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► **COVER:** 'Nouveau niche' by Patrick Morgan, inspired by the Perspective on p725.



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**D**iverse mechanisms contribute to evolution at the levels of genes and genomes, but we are far from a complete understanding of their relative importance. Three articles in this issue look at very different processes that have shaped eukaryotic genomes.

The duplication of entire genomes has the potential to contribute to evolution in several ways. But the retention of whole-genome duplications seems to have been rare, which has led to the suggestion that they are an evolutionary dead end. In their Opinion article on p725, Van de Peer and colleagues argue instead that whole-genome duplications offer important evolutionary opportunities, but that these only come into play following dramatic ecosystem upheavals.

Another mechanism that can have widespread effects on genomes is the activity of transposable elements. As Cordaux and Batzer discuss in their Review on p691, increasing evidence suggests that retrotransposons have markedly affected human gene and genome evolution. The extent of this contribution will be revealed as more human and non-human primate genomes are characterized using high-throughput technologies.

Less widely appreciated is the potentially large impact of erroneous protein synthesis on evolution, as discussed by Drummond and Wilke in their Review on p715. Further work will be needed to determine the rate at which these errors occur and to understand how cells cope with and even take advantage of them.

This issue also contains the first of a series of articles on the applications of next-generation sequencing technologies (<http://www.nature.com/nrg/series/nextgeneration>). The Review by Park on p669 explores the advantages of ChIP-seq for profiling patterns of protein binding and histone modification across genomes.

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