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A preliminary study on human Y-DNA haplogroup M20 in Sinhalese male individuals

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Origin of Sinhalese, the major ethnic population in Sri Lanka, is controversial according to the Sri Lankan historical evidences and hence, this is a preliminary approach of investigate the paternal inheritance of Sinhalese individuals in a scientific aspect. Sinhalese are known as either descent of Aryans, Prince Vijaya and his followers, who were migrated from West Bengal of India, or present generation of the trial inhabitants or a combination of both Aryans and native tribal population. Haplogroups are derived from a combination of single nucleotide polymorphism unique to a population. M20 is identified as a Y haplogroup which is frequent in South Asia, including India Since mainly males were migrated from India in many instance origin of Sinhalese, the major ethnic population in Sri Lanka, is controversial according to the Sri Lankan historical evidences and hence, this is a preliminary approach of investigate the paternal inheritance of Sinhalese individuals in a scientific aspect. Sinhalese are known as either descent of Aryans, Prince Vijaya and his followers, who were migrated from West Bengal of India, or present generation of the trial inhabitants or a combination of both Aryans and native tribal population. Haplogroups are derived from a combination of single nucleotide polymorphism unique to a population. M20 is identified as a Y haplogroup which is frequent in South Asia, including India Since mainly males were migrated from India in many instances; present study mainly designs to analyze more prevalent Y haplogroup in India in view of studying paternal inheritance of Sinhalese individuals. Here, we used few male samples (N=5) which were already screening for Alu polymorphisms. Polymerase chain reaction (PCR) was carried out using sequence specific primers to amplify the specific region for M20 haplogroup. Prior to the amplification of samples, primer was optimized for annealing temperature and magnesium ion concentrations. Followed by each PCR, products were confirmed with 50 bp ladder in agarose electrophoresis. Then the PCR products were purified and direct sequencing was carried out In ABI 3500Dx Genetic analyzer. Hereafter generating sequencing results were analyzed using BioEdit and Ensemble applications. Those analysis states that the respective polymorphism A to G at 19571568 positions about GRC h38/h38 was not detected in present study. However, further analysis should be carried out using a larger number of samples to obtain valid conclusions.

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