Hoverfly research within WildPosh project

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BACKGROUND

WildPosh is a multi-actor, transdisciplinary project aiming to improve the assessment of pesticide exposure risks to wild pollinators and to support the long-term sustainability of pollinators and pollination services across Europe.

Consortium

14 Institutions 9 Countries

Structure

9 Work Packages

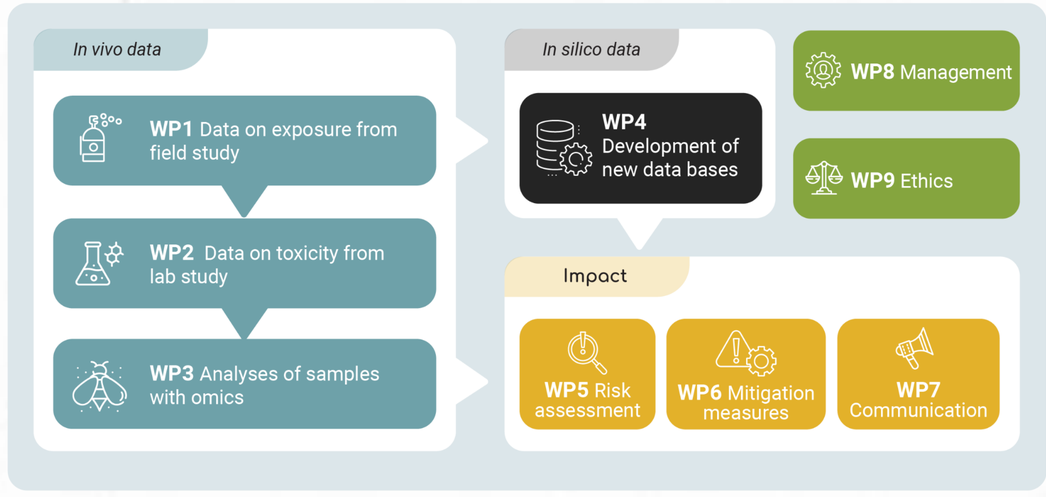
Duration

4 Years (January 2024–December 2027)





WILDPOSH WORK PACKAGE FRAMEWORK



Parallel evidence streams supporting improved pesticide risk assessment

Monitoring & exposure

Goal: Identify contamination sources and pesticide exposure routes in hoverflies

- Hoverfly sampling across agricultural landscapes
- Residue analyses of nectar, pollen and plant material
- Identification of contamination sources and exposure pathways
- Linking exposure patterns to landscape and crop characteristics

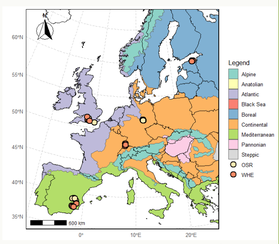


Figure 1: European map with a bioclimatic stratification showing the approximate locations of the oilseed rape (OSR) and wheat (WHE) sites within the WildPosh project.

Toxicity testing

Goal: Evaluate lethal and sublethal effects of pesticides on hoverflies to support improved risk assessment

- Acute contact and oral toxicity assays were conducted on several hoverfly species
- Test species included *Eristalinus aeneus*, *Myathropa florea* and *Eristalis arbustorum*, with additional pilot studies conducted on *Eupeodes corollae* and *Cheilosia* sp.
- Adults were evaluated for both lethal and sublethal effects
- Tested compounds included three different pesticides, individually and in mixtures
- Mortality, behavioural disruption and other sublethal responses were monitored over time
- Species-specific and sex-specific sensitivity differences were assessed through LD_{50} experiments
- Wing fluctuating asymmetry (FA) was assessed as an indicator of morphological responses to pesticide exposure

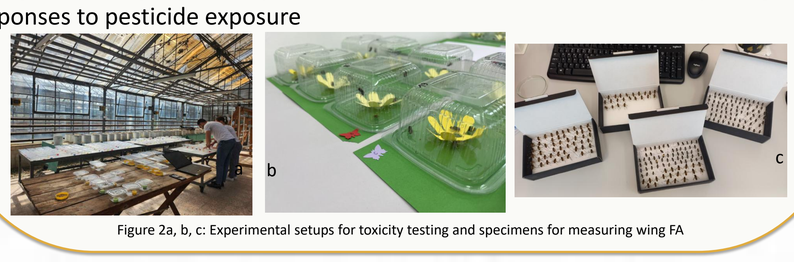


Figure 2a, b, c: Experimental setups for toxicity testing and specimens for measuring wing FA

