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GENOMICS

Slimy mucus? Decode it, idiot!

The amoeboid protozoan *Dictyostelium discoideum* is a strange beast, not just for its ability to transform from a unicellular to a multicellular state, but because, for a simple model organism, it carries many genes homologous to those of higher eukaryotes. For 50 years, this species has helped to shed light on basic cellular processes such as signalling, motility, adhesion and interaction. Now, with the sequencing of its 34-Mb genome, it could further aid the understanding and application of these processes in medical research, as well as answering fundamental questions about multicellular development. And, as one of the authors notes, the anagram of its name (see title) was auspicious for the whole project.

Dictyostelium discoideum has six chromosomes, but hereditary information is also contained on a multicopy 90-kb extrachromosomal element (which carries the rRNA genes) and a 54-kb mitochondrial genome, both of which have already been sequenced. This makes the *D. discoideum* genome 10 times larger than that of bacteria and three times the size of the yeast genomes sequenced so far. The International Sequencing Consortium shotgun-sequenced each of the chromosomes separately, and in the process had to overcome the challenge presented by the high (78%) A + T content of the DNA. The predicted number of genes (~12,500) is nearer to that of many higher eukaryotes, and a rela-

tively high proportion of the genome (62%) codes for proteins.

Surprisingly, over a third of the predicted *D. discoideum* proteins contain repetitive tracts of amino acids — a higher abundance than in any other sequenced organism. In humans, such repeats are associated with many diseases, making an understanding of these repeats and their functional consequences in *D. discoideum* an attractive goal. Roughly 3% of the genome seems to be involved in the production and export of many small molecules involved in defence and signalling — a rich seam of secondary metabolites which invites further study.

The phylogeny that the authors infer from the complete proteome extends earlier findings and shows that *D. discoideum* diverged from animals before animals diverged from fungi (and, contrary to many previous theories, after they diverged from plants). The proteins shared by these four taxonomic groups point to common mechanisms of cell movement, cell differentiation and tissue organization. The high number of these shared proteins indicates that their common ancestor had a larger genome than was previously thought.

The completion of the *D. discoideum* genome sequence is expected to lead to further advances in several research areas — its relatively complex genome and position on the evolutionary tree mark it out for comparative studies, whereas the cel-

lular mechanisms and developmental pathways it shares with higher eukaryotes lend themselves to the study of many human diseases.

David Stevens

References and links

ORIGINAL RESEARCH PAPER Eichinger, L. *et al.* The genome of the social amoeba *Dictyostelium discoideum*. *Nature* **434**, xxx–xxx (2005) [page nos to come]

WEB SITE

dictyBase: <http://dictybase.org>



Image courtesy of Paul Dear, MRC Laboratory of Molecular Biology, Cambridge, UK