

Y-chromosomal connection between Hungarians and geographically distant populations of the Ural Mountain region and West Siberia

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Figures



Figure S1. Map with sampling points.

Background maps from Surfer® (v.8, Golden Software, Inc, Golden, CO, USA).

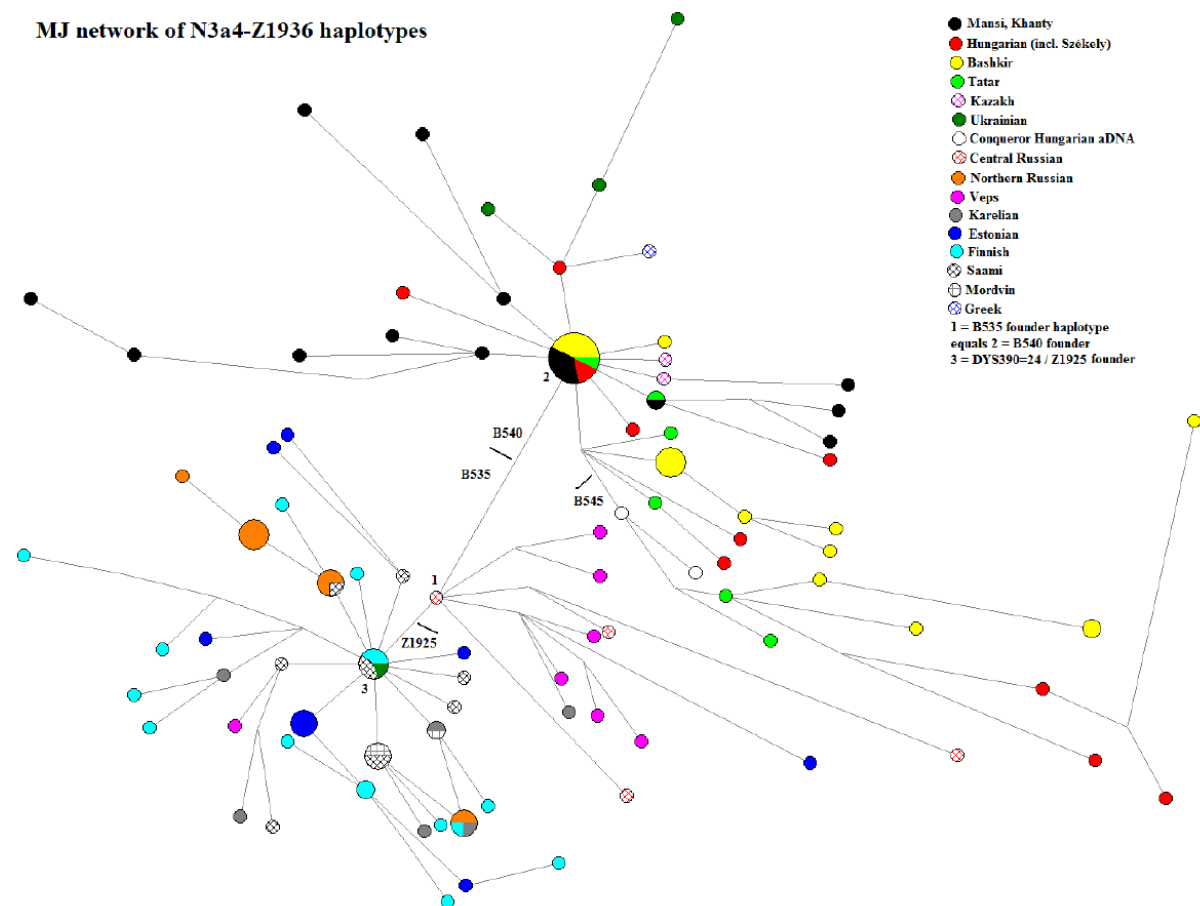


Figure S2. Network of N3a4 clade.

