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Evaluating the vulnerability of arthropod ecosystem service providers to pesticide exposure.

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DATA AVAILABILITY STATEMENT

The authors declare that the data supporting the findings of this study are available within the paper and its Supplementary Information files.

CONFLICTS OF INTEREST

Authors declare no conflict of interest.

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Abstract

Protecting arthropod species that deliver pest control and pollination services in agricultural landscapes requires methods that account for exposure, toxicological sensitivity and capacity for population recovery. We developed a trait-based vulnerability framework for representative above-ground arthropod families occurring in European crops and combined it with chemical-specific acute contact toxicity data to produce family-level, scenario-dependent vulnerability indices. Trait information describing habitat use, feeding guild, life cycle (breeding phenology and voltinism and dispersal mode was used to calculate a partial vulnerability index based on exposure and recovery. These trait scores were then integrated with measures of acute contact toxicity, expressed as lethal application rates, to derive chemical-specific vulnerability estimates under two exposure scenarios (canopy spray and soil contact). Trait-only screening identified many ground-associated predators (notably several spider families, ground beetles and rove beetles), certain parasitoid wasps and several Diptera as having higher vulnerability related to exposure and limited recovery relative to common regulatory test species. Adding toxicity data produced compound-dependent re-ranking. For a subset of insecticides, families such as ground beetles, ladybirds, certain parasitoids, pteromalid wasps, lacewings and some moths exhibited higher overall vulnerability than the standard surrogates. Canopy exposure produced slightly higher mean vulnerability overall, while soil exposure increased vulnerability of several ground-dwelling families. Data gaps in toxicological coverage and reliance on family-level trait aggregation constrain full implementation. We conclude that a tiered approach that uses trait-based screening to prioritise taxa for targeted toxicological testing will improve ecological relevance of risk assessment and better safeguard arthropod-mediated ecosystem services in agricultural systems.

Keywords: Non-target arthropods, vulnerability analysis, trait based, agriculture

1. Introduction

To meet the growing demand for food, agricultural production systems are increasingly focusing on enhancing productivity. This shift involves greater use of plant protection products (PPPs) and significant alterations to agricultural landscapes, both of which impact biodiversity (Raven and Wagner, 2021; Vanbergen et al., 2020). In PPP environmental risk assessment (ERA), emphasis is often placed on arthropod taxa that contribute to ecosystem services relevant for agricultural systems, such as biological control or pollination. Although this prioritisation reflects anthropogenic management goals, it provides a practical starting point for assessment. In addition, trait-based approaches offer an opportunity to move beyond predefined “important” taxa and identify vulnerable groups more systematically. Ecologically important arthropods, such as decomposers, natural enemies (i.e. predators and parasitoids of pest species) and pollinators, often share physiological and taxonomic similarities with insect pest species targeted by PPPs. As a result, these organisms may also be affected by PPP exposure, particularly by insecticides designed to act on broadly conserved biological pathways (Brock et al., 2021). Environmental Risk Assessment (ERA) aims to estimate the probability of adverse effects of chemicals on populations and ecosystems (Calow et al., 1997) and guidance has been developed for assessing the risk of PPP to non-target species, including arthropods (Adriaanse et al., 2022; EC, 2002; Maltby et al., 2021). However, assessing the potential impact of a vast array of toxic substances on the multitude of species potentially exposed, remains a significant challenge. Despite decades of research, current knowledge is largely limited to effects on standard test species (Candolfi et al., 1999), leading to uncertainty when evaluating the vulnerability of ecosystem service providers to PPP exposure (Van den Berg et al., 2021; Mata et al., 2024). To address these gaps, vulnerability frameworks explicitly combine exposure, intrinsic sensitivity and recovery potential to prioritise taxa for testing and conservation. We adopt and extend this multi-component approach, but stress that recovery should not be treated as an automatic outcome. Population recovery depends on species-specific traits (e.g., dispersal capacity, voltinism, fecundity, habitat specificity), landscape context (e.g., connectivity, source populations) and the frequency and magnitude of chemical exposure relative to species' life histories. Low recovery scores highlight where recolonisation or demographic rebounds are unlikely within management-relevant timescales. By treating recovery as a variable, the vulnerability analysis avoids assuming resilience, thereby strengthening the index's ability to prioritise taxa and guide targeted conservation or testing actions.

Vulnerability assessment is inherently complex, requiring multiple interacting factors to be considered (Yoshikawa et al., 2023). Under field conditions, the vulnerability of a species to pesticides depends primarily on their exposure, inherent sensitivity and recovery potential (Van Straalen, 1993). Agroecosystems support a large and highly interconnected diversity of species (Bakker et al., 2022; Billeter et al., 2008; Riedel et al., 2016; Sowa et al., 2025), which makes comprehensive species-by-species vulnerability assessment infeasible given the limited toxicity data available for most taxa. Moreover, direct effects on individual species can be amplified, dampened or redirected by changes in species interactions (e.g., predation, parasitism, mutualism, competition), which represent an important potential limitation of single-species assessments. The integration of trait-based approaches into risk assessment frameworks has been proposed to address data gaps (De Lange et al., 2012; Ippolito et al., 2012) and previous studies have demonstrated their value for predicting species sensitivity to pollutants (Baird and van den Brink, 2007; Spromberg and Birge, 2005). For example, body size has been identified as one potential factor influencing toxicological response (Glazier and Gjoni, 2024; Uhl et al., 2019). A range of candidate traits can be informative in this context. Life-history attributes (e.g., generation time, fecundity, voltinism), behavioural traits (e.g., diel activity, foraging range, nesting or sheltering habits), trophic and feeding guild, habitat specialization and microhabitat use, phenology, and physiological characteristics related to uptake and biotransformation (e.g., cuticle properties, lipid reserves, detoxification enzyme systems) all influence how a species encounters, absorbs and recovers from chemical stressors (Schmolke et al., 2021; EFSA, 2023).

Building on existing vulnerability frameworks, we investigate the relative vulnerability of above-ground arthropods that provide the ecosystem services of pest control and pollination, to PPPs. We focus on representative arthropod families in European agricultural landscapes (Sowa et al., 2025) and use ecological trait and chemical-specific toxicity data to compare the vulnerability of representative families and those of standard test species. By integrating exposure, recovery and sensitivity components into a comprehensive vulnerability index, we identify ecosystem service providers that are potentially at high risk from PPP exposure in European agricultural landscapes.

Our analysis uses acute contact mortality as a pragmatic, widely available endpoint for initial screening. However, sublethal responses and indirect effects resulting from species interactions, can substantially alter species- and community-level outcomes. These trait-based vulnerability scores are therefore a prioritisation tool, requiring additional toxicity, ecological or modelling data for detailed, management-specific risk assessments. We follow the ecological-vulnerability approach developed by De Lange et al. (2012), which treats vulnerability as a multi-component property that combines (i) likelihood of exposure, (ii) intrinsic sensitivity to the stressor and (iii) the capacity for recovery or adaptive response. Separating these components clarifies the ecological processes that underpin index scores and facilitates interpretation of relative vulnerability across taxa and service groups. Each component of the vulnerability framework incorporates distinct biological traits. However, whereas exposure and recovery components are determined by taxon-specific traits and are independent of the specific chemical being assessed, sensitivity is a function of taxon-specific traits and chemical-specific properties. Exposure was characterised using traits that determine contact probability and route of uptake, occupied habitat (e.g. above-ground plant parts or soil surface), dietary type (predator versus herbivore) and seasonal breeding period. Recovery was operationalised using pragmatic proxies that reflect population replacement potential and recolonisation capacity, including voltinism (i.e., multivoltine versus univoltine) and dispersal mode (e.g., walking, ballooning or flight). As noted above, population recovery is context dependent and the recovery index used here is a screening-level proxy intended to prioritise taxa for more detailed population- or landscape-scale assessment. Several traits that influence the toxicokinetics and toxicodynamics (TK/TD) of chemicals have been proposed as predictive measures of intrinsic sensitivity (Rubach et al., 2012; Rico et al., 2015; Dalhoff et al., 2020; Spurgeon et al., 2020; Brooks et al., 2024). However, the limited availability of TK/TD-linked traits, means that the approach is not applicable across large numbers of taxonomically distinct species, such as terrestrial arthropods. In such cases, toxicity data is used to assess sensitivity.

2. Methods

2.1. Data sources and extraction

2.1.1. Representative Non-Target Arthropods

A list of representative non-target arthropod (NTA) families for the ecosystem services of pest control and pollination in European agricultural landscapes was obtained from Sowa et al. (2025). This list, which includes taxa occurring in annual and perennial crops, comprises 27 representative families for pest control and 10 representative families for pollination (Table 1).

