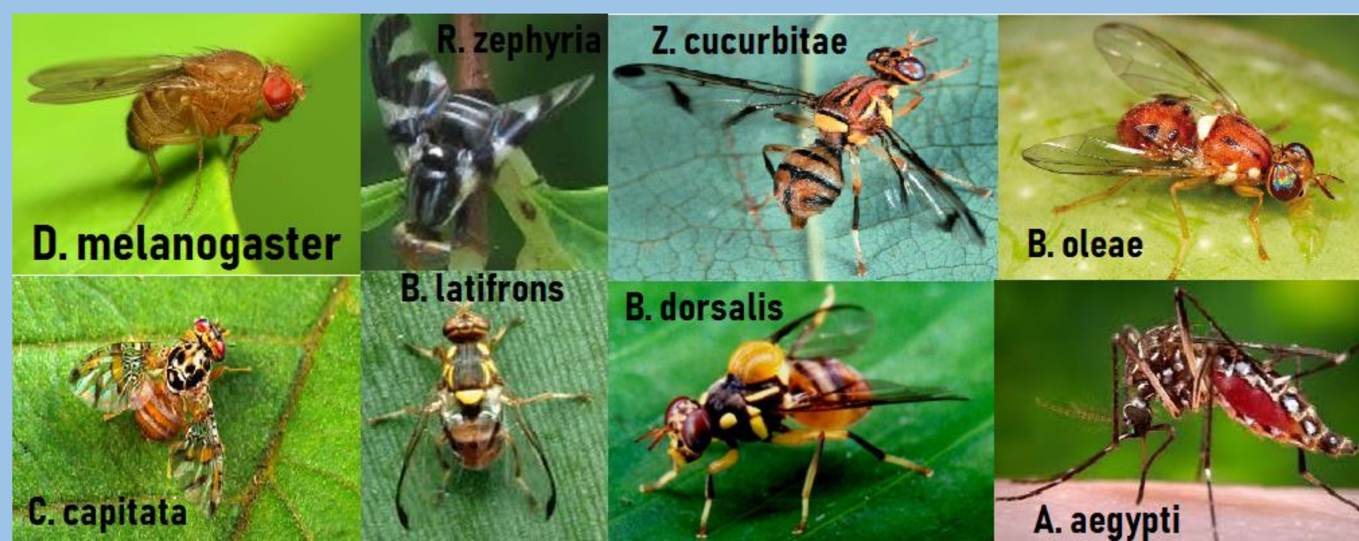
May 2019

Cytochrome P450 Protein Family 4 Conservation and Diversification Among Flies

Kevin Croft
Western Washinton University

Cytochrome P450 Family 4: Conservation, Duplication, and General Trends in Flies



Western Washington University – Biology Department
Produced by: Kevin Croft
Overseen by Dietmar Schwartz

Abstract: Commercial fruit pests, such as flies within the Tephritidae family, have a large economic impact on the global food supply due to their ability to infest a wide range of host plants. The genus Rhagoletis, which contains the apple maggot fly, has become an important organism for understanding the process of switching and adapting to new hosts. One enzyme group responsible for this ability in Rhagoletis flies is the Cytochrome P450 proteins. This superfamily of proteins is known to help organisms deal with various environmental stressors, such as detoxification of plant defensive compounds or insecticides. The Rhagoletis zephyria (the snowberry maggot) genome has recently be sequenced, providing a complete list of Cytochrome P450 gene sequences. Using MegaX and sequences from National Center for Biotechnology Information (NCBI), a maximum likelihood phylogenetic tree was generated to show potential conservation and diversification events, along with noticeable trends of Cytochrome P450 genes in the diverse subfamily 4. Testing will include Rhagoletis compared to other flies from families Tephritidae and Drosophilidae, while using mosquitos as an out-group. I hypothesize that Rhagoletis and other tephritids, as species that infest live well-defended fruit, will have a greater Cytochrome P450 diversity than Drosophila species surviving on yeasts in decaying fruit, as well the other flies seen as generalists possessing a higher variety of those defined as specialists, such as Rhagoletis.

Methods: Protein gene sequences were acquired from National Center for Biotechnology Information (NCBI), but only partials above 400 amino acids were used. All sequences were aligned using ClustalW with default settings, then a maximum likelihood tree was created in MegaX, using a bootstrap test of phylogeny with 100 replications, a Jones-Taylor-Thornton (JTT) model, gamma distribution rates among sites with 5 discrete categories, complete deletion for gaps/missing data, and the rest of the settings were left default. The yellow fever mosquito (Aedes aegypti) was used as an outgroup, along with a protein not found in the CYP4 family. Fly and mosquito taxa were colored for visual aid, along with labeled brackets.

Results: As expected, there is a small difference in the number of protein types between generalists such as C. capitata (13), B. dorsalis (13), Z. cucurbitae (12), B. latifrons (10) and specialists such as B. oleae (9). R. zephyria still has a large number (18) for being another specialist though. The protein diversity of D. melanogaster appears to be higher (22) than that of R. zephyria (18), as opposed to the hypothesized assumption. Conservation can be seen in most areas with greater than a single spaced bracket, disregarding duplicate genes within identical species. Duplication events are found within many taxa, along with partially mutated or lost intraspecies duplicates or “likes” in some flies. They could also be in the process of generating a pseudogene.

Discussion: Due to the limited categorization or defining of protein types among newly sequenced fly genomes, as well as this being a small sample size, it is a challenge to see or determine if such trends exist throughout the entire family. C. capitata is known to infest 362 plant types along potentially 212 more [1], B. dorsalis has been confirmed to infest 478 host plants [2], Z. cucurbitae (aka B. cucurbitae) has 136 known hosts [3], B. latifrons has 59 known hosts [4], and B. oleae only feeds on olives [5]. D. melanogaster may feed on yeasts and decaying fruit, but it seems to need a complex assortment of proteins to deal with the remaining compounds in fruits and/or toxins produced by yeast.

Conclusion: More fly genomes would be needed to form any definite conclusions, as well as confirming probable or predicted assumptions regarding protein types, but this analysis is a good start to an interesting understanding of fruit pests and their host-plant coevolution.

References:

[1] - Liquido, N., Mcquate, G., Hanlin, M., and Suiter, K. 2017. Host plants of the Mediterranean Fruit Fly, Ceratitis capitate. Tropical Crop and Commodity Protection Research. https://www.ars.usda.gov/research/publications/publication/?seqNo115=347486

[2] - Liquido, N., Mcquate, G., Birnbaum, A., Hanlin, M., Nakamichi, K., Inskeep, J., Ching, A., Marnell, S., and Kurashima, R. 2017. A review of recorded host plants of Oriental Fruit Fly, Bactrocera dorsalis. Tropical Crop and Commodity Protection Research. https://www.ars.usda.gov/research/publications/publication/?seqNo115=347371

[3] - McQuate, G.T., Liquido, N.J., and Nakamichi, K.A.A. 2017. Annotated World Bibliography of the Melon Fly, Bactrocera cucurbitae. Insect Mundi. Articles 0525-0527. http://journals.fcla.edu/mundi/article/view/0527

[4] - McQuate, G.T. and Liquido, N.J. 2016. Host plants of Solanum fruit fly, Bactrocera latifrons. Tropical Crop and Commodity Protection Research. https://www.ars.usda.gov/research/publications/publication/?seqNo115=336159

[5] – Daane, K.M. and Johnson, M.W. 2010. Olive fruit fly: Managing an ancient pest in modern times. Annual Review of Entomology 55: 151-169. https://www.ncbi.nlm.nih.gov/pubmed/19961328