



MOLECULAR EVOLUTION

Rearrangements for fitness

Chromosomal rearrangements can alter the karyotype of an organism without necessarily modifying the coding sequence. Their contribution to fitness has never been directly tested, as these rearrangements are accompanied by other genetic diversity in natural populations. A recent study in the fission yeast *Schizosaccharomyces pombe* has found that genome architecture is a selectable trait that interacts with the environment.

Avelar *et al.* observed natural karyotypic variation in wild *S. pombe* strains that results from chromosomal rearrangements, which led them to question how this type of genetic variation is maintained in these populations. Rearrangements that are maintained in the wild are not only associated with other forms of genetic diversity but are also the product of selection. To avoid these issues, the authors generated a strain in which rearrangements were engineered onto a standard genetic background. Surprisingly,

the rearrangements conferred meiotic defects on the engineered strain, which contradicted the maintenance of these rearrangements in wild populations.

To further probe why genomic rearrangements are maintained, the authors then assayed the rearrangement strain for growth defects under varying environmental conditions, including temperature and pH. The rearrangements conferred fitness effects that varied according to environmental conditions and were advantageous under some conditions; thus, there was a strong gene–environment interaction that overcame the meiotic defect.

The authors were then intrigued to know whether these advantageous rearrangements are destined to be fixed within the population. Under conditions that promoted asexual reproduction, the frequency of these rearrangements increased in mixed populations of wild-type and genetically rearranged cells. However, if sexual reproduction was allowed, then the frequency of the rearrangements was

close to its initial levels. Thus, the authors propose that this ‘antagonistic pleiotropy’ — the trade-off between growth and meiotic phenotypes — is able to maintain low-frequency chromosomal rearrangements in wild populations. Strikingly, maintenance of the rearrangements was dependent on their initial frequencies, and fixation may therefore depend on population structure in the wild.

Through a quantification of mRNA transcripts, the authors showed that gene expression patterns were globally altered. Thus, they suggest that these alterations in gene expression confer the resultant fitness effects.

This analysis suggests why chromosomal rearrangements are maintained in wild populations: the disadvantageous effects in meiosis are overcome by increases in fitness during mitotic growth. Whether these effects then have a role in speciation remains to be seen.

Hannah Stower

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ORIGINAL RESEARCH PAPER Avelar, A. T. *et al.* Genome architecture is a selectable trait that can be maintained by antagonistic pleiotropy. *Nature Commun.* <http://dx.doi.org/10.1038/ncomms3235> (2013)