

Genetic structure and relationships among populations of the subgenus *Protocamellia* in the southern area of Vietnam inferred by SSR analysis

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We are investigating genetic structure and relationships of *Camellia* species in Vietnam. Sixty two species were collected from natural habitats, in which, 36 species were obtained from Southern area. After 1990s, many new species have been reported from Vietnam, especially from southern area, therefore its origin is supposed to be more south than before thought to be. *Protocamellia* is considered to be most primitive in the genus *Camellia*, thus it is important to investigate the origin and evolution of the genus *Camellia*. In our project, 15 out of 62 species belonged to *Protocamellia*, especially 13 were collected from South. Here we introduce our results of population analysis using SSR markers in relation to the whole analysis using all accessions belong to 4 subgenera of the genus *Camellia*.

Thirteen SSR markers out of 107 SSR markers examined were proved to be applicable for this study. A total of 131 individuals from 17 populations of 13 *Protocamellia* species were collected by explorations, in which 99 individuals from 13 populations of 11 species were subjected to the population analysis. Structure analysis revealed subgenus *Protocamellia* was derived from two different ancestral genotypes. This may suggest that the subgenus *Protocamellia* is highly divergent. The result of genetic relationship analysis showed 2 clades of *Protocamellia*, corresponding to 2 ancestral genotypes. One genotype includes *C. dormoyana*, *C. luteocerata* and *C. bugiamapensis* which appeared nested each other on the phylogenetic tree. Further investigation, especially morphological observation will be required.