

Y-STR FREQUENCIES AND ADMIXTURE IN MALES OF THE ALEUTIAN ISLANDS

Reena Roy¹, Rohina Rubicz², G. Su³, Ranjan Deka³, Victor Spitsyn⁴, Kristin Melvin², Karlyn Rensing¹ and Michael H. Crawford²

¹*St. Louis County Police Crime Lab, St. Louis, MO*

²*Department of Anthropology, University of Kansas, Lawrence, KS*

³*Department of Environmental Health, University of Cincinnati Medical Centre, Cincinnati, OH*

⁴*Russian Academy of Medical Sciences, Moscow, Russia*

Aleut males residing throughout the Aleutian Islands were characterized for 17 Y STRs, including: DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385a/b, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, and Y GATA H4. Thirty-four unique haplotypes were observed from a sample size of 52. Markers DYS448, DYS456, DYS458, DYS635, and Y GATA H4 were excluded and comparisons were made with Aleuts from Bering Island, Russians, Even, and Koryak. An R-matrix analysis using the 5 populations and 16 alleles from 11 loci indicated the Aleutian Aleuts were closer to Russians than to the Bering Island Aleuts (with the first 3 eigenvectors accounting for 93.6% of the total variation), indicating substantial non-Native gene flow through the paternal side into this population. This is in contrast to previous studies using maternal markers (restriction fragment length polymorphisms and HVS-1 sequences) which demonstrate the exclusive presence of Native American haplogroups A and D. Non-Native male admixture into this population has been documented beginning shortly after the discovery of the Aleutian Islands by Russians in the mid-1700's, first by Russian fur traders, and later through Scandinavian fishermen.