



Identical cropping systems lead to varying insect communities and associated plant traces across four sites in Hesse

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Sampling Sites

As part of the project “Transformative Intercropping Systems for One Health” (TRIO), this study investigates the effects of strip cropping systems on **insect diversity** and their **retrospective plant visits**. The sampling sites are situated in the state of **Hesse, Germany (Fig. 1)**. At each of the four sites the **identical experimental scale cropping system** is implemented, consisting of spring wheat, coriander, and caraway strips. The sites vary in **local climate, soil types and surrounding landscape** and are either farmed **organically (DFH, FOR)** or **conventionally (WBG, GGE)**.

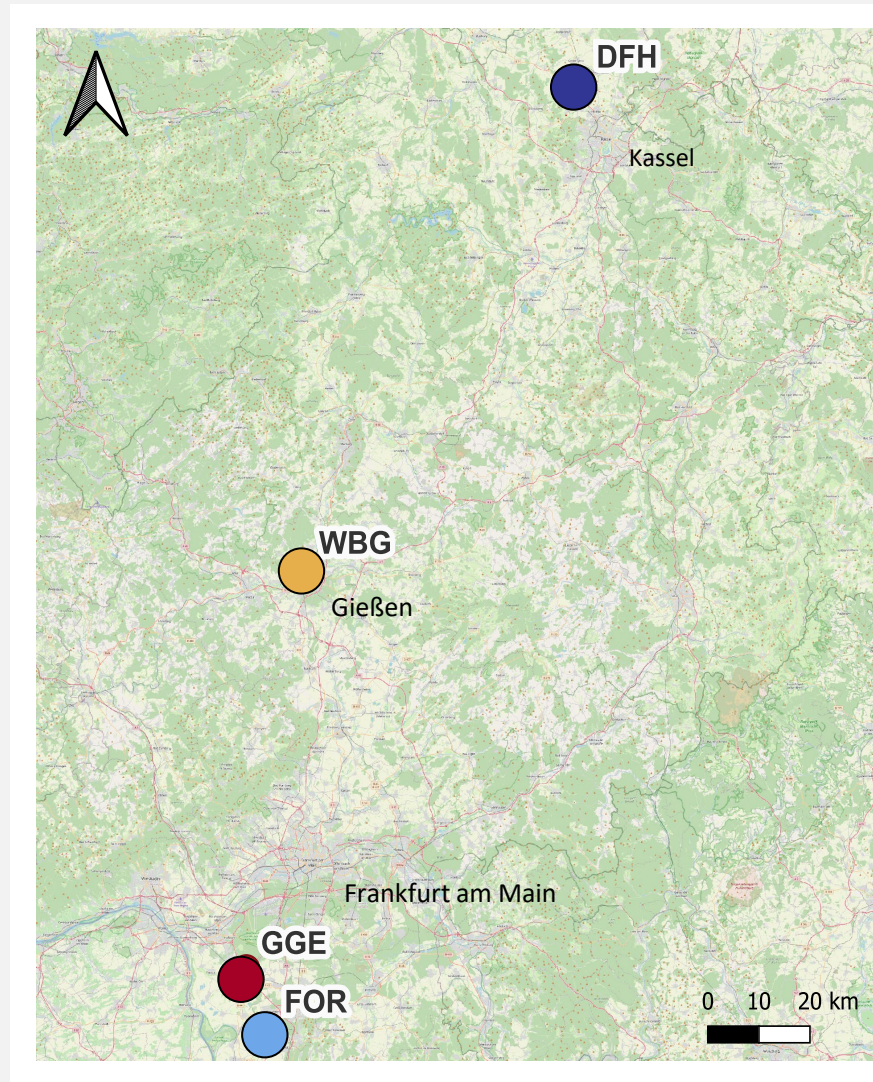


Fig. 1: TRIO sampling sites in Hesse, Germany.

Methodology

The **insect diversity** and **plant visit patterns** were examined using sweep netting along transects during the **flowering of coriander in July 2024**. Each transect was sampled for 2 minutes, repeated 20 times per site. To **avoid contamination**, a sterile net was used for every transect. Further **laboratory analysis (metabarcoding)** was carried out under sterile conditions for plants and semi-sterile for insects (Fig. 2).

