

Fungi and the bare necessities of life

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Sometimes progress in mycology is so significant that it contributes to understanding in the wider scientific arena. To reflect this, an *ad hoc* series of articles will be published in the *Mycologist* outlining examples of when this has occurred. This, the first of these articles, examines work by Katinka and co-workers who have published a summary of findings about the genetic code (genome sequence) of the fungal parasite *Encephalitozoon cuniculi* (*Nature* 414: 450-453; 22/11/2001). Katinka *et al.* found that although fungi are complex organisms, the cellular machinery required to make a fungus can be very simple.

Encephalitozoon cuniculi is an obligate intracellular parasite that infects many animals, including man. It has a biphasic life-cycle, alternating between a wall-less phase and walled spores. Germinating spores inject their contents into host cells. Although *E. cuniculi* was originally thought to be a 'primitive' protist, early molecular studies indicated that it was really a fungus in disguise. It has long been known that *E. cuniculi* had dispensed with many of its metabolic functions, lacking the cellular structures required for normal respiration (mitochondria) and stress management (peroxisomes). An inspection of the complete genetic code of this organism provides some remarkable insights into how such a reduction has been achieved and what the limits are on coding capacity.

From the complete genetic sequence, researchers have reconstructed the organism's metabolic capabilities. The sequence encodes most of the enzymes known to be required for the replication of the genetic material. However, there is no evidence of the genes present in most other organisms that are required to replicate viruses. The code also contains rudimentary information for the metabolism of chitin, biosynthesis of cell wall materials (including the capacity for N-glycosylation and o-linked mannosylation), trehalose metabolism and a polarized secretory apparatus, all underpinning a fungal affinity for this organism.

By virtue of its parasitic life-style, many metabolic functions have been dispensed with; there are hardly

any genes for amino acid, nucleic acid or fatty acid biosynthesis. To compensate for such deficiencies there are genes for many different classes of transporter protein. Surprisingly, some components of the mitochondrial apparatus are still required, but there is no respiratory electron transport chain as such. The absence of many genes normally associated with cell signalling is particularly intriguing – hinting at the relatively small number of regulatory steps that need to be integrated in order to produce a 'complex' functional cell.

Remarkably, even the gene sequence of this organism has been stripped to the bare essentials. The full sequence is only 2.9 million bases in length (compared to about 4.6 million bases in the bacterium *Escherichia coli* and 16 million bases for yeast) and encodes for only 1,997 proteins (cf 6500 in yeast; 30,000+ in humans). There is no room for 'junk' in the sequence. The average distance between genes is very short (only 129 bases), and even the genes themselves are short (typically 15% shorter than their counterparts in yeast).

The paper is just one of many where fungal biology is leading the way forward in addressing fundamental questions in the life-sciences. Whilst several research groups have set out to experimentally identify the minimum set of instructions required to build an organism, it would appear that a 'simple' fungus is already able to provide the answer.

Reference

Katinka, M., Duprat, S., Cornillot, E., Méténier, G., Thomarat, F., Prensier, G., Barbe, V., Peyretaillade, E., Brottier, P., Wincker, P., Delbac, F., El Alaoui, H., Peyret, P., Saurin, W., Gouy, M., Weissenbach, J., & Vivarès, C.P. (2001). Genome sequence and gene compaction of the eukaryote parasite *Encephalitozoon cuniculi*. *Nature* **414**: 450-453.

Further information about this paper can be found on the *Nature* website at <http://www.nature.com>