# LIFE + BIODIVINE - Arthropods protocol

Overview

In the BioDiVine project, a simple biodiversity assessment protocol is used (parataxonomy) for monitoring arthropods. It is composed by a non-selective trapping system, and a sample analysis procedure called RBA (Rapid Biodiversity Assessment) [1]. It has been shown that in particular cases, RBA can be used to assess biodiversity on a site[2][3].

Trapping System

Two complementary traps are used (figure 1): a "combi" - trap which is aiming mainly at flying arthropods, and a pitfall trap which collects mostly ground dwelling arthropods. Sampling of several pests (berry moths, leafhoppers) is often performed on the same site. Samples are collected weekly for 10 weeks, from April to July.

Combi-trap: Interception of flying arthropods by two transparent sheets, and attraction by the yellow funnel

Combi-trap (left), pitfall trap (bottom right) and pest monitoring trap (right)
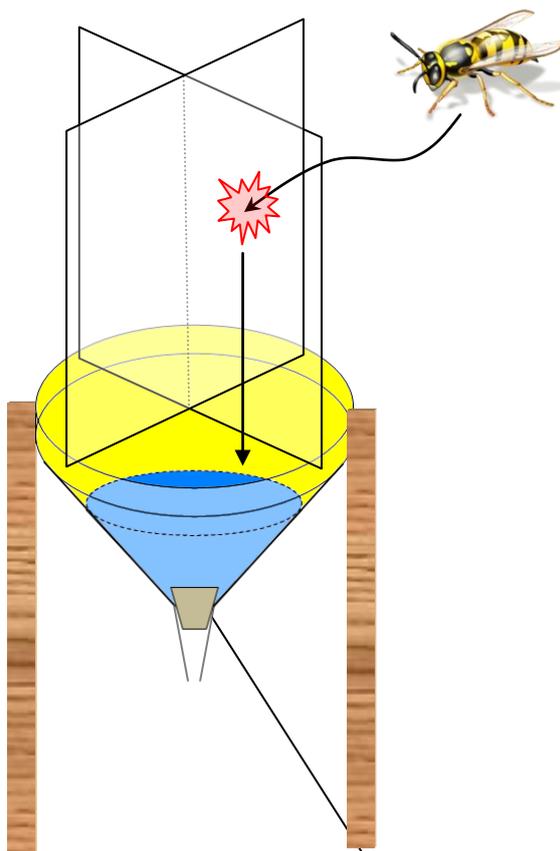
Pitfall trap : ground arthropods fall into the funnel and collection bottle
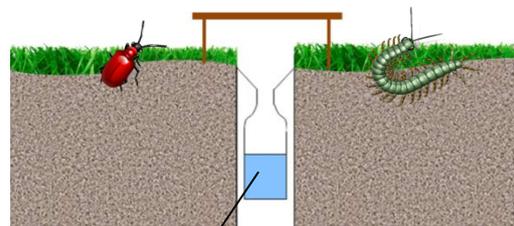
Water + 5% of Salt and a few drops of soap

Figure 1: Traps used for monitoring arthropods

[1] **Oliver I, Beattie J,** 1993, A possible Method for the Rapid Assessment of Biodiversity, published in *Conservation Biology Volume 7*

[2] **Duelli P., Obrist M.K.**, 2005, "Rapid Biodiversity Assessment" (RBA) : Une méthode avantageuse et économique pour l'appréciation de la diversité locale des arthropodes mobiles, published in *Les cahiers de la FAL 56*

[3] **Obrist M.K., Duelli P.**, 2010, "Rapid biodiversity assessment of arthropods for monitoring average local species richness and related ecosystem services", published in *Biodiversity Conservation 19*

RBA method

RBA is a simple method which enables to estimate biodiversity without the need of taxonomy.

It consists in the sorting of **morpho-species (or morpho-types to avoid confusion with real species)** instead of real species. Identification up to order level is done first. Then, two or more specimens are considered as belonging to one morpho-type if an observer (with basic entomological knowledge) cannot see any morphological difference (figure 2).

Each morpho-type is recorded with the order information, plus one identification number. A reference collection (of several specimen per morpho-type) prepared on each site allows to be consistent among the study.
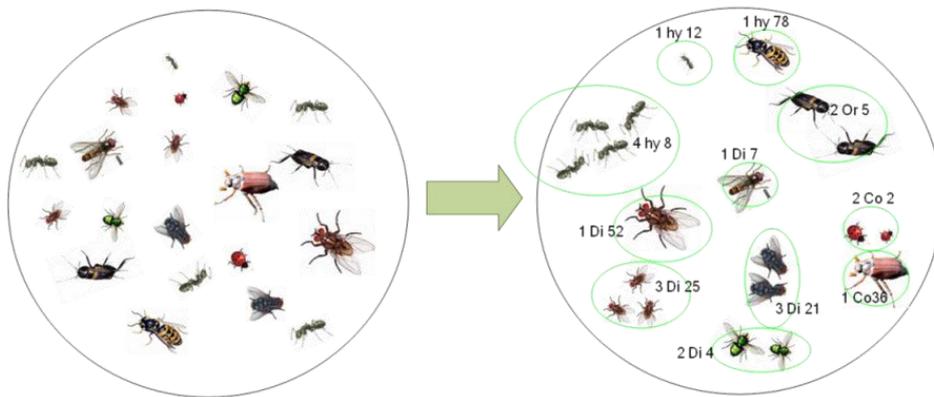

Figure 2: A raw sample (left) of 20 specimens (abundance) , sorted out in 11 morpho-types (estimated richness) and their "reference codes".

Counting morphotypes and specimens for each sample allows calculating the main indexes (approximate richness, shannon, simpson…).

Problematics and trap networks

Biodivine project aims to best understand the repartition of biodiversity in vineyard landscapes and set up the most efficient conservation actions. The first year of monitoring (2011) is dedicated to habitats, and their "biodiversity value" for vineyard landscape. Traps are set up directly into the main habitats present on each demonstration site. (figure 3).

Forest	Vineyard	Meadow	Orchard	Hedgerow

Figure 3: Traps in main landscape elements, Costières de Nîmes, 2011

In 2012 and 2013, the composition of landscape and its effect on the vineyard-plots biodiversity are tested. Therefore, traps are set up into vine plots exclusively, and landscape elements are recorded and quantified by mapping habitats (GIS). The traps are separated by at least one kilometer to allow a large-scale landscape analysis (figure 4).
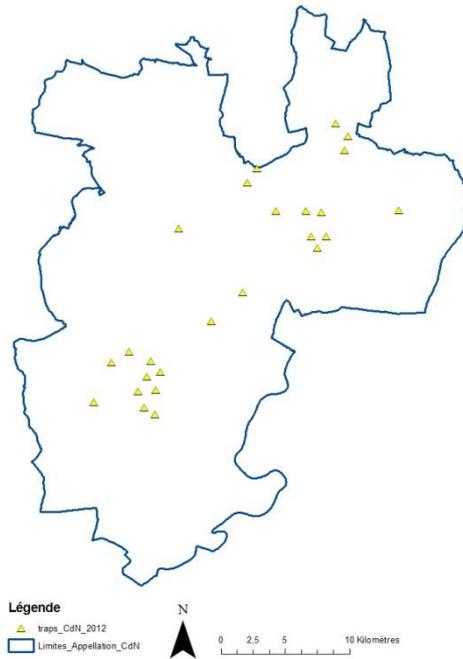

Figure 4: Example of the 2012-2013 network in Costières de Nîmes