



Based on SSR markers and A Model-based Genetic Clustering Method

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Introduction

Arabica coffee (*Coffea arabica* L.) plays an increasingly significant contribution to coffee industry in Thailand. Currently, the main important issues are continuously lost the trust resistance genes due to breeding of the new varieties and an increase in population sizes in the country. This study aimed to investigate the genetic variability and genetic structure of Thai Arabica Coffee hybrids (*Coffea arabica* L.) based on SSR markers and a Model-based genetic clustering method^{1,2}.

Materials/Methods

The 67 coffee hybrid accessions together with 25 derived-spontaneous accessions maintained at the Royal Agricultural Research Center, Chiangmai, Thailand were assessed genetic variability and structure using 21 simple sequence repeat (SSR) markers and explored with the distance-based clustering and the structure-based methods.

Conclusion/Perspectives

Based on these findings, it is possible to minimize duplication and assist in the establishment of core collections that are representative of the full range of genetic variability. This information will provide coffee breeders with more efficient strategies for exploiting available germplasm resources in Thailand as well as informative data for varietal registration and identification.

References:

Pritchard JK, Stephens M and Donnelly P. 2000. Inference of population structure using multilocus genotype data. *Genetics* 155: 945–959.
 Falush D, Stephens M and Pritchard JK. 2003. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164: 1567–1587.

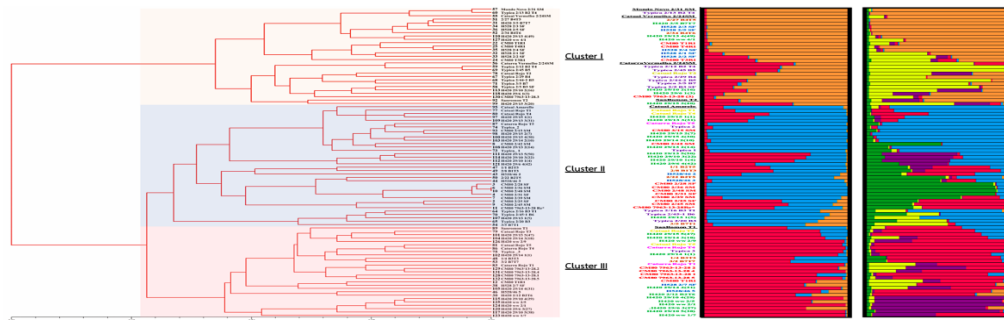


Figure 1: Phylogenetic tree based on UPGMA and genetic structure of 92 coffee accessions at K=3 and K =6. **Notice:** Red, green, blue, orange, yellow, pink represented CM80, H420, H528, Typica, F1 hybrids, Catuai, Caturra, respectively. Underline indicated the sample less than 2 accessions.

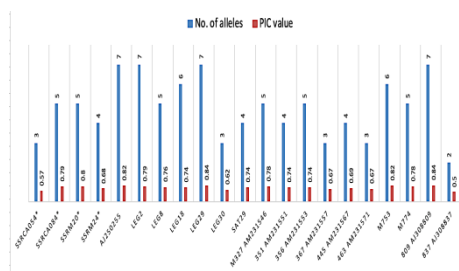


Figure 2: Number of alleles and PIC of the 21 SSR primers



Figure 3: The PCoA plot based on genetic distance **Notice:** Red, green, blue, orange, yellow, pink represented CM80, H420, H528, Typica, F1 hybrids, Catuai, Caturra, respectively. Underline indicated the sample less than 2 accessions.

Results/Discussion

All selected markers showed polymorphism with totally 100 alleles. The average number of alleles per locus was 4.7 and the average polymorphism information content (PIC) was 0.73 (Figure 2), showing the same range with those previously reports in the literature. The average genetic similarity based on Jaccard's similarity coefficients was 0.60 and ranged from 0.20 -1.0 (Figure 1).

The analysis of PCoA plot (Figure 3) and UPGMA tree showed three main clusters. The result revealed that the genetic clustering of the varieties or accessions was (Figure 1) correlated with their original varietal classifications. Therefore, the model-based clustering was applied to confirm the distance-based clustering and to more deeply understand the genetic variability and populations sub-structure within populations. The model-based analysis inferred three main genetic structures groups [K = 3] as the most suitable cluster and six sub-populations [K = 6] which provides a strong evidence of population substructure in *C. arabica* hybrids in Thailand (Figure 1).