Improving Honey Bee Health by Using Systems Biology Approach

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PURE PROGRAM FOR UNDERGRADUATE RESEARCH

ABSTRACT

Honey bees (*Apis mellifera*) around the world are declining, and this decline is caused by several environmental factors. Many studies have been conducted to determine how these factors (disease conditions, pesticides) affect bee health, but most factors are studied in isolation under controlled laboratory settings. In our project, we aim to integrate the bee's exposome with disease and pesticide data to identify biomkarkers, potential causes, and novel synergistic interactions responsible for bee health decline. To identify these asscoiations, across datasets, we used Mass Profiler Professional (MPP) bioinformatics software. We identified 31 compounds that could serve as biomarkers for monitoring bee health, several of which are found in highly conserved fatty acid metabolic pathways, suggesting that these may be used as robust biomarkers of bee health.

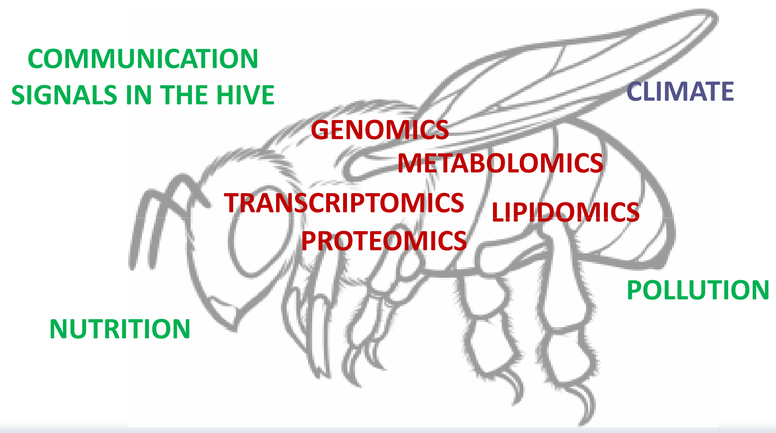
INTRODUCTION

• Honey bees are critical for agriculture and food production, their health is in decline. [1]

• There are many internal and external exposures that affect honey bee health such as parasites, fungicides, pesticides, etc. [2]

•How they interact with each other that causes health decline is unknown.

•The exposome (see below) takes into account all of the exposures that impact on an individual over a lifetime and this can be integrated with other –omic datasets to increase the understanding of environment that causes a decline in health. [3]

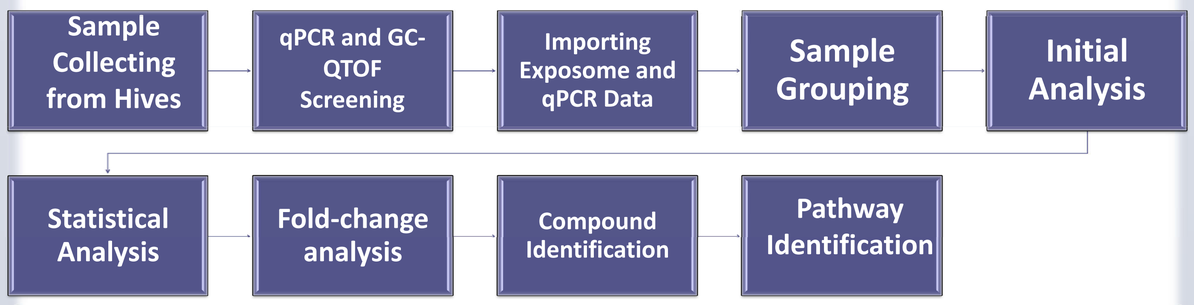


OBJECTIVES

• To integrate exposomic data with disease, pesticide, and health data to identify potential biomarkers that predict bee health decline

• To perform a KEGG pathway analysis to reveal insights to the underlying mechanisms causing a decline in bee health

MASS PROFILER PROFESSIONAL (MPP) METHODOLOGY



Box 1 - 30 bee hive samples were collected from the Philadelphia area
Box 2 – Samples were screened for diseases using qPCR and PCR, exposomes were generated using GC-QTOF analyses.
Box 3 - PCR and exposome data was imported to MPP software.
Box 4 - Samples were grouped as high, medium, and low based on health indicies.
Box 5 - Initial analysis parameters included a minimum abundance level of 5000 counts, minimum and maximum retention time values are adjusted to 15 and 37 minutes, respectively. Entities were baselined to the median value.
Box 6 - Statistical analysis - a One-Way ANOVA with Unequal Variance was applied. For multiple comparisons, we applied a Tukey test with Benjamin Hochberg (FDR) correction for multiple testing. The p-value cuf-off was set as 0.05.
Box 9 - After fold-change analysis, all of the entities were searched within the KEGG Pathway Database to indentify potential pathways that may have been disrubted from the respective stressors.

RESULTS

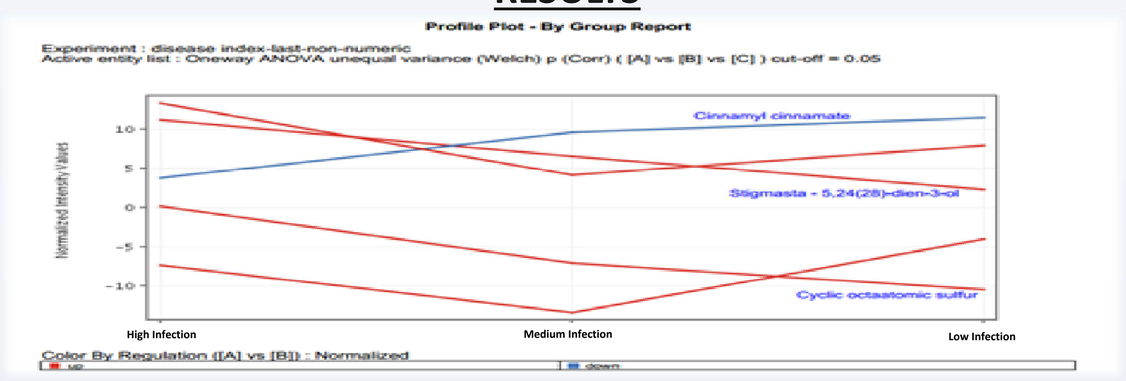


Figure 1: Fold Change Analysis of Disease Index Data:5 compounds were identified. Only 1 compound was down-regulated from high infection to low infection, the other two compounds were up-regulated.

