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How microsporidia evolve

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Genomes within a group of eukaryotic obligate intracellular parasites - the microsporidia - are changing very slowly, even as the genes within them are evolving at a "strikingly high" rate, according to a study in the latest edition of Current Biology. The evolution of eukaryotic genomes usually correlates with the rate of sequence evolution, but the results of this study show that genomes do not necessary evolve in a clock-like fashion, say the authors (*Curr Biol* 2004, **14:**891-896).

Patrick Keeling at the University of British Columbia and colleagues randomly sequenced 685,000 base pairs of the microsporidian *Antonospora locustae* genome. They compared the organization of 183 genes found there with the recently completed genome sequence of the distantly related human parasite *Encephalitozoon cuniculi,* also a microsporidium. The degree of conservation of gene order between the two species was measured as the percentage of gene couples - pairs of genes adjacent to each other - that were couples in both species.

In over 94 *A. locustae* gene couples, 13% were also adjacent in *E. cuniculi*, an additional 17% were close neighbors in *E. cuniculi*, and 43% of the *A. locustae* couples are located on the same chromosome in *E. cuniculi.* The level of gene order conservation between these microsporidia (13%) is almost 1.5-fold higher than that between *Saccharomyces cerevisiae* and *Candida albicans* - 9% - ascomycetes that are the closest relative to the microsporidia and that the authors say can provide a valid comparison of the data.

Moving genes around is a random process, so one would guess that the organization of two distantly related genomes would be completely randomized, said Keeling. "The overall genome structure was maintained a lot more than we would have expected," he said.

In contrast, the levels of sequence conservation between microsporidian SSU rRNA are 10-fold lower than those between *C. albicans* and *S. cerevisiae.* "There's a bit of a paradox in these genomes, that at one level the genes themselves are evolving very rapidly, but then the whole genome as an entity of itself is evolving very slowly," Keeling said.

Keeling said that this was likely to be a function of the force of compaction in these specialized reduced genomes because genome reorganization - a stochastic process - requires sequences to be broken. "Finding a place in [the microsporidial] genome to break is virtually impossible, because... if you just throw darts at the genome, everywhere you hit is important," he said.

The team's conclusions are reinforced by the fact that the comparison between the 183 genes of *A. Locustae* - 5.4 megabase pairs in size - and the 2,000 genes of *E. cuniculi* (2.8 megabase pairs) shows a similar gene density, Christian P. Vivarès, program director at the Centre National de la Recherche Scientifique at the University of Clermont, France, told us in an E-mail.

But Laurence D. Hurst said that this paper merely repeats on a small scale the work published by his own group 2 years ago. "What we did was more or less what [the authors] did, only we did it on a whole genome, comparing yeast [*S. cerevisiae*] to C*andida* [*albicans*]," said Hurst, professor of evolutionary genetics at the University of Bath.

"I have shown previously that in yeast, the probability that two genes that reside as pairs are also pairs sitting next to each other in *Candida* (400 million years away) is strongly coupled to the degree of regional compaction of the genome - for example, intergene distance is a very strong predictor," Hurst, who was not involved in the study, wrote in an E-mail. "Overall, then, we expect a relationship between genomic compaction and the degree of rearrangement within and between genomes."

But Keeling said that the paper showed something "quite different" - that "it may be a minor effect in yeast and *Candida,* but it's probably a major effect when you start ratcheting down your genome size by compaction."

References

1. *Current Biology*, [http://www.current-biology.com]

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4. Laurence D. Hurst, [http://www.bath.ac.uk/bio-sci/hurst.htmc]

5. Natural selection promotes the conservation of linkage of co-expressed genes