Laboratory work

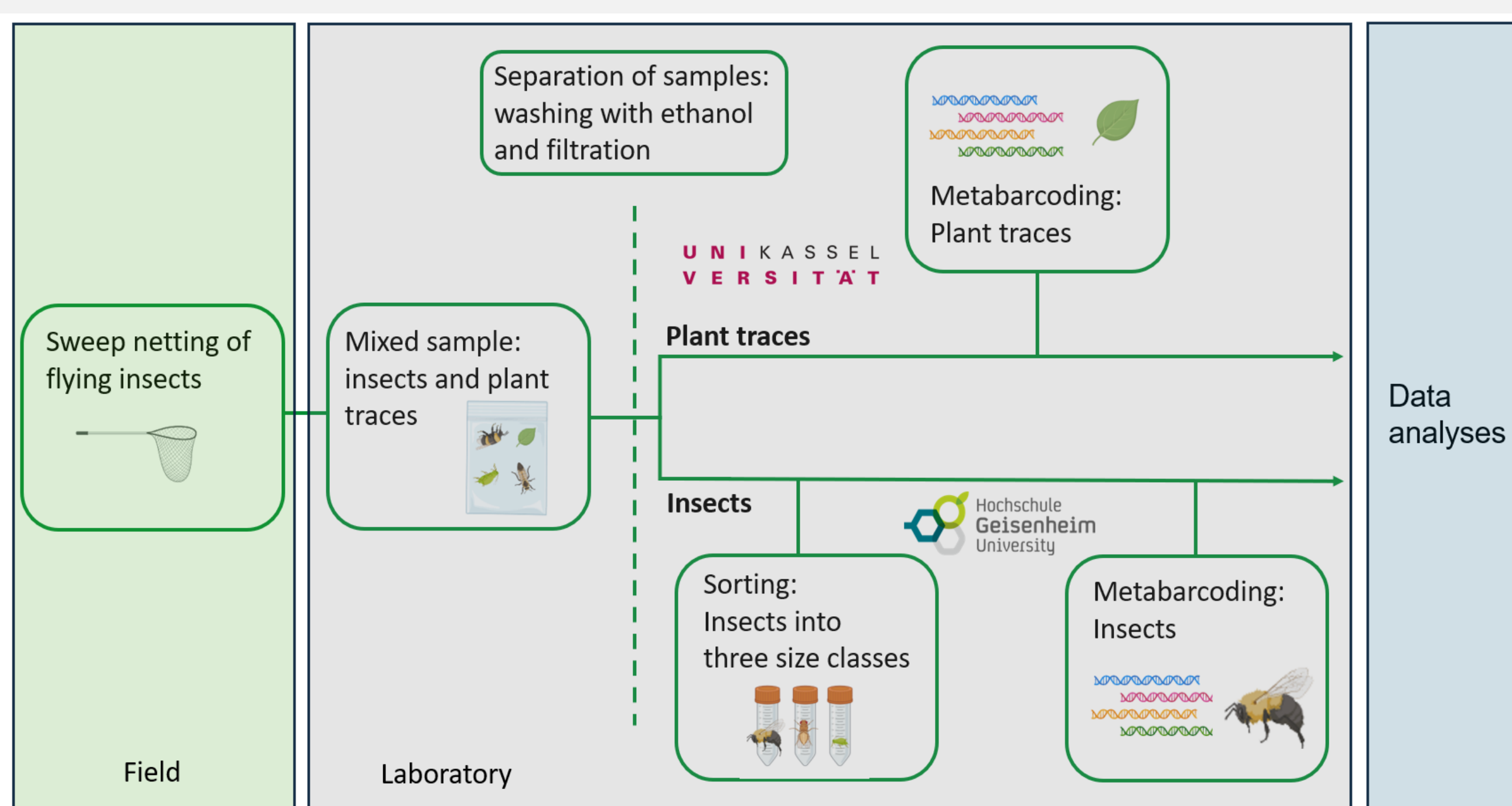


Fig. 2: Methodological overview. To avoid contamination, separation of samples and metabarcoding of plant traces was carried out in a clean lab under sterile conditions. For insect metabarcoding the COI barcode was used, for plant traces the ITS2 barcode, respectively. PCR was performed with three replicates per sample.

