

## **DNA ANALYSIS OF THE HUMAN REMAINS FOUND ON THE VASA WARSHIP**

Magdalena M. Buś<sup>1</sup>, Fred Hocker<sup>2</sup>, Maria Lembring<sup>1</sup>, and Marie Allen<sup>1</sup>

<sup>1</sup> Department of Immunology, Genetics and Pathology, Biomedical Centre (BMC), Uppsala University, Husargatan 3, S-751 08 Uppsala, Sweden.

<sup>2</sup> The Vasa Museum, National Maritime Museums, Galärvarvsvägen 14, S-115 21 Stockholm, Sweden

Corresponding author: Marie Allen, Department of Immunology, Genetics and Pathology, Biomedical Centre (BMC), Uppsala University, Husargatan 3, S-751 08 Uppsala, Sweden, e-mail: marie.allen@igp.uu.se

The Swedish Royal Warship Vasa capsized on her maiden voyage on the 10 August 1628, shortly after she left the harbour of Stockholm. In 1961 Vasa was salvaged from the Baltic Sea, and skeletal remains from approximately 15 individuals were found scattered in and around the ship. After osteological analysis the skeletons were buried in a cemetery in 1963. When the remains were initially found, the skeletons were in quite good condition and seemed well preserved. However, the skeletons are likely to have been further damaged and progressively degraded during the period in the grave. The grave was reopened in 1989 for further osteological and archaeological analysis. To confirm that the remains found outside the ship were from the same time period as the victims of Vasa, a C14 analysis was performed. Recently, teeth and bone samples were taken for mitochondrial DNA analysis.

The aim of the mtDNA study was to perform a realistic estimate of the number of individuals that perished with the Vasa warship. A second objective was to investigate if some of the individuals were possible siblings, due to the morphological features, certain anomalies of the skulls and similar age of these individuals. As the samples are likely to be degraded, the mitochondrial D-loop region comprising two hypervariable fragments (HVI and HVII) were sequenced. The mtDNA analysis is more likely to yield information from degraded samples due to the high copy number per cell. Several protocols for DNA extraction, amplification, purification, and sequencing were evaluated and improved during the investigations and later used for the final analysis. Despite the age of the samples, the fact that they have been in seawater for 333 years, and long deposition of remains in soil, DNA amplification and sequencing that produced data of good quality was possible.

There is limited research performed regarding how long DNA can survive in seawater. This study shows that human remains immersed for over 300 years can still provide a source of amplifiable DNA. The data indicate possible relationships between individuals, and could also connect morphologically unidentified remains to each other. Moreover, unique haplotypes of some individuals, and their attribution to rare haplogroups indicated a likely area of origin. Several new reagents were tested in the study, and improvements in the protocols of molecular analyses had crucial impact on the success. The used methodology can therefore be useful in future DNA investigations of severely degraded skeletal remains from water and/or soil environments.