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Understanding the molecular machinery in agrochemical detoxification

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Pollination is a vital ecosystem service as it is key for the reproduction of flowering plants, including important agricultural crops. The eusocial western honey bee, Apis mellifera, is the only honey bee in North America and is the primary managed pollinator in the world. Unfortunately, honey bees are susceptible to a wide range of interacting stressors, including chemicals used in agriculture. The use and overuse of agrochemicals present a current threat to honey bee populations. It can be difficult to disentangle and identify specific stressors that affect a particular colony. Therefore, research is needed to understand how agrochemicals operate to affect bee mortality, how honey bees detoxify the many agrochemicals found in their environment, and the degree to which genetics contributes to resistance. However, much of the literature about how honey bees metabolize toxic chemicals is founded on homology to other insects. Studies directly linking exposure to agrochemicals and the elicited changes in gene expression are needed to improve our comprehension of the honey bee detoxification system. We are presenting the largest RNA-Seq study on honey bee toxicology, including the effect of 18 different agrochemicals from 5 classes, across 3 tissue types totalling 99 experimental contrasts. Here we show that each chemical produces both common and unique patterns of gene expression. Furthermore, detox gene regulation occurred in all tissue types and was present in all chemical classes, e.g., insecticides and herbicides. Alarmingly, this trend was prominent for amitraz and oxytetracycline, both used as treatments in commercial beekeeping. Our research addresses several questions in the field and provides important knowledge that can be mobilized to improve honey bee health and potentially the health of other native pollinators. Promoting agrochemical awareness and potential breeding practices for agrochemical resistance.