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Evidence of Interbreeding between Homo sapiens and Neanderthals in Melanesia

by Karen Goto

(Biology 1151)

ABSTRACT

Remains of an ancient *Homo sapiens* were recovered in Melanesia. The remains offered insight into interbreeding between Neanderthals and *H. sapiens*. The possibility of this is focused on the presence of STAT12 gene profile using electrophoresis. DNA fingerprinting was done to compare the remains with Neanderthals. Human contemporaries from the local regions of Asia were also included to examine the possibility of Neanderthal DNA. Comparison showed that the remains recovered from Melanesian had the gene variation possessed by the Neanderthal. No other matches were found. The skeletal remains were of a female of an estimated age of seventeen to mid-twenties. Findings support that there has been interbreeding between the two hominins; however, more evidence is needed of where interbreeding occurred based on migration patterns. In addition, this gene variation could have risen from multiple mutation events or from interbreeding between modern humans and a descendent or close relative of the Neanderthals.

INTRODUCTION

Homo sapiens first appeared in the fossil record from about 200,000 years ago. A close relative, the Neanderthals, appeared in fossil record about 230,000 years ago and went extinct about 30,000 years (Sankararaman et al 2012). Multiple questions revolve around the human species regarding its classification and possible ancestors. An ongoing debated question involves the relationship and the potential interbreeding between the modern human and Neanderthals. There is direct evidence in proving that sequenced Neanderthal DNA is very similar to nuclear DNA of living *H. sapiens*. More specifically, a gene variation STAT12 in modern humans appears to have been inherited from interbreeding with Neanderthals. Neanderthals occupied Europe and Western Asia; which eventually was colonized by *H. sapiens*. Numerous studies have proven that Europeans are known to carry a higher frequency of this gene variation; thus, the question was whether there is presence of this similar DNA in different parts of Asia.

Recent excavations in Melanesia uncovered the skeleton of an ancient human. The interest was if the remains showed evidence of Neanderthal DNA. DNA fingerprinting was used to compare the DNA profiles of the remains, the Neanderthals and 4 human contemporaries from Philippine, China, Australia, and Polynesia for evidence of species interbreeding. Additional objectives of the study were to determine determining the gender, age at death, and cause of death of the individual whose remains were found.

METHODS

Carbon-14 dating was used to find the age of the remains using five bone fragments. Samples of STAT12 were collected from the human remains, a Neanderthal and the 4 human contemporaries in a blind experiment. The DNA samples were collected using the Eco RI/PSH restriction enzyme and separated by horizontal electrophoresis (Bio-Rad Laboratories, LTP, Hercules, CA).

Gender was determined by looking at the pelvic girdle and sacrum. The teeth were used to estimate the age of the remains. Cause of death was determined by considering the time and place of the skeleton excavated and observations of the skeleton for potential marks that can indicate injury fatal for death.

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RESULTS AND DISCUSSION

The STAT 12 gene profile matched between the ancient remains and the Neanderthal (Figure 1). This finding is consistent with interbreeding between Neanderthals and *H. sapiens* in Melanesia. The remains dated to $42,143 \pm 102.3$ years (mean \pm standard deviation, n=5).

The pelvis of the remains was circular and broad, and the sacrum tilted back which identified the gender as female (Tortora and Derrickson 2009). The presence of a third molar indicated that the individual is at least 17 years old. The spinal cord showed no wear or any evidence of arthritis that is present in older individuals and the collarbone has not completed fusion so the individual's age can range from 17 years old to late 20's.

The skeletal remains showed a crack in the jaw that could have impeded this individual from being able to eat properly which could have eventually led to death from malnutrition. However, it was unknown if any of these injuries occurred before death. The missing parts of the skeleton could be explained due to natural causes over the 42,143 years. Hence, cause of death could not be determined.

The presence of the gene variation in the Melanesian remains suggests interbreeding between Neanderthal and H. sapiens in the South Pacific islands. With 170,000 years of both species' simultaneous existence, there was also overlap in geographical distribution. If interbreeding occurred, the group must have been very small due to such a small percentage of STAT12 in human contemporaries and due to small population densities of the Neanderthals as they were close to extinction (Neves and Serva 2012). However, there are other possibilities that could have resulted in a similar gene between Neanderthals and Homo sapiens. One possibility is multiple episodes of similar STAT12 mutations. Alternatively, the STAT 12 variant may have come from a close relative of Neanderthals. The number of hominins is still a debate with some recognizing over 20 hominin species and others declaring only a few. Excavations in the Denisova cave recovered remains that, when compared in an analysis of nuclear genomes, show levels of gene flow similar to Neanderthal and H. sapiens (Bokma et al 2012). Another group, the Denisova hominins, show similarities with the Neanderthals and human contemporaries suggesting other hominins that could be closely related to the Neanderthals. Finally, it is unknown when the Neanderthal DNA was introduced to Homo sapiens. Migration of an ancestor to the ancient human observed in H. sapiens could have accounted for the gene.

LITERATURE CITED

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Wells	Samples
2	Neanderthal
3	Philippines
4	China
5	Melanesia
6	Australia
7	Polynesia

Figure 1. Gel extracted from horizontal electrophoresis.

Figure 2. Skeletal remains recovered.



Figure 3. Close up of the teeth