2.1.2. Traits and toxicity data

Trait information was obtained from a comprehensive database on NTA communities in European arable crops (Riedel et al., 2016) supplemented with specific literature searches. The Riedel et al. (2016) database includes data on over 4,000 arthropod species sampled across 37 European countries. It includes information on habitat preference (e.g., below-ground, soil surface, above-ground plant parts, aquatic or unknown), ecological function classification (including predator, herbivore, decomposer, parasitoid, aquatic non-predator, pollinator, or unknown) and feeding guild (such as hosts parasitized or plant parts consumed) across both juvenile and adult life stages (Supplementary Information S1).

Acute toxicity data were sourced from EFSA reports, the U.S. EPA ECOTOX database (US EPA, 2024) and two European projects (GETREAL (Duque et al., 2024) and EcoStack (Blanco-Moreno et al., 2024)) (Supplementary Information S2). Data were collated for a single exposure route (i.e. surface contact) and chemicals were selected for further analysis based on taxonomic coverage within an exposure route: i.e. the 50% lethal rate (LR50) data for at least 10 species and six arthropod families, including representative families and the Tier 1 standard NTA test species *Typholodromus pyri* (Phytoseiidae) and *Aphidius rhopalosiphi* (Brachionidae).

All LR50 values were standardized to units of grams per hectare (g/ha). When multiple LR50 values were reported for a given species within a single study, the lowest value was selected to represent the most conservative estimate of sensitivity and to avoid the influence of resistant NTA strains. For taxa with data originating from multiple independent studies, species-specific geometric mean LR50 values were calculated. Species-specific LR50 values were used to derive family-specific geometric mean LR50 values. Log-normal species- and family-level sensitivity distributions were produced using the ssdtools package in R (Thorley et al., 2025).

2.2. Vulnerability index calculation

Vulnerability analysis was conducted for all representative families for which representative genera had been identified by Sowa et al. (2025). Partial vulnerability indices focusing on exposure and recovery (I_{E+R}), were calculated using trait data for representative genera within representative families (Supplementary Information S1). Members of the family Syrphidae contribute to pest control as larvae and to pollination as adults. Indices were therefore derived separately for each life stage and hence function. Complete vulnerability indices (VI) including exposure, recovery and sensitivity, were calculated by combining trait data and toxicity data.

2.2.1. Trait scoring and normalization

Trait scoring follows the semi-quantitative, ordinal approach where ecological states are mapped to reproducible vulnerability scores and subsequently normalized for index aggregation. Exposure and recovery traits were classified into discrete classes and mapped to standardized scores in the interval 0-1, where 1 represents maximum potential contribution to vulnerability for that trait and 0 is minimum potential contribution to vulnerability (Table 2).

Two exposure scenarios were considered: canopy and soil. The canopy exposure scenario assumes higher exposure for taxa associated with the canopy or aerial habitats, as would be the case with a foliar spray application. The soil exposure scenario assumes higher exposure for ground-dwelling taxa, as would be the case for soil-directed applications. Vulnerability components were compared across both exposure scenarios.

For toxicity (continuous variables), Min–Max normalization was applied to rescale values to [0, 1] as:

$$x' = \frac{x - x_{min}}{x_{max} - x_{min}}$$

where x' is the normalized value, x is the original value, x_{min} is the minimum value and x_{max} is the maximum value in the dataset.

The preprocessing steps applied to the toxicity data were: log10 transformation to reduce heteroscedasticity, addition of a constant value (i.e. 4) to avoid negative values after transformation, and Min–Max normalization followed by inversion consistent with the other vulnerability metrics so that lower LR50 (higher sensitivity) mapped to higher potential vulnerability scores. Family-level geometric means (or multisource geomeans when data existed across sources) were assigned to genera when genus-level data were absent; absence of family-level data led to exclusion from toxicant-specific analyses.

2.2.2. Weighting schemes

Once scores have been assigned to individual traits, they need to be combined and weighted to derive the vulnerability indices (I_{E+R}, VI). De Lange et al. (2012) presented differential weighting of traits within and across vulnerability components. Differential weightings were based on expert judgement and are consequently subject to bias. A more parsimonious approach is to give equal weight to traits within components and to weight components equally. Both approaches were applied (Table 3).

3. Results

3.1. Partial vulnerability index (I_{E+R})

Indices combining exposure and recovery traits (I_{E+R}) were calculated using trait data for representative genera within representative families. Indices were calculated for 34 representative arthropod families (26 pest-control families and 8 pollination families). Cantharidae (soldier beetles), Megachilidae (solitary bees) and Erebidae (moths) were omitted from the analysis as no representative genera were identified by Sowa et al. (2025). There was a strong positive correlation between I_{E+R} indices calculated using either the equal weighting or differential weighting methods for both the soil and canopy exposure scenarios ($r \geq 0.95$, $n = 34$), consequently only results for the equal weighting method are presented here. The differential weighting approach is presented in the Supplementary Information (Fig. S1.1).

Under both exposure scenarios, I_{E+R} was significantly higher for pest-control families than for the pollination families (Two-way ANOVA: $F = 4.7$, d.f.= 1,64, $p = 0.034$) and for ground-dwelling compared to foliar-dwelling families ($F = 18.95$, d.f. = 1, 64, $p = 0.08$) (Fig. 1). In neither case was there a significant overall effect of exposure scenario on I_{E+R} ($F \leq 2.21$, d.f. = 1, 64, $p > 0.142$), although the difference between foliar and ground-dwelling families under the soil exposure scenario was statistically significant (Fig. 1b).

A comparison of family-specific I_{E+R} values with I_{E+R} values for standard species (Fig. 2) shows that only one family, Aeolothripidae (thrips) had a lower I_{E+R} value than *A. rhopalosiphi* under either scenario, indicating that the majority of representative NTA families were more vulnerable with respect to exposure and recovery traits, than *A. rhopalosiphi* (Fig. 2a). The pattern was more variable for the *T. pyri* comparison (Fig. 2b). Most spider families, ground-dwelling beetles (Carabidae, Staphylinidae), dance flies (Hybotidae) and one family of parasitic wasp (Pteromalidae) had higher I_{E+R} values than *T. pyri* under both exposure scenarios indicating greater vulnerability with respect to exposure and recovery traits than the standard species. However, lepidopterans, thrips, ladybirds (Coccinellidae) and most families of dipterans, hemipterans and hymenopterans had lower I_{E+R} values under both exposure scenarios. Ground-dwelling ants (Formicidae) and tangle-web spiders (Theridiidae) had a lower I_{E+R} than *T. pyri* under the canopy exposure scenario, but a greater value, and hence potentially more vulnerable, under the soil exposure scenario.

3.2. Chemical-specific sensitivity

Surface contact LR50 data meeting our inclusion criteria were available for 13 insecticides including organophosphates (chlorpyrifos, diazinon, dimethoate, malathion), pyrethroids (bifenthrin, cyfluthrin, λ-cyhalothrin, cypermethrin, deltamethrin, esfenvalerate), carbamates (carbaryl, methomyl) and a neonicotinoid (imidacloprid). Toxicity data were available for species belonging to nine of the 10 orders covered by representative families (no data for Thysanoptera), but data availability for representative families varied considerably between major taxonomic groups (Fig. 3a) and between insecticides (Fig. 3b). Family-level LR50 values were computed for 55 arthropod families, of which 22 were designated representative families. Across all 13 insecticides, representative families had higher sensitivity than non-representative families (nested ANOVA F = 2.32, df = 13, 126, p = 0.008), although within chemicals, this effect was only statistically significant for dimethoate and malathion ($t \geq 2.48$, $df \geq 8$, $p \leq 0.028$). For both chemicals, representative families were the most sensitive (i.e. lowest LR50 values, Fig. 3c).

Standard test species data were available for all selected chemicals, enabling cross-family comparison. Specifically, *Typhlodromus pyri* LR50 data were available for all 13 insecticides, whereas *Aphidius rhopalosiphi* data were available for all substances except esfenvalerate. Standard test species had the lowest LR50 values for four of the study insecticides and the families to which they belong, Phytoseiidae and Braconidae, were the most sensitive families for nine of the insecticides. For the remaining insecticides, the most sensitive species were other parasitic wasps (Pteromalidae, Eulophidae) or ladybirds (Coccinellidae). The exception was λ-cyhalothrin where a pest species of weevil (Curculionidae) was the most sensitive species tested, but Phytoseiidae was the most sensitive family (Table 4).

For four of the nine insecticides, where non-standard species had the lowest LR50 values, the difference compared to standard species was less than fivefold. (Table 4). The five insecticides with substantially higher sensitivity were chlorpyrifos, cyfluthrin, bifenthrin, λ-cyhalothrin and methomyl (Fig. 4).

3.3. Vulnerability Index (VI)

Chemical-specific vulnerability indices (VI) that integrate exposure, recovery and chemical sensitivity were computed for 21 representative families for which both trait and toxicity data were available. Mean family VI was consistently higher for the canopy exposure scenario across all 13 insecticides (Paired t-test, t = 7.22, n = 13, p <0.001), although the magnitude of the difference was small (i.e. 0 - 14%).

