Combined use of STRs and mtDNA genetic profiles for the identification of Korean War victims

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An effort to establish a database of mitochondrial DNA control region sequences (HV1 and HV2) using skeletal remains of war victims killed in the Korean War (1950-1953) and bloods from suspected war-bereaved families has been made since the beginning of the national project, “The Excavation on Casualties from Korean War” in 2000. According to the circumstantial evidences and the matching results of mtDNA genetic profiles, some of missing casualties were identified and returned to their families. However, relatively high mitochondrial HV1/HV2 haplotype frequencies in particular haplotypes suggest the need for additional genetic analyses to better identify individuals with scientific exactitude. In this regard, additional autosomal STR typing analyses were carried out using PowerPlex16 and miniSTR (by Butler JM). As old skeletal remains contain degraded genetic materials, miniSTR system which was developed to produce PCR fragments with reduced STR amplicon length was employed efficiently. Here, we report the use of additional STR typing on confirmation of genetic relationship between missing casualties and their bereaved families which was revealed by comparison of mtDNA genetic profiles. The strategy of combined use of STR information with sequence polymorphisms in mitochondrial HV1 and HV2 region will be greatly helpful to the effort of identifying missing casualties of Korean War.