|  |  |
| --- | --- |
|  | **Research Networking Programmes** |
|  |
|  |

**Short Visit Grant**  **or** **Exchange Visit Grant**

***(please tick the relevant box)***

**Scientific Report**

**Scientific report (one single document in WORD or PDF file) should be submitted online within one month of the event. It should not exceed eight A4 pages.**

***Proposal Title****:* Autenthification of ancient DNA molecules in genomic studies of Pleistocene macromammals

***Application Reference N°:*** 5882

1. **Purpose of the visit**

The main purpose of the visit was the analysis of ancient DNA molecules from Pleistocene macrommals -particularly brown bears-, in order of identifying patterns of molecular damages that are specific of ancient DNA. The identification of that patterns are relevant to two main puposes in the genetic analysis of ancient remains: first, in order to distiguish real polymorphisms from molecular alterations that ocurred after morten and so, to accurately assign the genotypes. Second, to autenthify the antiquity of the molecules and distinguish them from modern contaminants, which would not display these patterns.

1. **Description of the work carried out during the visit**

Ten ancient samples of brown bear, ranging on age from 10,000 to 4,0000 yBP have been studied during this visit. All of the samples are originally from Spain and have been studied at genetical level in Professor Michael Hofreiter's lab in the University of York, which is my current employer. We performed enrichment techniques based on hybridization capture and subsequent next generation sequencing (NGS), from which we recovered the completed mitochondrial DNA from all the ten samples of brown bear. However, before proceeding with the haplotype assigment it is crucial to distinguish the original polimorphism from post morten molecular damages.

During this short visit at the Center of GeoGenetics in the University of Copenhagen I have been trained on the use of MapDamage. This is a software specifically developed to identify and provide statistical estimates of the main patterns of damage in ancient DNA molecules: the average length of the molecules, which is expected to get shorter over time; and the citosine deamination rate, which has been observed to increase at the end of ancient DNA fragments.

1. **Description of the main results obtained**

The mitochondrial DNA sequences obtained from the ten samples of bear were analyzed with the software MapDamage. As result it generates a graphical representation of the deamination patterns as well as the fragment size distribution of the NGS data from each of the samples. Deamination ratios were observed to be high at the 5' end, as expected from ancient DNA molecules, while the deamination ratios at the 3 ' were lower, which in the case of these samples was explained by an effect of the capture technique employed for the enrichment of mithocondrial DNA. The clear

increase in cytosine deamination towards the 5 ́ was taken as a solid probe of the antiquity of the molecules. As well as, the average fragment size of the molecules, which was around 50-70 bp.

1. **Future collaboration with host institution (if applicable)**

Other samples from Spain have been analyzed in York and NGS data from them is now available. We are planning further collaborations to work on the analysis of these sequences, which would include prehistoric human samples from the same geographical areas than the old brown bears.

1. **Projected publications / articles resulting or to result from the grant *(ESF must be acknowledged in publications resulting from the grantee’s work in relation with the grant)***

The genetic data of the ancient brown bears from Spain will be write to be publish in a science journal (Molecular Ecology as possible journal on the topic). ESF will be acknowledged in the resulted publication.

1. **Other comments (if any)**

On the 13th of November and applied to postpone the starting date of the visit to the 4th of December. I was comunicated by email that the change of the dates for the visit was accepted (from the 4th to the 10th of December 2013).