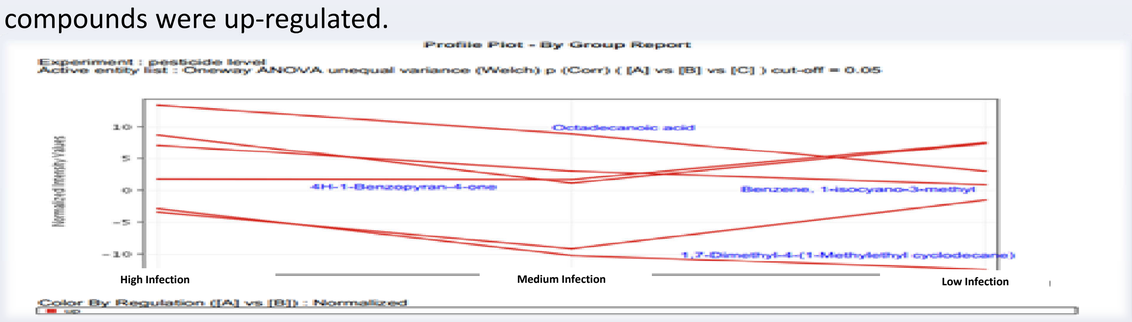


Figure 2: Fold Change Analysis of Pesticide Index Data: 6 entities were identified. Since 4 of the compounds show consistency from high infection to low infection, those compounds are highlighted. All of the compounds were down-regulated from high to low pesticide exposure.

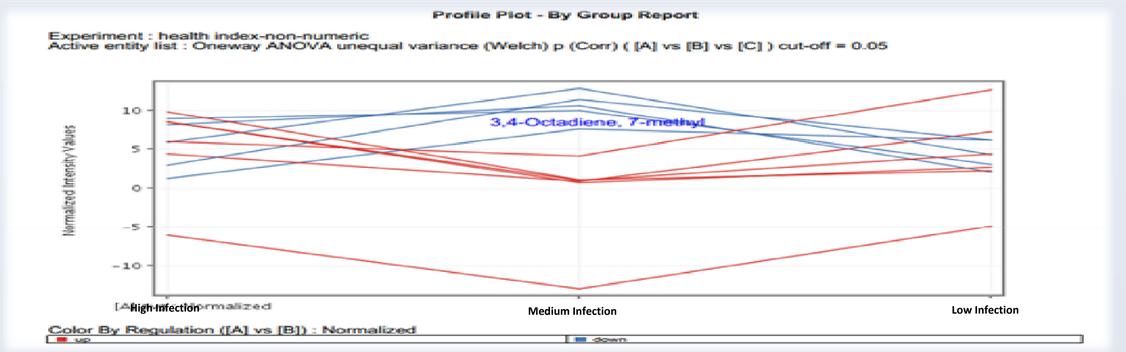


Figure 3: Fold Change Analysis of Health Index (Disease + Pesticide Index) Data: 11 compounds are identified. Only one of them showed a consistent down regulation when going from high to low health.

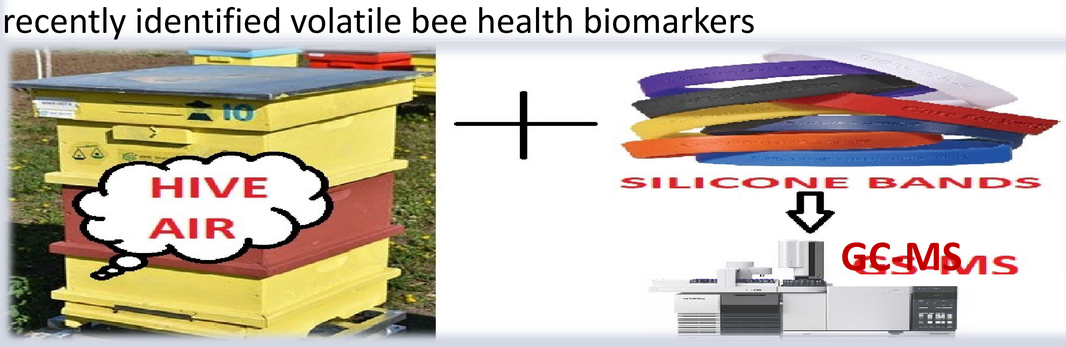
CONCLUSIONS

We identify several potential biomarkers that might be robust indicators and predictors of bee health and its delcine. We have yet to place these in several types of metabolic pathways to determine if they have synergistic effects on particular metabolic pathways.

So far we have identified some biomarkers that have roles in phototransduction, unsaturated fat biosynthesis, and fatty acid degredation.

FUTURE WORK

• Develop a silicone band absorbent technology to constantly monitor bee health in a cost-effective manner by screening for some of the recently identified volatile bee health biomarkers



ACKNOWLEDGEMENTS

Special thanks to other Mayack Lab members; Asal Ghaffari, Yasameen Koperly and Dalya Koperly for their great contributions for the project.

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