Under the canopy exposure scenario, all families, except Nymphalidae, were more vulnerable than *A. rhopalosiphi* for at least one chemical (Fig. 5a). In contrast, 10 families were more vulnerable than *T. pyri* for at least one chemical (Fig. 5b). Six representative arthropod families had a higher vulnerability than both standard species for at least one insecticide: Carabidae (imidacloprid), Coccinellidae (methomyl, cyfluthrin), Eulophidae (imidacloprid), Pteromalidae (imidacloprid, cyfluthrin, dimethoate, malathion, methomyl), Chrysopidae (imidacloprid) and Noctuidae (imidacloprid and carbaryl). Three of these cases were wholly expected as members of the family (Pteromalidae) had a higher I_{E+R} value and lower LR50 values than either of the standard test species to cyfluthrin, malathion and methomyl. In the remaining cases, the overall vulnerability was a balance between toxicological sensitivity (LR50 value) and partial vulnerability based on exposure and recovery traits (I_{E+R}). Greater toxicological sensitivity (i.e. lower LR50, lower I_{E+R}) resulted in higher vulnerability of Coccinellidae to methomyl and cyfluthrin, and of Eulophidae to imidacloprid. In contrast, higher partial vulnerability (i.e. higher I_{E+R}, higher LR50) resulted in higher vulnerability of Carabidae to imidacloprid. The remaining cases were either ‘lower LR50, lower I_{E+R}’ or ‘higher I_{E+R}, higher LR50’ depending on the standard test species.

Increased I_{E+R} values of ground-dwelling NTAs under the soil exposure scenario (see supplementary information S1.2), resulted in two additional families having higher vulnerabilities than either of the standard test species: Staphylinidae (chlorpyrifos, λ-cyhalothrin) and Formicidae (chlorpyrifos, dimethoate, malathion). It also increased the number of insecticides for which carabid beetles were more vulnerable than either test species (i.e. imidacloprid, chlorpyrifos and λ-cyhalothrin).

4. Discussion

We asked whether combining trait-based partial vulnerability metrics (exposure + recovery; I_{E+R}) with chemical-specific toxicological sensitivity (LR50-derived scores) produces a more realistic, policy-relevant prioritisation of NTA families in European cropping systems than reliance on standard regulatory test species alone. The combined approach produced three clear, inter-related outcomes. First, trait-only analysis (I_{E+R}) flagged several representative families (notably many spider families, ground beetles (Carabidae), rove beetles (Staphylinidae), Hybotidae and several parasitoid wasp groups) as more potentially vulnerable than common regulatory test species. Second, when chemical-specific sensitivity was added, family rankings shifted in a chemical-dependent way: for several families the addition of LR50 information caused them to rank as more vulnerable than the standard species for at least one insecticide. Third, the magnitude and even the direction of those re-rankings depended jointly on trait profiles (habitat association, dispersal, voltinism) and on the chemical identity/class. In short, exposure and recovery traits can identify potentially vulnerable taxa, but toxicological information is necessary to quantify chemical-specific vulnerabilities, a critical point for protecting the ecosystem services of pest control and pollination (Knapp et al., 2023).

Our results are consistent with previous studies demonstrating the predictive value of trait-based vulnerability frameworks (De Lange et al., 2012; Sgolastra et al., 2019; Schmolke et al., 2021). Trait-based screening provides an efficient means to flag families likely to have elevated exposure or reduced recovery capacity (De Lange et al., 2012), while mechanistic links to TK/TD processes explain why trait signals sometimes fail to predict chemical sensitivity (Rubach et al., 2012). Our results are complementary showing that I_{E+R} is a powerful first filter, but LR50 data are needed to make compound-specific risk judgments (Van den Brink et al., 2013).

Three patterns emerge from the I_{E+R} data that are useful for generalizing vulnerability across families. (1) The higher I_{E+R} values observed for many ground-dwelling families do not arise solely from the soil-exposure scenario. Rather, the results show that this pattern is consistent across both exposure scenarios. Only one family (Thripidae) had partial vulnerability (I_{E+R}) values lower than *A. rhopalosiphi* and most spider families, ground-dwelling beetles (Carabidae, Staphylinidae), dance flies (Hybotidae) and one parasitoid wasp family (Pteromalidae) had higher I_{E+R} values than *T. pyri* under both exposure scenarios. They therefore had greater trait-based vulnerabilities than both standard regulatory species. Although exposure traits were parametrized such that soil-associated states score higher in the soil scenario, this methodological feature does not fully explain the consistent elevation of I_{E+R} for these taxa across scenarios. Instead, their trait combinations, ground association, limited aerial dispersal and lower voltinism, produce robustly higher partial vulnerability scores regardless of scenario. Scenario-specific effects still occur and switching scenarios alters rank order for some taxa and chemicals. Together, these results indicate that while scenario choice shapes relative differences, the identification of high-vulnerability families is not an artefact of one scenario, but a scenario-robust outcome of their underlying trait profiles (Schmolke et al., 2021). (2) Low dispersal and univoltinism amplify vulnerability. Families lacking aerial dispersal or with few generations per year score higher because recolonization and population recovery after a local impact are constrained (Kotiaho et al., 2005; Essens et al., 2017). (3) Canopy association increases exposure but interacts strongly with recovery traits. Aerial dispersal (e.g. flight or ballooning) and multivoltinism typically buffer canopy-associated families from high I_{E+R}. These three rules-of-thumb were robust across the two weighting strategies we tested and therefore provide a compact way to identify families likely to be trait-vulnerable in agroecosystems.

Scenario choice (canopy versus soil contact) influenced vulnerability index (VI) outcomes and should be treated explicitly in vulnerability assessments. Across the insecticides we analyzed mean VI values were generally higher for the canopy scenario, although differences were modest. However, the results show that switching to the soil scenario increases VI for several ground-dwelling families for specific chemicals: Staphylinidae showed higher VI than both standard species for chlorpyrifos and λ-cyhalothrin, Formicidae exceeded both standard species for chlorpyrifos, dimethoate and malathion, and Carabidae exceeded both standard species for imidacloprid, chlorpyrifos and λ-cyhalothrin. These scenario-dependent shifts in VI identify families whose relative vulnerability changes with the exposure pathway, even though many high-vulnerability families remain elevated under both scenarios. Consequently, vulnerability outputs should report scenario dependence and justify the choice of any single scenario rather than collapsing across pathways, as this avoids misclassifying families whose ecology makes them sensitive to exposure-scenario choice (EFSA 2015; Wheatley et al., 2017).

Ground beetles, rove beetles, predatory mites and certain parasitoids repeatedly emerged as taxa whose loss would threaten in-field pest suppression, potentially leading to increased pest outbreaks and greater reliance on chemical control measures (Landis et al., 2000). Given the role of these species in maintaining ecosystem resilience, their decline could have cascading effects on both biodiversity and crop yields (Allen-Wardell, et al., 1998). The functional loss of NTAs due to pesticide exposure could also reduce ecosystem stability, as declining predator populations may allow pest species to proliferate unchecked (Bianchi et al., 2006).

A critical aspect of our findings is the evaluation of standard test species. Traditionally, species such as Phytoseiidae and Braconidae have served as proxies for broader NTA risk assessments (EC 2024). While those species remain useful for Tier-1 screening to provide a baseline for ERA, by themselves, they may not adequately capture the diversity of vulnerability across compound classes or functional groups. Under the canopy exposure scenario, six representative arthropod families exhibited higher VI than both standard species for at least one insecticide e.g. Carabidae (imidacloprid), Coccinellidae (methomyl), Eulophidae (imidacloprid), Pteromalidae (cyfluthrin), Chrysopidae (imidacloprid), and Noctuidae (carbaryl). Under the soil exposure scenario, two additional ground-dwelling families exceeded the VI of both standard species for specific chemicals: Staphylinidae (chlorpyrifos) and Formicidae (malathion). These VI-based outcomes show that reliance on Phytoseiidae and Braconidae alone can miss families more vulnerable to particular compounds or exposure routes. Accordingly, surrogate selection should be informed by VI (and its scenario dependence) by using a stepwise approach in which trait-based VI screening identifies candidate families and second VI refines their chemical-specific vulnerability.

Introducing sensitivity proxies of chemical - specific toxicity data markedly refined the vulnerability rankings. Chemical identity proved to be a major driver of these re-rankings. Different insecticide classes produced strongly taxon-specific sensitivity patterns: pyrethroids such as λ-cyhalothrin were especially toxic to mites, bugs (Anthocoridae) and some beetles (pest species from Curculionidae family), neonicotinoids like imidacloprid disproportionately affected several parasitoids families (e.g. Eulophidae, Pteromalidae, Scelionidae, Trichogrammatidae) and moths (Noctuidae), and carbamates (i.e. methomyl) showed heightened toxicity to ladybirds. These differences underscore that surrogate species selection for regulatory testing cannot be one-size-fits-all and a reliance on Phytoseiidae and Braconidae in Tier 1 assessment may underestimate the sensitivity of other functionally important taxa.

