Biomedical Research & Therapy

ISSN: 2198-4093
www.bmrat.org

POSTER

Variation of mitochondrial DNA HV1 and HV2 of the Vietnamese population

Linh Nguyen Quy, Le Anh Tuan Pham, Anh Hong Trinh, Thuy Thi Nguyen, Thinh Huy Tran, Anh Van Tran, Hinh Duc Nguyen, Van Thanh Ta, Van Khanh Tran

Hanoi Medical University, Hanoi, Vietnam

Abstract

The sequence polymorphism of mitochondrial DNA (mtDNA) hypervariable Segment 1 (HV1) and hypervariable Segment 2 (HV2) are studied and applied to genetic diversity and human evolution assessment, forensic genetics, consanguinity determination, and mitochondrial disease diagnosis.

Nucleotide sequence variations in HV1 and HV2, two hypervariable segments of the noncoding control region of human mitochondrial DNA (mtDNA), in selected ethnics of the Vietnamese population were elucidated through sequencing. In this study, we define the variations of HV1 and HV2 of 517 unrelated Vietnamese individuals in Kinh, Muong, Cham, and Khmer ethnic. We found 50 haplogroups: F1a haplogroup frequency is the highest at 15.7%; B5a haplogroup frequency is 10.8%, M haplogroup frequency is 8.9%, M7b1 haplogroup frequency is 7.7%; B6, D4e, D5a, E, F1c, F2a, F3a, G2a, M9b, N, N21 and U5a haplogroup frequencies are the lowest (1%). The frequency of SNP A263G are 100%; A73G is 99.6%, 315insC is 96%; 309insC is 56%; C16223T is 41%, and T16189C is 39%. We have assessed the genetic polymorphism of mtDNA HV1 and HV2 of 517 Kinh, Muong, Cham, Khmer ethnic samples.

*For correspondence:

tranvankhanh@hmu.edu.vn

Competing interests: The authors declare that no competing interests exist.

Received: 2017-07-13
Accepted: 2017-08-04
Published: 2017-09-05

Keywords

Mitochondrial DNA, hypervariable region HV1, HV2, Vietnamese

Funding

References