

Annex 4:

CONTRAT N° B2/191/P1/ISeBAF

Insect Service and Biodiversity in Agroecological Farming

BELSPO programme manager: Aline van der Werf

4th meeting of the project follow-up Committee

Tervuren

June 26th 2025

Designated experts:

Marc De Meyer, Senior Scientist, taxonomist, RMCA

Kurt Jordaen, Senior Scientist, taxonomist, RMCA

Achik Dorchin, FEDtWIN researcher UMons / RMCA

Steven Janssen, Senior Scientist, Botanical Garden Meise

Participants project consortium:

Ramadhani Majuba - project coordinator (international cooperation), Sokoine University of Agriculture (SUA, Tanzania)

Sija Kabota - project PhD student SUA

Massimiliano Virgilio - project coordinator, Royal Museum for Central Africa (RMCA)

Jean-Luc Boeve - project partner, Royal Belgian Institute of Natural Sciences (RBINS)

Julien Gaspar – project post-doc researcher, RBINS

Gontran Sonet - JEMU, RBINS

Nicolas Vereecken - project partner, Université Libre de Bruxelles (ULB)

Oumayma Ishane - project PhD student, ULB

This document provides an overview of the ISeBAF project activities 2024-2025, as presented by the project partners and a minute of the discussion which followed with the designated experts.

Tervuren, 27th June 2025

Massimiliano Virgilio



Minute of the discussion between the designated experts and the project consortium.

Project PhD students at SUA and ULB presented their findings, followed by Julien Gaspar and Gontran Sonet (RBINS)

Sija Kabota (SUA)

Over the past year, Sija Kabota and the SUA team have used high-throughput metabarcoding to characterize pollen loads gathered from hoverflies and honeybees within the ISeBAF experimental setup. By targeting and sequencing the *rbcL* gene from pollen grains washed off insect bodies, they detected more than 300 distinct plant taxa. The results reveal clear differences in foraging behavior: hoverflies exploited a wider variety of floral resources, whereas honeybees focused primarily on cucurbit crops. In addition, male and female hoverflies of the dominant species exhibited different pollen profiles, indicating sex-related variations in flower visitation.

Comment from JLB: please specify the exact number of hoverfly specimens analyzed, broken down by taxon, as well as the total number of flower-fly species included in the dataset, to clarify sampling depth and taxonomic coverage.

Julien Gaspar & Gontran Sonet (RBINS)

Over the last year, Julien Gaspar and Gontran Sonet have quantified the phylogenetic diversity of wild-bee communities in the ISeBAF experimental plots using two complementary molecular approaches:

- Shallow & wide dataset (COI DNA barcoding): they sequenced the COI barcode region for a broad suite of bee specimens and used those data to calculate community-level phylogenetic diversity indices across treatments (highlands vs. lowlands; agroecological vs. conventional farms).
- Narrow & deep dataset (UCE capture): focusing on a targeted subset of taxa, they applied ultra-conserved-element (UCE) target capture to generate a high-resolution dataset. From these loci, they derived the same phylogenetic diversity metrics.

Both approaches revealed complex, treatment-dependent patterns of phylogenetic diversity, with different responses to elevation and management practices.

Oumayma Ishane (ULB)

Over the past year, Oumayma Ishane and her ULB team have developed spatially explicit models to unravel how landscape configuration and composition influence wild-bee diversity across the ISeBAF plots. Using high-resolution land-use maps and field-survey data, they derived key structural metrics at multiple spatial scales.

Discussion (NV, JL, GS, JG): The team discussed optimal strategies for combining ULB's spatial-model outputs with RBINS's phylogenetic diversity estimates.

Comments and recommendations by the experts

Marc De Meyer, Kurt Jordaeans: suggestions to the project consortium on how to support outreach to the general public with the possible involvement of the publication service of RMCA and involvement of SUA in translating a booklet in prep in Kiswahili. The consortium explored adapting the wild-bee identification fact-sheets into outreach materials for university students, NPPO officers, and the general public, and discussed leveraging existing networks (e.g., agricultural extension services and academic partners) to ensure broad distribution.

Achik Dorchin provided suggestions on how to interpret species accumulation curves more effectively and wondered whether the project could propose approaches to identify the wild

bee species that contribute most to differences in community structure across experimental treatments, such as between highland and lowland sites or between agroecological and conventional farms.

Discussion initiated by **MDM, KJ, AD** on the criteria used to select target wild bee species for the phylogenomic analyses. GS explained that, regardless of the available life history information for some of the selected species (e.g. the specialisation of *Hypomalictus* on cucurbit crops), an exploratory approach was adopted for the characterisation of phylogenomic diversity. Species were selected among the most dominant wild bees to ensure sufficient replication across experimental plots and to capture the main ecological strategies represented in the communities.

Discussion (**NV, KJ, AD, MV**) on the optimal approach to extrapolate quantitative and semi-quantitative comparisons from metabarcoding data. Key points included the need for appropriate data standardization methods and the identification of suitable statistical frameworks to account for variability in sequencing depth, potential amplification bias, and differences in sample composition across treatments.