

HIGHLIGHTS

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GENOMICS

Neurospora: ripped from the headlines

Without model organisms, there would be no genetics as we know it today. Thanks to the relatively new field of genomics, we are now pairing the genetic code of our favourite organisms with years of research from classical genetics. So, it is fitting that in the 24 April issue of *Nature*, almost exactly 50 years after the publication of the structure of DNA, we learn the genetic code of one favourite model organism — *Neurospora crassa*.

The filamentous fungus *Neurospora*, the genome of which is 40 Mb and encodes ~10,000 proteins, has been studied by geneticists for almost a century, and unwittingly grown by many people as common orange bread mold. Beadle and Tatum used *Neurospora* for their Nobel-Prize-winning 'one gene, one enzyme' hypothesis in the 1940s. More recently, *Neurospora* has enjoyed a renaissance as an epigenetic model, owing to its fascinating defence mechanism against gene duplication. This phenomenon, known as repeat induced point mutation (RIP), has presumably had profound effects on the genomic history of the fungus. Within one passage through a sexual cycle, newly duplicated sequences larger than ~400 base pairs undergo CpG methylation throughout, resulting in as many as 30% of the cytosines being mutated on replication.

Cytosine methylation is just one feature that *Neurospora* shares with higher organisms; the genome sequence shows it also has a detailed

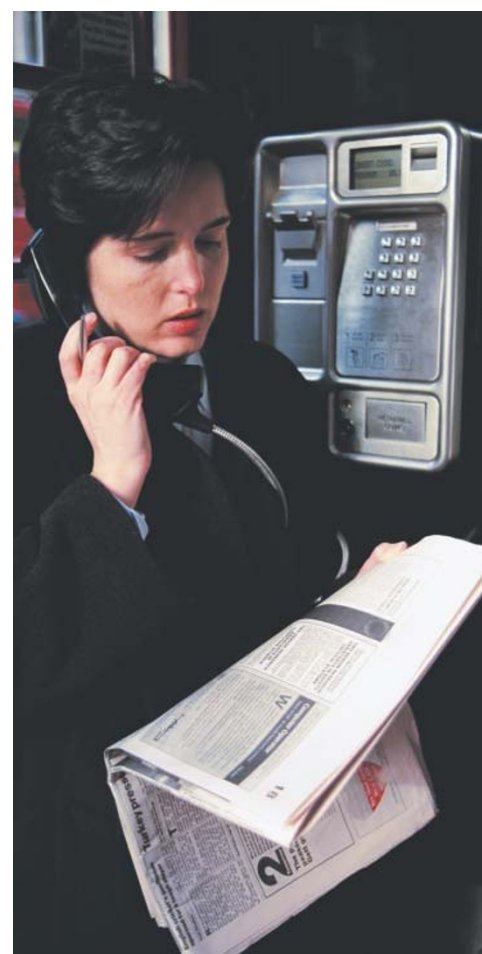
circadian-rhythm system and complex signalling networks, which possibly include the existence of an extracellular cAMP signalling pathway never before seen in any fungi. Yet compared to other organisms the genomes of which have been sequenced, *Neurospora* has almost no similar genes in multigene families. In their analyses of the genome, Galagan *et al.* propose that the particular rapid mutation unique to RIP has forced the fungus to evolve not by duplicating its genes, as many organisms do, but instead by inventing new genes with little similarity to each other.

But evolution is often a war, and the organism gains from RIP the ability to fight off invading DNA. In an accompanying work, Selker *et al.* isolate the methylated component of the *Neurospora* genome, and conclude it is made up almost exclusively of RIPped sequences. In effect, the genome is littered with the debris of potential invaders, such as retrotransposons, which have all been RIPped to death. So, the fungus might have traded the protection of its current genome for the possibility of evolving into who knows what? We will soon know more, as researchers come full circle in translating the genomic information into new studies of this old friend.

Chris Gunter,
Associate Editor, *Nature*

References and links

ORIGINAL RESEARCH PAPERS Galagan, J. E. *et al.* The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature* 24 April (2003) (10.1038/nature01554) | Selker, E. U. *et al.*



The methylated component of the *Neurospora crassa* genome. *Nature* 24 April (2003) (10.1038/nature01564)

WEB SITES

Whitehead Neurospora database: www-genome.wi.mit.edu/annotation/fungi/neurospora
Neurospora at the Fungal Genetics Stock Center: <http://www.fgsc.net/ncrassa.html>
NCBI Neurospora genome: www-genome.wi.mit.edu/annotation/fungi/neurospora