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Terrestrial Biodiversity and Ecosystems

Usage of Environmental DNA (eDNA) for Pest Monitoring: A Case Study with Rapeseed (*Brassica napus*)

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Venue: Auditorium, 1st Floor,
Interdisciplinary Research Building
跨領域科技研究大樓1樓演講廳

Host: Dr. Jen-Pan Huang 黃仁磐副研究員

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Abstract

Environmental DNA (eDNA) metabarcoding is immensely revolutionizing biomonitoring. By using DNA shed by organisms and released into the surrounding environment, it is possible to consider presence or absence of species and, potentially, also abundance and interactions (e.g., plant-herbivore). Such traits make eDNA analyses also employable in an agricultural setting; specifically, pests can be detected by extracting eDNA from plant themselves or even by analyzing eDNA collected passively (e.g., through air sampling) in agricultural areas. This could be useful for facilitating pest detection and management before the infestation becomes evident (i.e., visible), given the power of eDNA of detecting species at early non-evident (e.g., larvae inside plants) stages or when their abundance is still low. Additionally, eDNA metabarcoding could potentially evaluate the presence of SNPs associated with pest resistance and track parasitoids that could be useful for biological control.

For evaluating the potential usage of eDNA for arthropod pest monitoring, we designed a sampling trial in three different rapeseed (*Brassica napus*) fields in Luxembourg; rapeseed is an important crop species in Central Europe, and the selected fields have been monitored for arthropod pest species by local researchers for the past twenty years by yellow pan traps. After collecting, we evaluated: 1) pest presence and detection through eDNA compared to pan traps used in our same collecting period; 2) the potential usage of eDNA for pest resistance detection; 3) evaluation of the presence of parasitoids. For what concern the first part, we show how eDNA not only detects more species than pan traps (which are biased toward taxa that attacks flower), but it also helps to detect cryptic pest species are potentially confused with congeneric ones, while also tracking species not reported for the Luxembourg area, albeit it suffers from potential metabarcoding caveats (e.g., lack of reference data leads to non-detection of species). For the second point, although performance was inconsistent among samples and primers, we were able to detect SNPs associated with resistance to a widespread used class of pesticides (pyrethroids). According to our data, such resistance seems also to be widespread in Luxembourgian Cabbage Stem Flea Beetles (CSFB; *Psylliodes chrysocephala*), suggesting a potential non-usefulness of certain pesticide applications. Finally, it seems to be possible to use eDNA metabarcoding for tracking potential agriculturally useful parasitoid, given both eDNA and bulk specimens' results.

Our data will be potentially useful for the employment of eDNA for agricultural pest monitoring. In addition, we plan to develop tools for the detection of pest species which could also be used by farmers for managing crops.