A common critique of surrogate selection is that representative families might be less sensitive than many functionally important taxa, so reliance on them could fail to protect vulnerable service providers (Banks et al., 2014). However, our analyses do not support that assertion: representative families in our dataset were, on average, more sensitive across the set of chemicals tested, and this pattern was statistically significant for some insecticides (notably dimethoate and malathion). Importantly, vulnerability is a compound metric that combines exposure, recovery and sensitivity: a family with relatively low toxicological sensitivity can still rank highly if its I_{E+R} is large, and conversely a family with strong recovery traits may still be vulnerable if its LR50 is unusually low. Representativeness alone is insufficient as a guarantee of conservatism. Surrogate selection should combine trait-based screening to flag likely at-risk functional families and targeted LR50 testing to confirm chemical-specific sensitivity, ensuring that decision-making captures both ecological function and compound-specific risk. The varying sensitivity patterns further support the argument that ERA should incorporate taxon-specific vulnerabilities rather than assuming a uniform response across NTAs (Rubach et al., 2012).

We tested two plausible weighting strategies for trait components (equal weighting and a biologically informed differential weighting) and found I_{E+R} outcomes to be highly correlated across approaches indicating that the precise, reasonable choice of weights had little effect on the relative ordering of families. The availability of exposure and recovery trait data for the representative families was comparatively comprehensive, and the approach could readily be extended to include additional traits where appropriate data exist. Vulnerability indices are generated by weighting trait scores within and between components (exposure, recovery and sensitivity); De Lange et al. (2012) used differential weighting based on expert judgement, which can introduce bias, whereas equal weighting is a more parsimonious choice for broad screening. In our analyses, exposure scenario (canopy versus soil) had a greater influence on VI outcomes than modest, biologically plausible changes in weighting. That said, weighting schemes could matter in other datasets or when trait measurements are uncertain; improving trait coverage and the biological basis for trait assignments remains a priority.

From a regulatory perspective, our findings support a tiered, compound- and scenario-aware approach to environmental risk assessment that combines ecological and toxicological evidence. Standard test species remain valuable for initial screening, but they should be complemented by trait-based I_{E+R} prioritization (to identify ecologically important, scenario-robust families) and by targeted LR50 screening that explicitly covers taxa known to be toxicologically sensitive even when trait-vulnerability is low. In our dataset, such taxa include ladybirds (Coccinellidae) and several non-Braconid parasitoid wasps (e.g., Eulophidae), which in some cases showed very low LR50s despite modest I_{E+R} scores. Immediate toxicology priorities are Hybotidae and several spider families; prioritization lists derived solely from toxicity databases risk missing trait-vulnerable taxa because of current data bias. We also recommend that vulnerability outputs explicitly report exposure-scenario dependence (canopy vs soil) so that risk managers can see when rankings are robust and when they are contingent on particular exposure routes. Finally, where feasible, augmenting trait data with mechanistic TK/TD-linked physiological measurements (e.g. metabolic/detoxification capacity) would reduce reliance on LR50 proxies and increase the mechanistic interpretability of the combined vulnerability index.

Limitations of our study include LR50 data gaps, reliance on family-level (rather than species-level for many taxa) trait assignments and the pragmatic simplifications inherent in exposure-scenario parameterization. LR50 records were uneven across chemicals and taxa: λ-cyhalothrin dominates our toxicity database while many common compounds and entire clades, e.g. numerous Diptera and thrips are poorly represented. For arthropods contributing to pest control, missing LR50 data was particularly acute for Hybotidae and for many spider families. For arthropods contributing to pollination, missing LR50 data was an issue for lepidopterans, non-apid bees and hoverflies. Importantly, the I_{E+R} calculations depend on the prior identification of representative genera within families, however we omitted several families (e.g. Cantharidae, Megachilidae, Erebidae) because no representative genera were available. The lack of LR50 data meant that it was not possible to produce a chemical-specific vulnerability analysis for all families. The practical consequences are twofold. First, families that are identified as high priority based on their trait profiles remain potential priorities until toxicological confirmation is available. Second, the subset of families included in chemical-specific comparisons is biased toward better-studied groups (parasitoids, beetles, mites), which can distort conclusions about which service-providing families are most at risk across chemical classes.

The LR50 values used in our analysis were compiled from multiple independent laboratory studies that potentially differed in experimental design and hence included sources of variation that are not controlled for. The analysis focused on acute toxicity resulting from surface contact with individual active substances. This was a pragmatic decision driven by data availability. Sensitivity ratios generated using data from standardised laboratory studies provide a measure of relative sensitivity, which may be modified under field conditions. However, their role in this study was to highlight cases where non-standard taxa appear substantially more sensitive than commonly used regulatory surrogate species. The approach provides an important priortisation tool for subsequent investigations, and with sufficient data, future iterations of the framework could incorporate additional endpoints, alternative exposure routes and chemical mixtures.

Aggregating at the family level was a pragmatic choice to increase comparability and regulatory relevance, but it can conceal species-level outliers. We parameterised exposure scenarios so that soil-associated trait states received higher exposure scores under the soil scenario and foliar/plant-associated states received higher scores under the canopy scenario and we tested the sensitivity of I_{E+R} and VI rankings to alternative parameter and scenario assumptions. These sensitivity checks show that many high- I_{E+R} families remain elevated across plausible parameter sets, but that switching scenarios or altering exposure parameterisation can change rank order for particular taxa and chemicals, which is why we report scenario dependence and give concrete examples in the results. Even so, the combined trait plus LR50 framework produced robust, policy-relevant outputs: it consistently identified families with high trait-vulnerability across scenarios, revealed chemical-specific re-rankings that flag concrete testing priorities and generated a concise, actionable list of taxa and chemicals warranting targeted LR50 assays.

Increasing taxonomic coverage of LR50 studies, improving trait databases (especially for understudied Diptera and arachnids) and incorporating empirically derived exposure metrics (residue dissipation on different microhabitats, airborne drift models for canopy exposure) would all strengthen future applications. Moreover, explicitly adding TK/TD traits (and combining these with phylogenetic and genomic information) could ultimately enable a more predictive approach to species sensitivity (Spurgeon et al., 2020; Van den Berg et al., 2021), but such integrated databases are not yet available for many representative NTAs. For this reason, we recommend generating robust toxicological datasets for a taxonomically diverse suite of representative taxa, including foliar and ground-dwelling spiders, ground-dwelling beetles (e.g. Carabidae, Staphylinidae), ladybirds (Coccinellidae), dance flies (Hybotidae), hoverflies (Syrphidae), lacewings (Chrysopidae), ants (Formicidae), solitary bees and lepidopterans (moths and butterflies), so that trait-identified priorities can be validated and TK/TD-informed models can be developed. However, it is important to remember that proxies may not fully capture interspecific variability in toxicokinetics and detoxification mechanisms. For example, while smaller-bodied insects generally exhibit higher sensitivity due to greater relative exposure, some species possess enhanced detoxification enzymes that mitigate pesticide effects (Nagloo et al., 2024).

Validation of the proposed framework requires datasets that combine standardized toxicity measurements across multiple taxa and chemicals with field observations of population responses under realistic exposure conditions. Such integrated datasets remain rare for terrestrial arthropods in agricultural systems. Consequently, the framework should be viewed primarily as a prioritization and hypothesis-generating tool that identifies taxa likely to warrant further toxicological testing or ecological monitoring. Future work could evaluate its predictive performance by comparing vulnerability rankings with standardized laboratory toxicity datasets, semi-field experiments or long-term monitoring of arthropod communities exposed to known pesticide regimes.

In conclusion, integrating trait-based vulnerability screening with chemical-specific toxicological data provides a more ecologically realistic and operational framework for assessing risks to non-target arthropods that deliver key ecosystem services in European agroecosystems. Our results show that standard test species are not necessarily the most vulnerable representatives of above-ground NTAs: depending on the insecticide and exposure route, non-Braconid parasitoid wasps, ladybirds (Coccinellidae), ground and rove beetles (Carabidae, Staphylinidae), ants (Formicidae), lacewings (Chrysopidae) and several moth taxa can exhibit higher vulnerability than regulatory surrogates. Recognizing these differences is essential for evaluating risks to the ecosystem services of pest control and pollination. By broadening the range of test species (EC, 2024), aligning surrogates with compound-specific toxicity patterns, and investing in targeted testing for trait-identified high-risk taxa, regulatory frameworks can more effectively safeguard the ecosystem services that underpin agricultural productivity (Allen-Wardell et al., 1998; Bianchi et al., 2006; Landis et al., 2000). The combined trait–toxicology framework identifies which service-providing families are likely to be most at risk, highlights when vulnerability is scenario-dependent and produces concrete priorities for targeted LR50 testing. Although current data gaps limit full implementation, this structured, evidence-based approach provides a pragmatic way to refine surrogate selection, strengthen protection goals for ecosystem services, and increase confidence in the ecological relevance of ERA for PPPs.