Transcriptomics & genomics

Goal: Decipher molecular and genetic responses of hoverflies to pesticide exposure

- *Myathropa florea* as a model species for omics and genomics studies
- Transcriptomic profiling of cypermethrin-exposed individuals
- Functional annotation of the existing *M. florea* genome assembly
- Integration of transcriptomic and genomic datasets to investigate pesticide susceptibility

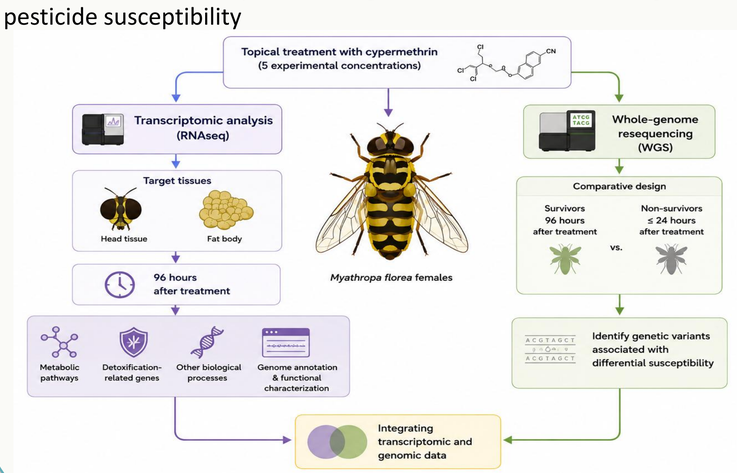
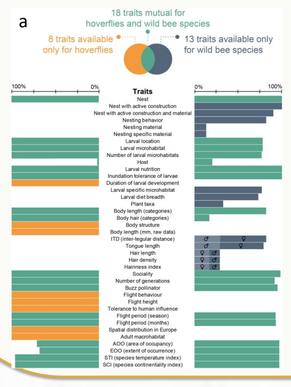


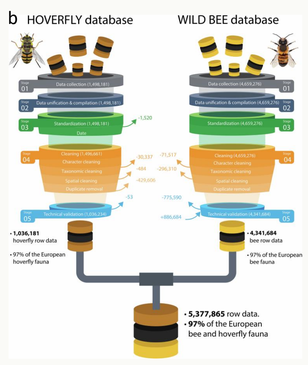
Figure 4. Overview of transcriptomic and genomic approaches used to investigate hoverfly responses to cypermethrin exposure

Traits & distribution

Goal: Develop harmonised trait and distribution datasets to support large-scale ecological modelling and pesticide risk assessment

- Expansion of existing European hoverfly trait datasets with exposure- and sensitivity-related characteristics
- Compilation of harmonised distribution records from different sources
- Development of FAIR and Darwin Core–compliant biodiversity data resources
- Integration of trait and distribution data for ecological modelling





Data descriptors published in Scientific Data, representing first part of the data collection:

a) Sentil, Miličić, Benrezkallah et al. (2026) Synthesised database of wild bee and hoverfly records in Europe
b) Miličić, Sentil et al. (2026) Trait Dataset for 3,000 European Wild Bee and Hoverfly Species

Further WildPosh additions

- Exposure-related traits
- Sensitivity-related traits
- Additional distribution records (100+ datasets)
- Data harmonisation and standardisation

Ecological modelling

Goal: Integrate exposure, toxicity and ecological data to support predictive risk assessment for hoverflies

- Integration of data generated across WildPosh work packages
- Development of landscape-scale pesticide risk models
- Prediction of pollinator responses under different environmental scenarios
- Support for evidence-based risk assessment and mitigation strategies

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WildPosh contributions to hoverfly risk assessment

EXPOSURE-INFORMED
Realistic exposure pathways

SPECIES-SPECIFIC
Beyond honeybee-based approaches

MECHANISTICALLY SUPPORTED
Molecular and genetic evidence

DATA-DRIVEN
Traits, distributions and risk modelling

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