

Random amplified polymorphic DNA (RAPD) markers reveal genetic relatedness of tea (*Camellia sinensis* L.) clones in Sri Lanka

Genetic relationships of tea clones representing, TRI recommended clones, estate selections and two known diverse varieties were assessed by RAPD screening with five primers selected by pre-screening 100 primers (Operon). DNA was isolated from by applying a CTAB based technique and amplified by RAPD-PCR following the standard protocol. The amplification products were checked and scored on agarose/ethidium bromide and Photoprint get Documentation system. Nei and Li genetic distances were calculated based on band sharing and a dendrogram was constructed to observe the pattern of clustering.

A high level of genetic diversity was observed with an average of 0.40 (TRI clones, 0.39 and estate selections, 0.33). TRI clones, TRI 3055 and TRI 4006 varied immensely and the only ASSam clone (TRI 2016) too varied considerably. The Japanese and Chinese varieties 'Yabukita' and "China" deviated more from RTI clones than estate selections. All estate selections clustered together with "Yabukita" and "China" and separated from the bulk of ASM4/10 derived TRI clones.

The TRI recommended clones and estate selections of tea are constitute by a broad genetic base comprising diverse tea collections from the Asian continent indicating good chances of further genetic improvement by hybridization. The genetic relationship of the 40 clones as revealed by RAPDs reflected a clear picture of the tea population structure in Sri Lanka more accurately than previous descriptions based on morphological or isozyme data. A more accurate assay using a much higher number of

primers (app. 200 polymorphic bands) is suggested for a much finer classification of the tea clones in Sri Lanka.