

MITO COMMUNICATION

Mito-communications

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Adding insult to injury: Transmissible cancer captures host mitochondrial genomes

Canine transmissible venereal tumour (CTVT) is a single-celled asexual cell lineage that causes cancer in various canines, and is one of only three known infectious cancers. Analysis of CTVT's nuclear genome shows that it is derived from a single canine cancer that existed around 6000 years ago (Rebbeck et al. 2009).

However, a recent analysis of CTVT mitochondrial genomes showed a surprising pattern (Rebbeck et al. 2011). Instead of forming a monophyletic group, CTVT mitochondrial genomes are scattered throughout the canine family tree (Rebbeck et al. 2011). That is, CTVT mitochondrial genomes are often more closely related to the mitochondrial genomes of their host canines than they are to each other.

The best explanation for this pattern is that CTVT lineages occasionally capture mitochondrial genomes from their hosts (Rebbeck et al. 2011). The reasons for this capture remain elusive, but the authors suggest

that it may occur because the drastic change from a free-living mammal into a pathogenic cancerous cell lineage has caused significant problems for CTVT in maintaining its mitochondrial genome. Mitochondria are the metabolic powerhouses of mammalian cells, and as a result their genomes are constantly exposed to damaging mutagens. Most mammals get around this problem by keeping a few copies of their mitochondrial genomes out of harm's way in the germ-line tissue. However, CTVT does not have a separate germ line and so its mitochondrial genomes are constantly exposed to damaging mutagens. This can lead to high mutation rates and a gradual loss of fitness. Thus, CTVT may gain fitness by occasionally replacing its own damaged mitochondrial genomes with those of its closely related hosts.

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Evolutionary diversification of birds in the Cretaceous

The fossil record indicates that most of the extant orders of birds first appeared in the early Palaeogene, leading to the hypothesis that birds underwent an evolutionary radiation after the mass extinction of

reptiles and other organisms at the end of the Cretaceous (Feduccia 1995). Numerous studies have tested this hypothesis using molecular-clock analyses of DNA sequences, with overwhelming support for gradual divergences among avian orders throughout the Cretaceous (e.g. Pereira and Baker 2006; Brown et al. 2008). However, the poor phylogenetic resolution among orders, even in analyses of large

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nuclear data sets (Hackett et al. 2008), is suggestive of a rapid radiation. This is similar to the situation observed for the origins of metazoan phyla at the base of the Cambrian (Rokas et al. 2005).

Pacheco et al. (2011) have recently revisited this issue by conducting a phylogenetic analysis of 80 complete mitochondrial genomes, 17 of which were newly sequenced. They concentrated on the neognaths, with the largely flightless ratites being excluded from their analyses. Most of the inferred inter-ordinal relationships were consistent with those obtained in previous phylogenetic studies of birds (e.g. Hackett et al. 2008). Unexpectedly, however, the authors found a sister relationship between shorebirds and pigeons, and between owls and parrots.

Pacheco et al. (2011) used several relaxed-clock dating methods to estimate the timescale of avian evolution. They found that basal divergences in Neoaves occurred in the Cretaceous; 22 lineages were estimated to have crossed the Cretaceous–Palaeogene boundary, surviving the Chicxulub impact. This points towards a gradual diversification of avian orders long before their appearance in the fossil record.

Substitution rates were found to vary substantially among lineages. This supports previous criticisms of the “universal avian mitochondrial clock”, which posits the existence of a constant substitution rate of approximately 1% per million years among avian

lineages (e.g. García-Moreno 2004). Of the protein-coding genes, *cox1* exhibited the least variation among lineages, but the standard deviation of the rate was still 23.7% of the mean.

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