

# GENOME AND CHROMOSOME EVOLUTION OF *Drosophila* SPECIES OF THE AMERICAS

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The genus *Drosophila* has long served as an important biological model system in evolutionary biology. It is a highly diversified genus in terms of genome size, chromosomal rearrangements, and ecology. The increasingly number of sequenced *Drosophila* genomes provides an opportunity to study diversification at both genomic and chromosomal levels. In this symposium, new studies, taking advantage of sequenced genomes, will address a range of topics. The presentations will concern *Drosophila* species native to the Americas. Cactophilic species of the *D. repleta* group have undergone rapid speciation and adaptation in both North and South America. These species have not only undergone major chromosomal changes, including rearrangements and centromeric differentiation, but adaptive evolution in detoxification and reproduction genes. The repleta group consists of two major radiations, one in North America and other in South America, providing a naturally replicated experiment. One speaker, Dr. Kuhn, will discuss chromosomal evolution in the South American species and another, Dr. Markow, will present about those in North America. Another classic set of species is *D. pseudoobscura pseudoobscura*, *D. p. bogotana*, and *D. persimilis*, from both continents. Their genomes reveal previously unknown patterns of introgression, the topic of the presentation by Dr. Machado. Critical to the rapid advances in genome sequencing is the need to properly assemble and annotate the new genomes so that meaningful comparative studies can be undertaken. Dr. Carvalho's presentation will address these issues.

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## GENOME EVOLUTION AND ADAPTATION IN CACTOPHILIC MEXICAN DROSOPHILA OF THE SONORA DESERT

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Over a hundred *Drosophila* species, primarily belonging to the repleta species group, have adapted to utilize rotting cacti as their breeding sites. These species occur in both North and South America, having undergone separate radiations. In Mexico, the species range from subspecies that utilize different host cacti to species that have diverged many millions of years ago. Each species has had to adapt to the unique chemistry of its own cactus host, and

in addition to the genes involved in these adaptations, the species are also separated by multiple chromosomal inversions. Chromosomal inversions as well as differences in detoxification genes, underly their adaptations and reproductive isolation from their relatives. The species, their evolutionary relationships and the genomic changes that have accompanied their radiation are presented.

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## **THE ROLE OF CHROMOSOMAL INVERSIONS ON PATTERNS OF GENOMIC DIFFERENTIATION IN THE *Drosophila pseudoobscura* SPECIES GROUP**

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Chromosomal inversions constitute an important genetic mechanism that allows species to persist in the face of gene flow. Theoretical models suggest that inversions facilitate the formation or persistence of new species by allowing genetic factors conferring species-specific adaptations or genetic incompatibilities to be genetically linked, which in turn reduces their introgression. These models about the nature of inversions are critical to understanding speciation and can be applied both to cases of primary divergence in sympatry and to the persistence of species following secondary contact. Consistent with those hypotheses, empirical studies across diverse taxa show that chromosomal regions inverted between species often exhibit both a disproportionate fraction of phenotypic variation associated with reproductive isolation and higher sequence divergence than collinear regions, as is the case of the North American sibling species *Drosophila pseudoobscura* and *D. persimilis*. These species constitute a classic model system in speciation research started by T. Dobzhansky in the 1930s. Their divergence started 0.5 to 1 million years ago, and occurred in the face of gene flow, with different genomic regions showing different patterns of introgression. We will present new genome sequence data outlining differences in the genome architecture of the species particularly around inversion breakpoints, and population genomic data describing patterns of genomic differentiation and introgression.

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## **AN IMPROVED GENOME ASSEMBLY FOR *Drosophila navojoa*, THE BASAL SPECIES IN THE MOJAVENSIS CLUSTER**

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Three North American cactophilic *Drosophila* species, *D. mojavensis*, *D. arizonae*, and *D. navojoa*, are of considerable evolutionary interest owing to the shift from breeding in *Opuntia* cacti to columnar species. The 3 species form the “*mojavensis* cluster” of *Drosophila*. The genome of *D. mojavensis* was sequenced in 2007 and the genomes of *D. navojoa* and *D. arizonae* were sequenced together in 2016 using the same technology (Illumina) and assembly software (AllPaths-LG). Yet, unfortunately, the *D. navojoa* genome was considerably more fragmented and incomplete than its sister species, rendering it less useful for evolutionary genetic studies. The *D. navojoa* read dataset does not fully meet the strict insert size required by the assembler used (AllPaths-LG) and this incompatibility might explain its assembly problems. Accordingly, when we re-assembled the genome of *D. navojoa* with the SPAdes assembler, which does not have the strict AllPaths-LG requirements, we obtained a substantial improvement in all quality indicators such as N50 (from 84 kb to 389 kb) and BUSCO coverage (from 77% to 97%). Here we share a new, improved reference assembly for *D. navojoa* genome, along with a RNAseq transcriptome. Given the basal relationship of the *Opuntia* breeding *D. navojoa* to the columnar breeding *D. arizonae* and *D. mojavensis*, the improved assembly and annotation will allow researchers to address a range of questions associated with the genomics of host shifts, chromosomal rearrangements and speciation in this group.

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