mtDNAPROFILER: A WEB-BASED MITOCHONDRIAL DNA SEQUENCE ANALYSIS TOOL

In Seok Yang, Hwan Young Lee, Woo Ick Yang, <u>Kyoung-Jin Shin</u> Department of Forensic Medicine, Yonsei University College of Medicine, 250 Seongsanno, Seodaemun-gu, Seoul 120-752, Korea

Mitochondrial DNA (mtDNA) has become a potent tool in population, medical and forensic genetics investigation. However, the analysis and comparison of mtDNA sequences may not be easy to do for researchers who are not familiar with mtDNA nomenclature conventions. Therefore, we developed a web program, mtDNAprofiler, which enables users to analyze and compare mtDNA sequences whether they are indicated as FASTA format or as revised Cambridge Reference Sequence (rCRS). The mtDNAprofiler consists of two systems; mtDNA nomenclature system by alignment with the rCRS, and mtSNP conversion and comparison system. mtDNA nomenclature system sequentially performs range determination and mtSNP calculation for input sequences followed alignment with the rCRS. In mtSNP conversion and comparison system, conversion mode allows mtDNA data indicated as a difference to the rCRS to be converted to FASTA sequence so that all the difference-coded mtSNP data followed various alignment rules may be easily used for further analyses. Comparison mode provides comparison results between two mtSNP data gathered independently or generated by different alignment rules, thereby ensuring the validity of the input mtSNP nomenclature. Therefore, the mtDNAprofiler will provide useful tools to characterize and analyze mtDNA sequences for researcher dealing with mtDNA.