy, being of great importance for breeding programs of coffee. Most of the traits which are economically important are quantitative and complex in nature and require whole genome coverage of markers thus, GS, through the calculation of genomic estimated breeding values (GEBVs), are becoming important and effective tools for plant breeding. In the case of GS, these markers are used to build a predictive model using individuals with known genotypic and phenotypic information. With this model, GEBVs for the desired trait can be calculated and used to rank the individuals with unknown phenotype for subsequent selection. GS is a new approach in coffee breeding that enable early selection of elite materials, maximizing genetic gains over generations. For this purpose, in this work, a large number of individuals and markers were selected to assess GS applicability in terms of selection response of the targeted traits and prediction accuracy in a population of *C. canephora*. Approximately 1,300 individuals of *C. canephora* from a breeding population located at Embrapa Cerrados (Planaltina, DF, Brazil) were selected and evaluated for characteristics such as productivity, fruit precocity, grain size, cherry fruit size and weight of 100 grains. DNA of each of the 1,300 individuals selected from the breeding population was extracted and the genotypic data were obtained with the 26K Axiom SNP array developed for *C. canephora*. The sampled population performed two functions at the same time, estimation and validation of the GS model. Prediction equations of GEBVs were constructed for each character of interest, predicted by RR-BLUP. Although GS studies have not yet been able to explain the total phenotypic variation, they have identified essential genomic regions, and for perennial species such as coffee, the use of GS can greatly increase selection efficiency, thus reducing the time to introduction of characteristics of interest.

Financial Support: Consórcio Pesquisa Café, INCT-Café (CNPq/Fapemig), CAPES –
Concentration area: Plant Breeding

¹ PhD Student in Plant Biotechnology, UFLA/Lavras, MG, Brazil – fearca14@gmail.com;

² Researcher, Cirad UMR DAP Montpellier – France;

³ Researcher, UFLA, Lavras, MG, Brazil;

⁴ Researcher, Embrapa Genetic Resources and Biotechnology, Brasília, DF, Brazil;

⁵ Researcher, Embrapa Coffee/Inovacafé, UFLA/Lavras, MG, Brazil.