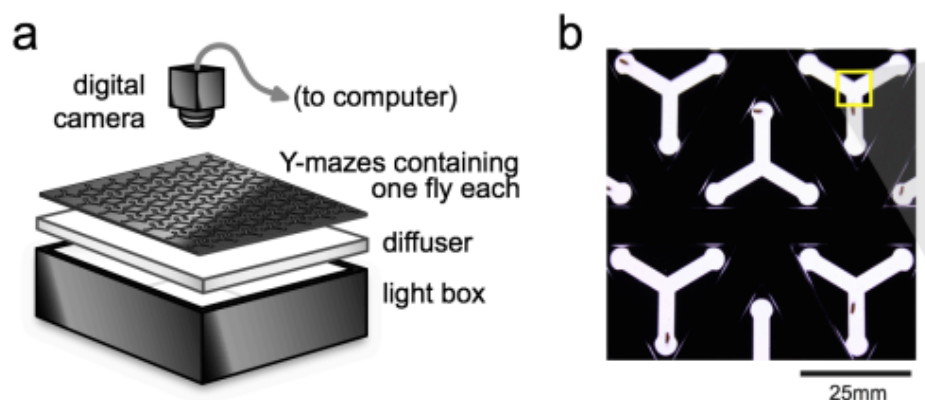


Behavioral individuality reveals genetic control of phenotypic variability

Posted on 3 March, 2015 by Noah Snyder-Mackler



High-throughput measure of *Drosophila* “handedness”. From Buchanan et al (2014), doi:10.1101/008565

Studies of animal personality (or, “behavioral syndromes”, if you choose your words carefully) are [so hot right now](#). One of the assumptions of such studies is that natural selection has somehow favored this behavioral variability/plasticity (and not just differences in means across genotypes). To date, however, no studies have shown a genetic basis underlying such intragenotypic phenotypic variability. Well, no studies until now...

A relatively new [preprint](#) from the labs of [Julien Ayroles](#) and [Benjamin de Bivort](#) measured behavioral variability in inbred *Drosophila* lines in order to determine the genetic basis of variability.

They used a very cool high-throughput behavioral assay to measure the “locomotor handedness” (i.e., whether or not they turned left or right in a Y-shaped maze; see picture above) of thousands of flies from 159 lineages. The powerful combination of the number of flies and isogenic lines allowed them to detect a heritable genetic basis for the variability in handedness.

This main finding has some pretty big implications for both evolutionary biology:

Within evolutionary biology, this is significant for understanding evolutionary trajectories or forces maintaining polymorphisms. An individual drawn from a high-variability genotype has the potential to explore a wider range of phenotypic space than one with a low-variability genotype.

and for understanding human disease (see also Supplementary Figure 5 in the manuscript):

In medical genetics, diseased states emerge beyond a phenotypic threshold, and high variability genotypes will produce a larger proportion of individuals exceeding that threshold than low variability genotypes, even if they have the same mean.

What genes predict variability in handedness? After finding heritability in variability, Ayroles et al went on

to conduct a very tiny (and, admittedly, underpowered GWAS) to try and pinpoint which variants were associated with the heritable variability. One gene, *Ten-a*, which passed their lenient p-value threshold, stuck out from the rest due because of its importance in *Drosophila* sensory integration and locomotion.

The authors used a few methods (RNAi, genetic deficiencies, and null alleles) to validate the effect of this gene on variability in handedness. Interestingly, they found some pretty good evidence linking *Ten-a* to variability in handedness: (i) knocking down (or out) *Ten-a* expression led to increased variation in handedness, and (ii) that this effect, which was measured in adult flies, could be induced by knocking down *Ten-a* expression during a specific 3-day window in development. And this 3-day window corresponded to a spike in *Ten-a* expression during normal fly development.

This study adds to an emerging body of work suggesting that in order to understand variation in complex traits, we must also understand the contribution of intragenotypic variability.

I think that it's fair to say that this manuscript will make pretty big waves once it hits the press.

REFERENCE

Ayroles JF, Buchanan SM, Jenney C, Skutt-Kakaria K, Grenier J, Clark AG, Hartl DL & de Bivort BL (2014) Behavioral individuality reveals genetic control of phenotypic variability, Cold Spring Harbor Labs Journals. [doi: 10.1101/009027](https://doi.org/10.1101/009027)

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About Noah Snyder-Mackler

I'm a postdoctoral fellow in the department of Evolutionary Anthropology at Duke University. Broadly, I study non-human primate genetics and genomics. More specifically, I'm interested in the interaction between behavior, genotype, and gene expression in response to social stress.

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