

Mothers on the move – thousands of complete mitochondrial sequences reveal the layered formation of the common maternal genepool of Finland and Estonia.

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We undertook a large-scale population-based examination of the maternal genepool of several populations residing in the Circum-Baltic Area. For this purpose, we collected over 6000 complete mtDNA sequences from Estonia, Finland, Sweden, Latvia and Poland with additional modern and ancient haploid genomes from published sources. We reconstructed maximum parsimony trees for all of these sequences and revealed shared monophyletic clusters common to the Circum-Baltic region. The shared mitochondrial genepool of Estonia, Finland and Sweden comprises temporally structured layers of maternal lineages stemming from the Late Neolithic to the Middle Ages. We discuss the association of some of these lineages with movement of peoples uncovered by archaeology and research on Y-chromosome and ancient DNA. We detect an increase in maternal effective population size during the Iron Age, coinciding with the diversification time of the Finnic languages. Contrasting the general notion of relatively homogenous mitochondrial genepool of Europe, the phylogeny-informed approach allows us to detect a geographic pattern previously associated primarily with male lineages. Almost 40% of Finnish mtDNA sequences belong to monophyletic clusters common with linguistically related Estonians, whereas below 8% are shared with geographically close Swedish population. In Estonia, roughly 15% of mtDNA sequences belong to shared Finnish-Estonian clusters, whereas 7% form common clusters with the Latvian samples. Despite known Swedish settlements from recent history, less than 2% of Estonian mtDNA samples form common clusters with Swedes.