MONITIETEINEN IHMISEN MONIMUOTOISUUS ESITELMÄSARJA
INTERDISCIPLINARY HUMAN DIVERSITY SEMINAR SERIES

The landscape of Y-chromosomal genetic variation in Finland

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Time: 11:45–12:15 coffee and tea served; 12:15–13:00 presentation
Location: Tauno Nurmela Hall, Main Building

Abstract

The human Y chromosome contains the longest non-recombining region in the human genome, allowing genetic variation within this segment to be transmitted directly from father to son. Over generations, the accumulation of mutations gives rise to distinct Y-chromosomal haplotypes and haplogroups, which have been widely used in population genetics and forensic research to reconstruct ancestry and population history.

In Finland, two major Y-chromosomal haplogroups, N1a1 (64%) and I1a (25%), capture the primary paternal substructure of the population, and are thought to reflect eastern and western ancestry contributions to the country. However, variation beyond these major lineages has remained largely unexplored.

In this talk, I present the most comprehensive analysis of Finnish Y-chromosomal variation to date, leveraging sequencing data from 1,802 geographically mapped Finnish Y chromosomes from the FINRISK cohort. By examining fine-scale subhaplogroup structure and its regional distributions, we refine our understanding of the Y-chromosomal gene pool in Finland and provide new insights into the genetic history of the Finnish population.

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