

# Genetic 'Rosetta Stone' unveiled in Nature

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Scientists have developed a new community resource that may act as a Rosetta Stone for revealing the genetic basis of traits and disease.

A new paper in *Nature* describes the *Drosophila* [Genetic](#) Reference Panel, or DGRP, which provides the highest-resolution view to date of the [genome structure](#) and variation in a population of 192 fruit flies with diverse traits.

The study was led by Trudy Mackay of North Carolina State University, in collaboration with the Human Genome Sequencing Center at Baylor College of Medicine and David Mittelman of Virginia Tech's Virginia Bioinformatics Institute, as well as a large group of researchers around the world.

"One of the grand challenges of biology is to understand how genetic variants and environmental factors interact to produce variation in complex phenotypes such as height, behaviors, and disease susceptibility within populations. This effort has been stymied by the lack of knowledge of all genetic variants in a population of a genetically tractable model organism. The DGRP sequences provide such a resource," Mackay noted.

It's been known for a long time that genes often work in concert to produce different effects, or phenotypes. But determining the exact contribution of these genes and genetic changes within them to animal traits remains a key challenge in genetics.

That's where model organisms like *Drosophila melanogaster* (the common fruit fly) shine. Using inbred strains of [fruit flies](#) in controlled environments, researchers can use whole genome data, which captures genetic changes at the nucleotide level, to better explain why strains exhibit variable traits. The DGRP acts as a “living library” of this information, helping researchers understand both common traits and rare variants.

Mittelman, with support from the NVIDIA Foundation's Compute the Cure Award, aided the study by analyzing genetic variation in the *Drosophila* population. “To truly exploit whole genome sequencing as a means of determining the basis for traits and disease, it is critical to develop methods for detecting all forms of genetic variation. In this study, we developed a method for measuring tandem repeat variation, which has been shown to modulate gene function, traits, and disease,” said Mittelman.

A companion paper describing this method has been recently accepted for publication which will enable others to exploit these tools in their research.

The study has far reaching effects that span animal breeding, pesticide development, and personalized medicine.

Provided by Virginia Polytechnic Institute and State University

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