

Development and Characterization of a True F₂ Population for Genetic and QTL Mapping in Arabica

C. NAGAI¹, M. R. JONES¹, A. E. BYERS¹, D. J. ADAMSKI¹, R. MING^{1,2}

¹Hawaii Agriculture Research Center, Aiea, HI, USA.

²University of Illinois at Urbana-Champaign, Dept of Plant Biology, IL, USA

SUMMARY

Arabica coffee is a perennial tetraploid species, and developing a mapping population is time consuming and costly. Limited genetic variation within *C. arabica* also delayed genetic map construction of this commercially important species. A segregating mapping population of Arabica coffee (*Coffea arabica* L.) was developed from a cross between the two varieties, Tall Mokka (MA2-7) and Catimor (T 5175-7-1). Tall Mokka and Catimor are distinctively different in cupping quality as well as leaf, bean, and tree morphology, including branch angle, sub-branching numbers, leaf length and width, cherry and bean size and weight. Difference in cupping quality of the two parents was confirmed by a professional coffee cuppers. An F₂ population was generated from two F₁ plants, H00-20-25 and H00-20-41, each producing 75 trees. This F₂ population was planted at HARC Kunia Station on Oahu in 2003. Phenotypic variations were detected and recorded on tree height and width, branch angle, leaf characteristics, cherry weight, and green bean weight. Cherry/green bean characteristics showed normal distribution. No difference in distribution patterns was found between two sub-populations originated from two F₁ trees. The variations of the true F₂ population were larger than those of the pseudo F₂ population as expected. Additional 200 F₂ seedlings were obtained, and are established in the field in 2006. A preliminary genetic linkage map was constructed using 797 polymorphic markers generated from 699 pairs of AFLP markers on the F₂- population of Arabica coffee. This map is being used for mapping of quantitative trait loci controlling source and sink traits.