# Evolutionary advantage of genetic recombination in the genome measured for first time

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UAB researchers have quantified one of the most important and hard-to-measure phenomena in molecular evolution: the effect of genetic recombination on a species' capacity of adaptation. The Genomics, Bioinformatics and Evolution research group, in collaboration with researchers in the universities of Sussex and Edinburgh, have quantified one of the most important and hard-to-measure phenomena in molecular evolution: the effect of genetic recombination on a species' capacity of adaptation.

There has been much discussion of the evolutionary role of genetic recombination: the exchange of parental genetic material that gives rise to new genetic combinations in offspring. Recombination is a practically universal phenomenon in living beings. In sexual organisms recombination occurs during the process of meiosis, which produces the sexual cells, and maintenance of this sophisticated mechanism, which systematises recombination to the whole genome, is the usual reason given for the preponderance of sex. But what exactly is the advantage of recombination? This work shows that genetic recombination facilitates adaptation and it estimates the evolutionary cost of its absence or depletion in a genome for the first time.

The fate of a new mutation in a genome is conditioned not only by the adaptive advantage or disadvantage that the mutation brings to its bearer, but also by the chromosomal context in which it appears. If a new

selected mutation is surrounded by others that are also exposed to selection, these mutations will interfere (compete) with each other as they do not segregate independently, so that joint selection will be less efficient than if selection acts on each mutation separately. This linkage cost, also known as Hill-Robertson interference after its discoverers, makes natural selection less efficient when it acts simultaneously on different linked sites.

In a previous work published in the journal *Nature*, the authors drew the first high-resolution map of the natural selection of a genome and proved that natural selection is ubiquitous in the genome of the species used as a model in genetics: the fruit fly Drosophila melanogaster. One implication of these findings is that at any one moment there will be linked genetic variants, exposed simultaneously to selection in the genome, and therefore selection will be sub-optimal due to the linkage cost. How can this cost be proved to really exist and, in particular, how can it be measured?

If linkage cost exists, wherever recombination is low there will be a greater density of selective variants that do not segregate freely, lowering the efficiency of the selection and therefore the adaptation rate. On the other hand, the regions of greater recombination will present higher adaptation rates. The first objective of the study was to determine whether the regions with a greater recombination rate experienced a higher genomic adaptation rate. To measure the genomic adaptation the researchers used sophisticated statistical methods from population genetics applied to data on genomic variation. The results showed a very positive correlation between recombination and adaptation, corroborating the existence of the linkage cost in the genome.

The surprise came when it was seen that the initially linear relationship between recombination and adaptation converged towards an asymptotic threshold as from recombination values equal to or above 2 cM/Mb

(centimorgans per megabase). This asymptote indicates that there is a threshold recombination value beyond which genomic adaptation reaches a maximum.

The existence of this threshold has two important consequences: (1) the linkage cost disappears beyond a recombination value, or in other words, the selected mutations act as if in practice they segregated independently. An infinite rate of recombination would not increase the adaptive rate of the genome more than a recombination value of 2 cM/Mb (the estimated threshold recombination). (2) the asymptote sets an optimal ceiling for the adaptation rate of a genome, its value being an estimation of the optimal adaptation rate, in the absence of the linkage cost.

Having defined the optimal situation, it is possible to estimate the linkage cost of a genome by analysing it. The researchers found that the D. melanogaster genome has an adaptation rate around 27% below the optimal adaptation rate, the rate it would have if the effects of the mutations did not interfere with one another.

This work, to be published next January in the prestigious journal *Molecular Biology and Evolution* also involved the study of other genomic determiners, like the rate of mutation and gene density over the rate of genomic adaptation. The Genomics, Bioinformatics and Evolution research group is formed by Sergi Hervás, Sònia Casillas, Marta Coronado, Isaac Noguera, David Castellano (lead author of the paper) and Antonio Barbadilla (principal researcher).

The genomics era has provided one of the most surprising examples of the power of natural selection, allowing us to detect the characteristic imprints that natural selection leaves on the genome. This work is also yet another step in the measurement of natural selection at the nucleotide, gene or genome level, as it addresses the question of how the

genomic context, whether the current rate of [recombination](#) or the rate of mutation, conditions the efficiency of [natural selection](#). The era of population genomics we are living in brings the promise of finally revealing the real nature of genetic variation.

Provided by Universitat Autonoma de Barcelona

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