



Research Networking Programmes

Short Visit Grant or Exchange Visit Grant

(please tick the relevant box)

Scientific Report

The scientific report (WORD or PDF file – maximum of eight A4 pages) should be submitted online within one month of the event. It will be published on the ESF website.

Proposal Title: Ancient DNA in conservation genomics: the ancient genome of the Iberian lynx

Application Reference N°: 5074

1) Purpose of the visit

My PhD. project investigates how genomic variation is shaped by genetic drift and selection in wild populations. To study the interaction between these two forces, we need a direct assessment of the magnitude of loss for both neutral and functional variation; and more importantly, we need to be able to distinguish an intrinsically low equilibrium diversity from a recent loss. The contrast of ancient genomic data with contemporary information will allow for a direct estimation of diversity and allele frequency change through time, for different types of variation and across loci and genomic regions. I am assessing these objectives using *Lynx pardinus* and *Lynx lynx* as model.

Framed in my PhD. project, the aim of my visit to Hofreiter's lab was to generate the first ancient whole genome sequence for the critically endangered Iberian lynx, *Lynx pardinus*.

I wanted to take advantage of Hofreiter's lab expertise on processing this material to be able to generate a library with an endogenous content high enough to make of shotgun sequencing a

cost-effective alternative, or at least that allows capture enrichment. The host lab is specially suited for this purpose, because they have fully implemented two recent technological developments that greatly improve the results obtained with ancient samples: a modified extraction protocol that preserve short- sequence and a more efficient single-strand library preparation.

2) Description of the work carried out during the visit

The work has been focus on DNA extraction and library preparation for the ancient samples available. We have focused our efforts on processing those samples that have shown promising results in previous analysis.

During my exchange, I built 70 libraries, processing a total of 20 ancient lynx samples. For 14 of those samples I performed two different protocols, with a bleaching pre-treatment before extraction, and without it. All the libraries were built with DNA extracted using Dabney method, and following the single-stranded library preparation protocol. 58 of the libraries have been test sequenced to check their endogenous content, 12 of them will be sequenced in the next weeks.

Besides, I have also worked in two extra objectives not previously defined in our proposal.

First, we have checked the endogenous content of some previously built historical libraries of *Lynx pardinus*, to assess which ones are suitable for whole genome analysis. I have also built a library for a *Lynx lynx* historical sample from the Iberian Peninsula.

Moreover, during these three months I had meetings and conversations about my research with members and visitors of Hofreiter's lab and Professor Hofreiter himself, that have been very valuable for the analysis of my data.

3) Description of the main results obtained

58 libraries have been test-sequenced to evaluate the endogenous content. Potential candidates have been identified, but further analyses are required. If there were any library with an endogenous content above 10%, that would be an ideal candidate to do shotgun sequencing. For values below that, we would make whole genome capture.

Future work will include those analysis as well as sequencing of 12 additional libraries that were built during the last week of exchange.

Regarding the analysis of the historical *Lynx pardinus* samples, we have identified potential candidates for shotgun sequencing that will help to complete the time line in our analysis.

The historical *Lynx lynx* library has also been test-sequenced and now we are performing the analysis to assess the endogenous content.

4) Future collaboration with host institution (if applicable)

Collaboration regarding this project will be maintained at least until publication of the data. We have not formally arranged any association regarding new projects, but we keep the door open to future collaborations.

5) 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*)

A projected article with the data generated thanks to this exchange will be prepared and submitted to a high-rank science journal. ESF will be acknowledged in the resulting publication.

6) Other comments (if any)