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Phylogenetics and Mitochondrial Evolution

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Message from the Guest Editors

The recent Nobel prize in Physiology and Medicine has been awarded to Swante Paabo for the research on human evolution, which cumulated in the discovery of gene exchange between human tree branches, e.g., modern humans and Neanderthals. This research critically depends on the methodology of sequencing ancient DNA, developed by the laureate. Today such analyses mostly employ nuclear DNA sequences. For some time, however, this field has been driven by phylogenic studies of mtDNA, which resulted, for example, in one of the most spectacular discoveries in this field, the recent Mitochondrial Eve. Interestingly, this discovery did not use ancient DNA sequencing. Today, when entire ancient nuclear genomes are commonly available for analysis, mtDNA seems doomed. However, mtDNA may still mainain its superiority in certain applications. Recently, 'intraorganismal' phylogenic analyses of mtDNA somatic mutations were used to follow somatic cell lineages in development. Similar approaches may be useful for studies of mtDNA bottleneck and inheritance.

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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