



Patterns of speciation in the transcriptomes of hybridizing wood ants: searching for the perfect hybrid

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The process of speciation is the fundamental biological process that underlies all novel biodiversity. Prior to its completion, diverging lineages that come into contact may still hybridize and experience gene flow. Speciation is often a gradual process, and hybridization was originally thought to be an antagonistic force to speciation, causing diverging lineages to homogenise once more. However, contemporary molecular techniques have revealed that many species pairs maintain some ability to interbreed throughout their divergence. Indeed, interbreeding between diverging lineages is likely a good source of novel and adaptive genetic variation. Theoretically, for diverging species to become distinct, there needs to be selection against hybrids, and other genotypically intermediate individuals. In *Formica* ants however, we have found a curious genetic pattern indicative of antagonistic selection between hybrids of different sexes. Previous studies have documented a population where hybrid females with certain genes are fitter than their counterparts. However, hybrid males born with same genes instead die during development. Thus, both the positive and negative consequences of hybridization are present simultaneously. My talk will describe how we examined the individual whole-body gene expression patterns of 62 larvae ants with known genotypes. This was done by constructing a de novo transcriptome, and then comparing the gene expression patterns of individuals with contrasting predicted fitness (i.e. those that die vs. those that will survive). These methods allowed us to uncover the genes that putatively underlie hybrid male death and hybrid female vigour. With this knowledge, we address what genes underlie hybrid fitness, and how the consequences of hybridization can be both positive and negative.