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**A New Method for Distinguishing Colony Social Forms of the Fire Ant *Solenopsis invicta***

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Two distinct forms of colony social organization occur in the fire ant *Solenopsis invicta*: Colonies of the monogyne social form are headed by a single egg-laying queen, whereas those of the polygyne social form contain multiple egg-laying queens. Recent studies have demonstrated that genetic variation at a single gene (*Gp-9*) is responsible for this major difference in social organization whereby all polygyne queens possess at least one *b*-like allele whereas monogyne queens lack such *b*-like alleles and instead harbor *B*-like alleles only. Extensive sequencing revealed that all *b*-like alleles in polygyne queens consistently contain three diagnostic amino acid residues: possession of only one or two of these critical residues is not sufficient for polygyny. We developed TaqMan assays to survey these critical sites and then validated our assays by surveying nests of known social form from the species' native South American range as well as by comparing our results to *Gp-9* sequence data from a subset of samples. Unlike previous assays, we show our method is sensitive, reliable, rapid, and accurate for determining colony social form, which is critical for planned and future studies aimed at better understanding the evolutionary genetics of social behavior in fire ants.

**A Systems Approach to Genetic Dissection of Complex Traits in *Drosophila melanogaster***

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Understanding how variation in sets of interacting transcripts affects organismal phenotypic variation is a critical challenge in contemporary quantitative genetics. We are using a systems genetics approach to explore this problem in *Drosophila melanogaster*. We derived 40 inbred lines and quantified the magnitude of genetic and environmental variation among these lines for a large number of physiological and behavioral phenotypes, including competitive fitness. We also performed whole genome transcriptional profiling of these lines. We performed analyses of variance for each gene to partition variation in transcript abundance into components attributable to the main effects of sex and line and the sex by line interaction. We found large amounts of genetic variation in transcript abundance, over 10,000 differentially expressed transcripts (FDR <0.001) which have high levels of broad sense heritability (over 5000 transcripts show  $H^2 > 0.5$ ) and large sex effects (> 13,000 transcripts). We then performed transcript-specific linear regressions on genetically variable genes, using fitness as a response variable. We identified 414 transcripts associated with variation in fitness. We then used the correlation structure between these phenotypically significant genes to construct gene co-expression networks, or modules of genetically correlated transcripts all associated with fitness. We uncovered networks associated with male mating behavior, oogenesis, and a large module involved in neural processes.

**Partial Behavioral Isolation Between DDT Resistant Populations and Their Unselected Controls Under Long Term Selection and Isolation in *Drosophila melanogaster***

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Three pairs of populations, in which one population of each pair has been selected for DDT resistance and the other maintained as an unselected control, were examined for behavioral isolation between the two populations of each pair. These populations have been under selection and isolated from each other for 49-56 years. Partial behavioral isolation has been reported in one of these pairs previously (91C and 91R; Boake *et al.*, 2003, *J. Evol. Biol.*, 16:83-90). We confirm these results and find another pair that also shows partial behavioral isolation (731C and 731R). The third pair shows no behavioral isolation (J1 and J2). The 91 and 731 populations are related closely in time and place of their founding populations. The J population was founded seven years after the other two, although from the same location. The origin of prezygotic isolation in long term isolated populations under strong selection in different directions is discussed.