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Population genomics of ancient DNA

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Ancient mitogenomes of Argentine Patagonia (6070-310 YBP) reveal the early contribution of lineages not previously found in South America

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Patagonia,
a *cul-de-sac* for the continental dispersal of *Homo sapiens* into the Americas, has been extensively analyzed by archaeologists and bioanthropologists. Despite its deep and rich archaeological record, the genetic make-up of its pre-contact inhabitants is barely known. We present the analysis of 19 mitogenomes recovered by NGS from archaeological sites in Central Patagonia (Chubut, Argentina). 15 are pre-contact samples, (6,010-770YBP), and four are samples from historical times (550-310YBP). Preservation of the samples was extraordinary, with endogenous DNA values up to 68%. Preliminary analysis indicates that mtDNA genomes from Central Patagonia belong to haplogroups B2 (21%), C1b (21%), C1c (5%), D1 (47%) and D4h3a (5%). This is surprising when compared with a database of >19,000 control region sequences and >2,100 mitogenomes of Native American origin: 1) While modern indigenous populations from Northern and Central Patagonia of Argentina and Chile derive 41-54% of their maternal lineages from clades B2i2 and C1b13, none of these are present in our dataset; 2) 75% of our B2 and C1b lineages share derived polymorphism with lineages so far known to be present only in modern Central-Western Argentina; and 3) although modern Patagonians carry the highest continental frequencies of D1g, the ancient set is enriched mostly in D1g5, a lineage widely distributed from South-Central Andes to Tierra del Fuego (including two samples with private motifs not described before). The upcoming analysis of the nuclear portion of these samples will help us better understand migratory and admixture processes in the Patagonian region.

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