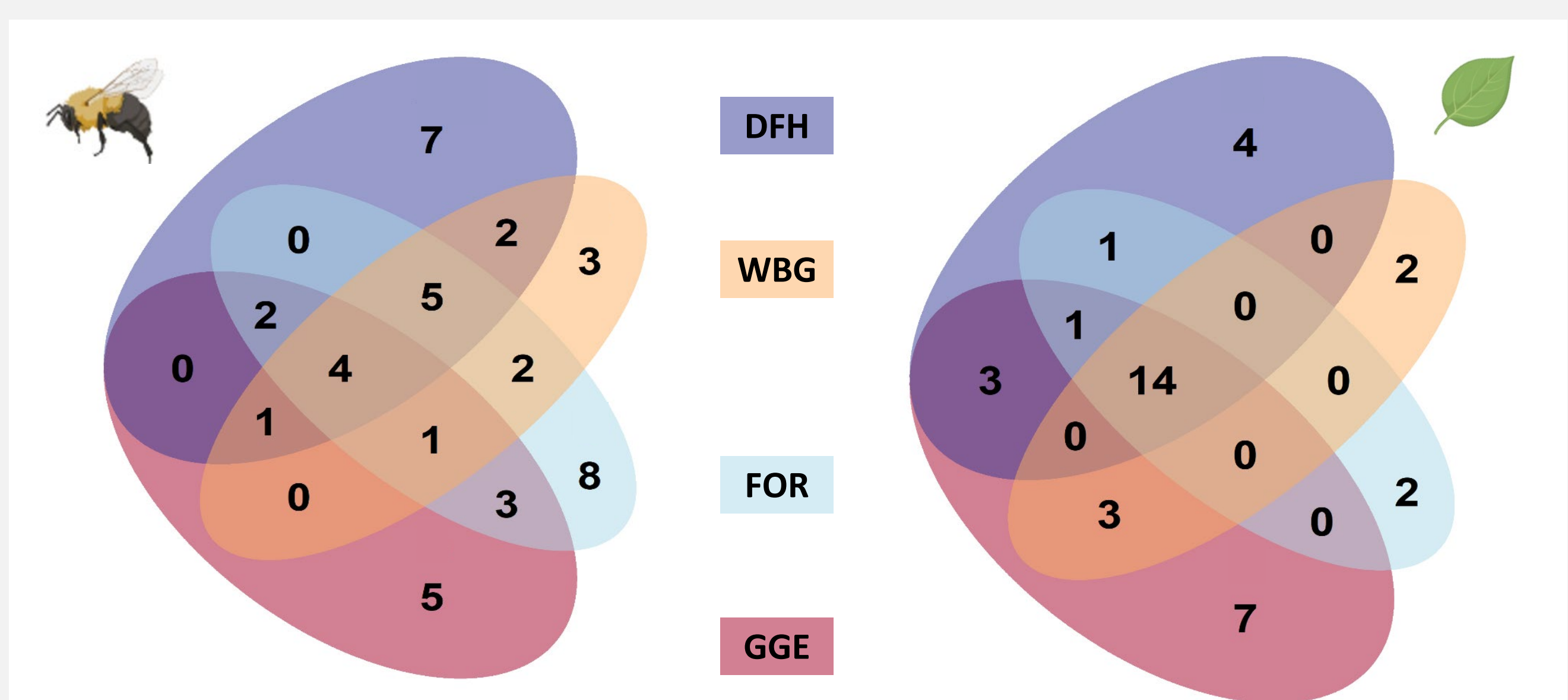


Fig. 3: Venn diagram indicating overlap of insect and plant family composition at trial sites during the flowering of coriander in July 2024. Insect families found at all sites: Coccinellidae, Muscidae, Syrphidae and Cicadellidae. Plant families found at all sites: Apiaceae, Asteraceae, Brassicaceae, Caryophyllaceae, Chenopodiaceae, Polygonaceae, Fabaceae, Fagaceae, Plantaginaceae, Euphorbiaceae, Poaceae, Papaveraceae, Rosaceae, and Urticaceae.

Data analyses

After Illumina MiSeq sequencing, the data sets were tested against **insect/plant reference databases** (Ratnasingham & Hebert 2007; Quaresma et al. 2024). Species lists were cleaned and quality filtered prior to data analyses. Species with fewer than 10 reads per sample were excluded from the analysis. Insect and plant families were summarized by site and converted into **presence/absence data**. Data visualization was performed in R using the packages *VennDiagram* and *networkD3*.

Key findings

Sweep netting together with metabarcoding revealed **distinct insect and plant community compositions** despite identical strip cropping systems. Preliminary analyses identified a total of **43 insect and 37 plant families (Fig. 4)**. The **organic farming site FOR** featured the most diverse **insect community**, though at **GGE (conventional)** the highest number of **plant families** were found. Further comparison showed an **overlap of 14 plant families** but only **4 insect families** between the sites (Fig. 3). This finding is consistent with previous studies, which found that the **landscape context**, such as the proximity to urban areas at GGE, is more **important** than local factors (Kennedy et al. 2013).

