CONTRAT N° B2/202/P2/InsectMOoD
Insect Museum Open -omic Database
BELSPO programme manager: Véronique Feys

1st meeting of the project follow-up Committee
(MSTeams, 1st of July 2021)

Participants:
Francesca Scolari – University of Pavia, InsectMOoD follow-up committee
Katerina Guschanski – Uppsala University, InsectMOoD follow-up committee
Peter Hollingsworth – Royal Botanic Garden Edinburgh, InsectMOoD follow-up committee

Massimiliano Virgilio - project coordinator, Royal Museum for Central Africa (RMCA)
Carl Vangestel - project partner, Royal Belgian Institute of Natural Sciences (RBINS)
Gontran Sonet - project collaborator, RBINS
Lore Esselens - project research assistant, RMCA
Jessica Ody – JEMU research assistant, RMCA

Meeting Report

A brief overview of the project timeline and implementation was provided by LE (see presentation attached to this report) with focus on:

- project structure and timeline
- sample age distributions in the tephritid and syrphid collections of RMCA
- methodological approach to wet lab pipelines
- methodological approach to the analysis of High Throughput Sequencing (HTS) performances
- expected outcome and valorisation of results

KG, PH and FS initiated discussion and provided input on

- destructive DNA extraction procedures and effects of sample age on proportions of endogenous vs contaminant DNA in Museum vouchers
- best practices for voucher cleaning and sterilization -> include PBS washing step before DNA extraction protocol to decrease contaminant DNA (if samples were collected > 10 years ago)
- fragmentation of degraded vouchers: retain smaller endogenous DNA fragments to distinguish from larger contaminant DNA fragments
- negative controls for DNA extraction and library preparation
- replicates vs pooling samples + use distinct species per batch
- include molecular identification and double indexing library preparation
- Use of Roche columns (High Pure Viral Nucleic Acid Large Volume Kit) as a possible alternative to the DNeasy Blood and Tissue Kit (Qiagen) columns to retain DNA fragments < 100bp
- Use of Qiagen kit for DNA extractions of sperm cells -> QIAamp DNA Mini or Micro kit as a suitable strategy to deal with low DNA concentrations
- MinElute columns (MinElute PCR Purification Kit from Qiagen) retain DNA fragments > 70bp -> in principle they could replace the DNeasy columns in the DNeasy Blood and Tissue Kit (Qiagen) protocol -> check DNA fragmentation as short fragments should be mostly endogenous and contamination is mostly about long fragments
- Library preparation: TRUSEQ Nano DNA Low Throughput Library Prep kit (Illumina) recommended for small yields of (degraded) DNA

- Control procedures in HTS and need for negative + positive controls (including library prep control + DNA extraction control)
- Suggestion for pilot on library preparation focusing on species with published/available reference genome

As a result of this discussion and following the recommendations from the follow-up committee, a pilot experiment was organized and will be carried out to test the possible effects of the use of different extraction protocols/columns on the final amount of DNA yielded from specimens of various populations

Tervuren 2 August 2021

Massimiliano Virgilio & Lore Esselens
Royal Museum for Central Africa