5. References

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Figure captions

Figure 1. Mean (+SE) IE+R for (a) pest control (solid bars) and pollination (open bars) families and (b) foliar dwelling (dark grey) and ground-dwelling (light grey) families, under canopy exposure or soil exposure scenarios. Letters above bars indicate results of Tukey pair-wise comparison test. Means that do not share the same letter are significantly different. IE+R was calculated using the equal weighting method.

Figure 2. Deviation from the partial vulnerability index (IE+R) of either (a) *Aphidus rhopalosiphi* or (b) *Typholodromus pyri* for arthropod families under the canopy exposure scenario (green) or soil exposure scenario (brown). Values greater than zero indicate the family-specific IE+R is greater than that of the standard species. The magnitude of deviation reflects the relative difference in trait-based vulnerability: for example, a value of 0.1 indicates a small increase in vulnerability relative to the standard species, whereas a value of 0.7 indicates a substantially higher vulnerability. IE+R calculated from exposure and recover traits using the equal weighting method, Syrphidae contribute to pest control as larvae (L) and pollination as adults (A) and hence IE+R calculated separately for each life stage.

Figure 3. Distribution of toxicity data for representative (black bar) and non-representative (white bar) arthropod families across (a) taxonomic orders and (b) insecticides. Numbers above bars denote total number of species. Also presented are (c) mean (+ 1 SE) family-level log LR50 values (g/ha) for representative (solid symbols) and non-representative (open symbols) families. Asterisk denotes significant difference between representative and non-representative families.

Figure 4. Species (a, c, e, g, i) and family (b, d, f, h, j) sensitivity distributions for arthropods exposed to insecticides where the LR50 value for most sensitive species was at least 5 times lower than the LR50 value for the most sensitive standard species. The curve represents the log-normal sensitivity distribution and the shaded area is the 95% confidence interval. Symbols are colour-coded by Order. Circles denote species belonging to representative families and triangles represent species belonging to non-representative families following Sowa et al. (2025). Standard test species, and the families to which they belong, are highlighted in red. Sensitivity distributions were produced using the ssdtools package in R (Thorley et al., 2025).

Figure 5. Chemical-specific vulnerability indices for arthropod families exposed to 13 chemicals expressed as deviation from vulnerability index (VI) of (a) *Aphidus rhopalosiphi* or (b) *Typholodromus pyri* under the canopy exposure scenario. Values greater than zero indicate the chemical-specific family VI is greater than that of the standard species. The study chemicals included organophospates (circles), pyrethroids (triangles), carbamates (squares) and a neonicitinoid (diamond). Corresponding data for the soil exposure scenario are presented in the Supplementary Information (Fig. S1.2).

Alt texts

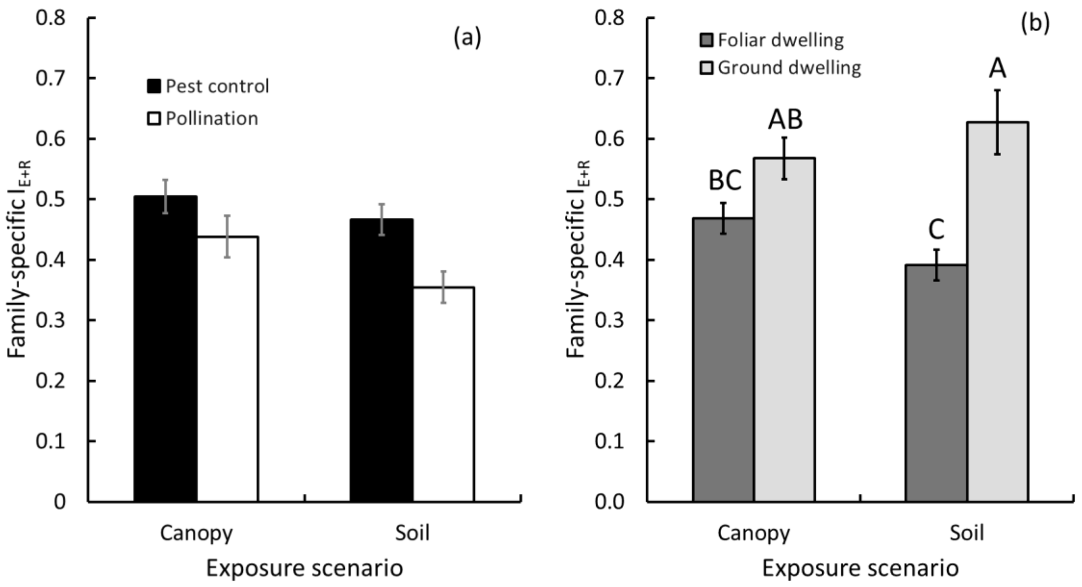
Figure 1. Bar chart comparing I_{E+R} values for pest control vs. pollination and foliar vs. ground-dwelling families under canopy and soil exposure. Pest control families have higher I_{E+R} than pollinators, and ground-dwelling families generally show higher IE+R than foliar-dwelling ones, with differences varying between canopy and soil exposure.

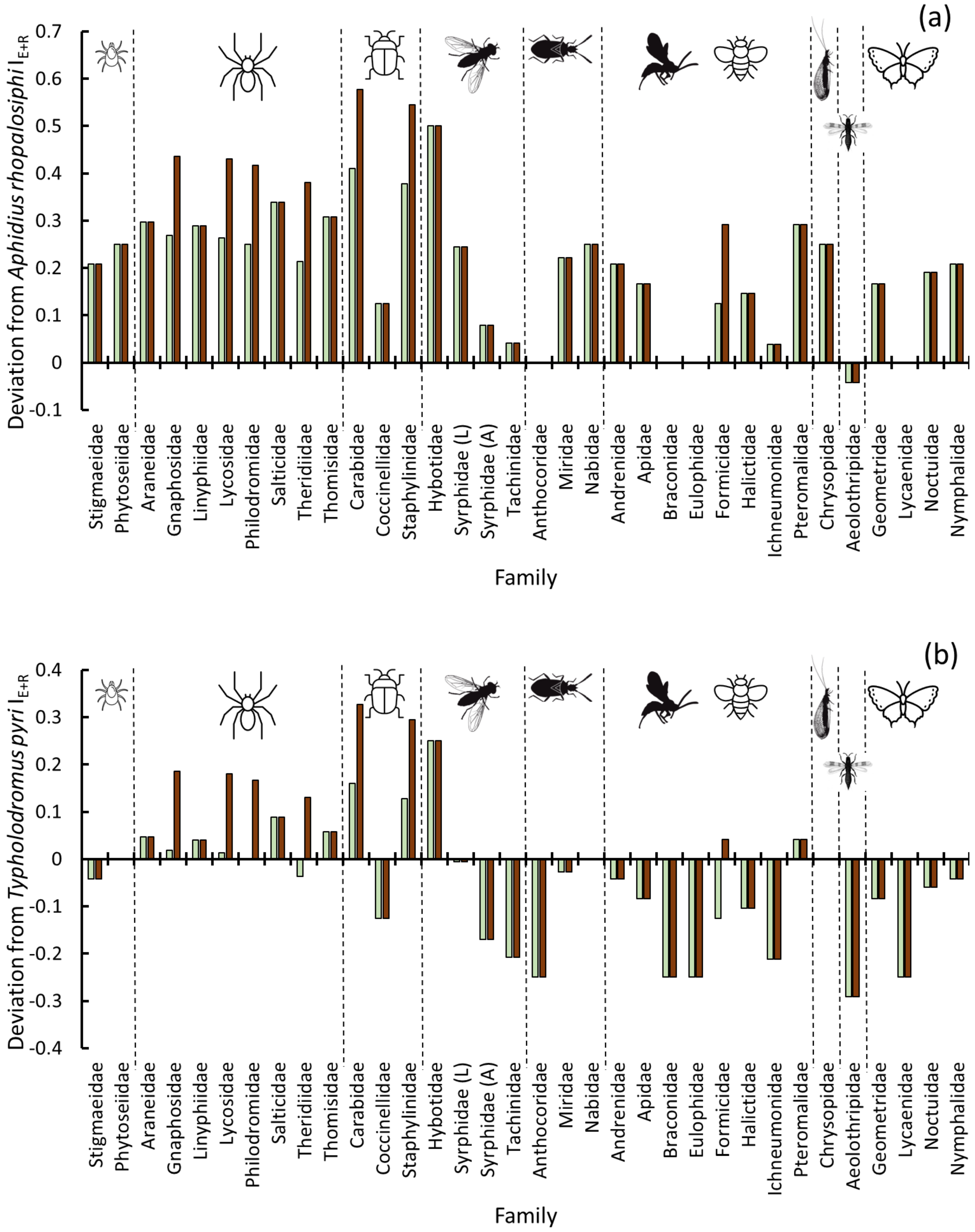
Figure 2. Bar chart showing how arthropod family vulnerability (I_{E+R}) differs from two reference species under canopy and soil exposure. Under canopy exposure, many arthropod families are more vulnerable than the reference species, while under soil exposure several families show reduced vulnerability, especially relative to *Typhlodromus pyri.*

