

When natural selection relaxes, genomes expand in flies!

A study carried out at LBBE, to be published in Molecular Biology and Evolution, reveals that mobile genetic elements accumulate in Drosophila genomes when natural selection becomes less effective, resulting in an increase in genome size.

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The size of genomes, i.e. the quantity of DNA in cells, which varies enormously between animals, essentially reflects the quantity of mobile genetic elements capable of replicating in genomes, often referred to as 'junk DNA'. Why do some species have larger genomes than others? Why do some species bear more junk DNA than others? French researchers have explored this question in flies of the genus Drosophila, relatives of the famous vinegar fly, a model organism in biology. The researchers analyzed the genome content of 76 Drosophila species, including 40 newly sequenced ones and estimated the strength of natural selection (through the analysis of over 2,000 genes). Their findings show that when natural selection is less effective — for example, in small populations — mobile genetic elements called transposable elements accumulate in greater numbers in genomes. This leads to a significant expansion in genome size. These results confirm a key prediction of the "nearly neutral" theory of evolution: in smaller populations, slightly harmful mutations — such as the insertion of these mobile elements — are more likely to escape natural selection and persist in the genome simply by chance, passed down from generation to generation. This discovery brings back into focus the importance of randomness (genetic drift) versus selection in the evolution of genome size.

More details in the full publication:

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