

Report on Workshop

Develop strategic priorities for DNA library creation of NH collections

at Museum für Naturkunde Berlin, 18-19 February 2016 (D 2.7)

The two-day workshop with 14 participants from 10 institutions involved in Task 2.2 ("Develop strategic priorities for DNA library creation of NH collections") had the aim of assessing the feasibility of creating DNA Libraries at institutional scale by European NH institutions and protocols for the common integration of those.

Background:

DNA libraries were suggested as a means of perpetuating DNA from rare specimens in NH collections (outcome of JRAs in S2).

Agenda (see meeting agenda for details):

- To obtain an overview of DNA library technology including costs and challenges; JRA leaders from S2 and other experts invited for this purpose.
- To discuss priorities for DNA library creation of NH collections.

Outcome:

- DNA libraries are an essential part of the NGS workflow and various alternative protocols exist, which each have specific advantages and disadvantages (for example, single strand versus double strand libraries, which differ in the DNA yield delivered (Hofreiter et al.)). The value of DNA libraries also critically depends on the DNA extraction method used.
- Technological change is rapid (e.g., switch from 454 to Illumina and soon presumably to long-read platforms), the costs per sample are still significant (c. 75-100 US\$/library). Furthermore, non-invasive techniques for DNA isolation are being refined continuously and this greatly influences the efficiency of DNA library construction.
- The discussion with the technical experts from the SYNTHESYS 2 JRAs and beyond clearly revealed that the systematic DNA library creation from NH collection samples independent of research projects is not a worthwhile endeavor due to costs and technological issues (it will be increasingly difficult, e.g., to analyze 454 libraries given that support for the system is discontinued and higher costs).
- However, DNA libraries created in the course of research projects involving specimens from NH collections should be databased (including all relevant metadata) and stored in DNA banks. This latter suggestion is now being taken up in a pilot study jointly with GGBN within the SYNTHESYS framework by RBGK (lead), BGBM, and MfN. This study will address an important gap in the sustainable archiving of genetic/genomic materials derived from NH collections and may set standards beyond the SYNTHESYS community.