SEQUENCING RELATIONSHIPS BETWEEN OF GENUS CAMELLIA (GREEN TEA) BASED ON THE CHARACTERISATION OF NUCLEAR ITS REGION

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ABSTRACT

The objective of this study was to verify genetic diversity of genus *Camellia*. This study used Blast data (NCBI) of ITS region (partial internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, partial 26S ribosomal DNA gene) for further analysis of studies. The mean nucleotide frequencies for thirty-one of genus *Camellia* are A = 18.2%, C = 35.0%, G = 32.3%, and T = 14.5%. There were a total of 695 positions in the final dataset. Total alignment length of genus *Camellia* is 695 positions, of which 44 are parsimony-informative, 117 variables, 69 singletons, 549 conserved, and 528 coverage (100%). Substitution pattern and rates were estimated under the Tamura-Nei (1993) model. Each entry is the probability of substitution from one base (row) to another base (column). The probability of changing from C to T(U) was 30.6 percent, higher than other substitution probabilities. The estimated Transition/Transversion bias (R) is 2.58. Number of segregating sites of genus *Camellia* was 117 and nucleotide diversity (π) was 0.033. Under the neutral mutation hypothesis, the probability that D is negative (-1.490) is small than 0.5.

Keywords: *Camellia***,** ITS region**,** nucleotide frequencies**,** substitution pattern**.**