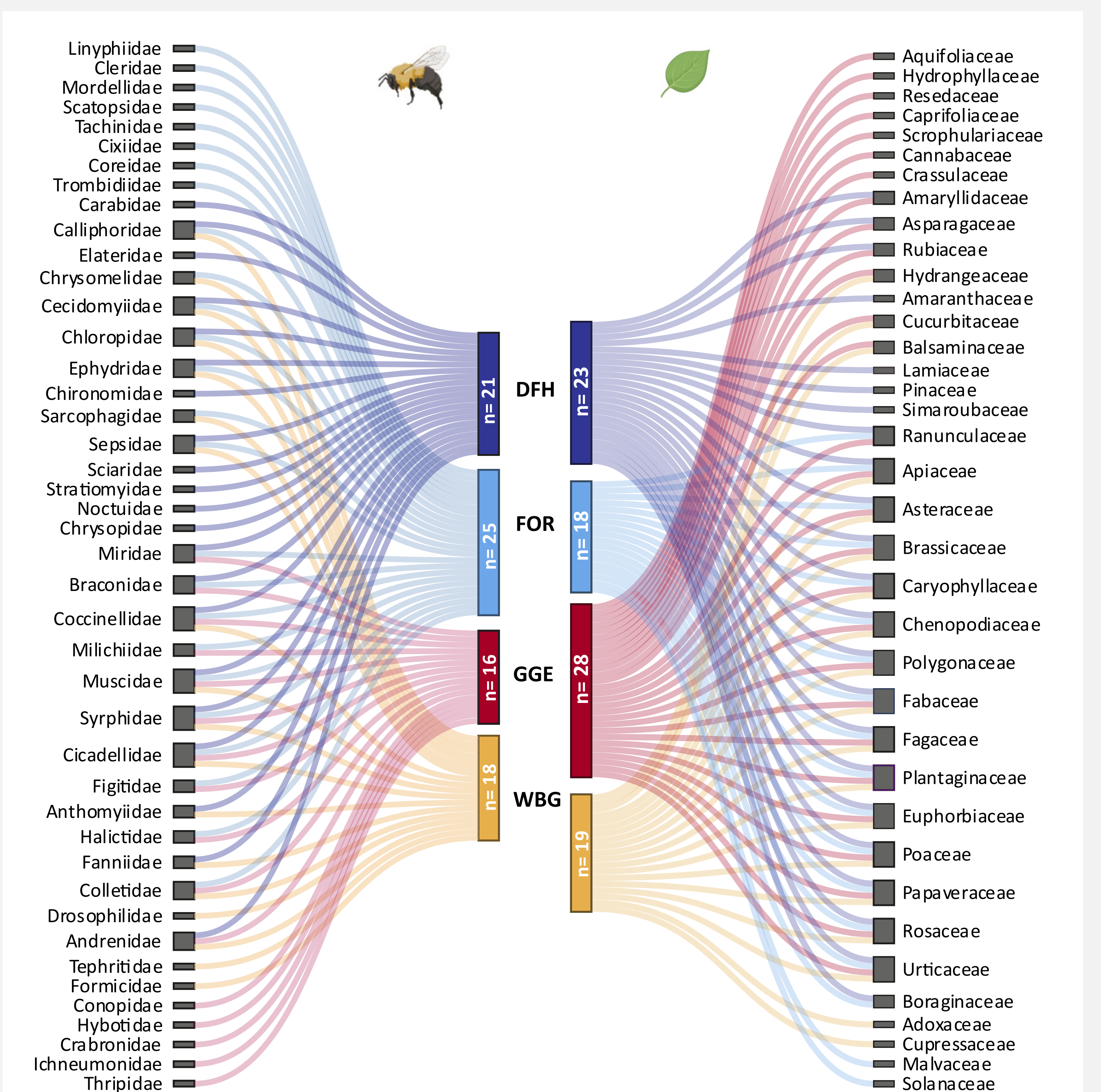


Fig. 4: Alluvial diagram depicting insect and plant families at the different trial sites during the flowering of coriander in July 2024. **Organic farming sites:** Domäne Frankenhausen (DFH), Forschungsring (FOR). **Conventional farming sites:** Groß Gerau (GGE), Weilburger Grenze (WBG). The block heights represent the number of families found at each site (n; and for each insect and plant family).

Future work will look at species level identification to gain a deeper insight into insect and plant community composition, interdependencies and their traits. Furthermore, a habitat and vegetation analysis of the surrounding area, as well as a crop specific comparison of insect and plant visitation will be carried out.