EEOB 563 Project Proposal

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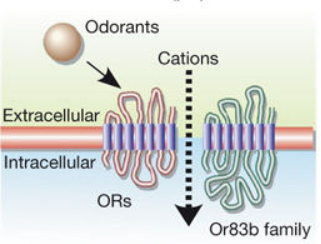
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The fig tree and its fig wasps pollinators are an example of a highly coevolved mutualistic system with each fig species producing a unique blend of volatile chemicals to attract its specific wasp pollinator to receptive inflorescences, and each pollinator species recognizing the volatile blend of its specific host (Weiblen, 2002). This specificity is not typically a result of rare chemical compounds being produced, but rather unique blends and ratios of common volatiles. The pattern of volatiles is sensed by pollinating fig wasps using the five major chemosensory gene families in insects. Of these gene families, it is the odorant receptors (OR), ionotropic receptors (IR), odorant binding proteins (OBP) and chemosensory proteins (CSP) in antennal tissues that are involved in the detection of volatile molecules. The presence of these four olfactory multi-gene families has been confirmed in an Old World pollinating fig wasp (*Ceratosolen solmsi*), with whole genome sequencing revealing a substantial contraction in OR and OBP gene diversity in this host specialist relative to other Hymenoptera (ants, bees, and wasps) (Xiao et al., 2013).

Of all of the families, the odorant receptor (OR) family is the largest and most diverse. Insects typically have anywhere from 60-400 OR gene family members, of which can be divided into three distinct groups: ligand-selective ORs that respond to general odorants, ligand-sensitive ORs that are pheromone specific, and a single highly conserved obligate co-receptor known as Orco (Nakagawa, Pellegrino, Sato, Vosshall, & Touhara, 2012). As an example, in the well-studied Hymenopteran model system, the parasitic wasp *Nasonia vitripennis,* has 301 odorant receptors (75 of which are pseudogenes). Whereas, in contrast, the Old World fig wasp *Ceratosolen solmsi* has only 46 OR family members and 2 pseudogenes (Xiao et al., 2013).

ORs are expressed in the olfactory neurons of the antennae’s olfactory sensilla (primarily the basiconic and trichoid sensilla) and are characterized by their seven transmembrane (7-TM) domain with an intracellular N-terminus and extracellular C-terminus (Engsontia, Sangket, Chotigeat, & Satasook, 2014). The one to three odorant receptors function with a highly conserved odorant receptor coreceptor (Orco) to form a ligand-gated cation channel, binding lipophilic volatiles such as aromatics, terpenes, and fatty acid derivatives (Montagné, De Fouchier, Newcomb, & Jacquin-Joly, 2015) as well as polar ligands such as esters and alcohols (Silbering et al., 2011).

**Fig 1.** Schematic model of ligand gated ion channel OR+Orco (Or83b) complex (Sato et al., 2008)



Although it is known that the odorant receptor family plays a very important role in the recognition of the receptive fig host, it is not well understood which of the odorant receptor subfamilies play an important role in that recognition and if the members of those subfamilies share a common function, recognizing the same odorant. There are also parasites in the system that must recognize the same bouquet of the receptive host as the pollinators. In theory, even though these wasps are not closely related at all to one another, the wasps must recognize the same volatiles. If the odorant receptor gene families of the parasites and the pollinators of the system are compared phylogenetically, we would expect that there would be similar behavior shared between them.

To test this, pollinators and parasites of a single system will be sequenced and then assembled. Genes will be called and annotated from these assemblies. The odorant receptors can then be identified using BLAST and fellow Hymenopteran OR genes as a database. These identified genes can then be aligned with the other known Hymenopteran OR genes and a phylogenetic tree built using maximum likelihood methods. For the sake of this course, I am going to focus on using the *F.petiolaris* pollinator *Pegoscapus* and two nonpollinators, *Idarnes LO1* and *Heterandrium A*. These three species are in no way closely related, but all recognize the host *F.petiolaris* and this should be reflected in the genes clades that are retained or expanded upon.In addition to this, I will look into the function of the genes within a clade/ family and see if the function is retained among them and that they are likely to recognize the same volatile.

Sources:

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