Determining the extent of genomic incompatibilities is a pivotal issue in understanding the process of speciation. Here, we present a new perspective by shifting the focus from the species divergence at the DNA sequence level to the fitness and functional aspects of foreign genomic introgression. To illustrate our point, we perform a 20-generation competition experiment between introgressed random genomic segments of *Drosophila sechellia* and their *D. simulans* counterparts in the genetic background of *D. simulans*. The result reveals that, even at the early stages of speciation, there are virtually always detrimental fitness consequences to introducing random foreign elements from one genome to another. This implies that incipient speciation may be characterized by widespread accumulation of genomic incompatibilities rather than a few isolated genes. This study shows that we should move beyond the sterility and inviability assays in order to understand the full extent of genetic incompatibilities during speciation.

**Incompatibility and Competitive Exclusion of Genomic Segments between Sibling *Drosophila* Species**

*Shu Fang, Roman Yukilevich, Ying Chen, David A. Turissini, Kai Zeng, Ian A. Boussy, and Chung-I Wu, PLoS Genetics 2012, 8, e1002795. doi:10.1371/journal.pgen.1002795*

All *Drosophila sechellia* introgressed alleles in the genetic background of *D. simulans* rapidly decrease in frequency.