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NEWS AND COMMENTARY

Mitochondria and the W chromosome

Low variability on the W chromosome in birds is more likely to indicate selection on mitochondrial genes

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The energetic efficiency of mitochondria in birds capable of flight (Hickey, 2008) frames two predictions to test whether avian mitochondria are responsible for the low variation of the W chromosome of birds, rather than being passive victims of maternal linkage, as concluded by Berlin *et al*. (2007).

There is a general, erroneous, assumption that mutations in mtDNA are not subject to intense selection; that mitochondrial genes do no more than 'housekeeping'. Yet efficient respiration is crucial for cells, and inefficiencies are punished directly through the loss of cytochrome *c* and apoptosis. As Bazin *et al*. (2006) point out, 'mtDNA appears to be anything but a neutral marker and probably undergoes frequent adaptive evolution'.

The mitochondrial genome is practically immune to decay over evolutionary time, despite a mutation rate that is 10–20 times faster than nuclear genes in vertebrates, and little, if any, recombination. Obviously, birds fly as well now as they did 65 million years ago, and need pristine mitochondria to do so. The mitochondrial genome presumably evades decay because it is small and under intense selection pressure. Such selection presumably operates during early embryonic development, where mitochondrial function apparently determines whether an embryo develops further or is eliminated (Dumullard *et al*., 2007).

The question is, why, in birds, is there so little variety on the W chromosome? In an earlier paper, Berlin and Ellegren (2004) express puzzlement, and argue for a selective sweep (but exclude sexual selection) on the W chromosome. They tested this idea in the present paper, arguing that a selective sweep on the W chromosome should be reflected, via strict maternal linkage, in a lower variation of mitochondrial DNA. But as Marais (2007) observes in a commentary, the same argument applies equally in reverse—strong selection on mitochondrial genes should purge the W chromosome of variation.

The high energy demands of flight must place a stronger selection pressure on mitochondrial genes than that occurs in flightless animals. The aerobic power of flight muscle in bats and birds is 2.5–3 times greater than that of non-flying mammals of similar size (Maina, 2000). This extreme aerobic capacity is attained partly by increasing the number of respiratory complexes, and optimizing the kinetic properties of key respiratory enzymes. The closer that respiratory function approaches an optimum, the less variation one would expect in mtDNA (either from 'genetic draft' or purifying selection). Restricted variation is exactly what Berlin *et al*. (2007) report.

In the context of optimizing mitochondrial genes for high aerobic capacity, it is an interesting possibility that low rates of free-radical leak in birds (Barja, 2007; Lambert *et al*., 2007) may have evolved in part to preserve mtDNA adaptations for flight in the face of Hill–Robertson effects; low free-radical leak would then contribute incidentally to the exceptional longevity of birds and bats.

Because the respiratory complexes are encoded by two genomes that must work together (the nuclear and mitochondrial genomes) there is generally very strong selection for intergenomic coadaptation (Burton *et al*., 2006). Optimizing the sequence of mtDNA counts for nothing if the nuclear genes are not under equally stringent selection. This leads to a specific prediction: in birds there should be less variation in nuclear genes that encode mitochondrial respiratory proteins, regardless of chromosomal location. Such restricted variation should apply most to subunits that interact directly with mitochondrial-encoded subunits such as cytochrome *c*. In contrast, the absence of Hill–Robertson effects on nuclear chromosomes predicts the opposite—there should be more variation in nuclear-encoded respiratory proteins.

A second prediction concerns the mitochondrial bottleneck. During embryonic development, the bottleneck lowers mtDNA diversity by restricting the copy number of mtDNA to a bare minimum in primordial oocytes, then amplifying this tiny population to 100 000 copies in the mature oocyte (Shoubridge and Wai, 2007). As a result, individual oocytes are typically homoplasmic for mtDNA, the function of which is presumably subjected to selection during embryonic development.

The stringency of the mitochondrial bottleneck varies with factors like litter size (Krakauer and Mira, 1999). In principle, the bottleneck should also vary with aerobic capacity. High aerobic capacity requires rigorous mitochondrial selection, demanding a tighter bottleneck. If there is heavier selection on mtDNA in birds than in mammals, there should also be a tighter bottleneck (specifically fewer copies of the mitochondrial genome in primordial oocytes). If this is the case, the lack of variation on the W chromosome is more likely to indicate Hill–Robertson effects resulting from selection on mitochondrial genes.

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Barja J (2007). Mitochondrial oxygen consumption and reactive oxygen species production are independently modulated: implications for aging studies. *Rejuv Res* **10**: 215–223.

Bazin E, Glémin S, Galtier N (2006). Population size does not influence mitochondrial genetic diversity in animals. *Science* **312**: 570–572.

Berlin S, Ellegren H (2004). Chicken W: a genetically uniform chromosome in a highly variable genome. *PNAS* **101**: 15967–15969.

Berlin S, Tomaras D, Charlesworth B (2007). Low mitochondrial variability in birds may indicate Hill–Robertson effects on the W chromosome. *Heredity* **99**: 389–396.

Burton RS, Ellison CK, Harrison JS (2006). The sorry state of F2 hybrids: consequences of rapid mitochondrial DNA evolution in allopatric populations. *Am Nat* **168** (Suppl 6): S14–S24.

Dumullard R, Duchen M, Carroll J (2007). The role of mitochondrial function in the oocyte and embryo. *Curr Top Dev Biol* **77**: 21–49.

Hickey AJR (2008). An alternate explanation for low mtDNA diversity in birds: an age-old solution? *Heredity* **100**: 443.

Krakauer DC, Mira A (1999). Mitochondria and germ-cell death. *Nature* **400**: 125–126.

Lambert AJ, Boysen HM, Buckingham JA, Yang T, Podlutsky A, Austad SN *et al*. (2007). Low rates

of hydrogen peroxide production by isolated heart mitochondria associate with long maximum lifespan in vertebrate homeotherms. *Aging Cell* **6**: 607–618.

Maina JN (2000). What it takes to fly: the structural and functional respiratory refinements in birds and bats. *J Exp Biol* **203**: 3045–3064.

Marais GAB (2007). The Hill–Robertson effects extend from nucleus to mitochondria. *Heredity* **99**: 357–358.

Shoubridge EA, Wai T (2007). Mitochondrial DNA and the mammalian oocyte. *Curr Top Dev Biol* **77**: 87–111.

Editor's suggested reading

Charlesworth D (2006). Population genetics: using recombination to detect sexual reproduction: the contrasting cases of Placozoa and *C. elegans*. *Heredity* **96**: 341–342.

Comeron JM, Williford A, Kliman RM (2008). The Hill–Robertson effect: evolutionary consequences of weak selection and linkage in finite populations. *Heredity* **100**: 19–31.

Handley LJL, Hammond RL, Emaresi G, Reber A, Perrin N (2006). Low Y chromosome variation in Saudi-Arabian hamadryas baboons (*Papio hamadryas hamadryas*). *Heredity* **96**: 298–303.

Ogata M, Hasegawa Y, Ohtani H, Mineyama M, Miura I (2008). The ZZ/ZW sex-determining mechanism originated twice and independently during evolution of the frog, *Rana rugosa*. *Heredity* **100**: 92–99.