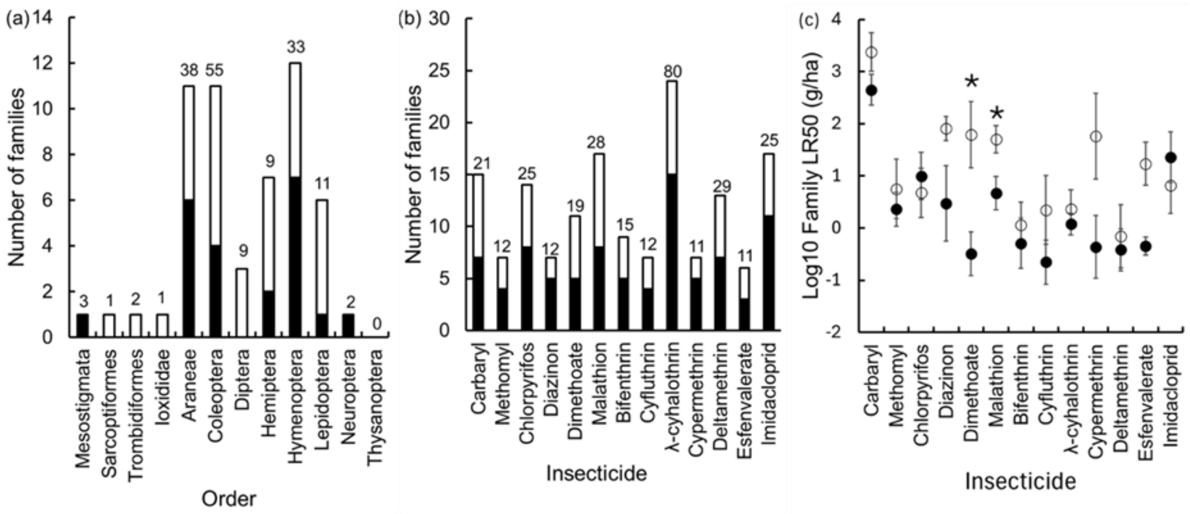
Figure 3. Representative and non-representative families differ in available toxicity data and mean sensitivity, with a significant difference in log LR50 values. Representative families dominate available toxicity data and show significantly different sensitivity, with generally higher log LR50 values than non-representative families.

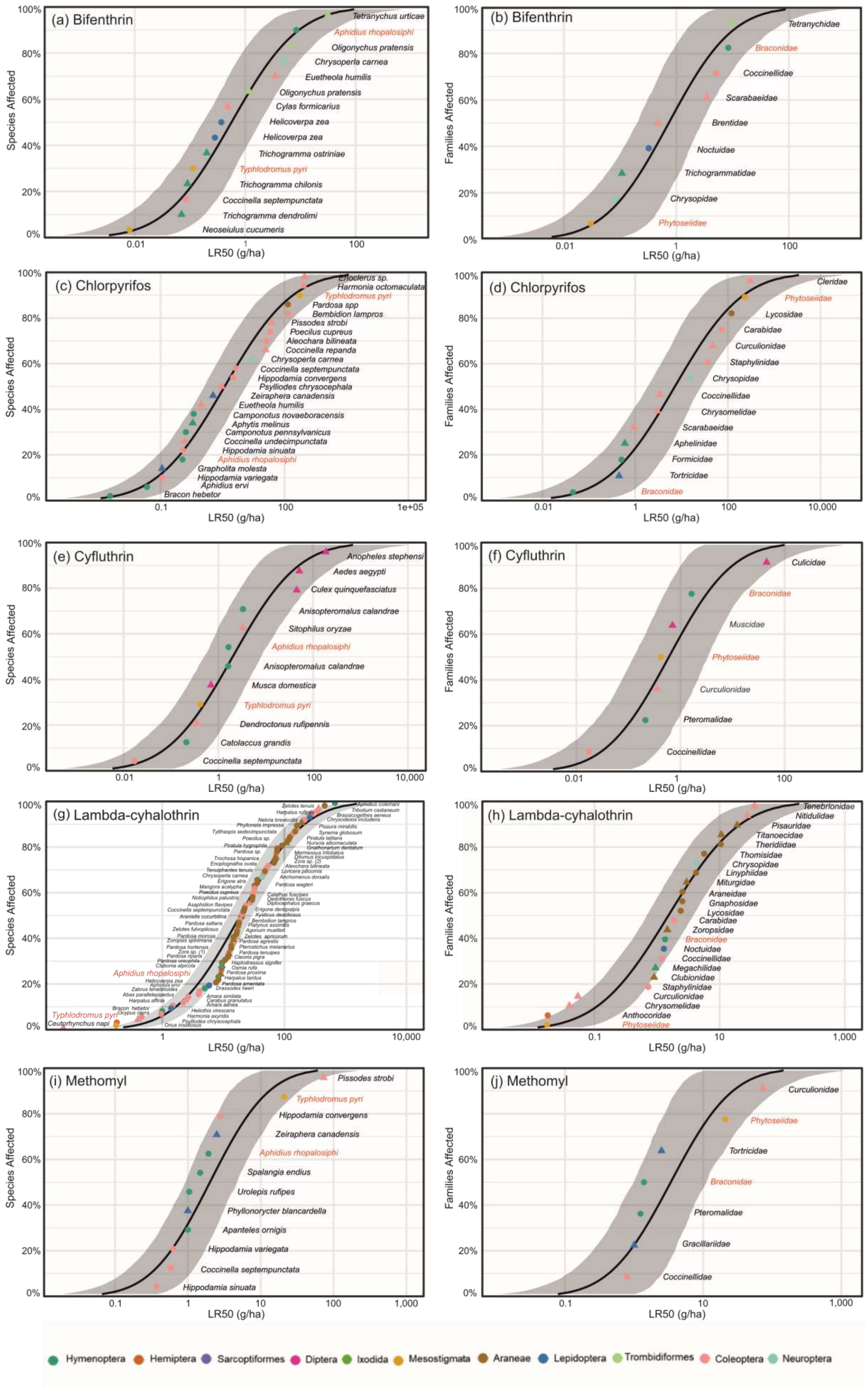
Figure 4. Species and family sensitivity distribution curves for five insecticides, showing the distribution of affected species as LR50 increases (g/ha).

Figure 5. Chemical-specific vulnerability indices for 13 chemicals under canopy exposure, showing deviations from two reference species. In comparison with *Aphidius rhopalosiphi* many families show increase in their sensitivity whereas in other comparison (*Typhlodromus pyri*) opposite (decrease).


(a)
Family-specific I_{E+R}
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
■ Pest control
□ Pollination
Canopy
Soil
Exposure scenario
(b)
Family-specific I_{E+R}
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
▨ Foliar dwelling
□ Ground dwelling
BC
AB
C
A
Canopy
Soil
Exposure scenario


(a)
Deviation from *Aphidius rhopalosiphi* I_{E+R}
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
-0.1
(b)
Deviation from *Typholodromus pyri* I_{E+R}
0.4
0.3
0.2
0.1
0
-0.1
-0.2
-0.3
-0.4
Stigmaeidae
Phytoseiidae
Araneidae
Gnaphosidae
Linyphiidae
Lycosidae
Philodromidae
Salticidae
Theridiidae
Thomisidae
Carabidae
Coccinellidae
Staphylinidae
Hybotidae
Syrphidae (L)
Syrphidae (A)
Tachinidae
Anthocoridae
Miridae
Nabidae
Andrenidae
Apidae
Braconidae
Eulophidae
Formicidae
Halictidae
Ichneumonidae
Pteromalidae
Chrysopidae
Aeolothripidae
Geometridae
Lycaenidae
Noctuidae
Nymphalidae
Family


