

## B64 The Biogeographic Origin and Genetic Characteristics of the Peopling of Jeju Island Based on Lineage Markers

*Sohee Cho, PhD\**, Seoul National University College of Medicine, Seoul 03080, SOUTH KOREA; *Soong Deok Lee, PhD*, Seoul National University, Department of Forensic Medicine, Seoul, South Korea 110-799, SOUTH KOREA

**Learning Overview:** After attending this presentation, attendees will understand the biogeographic origin and genetic characteristics of a relatively isolated population within Korea residing in an island apart from the mainland of Korea called Jeju Island and the power of lineage markers to infer the genetic origin or characteristics of populations.

**Impact on the Forensic Science Community:** This presentation will impact the forensic science community by presenting genetic evidence for an isolated population within Korea reflecting its historical background and geographical location, which is important to be considered in a forensic application.

Jeju Island is the largest island of Korea, located southwest of the Korean Peninsula, and has built a unique history and culture distinguished from other provinces within the mainland of Korea. Jeju Island has actively interacted with neighboring countries, probably due to its geographical location of the central region of East Asia, and also has been influenced by the Northeast regions, such as Mongolia. In various studies, much evidence of Mongolia's influence on Jeju Island has been found in their language, customs, and food, but little research has been conducted on genetic approaches so far. Lineage markers on Y-chromosome and mitochondrial DNA are useful in inferring paternal and maternal lineages of populations, respectively, and can be of help in understanding the biogeographic origin of peopling of Jeju Island.

This study analyzed data of Y-chromosomal Short Tandem Repeats (Y-STRs) of 615 males and mitochondrial DNA haplogroups of 799 individuals in Jeju Island using statistical methods, including pairwise  $R_{st}$  and  $F_{st}$ , Analysis of Molecular Variance (AMOVA), and Metric Multidimensional Scaling (MDS) analyses, with collected reference data of Korean populations within different provinces and other countries.

The results from Y-STR analysis presented that low diversity of Y-STR haplotypes, strong association with surnames, significant genetic difference among other males within different provinces of Korea, and common genetic variations known to be predominant in Mongolian people. Statistical analysis of mitochondrial DNA haplogroup showed that low diversity of haplogroup and high frequency of haplogroup Y was mostly prevalent in ethnic populations around the Sea of Okhotsk in Northeastern Asia. All these results could indicate that a genetic substructure of Jeju Island may exist, possibly due to genetic drift acting on this somewhat isolated island. In addition, it is believed that the peopling of Jeju Island may be genetically influenced by northern regions such as Mongolia, which can be supported by the fact that Jeju Island has historically had a close relationship with the Yuan Dynasty established by a leader of the Mongol people during the Koryo Dynasty of Korea. The present study provided genetic evidence on a unique background of peopling in Jeju Island distinguished from the mainland of Korea, and this should be taken into account for forensic application, including the establishment of forensic databases for disaster victim identification, such as the Jeju 4.3 incident.

### Jeju Island, Y-STR, Mitochondrial DNA Haplogroup