The network was constructed with Network 4.6.1.1 software by applying median joining algorithm and using haplotypes of 16 Y STRs (Supplementary Table S4).

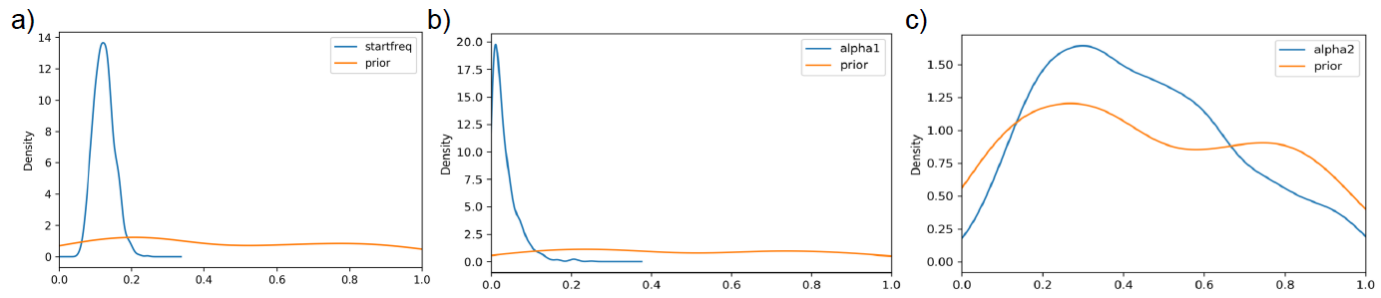


Figure S3. The posterior and prior distributions from Model C.

a) Haplotype frequency of Siberian populations which contributed to Europeans and Hungarians. b) Admixture proportion from Siberian to Europeans and c) Admixture proportion from Siberian to Hungarians. Posterior distribution in blue and prior distribution in orange.

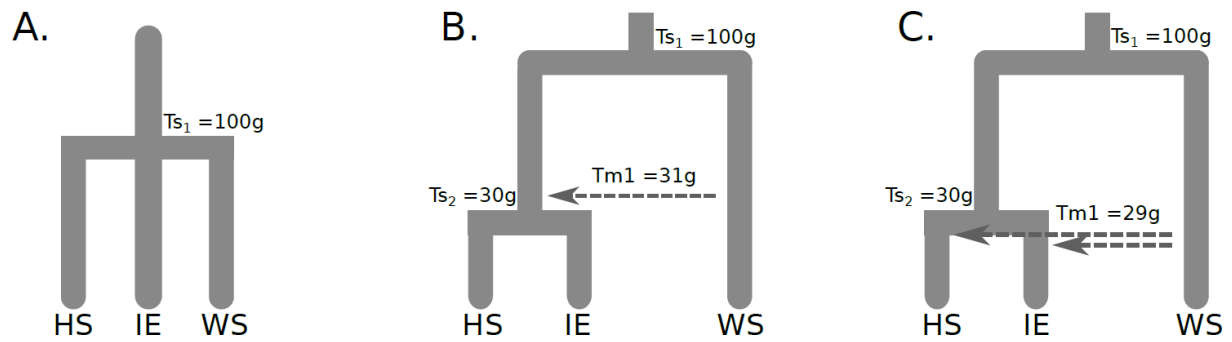


Figure S5. Overview of the simulated models A, B and C using the resampling approach.

Abbreviations: Ts: Time of split, Tm: Time of migration, HS: Hungarian Sekler, IE: Indo-European, WS: West Siberian.

Tables

Table S1. Mutation list for phylogenetic tree of N3a4

Table S2. Age estimates of N3a4 sub-clades according to Figure 2

Table S3. Geographic distribution of hg N2a1 and N3 subclades

Table S4. N3a4 STR haplotypes

Table S5. Locations of populations for local B539 surfer map

Table S6. List of re-sequenced samples and their geographic affiliations

Table S7. Specifications for SNPs used to genotype population samples