Unique mitochondrial DNA in highly inbred feral cattle

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The Chillingham herd of wild Northumbrian cattle remains viable despite over 300 years of in-breeding and a near-homozygous nuclear genome. Here we report the complete mitochondrial DNA sequence using ultra-deep next generation sequencing. Random population sampling of ~10% of the extant herd identified a single mtDNA haplotype harbouring a unique bovine variant present in all other higher mammals (m.11789C/Y421H) which may contribute to their survival.

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Given the phylogenetic relationship between these different species (Fig. 1b), m.7851C is likely to be a recurrent mutation. This is similar to other B. taurus breeds, which harbour 5 +/− 1.06 unique mtDNA variants (Achilli et al., 2008). Based on a phylogenetic mutation rate of $2.043 \pm 0.099 \times 10^{-8}$/base-pair/year for the mtDNA coding region (15,247 bp) (Achilli et al., 2008), the herd is predicted to have a
common maternal T3 ancestor ~12,000 years ago, in keeping with the Neolithic domestication of European founder cattle in the Fertile Crescent.

Inbreeding is generally found to reduce fitness in both farmed and wild animals (Visscher et al., 2001), so the continued survival of the isolated Chillingham herd suggests that deleterious alleles have been purged from the population. It is conceivable that the divergence of the Chillingham mtDNA genome contributes to the herd viability. This could, in part, be due the presence of m.11789C (Y421H), which resides in a highly conserved region of the complex I ND4 respiratory chain subunit. The histidine residue found in the Chillingham cattle is the sole allele in almost all other higher mammals (including domesticated sheep and horses), but not in modern bovine lineages (Supplementary Fig. 2), and is in a region sensitive to pathogenic mtDNA variation in humans (Taylor and Turnbull, 2005). Thus, m.11789C is likely to have a functional effect. This could occur directly through complex I activity, or indirectly though the nuclear genome, given evidence that mtDNA substitution drives the adaption in nuclear-encoded respiratory chain proteins in other species (Blier et al., 2001). Whichever is the case, since all are healthy, the Chillingham-specific variant could optimize the aerobic synthesis of adenosine triphosphate, and thus promote herd viability in the context of an otherwise invariant nuclear genome.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.mito.2012.05.003.

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