 Norwegian Genetic Profile Part 13: GENETIC HOMOGENEITY IN NORWAY

The relative homogeneity of Norway's population is a matter of historical record, and is confirmed by genetic testing.


1: Eur J Hum Genet. 2002 Sep;10(9):521-9

Different genetic components in the Norwegian population revealed by the analysis of mtDNA and Y chromosome polymorphisms.


The genetic composition of the Norwegian population was investigated by analysing polymorphisms associated with both the mitochondrial DNA (mtDNA) and Y chromosome loci in a sample of 74 Norwegian males. The combination of their uniparental mode of inheritance and the absence of recombination make these haplotypic stretches of DNA the tools of choice in evaluating the different components of a population's gene pool. The sequencing of the Dloop and two diagnostic RFLPs (AluI 7025 and HinfI at 12 308) allowed us to classify the mtDNA molecules in 10 previously described groups. As for the Y chromosome the combination of binary markers and microsatellites allowed us to compare our results to those obtained elsewhere in Europe. Both mtDNA and Y chromosome polymorphisms showed a noticeable genetic affinity between Norwegians and central Europeans, especially Germans. When the phylogeographic analysis of the Y chromosome haplotypes was attempted some interesting clues on the peopling of Norway emerged. Although Y chromosome binary and microsatellite data indicate that 80% of the haplotypes are closely related to Central and western Europeans, the remainder share a unique binary marker (M17) common in eastern Europeans with informative microsatellite haplotypes suggesting a different demographic history. Other minor genetic influences on the Norwegian population from Uralic speakers and Mediterranean populations were also highlighted.

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The "minor genetic influences from Uralic speakers" mentioned in this report above, is a reference to the 5.7% incidence of the 'Tat-C' marker found in Norway:

http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6T6W-42HFP9C-1&_coverDate=04%2F01%2F2001&_alid=112088375&_rdoc=1&_fmt=&_orig=search&_ collapse=1&_sort=d&view=c&_acct=C000050221&_version=1&_userid=10&md5=beb708cfdec936cc7ef8783f96606cb5

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Y-chromosome variation in a Norwegian population sample

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Abstract

Y-chromosome DNA profiles are promising tools in population genetics and forensic science. Here we present DNA profiles of 300 unrelated Y-chromosomes of Norwegian origin. The profile is composed of eight short tandem repeats (STRs) and one single nucleotide polymorphism (SNP). In more than 2/3 of the haplotypes the modular structure in the 5' end of the minisatellite locus DYF155S1 was revealed by minisatellite variant repeat
PCR (MVR-PCR) These haplotypes were also typed for deletions of fragment 50f2C (DYF155S2). Allele distribution and paternity exclusion parameters are given for each marker. The degree of haplotype diversity and its implication for statistics are evaluated. In the 300 samples 177 different haplotypes were encountered, of which 137 were observed once only. Analysis showed that the main source of variation is within the population. The Fst values were less than 0.015 in general. Haplotype grouping by the SNP demonstrated two haplogroups (Tat/T and Tat/C). Haplogroup Tat/C -- found in 5.7% of the present material -- is the same haplogroup as encountered in 60% of Finnish males [Am. J. Hum. Genet. 62 (1998) 1171]. Mutation analysis in 150 father/son pairs (a total of 1200 meiotic events) revealed an average mutation frequency of 0.0042 (95% CI 0.0014-0.0097).

The 'Tat-C' marker and its origin is discussed in the next section here.


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