GENOME EVOLUTION

Long way for a shortcut

The easiest way to create new genes is to duplicate the ones that are already there, and the quickest way of doing this for many of them is to duplicate the whole genome. This can then be shrunk back down to its previous size while sporting a new collection of genes. This simple theory, which Susumo Ohno proposed more than 30 years ago, has now been validated in yeast by 2 groups that have compared the genome of the most commonly studied member of this taxon, *Saccharomyces cerevisiae*, with that of its two close relatives.

Finding conclusive evidence of whole-genome duplication (WGD) in *S. cerevisiae* has been a fruitless task, as most duplicated regions have diverged beyond recognition. What is needed is a yeast species that diverged from *S. cerevisiae* before the duplication took place — because if WGD really occurred, any one region in this species would have two corresponding regions in *S. cerevisiae*. As one of almost any two duplicated genes in *S. cerevisiae* has been lost as the genome returned to its pre-duplication size, regions of homology for each ancestral segment would alternate between the two copies in *S. cerevisiae*. This pattern is exactly what was seen in the genomes of the yeasts *Kluyveromyces waltii* and *Ashbya gossypii*, which were sequenced and analysed by Manolis Kellis and co-workers and by Fred Dietrich and colleagues, respectively.

Kellis *et al.* identified 253 blocks in *K. waltii* that could each be matched to two regions in the *S. cerevisiae* genome. These blocks — which tiled 85% of the *K. waltii* genome and were spread across all chromosomes — were then used to match up the long sought-after sister regions in *S. cerevisiae* that evolution had caused to drift apart. A total of 145 such

sister blocks were found, corresponding to 457 gene pairs. So here is the first conclusive evidence that WGD occurred in yeast — but what happened next? Of the 457 gene pairs, 17% evolved more quickly than their counterparts in *K. waltii*, and the fact that most cases of accelerated evolution involved only one of the gene duplicates supports the popular idea that duplication leaves one gene copy free to diverge.

The sequencing and genome annotation of *A. gossypii* by Dietrich *et al.* led to the same conclusion. Ninety-five percent of all open reading frames in *A. gossypii* have homologues in *S. cerevisiae* and most of these are arranged in a conserved linear order. These syntenic regions were used to build a detailed map of ancient *S. cerevisiae* gene order that also provided definitive proof for the occurrence of WGD in the *S. cerevisiae* lineage after it split from its common ancestor with *A. gossypii*.

This work has settled the long-standing controversy over how to interpret the presence of duplicated blocks in the *S. cerevisiae* genome: are they evidence of WGD or were they caused by local duplications? Although Ohno's idea was an appealing one, it didn't necessarily describe the most plausible means of evolutionary innovation — after all, WGD takes the genome for a rather rocky ride. Now that this case has finally been closed, researchers can turn their attention to resolving similar issues in vertebrates, where the debate is still alive.

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References and links

ORIGINAL RESEARCH PAPERS Kellis, M. *et al.* Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae*. *Nature* 7 Mar 2004 (doi:10.1038/nature0224) | Dietrich, F. S. *et al.* The *Ashbya gossypii* genome as a tool for mapping the ancient *Saccharomyces* genome. *Science* 4 Mar 2004 (doi:10.1126/science.1095781)

IN BRIEF

EVOLUTION

Dispersed male networks in western gorillas.

Bradley, B. J. *et al. Curr. Biol.* **14**, 510–513 (2004)

Kin-selection theory, which is used to explain in evolutionary terms why individuals tend to favour relatives, has rarely been seen as relevant to interactions among social groups. Bradley and her colleagues typed groups of western gorillas at ten microsatellite loci. Single males leading social groups were usually related to nearby males. So, kin-selection might explain why interactions between males from different groups are often non-aggressive and why male western gorillas (and humans) tend to remain near to where they were born.

PLANT GENETICS

The wheat *VRN2* gene is a flowering repressor down-regulated by vernalisation.

Yan, L. *et al. Science* **303**, 1640–1644 (2004)

Prolonged exposure to low temperatures (vernalization) is required to prompt flowering after winter in wheat varieties that are planted in autumn. *VRN2* is the key gene that represses flowering until spring in such varieties. Yan *et al.* mapped *VRN2* in wheat to a region that contained three candidate genes. Confirmation that one of these (*ZCCT1*) was *VRN2* came from wheat and barley strains in which its expression was absent or knocked-down: these strains do not require vernalization for flowering.

DEVELOPMENTAL GENETICS

Control of fruit patterning by *INDEHISCENT*.

Liljegren, S. L. & Roeder, A. H. *et al. Cell* **116**, 843–853 (2004)

The *Arabidopsis thaliana* fruit grows after fertilization and encases the growing seeds. The seeds are dispersed when the seedpod opens and a spring-loaded mechanism scatters them. This paper reports the characterization of the *INDEHISCENT* (*IND*) gene, which was identified in a genetic screen for mutants that affect seed dispersal and that encode an atypical bHLH protein. *IND* is required for patterning the three cell types that are needed for fruit opening, which was previously believed to directly require the gene *FRUITFULL*.

TECHNOLOGY

Controlling transgene expression to study *Xenopus laevis* metamorphosis.

Das, B. & Brown, D. D. *Proc. Natl Acad. Sci USA* **101**, 4839–4842 (2004)

To extend the application of sperm-mediated transgenesis in *Xenopus laevis*, Das and Brown have used two well-known binary-inducible gene-expression systems (one controlled by doxycyclin and the other by a progesterone analogue). *X. laevis* that carry inducible lethal transgenes can now be grown to maturity and bred to produce F₁ progeny; the transgenes can then be induced when required.