# THE MITOCHONDRIAL DNA ANALYSIS OF ARCHIVAL SALIVA SPECIMENS FROM CENTRAL ASIA

Igor Ovchinnikov
Department of Biology and The Forensic Science Program, University of North Dakota, Grand Forks,
ND 58202, USA

Central Asia is a vast territory stretching in latitude from the Caspian Sea on the west to Mongolia and the northwestern part of China on the east. In longitude, Central Asia extends from the belt of Eurasian steppes on the north to the mountains of the Kopetdag, Pamir, and Himalayas, which separate Central Asia from South Asia. Central Asia, its people and states have played important roles throughout all human history. It was the crossroads of numerous migrations, civilizations, states and cultures, which arose and vanished between Europe and eastern Asia. Central Asia today is also a politically unstable region. This project will contribute to the ongoing efforts in understanding the routes of human migrations and global human diversity as well as generate a database of forensic genetic markers for populations in Central Asia. These markers are necessary in forensic applications for calculation of match probability between two random biological specimens in the geographic region.

The entire hypervariable regions I and II (HVRI and HVRII) of mtDNA have been sequenced from the Central Asian collection of the archival saliva specimens of anonymous unrelated adult donors collected in 1997 and 1998. This collection included 140 samples from Turkmenistan and 100 samples from Tajikistan. The mtDNA sequences were obtained from 82% of specimens. The basic population indices demonstrated a demographic scenario with the evidence of population expansion for both populations. The genetic distance based on the mtDNA sequences indicated that the Turkmen and Tajik populations cluster with several groups from the Caucasus (Armenian, Georgian, Kabardinian) and southern Europe (Tuscanian). Both populations also possessed an admixture of the mtDNA lineages from the eastern and southern Asia. The AMOVA analysis showed that the distribution of the mtDNA sequences within the Turkmen and Tajik populations is not structured according to tribal affiliation or geographical origins. The relatively homogeneous mtDNA diversity in these groups diminished the effect of population stratification on the probability of the DNA evidence.