(a)
Number of families
14
12
10
8
6
4
2
0
3
1
2
1
38
55
9
9
33
11
2
0
Mesostigmata
Sarcoptiformes
Trombidiformes
Ioxididae
Araneae
Coleoptera
Diptera
Hemiptera
Hymenoptera
Lepidoptera
Neuroptera
Thysanoptera
Order
(b)
Number of families
30
25
20
15
10
5
0
21
12
25
12
19
28
15
12
80
11
29
11
25
Carbaryl
Methomyl
Chlorpyrifos
Diazinon
Dimethoate
Malathion
Bifenthrin
Cyfluthrin
λ-cyhalothrin
Cypermethrin
Deltamethrin
Esfenvalerate
Imidacloprid
Insecticide
(c)
Log10 Family LR50 (g/ha)
4
3
2
1
0
-1
-2
*
*
Carbaryl
Methomyl
Chlorpyrifos
Diazinon
Dimethoate
Malathion
Bifenthrin
Cyfluthrin
λ-cyhalothrin
Cypermethrin
Deltamethrin
Esfenvalerate
Imidacloprid
Insecticide


(a) Bifenthrin
Species Affected
100%
80%
60%
40%
20%
0%
Tetranychus urticae
Aphidius rhopalosiphi
Oligonychus pratensis
Chrysoperla carnea
Euetheola humilis
Oligonychus pratensis
Cylas formicarius
Helicoverpa zea
Helicoverpa zea
Trichogramma ostriniae
Typhlodromus pyri
Trichogramma chilonis
Coccinella septempunctata
Trichogramma dendrolimi
Neoseiulus cucumeris
0.01
1
100
LR50 (g/ha)
(b) Bifenthrin
Families Affected
Tetranychidae
Braconidae
Coccinellidae
Scarabaeidae
Brentidae
Noctuidae
Trichogrammatidae
Chrysopidae
Phytoseiidae
(c) Chlorpyrifos
Eriocierus sp.
Harmonia octomaculata
Typhlodromus pyri
Pardosa spp
Bembidion lampros
Pissodes strobi
Poecilus cupreus
Aleochara bilineata
Coccinella repanda
Chrysoperla carnea
Coccinella septempunctata
Hippodamia convergens
Psylliodes chrysocephala
Zeiraphera canadensis
Euetheola humilis
Camponotus novaeboracensis
Aphytis melinus
Camponotus pennsylvanicus
Coccinella undecimpunctata
Hippodamia sinuata
Aphidius rhopalosiphi
Grapholita molesta
Hippodamia variegata
Aphidius ervi
Bracon hebetor
0.1
100
1e+05
(d) Chlorpyrifos
Cleridae
Phytoseiidae
Lycosidae
Carabidae
Curculionidae
Staphylinidae
Chrysopidae
Coccinellidae
Chrysomelidae
Scarabaeidae
Aphelinidae
Formicidae
Tortricidae
Braconidae
0.01
1
100
10,000
(e) Cyfluthrin
Anopheles stephensi
Aedes aegypti
Culex quinquefasciatus
Anisopteromalus calandrae
Sitophilus oryzae
Aphidius rhopalosiphi
Anisopteromalus calandrae
Musca domestica
Typhlodromus pyri
Dendroctonus rufipennis
Catolaccus grandis
Coccinella septempunctata
0.01
1
100
10,000
(f) Cyfluthrin
Culicidae
Braconidae
Muscidae
Phytoseiidae
Curculionidae
Pteromalidae
Coccinellidae
0.01
1
100
(g) Lambda-cyhalothrin
Zelotes tenuis
Aphidius colemani
Harpalus rufipes
Tribolium castaneum
Nebria brevicollis
Brassicogethes aeneus
Chrysodeixis includens
Phylloneta impressa
Pisaura mirabilis
Tytthaspis sedecimpunctata
Synema globosum
Poecilus sp.
Piratula latitans
Nurscia albomaculata
Piratula hygrophila
Gnathonarium dentatum
Pardosa sp.
Mermessus trilobatus
Trochosa hispanica
Diplocephalus tricuspidatus
Enoplognatha ovata
Zora sp. (2)
Aleochara bilineata
Tenuiphantes tenuis
Loricera pilicornis
Chrysoperla carnea
Anchomenus dorsalis
Erigone atra
Pardosa wagleri
Mangora acalypha
Poecilus cupreus
Calathus fuscipes
Notiophilus palustris
Oedothorax fuscus
Diplocephalus graecus
Asaphidion flavipes
Coccinella septempunctata
Erigone dentipalpis
Xysticus desidiosus
Araniella cucurbitina
Bembidion lampros
Pardosa saltans
Platynus assimilis
Zelotes fulvopilosus
Agonum muelleri
Pardosa morosa
Zelotes apricorum
Zoropsis spinimana
Pardosa agrestis
Pardosa hortensis
Pterostichus melanarius
Zora sp. (1)
Pardosa tenuipes
Pardosa riparia
Cleonis pigra
Pardosa oreophila
Clubiona alpicola
Haplodrassus signifer
Osmia rufa
Aphidius rhopalosiphi
Pardosa proxima
Harpalus tardus
Helicoverpa zea
Aphidius ervi
Pardosa amentata
Zabrus tenebrioides
Drassodex heeri
Abax parallelepipedus
Amara similata
Harpalus affinis
Carabus granulatus
Amara aenea
Bracon hebetor
Ocypus olens
Heliothis virescens
Typhlodromus pyri
Harmonia axyridis
Ceutorhynchus napi
Psylliodes chrysocephala
Orius insidiosus
1
100
10,000
(h) Lambda-cyhalothrin
Tenebrionidae
Nitidulidae
Pisauridae
Titanoecidae
Theridiidae
Thomisidae
Chrysopidae
Linyphiidae
Miturgidae
Araneidae
Gnaphosidae
Lycosidae
Carabidae
Zoropsidae
Braconidae
Noctuidae
Coccinellidae
Megachilidae
Clubionidae
Staphylinidae
Curculionidae
Chrysomelidae
Anthocoridae
Phytoseiidae
0.1
10
1,000
(i) Methomyl
Pissodes strobi
Typhlodromus pyri
Hippodamia convergens
Zeiraphera canadensis
Aphidius rhopalosiphi
Spalangia endius
Urolepis rufipes
Phyllonorycter blancardella
Apanteles ornigis
Hippodamia variegata
Coccinella septempunctata
Hippodamia sinuata
0.1
1
10
100
1,000
(j) Methomyl
Curculionidae
Phytoseiidae
Tortricidae
Braconidae
Pteromalidae
Gracillariidae
Coccinellidae
0.1
10
1,000
● Hymenoptera
● Hemiptera
● Sarcoptiformes
● Diptera
● Ixodida
● Mesostigmata
● Araneae
● Lepidoptera
● Trombidiformes
● Coleoptera
● Neuroptera

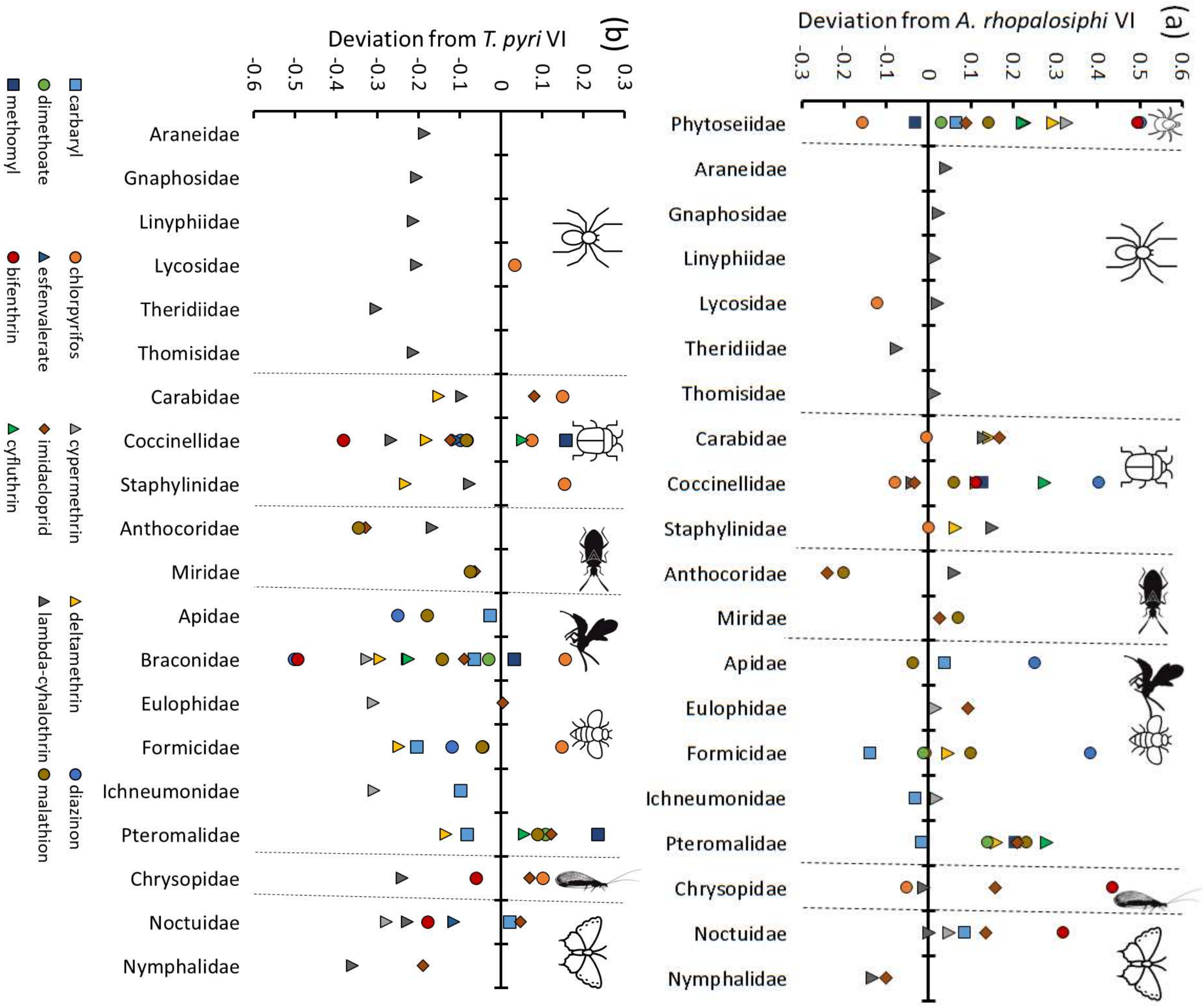
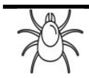
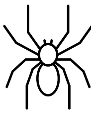

