BEESPOKE Frisian clay area: Pitfall trap protocol and analysis

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Problem: In the framework of the BEESPOKE project, general insect biodiversity plays an important role. Pollinators are important in agriculture, but also other groups are functional, for example as pest control species. Measuring pollinators and pest control species can be done in different ways. However, any measurement system has its own set of problems. Any method has particular biases, related to subjective observer differences, and/or specific aspects of objective catching methods. Insect catches are always biased towards certain species groups of interest, or favored by a particular catching method. We adopted yellow Sticky traps as a highly standardizable easy and cheap way to measure Insects (See factsheet on *BEESPOKE Sticky trap protocol and analysis*). However, Sticky traps of course have limitations and biases, and are currently not a widely used standard way of sampling Insects.

In order to see if flower strips change biodiversity in different groups of Insects, we also adopted other catching methods and other species groups of interest. In this Factsheet we explain the methods for our use of pitfall traps and the analysis.

Pitfall traps: Pitfall traps usually consist of small cups that are dug into the soil, with a catch and conservation fluid in it. Pitfall traps are in particular used for very mobile species: more active and moving species have a higher chance to be caught. Many of these are hunting species, such as spiders and Carabid beetles. We used standard plastic coffee cups of 180ml with a 7cm diameter which were cheap and easily attainable (see Figure 1).

Figure 1. Example of a dug in pitfall trap with catch in salt water, after a 2-day catching period.

Digging them into the soil was done by using a flower bulb planter or hand soil drill, without disturbing the soil outside of the hole as much as possible. Two cups were carefully embedded with the opening at the level of the mineral soil. The top cup could easily be emptied without disturbing the hole itself, and making repeated use of the same holes possible. Vegetation that could reach the inside of the cup was removed to prevent escape bridges. The cup was filled with salted water (100g/l) and a with a drop of dish washing detergent to break the surface tension.

The pitfall traps were always used for 2 days, which showed to yield reasonable catches after 2 complete daily cycles. In the BEESPOKE project, the same timing was used for sticky traps and pan traps.

Catches were gathered by removing any obvious debris and snails, and subsequent emptying the bowl over a standard plastic tea sieve, and storing the catch in a 60ml plastic container with a screw cap in 70% Ethanol until taxonomic determination.

Analysis: From these pitfall traps, we assessed quantitative biodiversity indexes by looking at variation at order and family taxonomic levels, and for a specific catchable and relevant species group: Carabid beetles. Carabid beetles are top predetors of the soil layer and are a group with pest control species.

These measures can be used to contrast species richness and diversity by seeing if more orders or more families (with higher diversity) occur, and if more of the relevant species (with higher diversity) make use of the location.

Methods. Pitfall trap catches were cleaned for any remaining soil and debris and transferred to a Petri dish, where the animals were isolated and determined to the nearest easily attainable taxonomic level, using a standard 10-40x binocular microscope. Species were determined using standard determination literature, adapted for the Dutch situation. Carabid beetles, and occasional bees, and butterflies were determined to species level.

Measures of insect number and diversity: From these data, measures for insect biodiversity were derived. These included numbers of individuals per class, order, family and species. For family and species level, also estimated species group numbers (Chao-1; Chao, A., 1984) and estimated biodiversity (Shannon entropy; Chao et al., 2013) were made, using the biodiversity calculation program SpadeR (Chao et al., 2015).

References

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