

Genetic variation in Sri Lanka

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Abstract

A population genetic study was designed to analyze genetic composition and population structure of the five main population groups (Sinhalese, Tamils, Moors, Burghers, and Malays) of Sri Lanka. Twenty-seven polymorphic and three monomorphic loci were examined in all five populations. Several genetic markers, including subtype variation of HP, TF, PI, GC, ORM, and PGMI, were analyzed for the first time and helped to clarify the range of genetic variation for Sri Lankan populations. Many genetic systems (Rh, JK, ACP, ESD, HP, C3, TF, and GC) showed a high level of variation among the populations of Sri Lanka. However, at the individual level the Burgher population (a hybrid group between the Dutch and Portuguese and the local Sinhalese) showed European features, but its gene frequencies were either intermediate to its parental populations or more similar to the local Sinhalese. In the F statistic analysis all populations showed positive F(IS) values, ranging from 0.0305 in the Burghers to 0.1084 in the Malays; however, for a large number of loci the F(IS) values for the Burghers were negative, indicating the possible hybrid nature of this population. In genetic affinity studies the Burghers, Moors, and Malays showed a greater degree of isolation, but compared with the possible populations of their origin, the five populations of Sri Lanka tended to show some degree of affinity to each other. Our analysis therefore suggests that there is little evidence of disruptive selection; however, restricted gene flow favors the change of allele frequency toward the local Sinhalese and Tamil populations