(a)
Deviation from *A. rhopalosiphi* VI
-0.3
-0.2
-0.1
0
0.1
0.2
0.3
0.4
0.5
0.6
Phytoseiidae
Araneidae
Gnaphosidae
Linyphiidae
Lycosidae
Theridiidae
Thomisidae
Carabidae
Coccinellidae
Staphylinidae
Anthocoridae
Miridae
Apidae
Eulophidae
Formicidae
Ichneumonidae
Pteromalidae
Chrysopidae
Noctuidae
Nymphalidae
(b)
Deviation from *T. pyri* VI
-0.6
-0.5
-0.4
-0.3
-0.2
-0.1
0
0.1
0.2
0.3
Araneidae
Gnaphosidae
Linyphiidae
Lycosidae
Theridiidae
Thomisidae
Carabidae
Coccinellidae
Staphylinidae
Anthocoridae
Miridae
Apidae
Braconidae
Eulophidae
Formicidae
Ichneumonidae
Pteromalidae
Chrysopidae
Noctuidae
Nymphalidae
■ carbaryl
● dimethoate
■ methomyl
● chlorpyrifos
▲ esfenvalerate
● bifenthrin
△ cypermethrin
◆ imidacloprid
▲ cyfluthrin
△ deltamethrin
▲ lambda-cyhalothrin
● diazinon
● malathion

Table 1. Representative above-ground arthropod families contributing to pest control and pollination in EU crop fields (taken from Sowa et al., 2025). Pest control families were divided into ground-dwelling (G) and foliar-dwelling (F). Syrphidae contribute to both pollination and pest control.

	Order	Family	Common name	Ecosystem service
	Mesostigmata	Phytoseiidae	mites	Pest control (F)
	Trombidiformes	Stigmaeidae	mites	Pest control (F)
	Araneae	Araneidae	orb-weaver spider	Pest control (F)
		Gnaphosidae	ground spiders	Pest control (G)
		Linyphiidae	money spiders	Pest control (F)
		Lycosidae	wolf spiders	Pest control (G)
		Philodromidae	running crab spiders	Pest control (G)
		Salticidae	jumping spiders	Pest control (F)
		Theridiidae	tangle web spiders	Pest control (G)
		Thomisidae	crab spiders	Pest control (F)
	Coleoptera	Cantharidae	soldier beetles	Pest control (F)
		Carabidae	ground beetles	Pest control (G)
		Coccinellidae	ladybirds	Pest control (F)
		Staphylinidae	rove beetles	Pest control (G)
	Diptera	Hybotidae	dance flies	Pest control (F)
		Syrphidae	hoverflies	Pest control (F) / Pollination
		Tachinidae	tachinid flies	Pest control (F)
	Hemiptera	Anthocoridae	minute pirate bugs	Pest control (F)

		Nabidae	damsel bugs	Pest control (F)
		Miridae	mirid bugs	Pest control (F)
	Hymenoptera	Andrenidae	mining bees	Pollination
		Braconidae	parasitoid wasps	Pest control (F)
		Apidae	bees	Pollination
		Eulophidae	parasitoid wasps	Pest control (F)
		Formicidae	ants	Pest control (G)
		Halictidae	sweat bees	Pollination
		Ichneumonidae	icheumonid wasps	Pest control (F)
		Megachilidae	solitary bees	Pollination
		Pteromalidae	parasitoid wasps	Pest control (F)
	Lepidoptera	Erebidae	moths	Pollination
		Geometridae	geometer moths	Pollination
		Lycaenidae	gossamer-winged butterflies	Pollination
		Noctuidae	owlet moths	Pollination
		Nymphalidae	brush-footed butterflies	Pollination
	Neuroptera	Chrysopidae	green lacewings	Pest control (F)
	Thysanoptera	Aeolothripidae	thrips	Pest control (F)

Table 2. Traits and standardized scores used to in the vulnerability analysis. A score of 0 represents minimum potential contribution to vulnerability and 1 represents maximum potential contribution to vulnerability. Scores are presented for the canopy exposure scenario and adjustments for the soil exposure scenario are presented in parentheses. Scores are modified from De Lange et al. (2012) (see Supplementary Information S1 for details).

	Trait	**Trait class**	**Standardized score**
Exposure	Habitat	In soil	0
		On soil	0.5 (1)
		On canopy or flying	1 (0.5)
	Food	Prey	0
		Nectar/pollen/seed	0.5
		Vegetation	1
	Breeding period	Autumn	0
		Summer/Autumn	0.25
		Spring/Summer/Autumn	0.5
		Summer	0.5
		Spring/Summer	0.75
		Spring	1
Recovery	Dispersion	Flying	0
		Ballooning	0.333
		Walking and flying	0.667
		Walking only	1
	Reproduction	Multivoltine	0

		Multivoltine/Univoltine	0.5
		Univoltine	1

Table 3. Weighting factors for individual traits used for vulnerability analysis. Values are given for a partial vulnerability index based on exposure and recovery (I_{E+R}) and for a complete vulnerability index based on exposure, recovery and sensitivity (VI). Differential weighting is from De Lange et al. (2012) for an insecticide scenario and considers exposure and recovery traits only (see Supplementary Information S1 for details).

Component	**Trait**	**Differential weighting (I_{E+R})**	**Equal weighting (I_{E+R})**	**Equal weighting (VI)**
Exposure	Habitat	0.25	0.167	0.111
	Food	0	0.167	0.111
	Breeding period	0.25	0.167	0.111
Recovery	Dispersion	0.25	0.25	0.167
	Reproduction	0.25	0.25	0.167
Sensitivity	Toxicity	-	-	0.333

Table 4. Species and families with the the lowest LR50 value for each of the 13 study insecticides. SR (sensitivity ratio) is the ratio between the lowest LR50 value and the lowest standard species LR50.

Chemical group	Insecticide	Lowest species LR50	SR	Lowest family LR50
Organophosphate	Chlorpyrifos	*Bracon hebetor* (Braconidae)	56	Braconidae
	Diazinon	*Coccinella septempunctata* (Coccinellidae)	3.5	Braconidae
	Dimethoate	*Aphidius rhopalosiphi* (Braconidae)	1	Braconidae
	Malathion	*Catolaccus grandis* (Pteromalidae)	4.7	Pteromalidae
Pyrethroid	Bifenthrin	*Neoseiulus cucumeris* (Phytoseiidae)	14.1	Phytoseiidae
	Cyfluthrin	*Coccinella septempunctata* (Coccinellidae)	24.7	Coccinellidae
	λ-cyhalothrin	*Ceutorhynchus napi* (Curculionidae)	7.3	Phytoseiidae
	Cypermethrin	*Typhlodromus pyri* (Phytoseiidae)	1	Phytoseiidae
	Deltamethrin	*Typhlodromus pyri* (Phytoseiidae)	1	Phytoseiidae
	Esfenvalerate	*Hippodamia convergens* (Coccinellidae)	1.7	Phytoseiidae

Carbamate	Carbaryl	*Aphidius rhopalosiphi* (Braconidae)	1	Braconidae
	Methomyl	*Hippodamia sinuata* (Coccinellidae)	5.2	Coccinellidae
Neonicotinoid	Imidacloprid	*Neochrysocharis formosa* (Eulophidae)	1.4	Eulophidae