

## Mito-communications

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### Understanding the origin of doubly uniparental inheritance in bivalves

In most animal species, offspring of both sexes inherit their mitogenome from their mother, whereas the father's mitogenome is never passed on. However, some bivalves have an intriguingly different mode of transmission known as doubly uniparental inheritance (DUI). In species with DUI, offspring of both sexes inherit the mother's mitogenome, but male offspring also inherit the father's mitogenome. Thus, males carry both the female-transmitted (F) and male-transmitted (M) mitogenomes, which predominate in the somatic and gonadal tissues, respectively (Garrido-Ramos et al. 1998).

In a new paper, Doucet-Beaupré et al. (2010) report the sequencing and analysis of six complete mitogenomes from three bivalve species that show DUI (i.e. they sequenced an F and an M genome from each species). A careful phylogenetic analysis, combined with consideration of the difficulty of evolving such an unusual mode of mitogenomic transmission, led the authors to suggest that DUI probably arose only once within the bivalves, but was lost at least three times.

The sequenced M mitogenomes show some unusual characteristics relative to the F mitogenomes, including an extension of the *cox2* gene (see also Walker et al. 2006) and a minor difference in the gene order. It would be fascinating to know whether these differences confer any advantages to the M

mitogenome (perhaps as a result of its limitation to only a few tissues) or whether they are simply the result of a reduced effective population size or relaxed selective constraint.

Doucet-Beaupré et al. (2010) found the astounding result that the average amino acid identity between the F and M mitogenomes is only 50%. That is, a single male individual from each of the studied species will be carrying two mitogenomes that differ at approximately 50% of the amino acid positions. It is not yet known how both of these apparently very different mitochondrial genomes manage to interact successfully with the nuclear genome. But this observation suggests that the DUI system of some bivalves may hold some interesting clues to understand how mitonuclear interactions operate.

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## Mitogenomic sequence from an ancient polar bear

The polar bear (*Ursus maritimus*) is one of the more well-known and charismatic members of the ursid family. Public interest in the polar bear has increased dramatically in recent times, with the species assuming a symbolic role in the context of anthropogenic climate change. A number of molecular studies have confirmed its status as comprising a subgroup of the brown bear (*Ursus arctos*), although the two are recognised as distinct species on the basis of various criteria.

Lindqvist et al. (2010) have sequenced the complete mitogenome of the oldest known sample of a polar bear, dated to about 110,000–130,000 years before present. The ancient specimen, which was discovered in the Svalbard archipelago, also represents the oldest dated material from which a complete mitogenome has been sequenced (for a recent review of ancient mitogenomic sequences, see Ho and Gilbert 2010).

To elucidate the phylogenetic placement of this ancient polar bear and to estimate the evolutionary timescale of the species, Lindqvist et al. (2010) sequenced six additional mitogenomes from modern polar bears and closely-related brown bears. This allowed the authors to produce an accurate and comparatively precise estimate of the timing of the origin of the polar bear lineage, improving upon other recent attempts that were based either on a fragment of the mitochondrial D-loop (Ho et al. 2008; Korsten et al. 2009) or on small number of representative mitogenome sequences sampled across ursid species (Yu et al. 2007; Bon et al. 2008; Krause et al. 2008).

The phylogenetic analysis of these sequences is particularly fascinating, showing that the ancient polar bear lies very close to the estimated timing of polar bear speciation. This might be a consequence of a bottleneck at speciation, which greatly increases the probability of concordance between genetic and

population divergence. Moreover, the ancient specimen has clear diagnostic features that confirm its alliance with extant polar bears, suggesting that morphological and physiological evolution was rapid and took place over a few tens of thousands of years.

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