

## Ancient Upper Mesopotamia, 10,000 years ago: first genomic impressions

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We present partial ancient genomes from 13 individuals from the Pre-Pottery Neolithic period of Çayönü Tepesi in present-day Diyarbakır, Turkey. The sample covers a 1,000 year range, between approximately 10,500-9,500 years ago, and represents the first ancient genome set yet published from Upper Mesopotamia. Pre-Pottery Neolithic Çayönü was a sedentary community, with largely hunter-gatherer subsistence, but at the same time heavily experimenting with crop cultivation and animal management. Neolithic Çayönü is also known for its remarkable cultural dynamism reflected in diverse architectural styles and changing mortuary practices. Our genome data suggest that the Çayönü population, most likely representing that of Upper Mesopotamia, emerged through admixture between groups from eastern and western Fertile Crescent, namely the Central Zagros and Central Anatolia/Levant, respectively. We find that the Çayönü genetic profile is the best candidate for "eastern" gene flow into Central Anatolia by the 7th millennium BCE, marking Upper Mesopotamia as a potential contributing ancestry source to sites such as Çatalhöyük. We further determine close genetic kinship among individuals co-buried underneath floors of domestic buildings, in support of the notion that household membership was related to biological family ties in the Pre-Pottery Neolithic, a pattern that appears to have changed in later sites such as Çatalhöyük and Barcın. Finally, using the genomic data and pedigree simulations we identify a possible third-generation migrant infant of likely Central Zagros descent in our sample, implying that the Çayönü community was open to immigration.

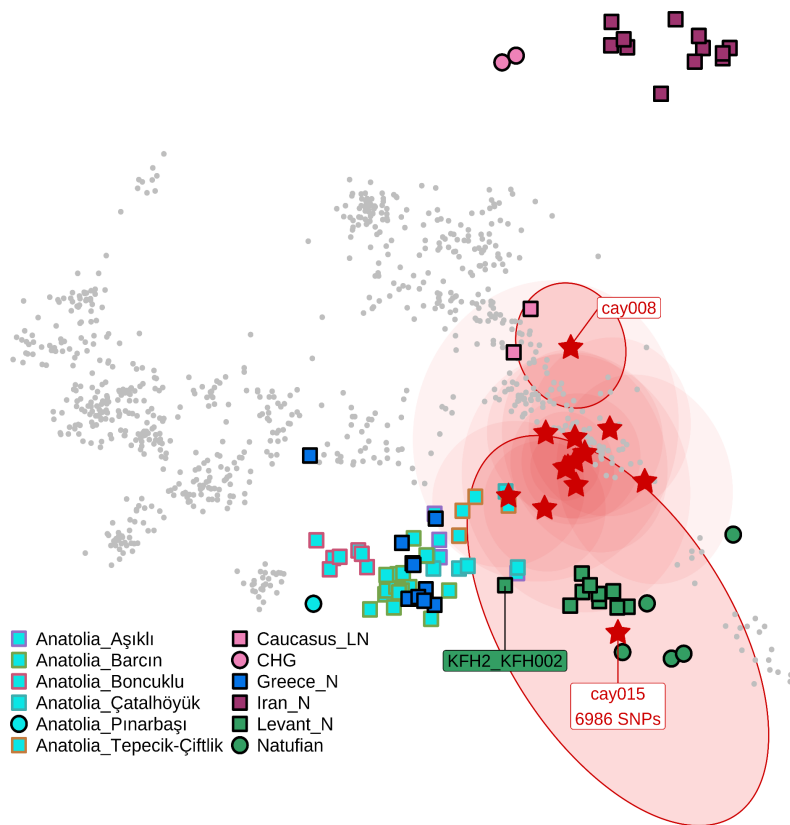


Figure 1: A principal component analysis of Çayönü genomes (red stars) and other early Holocene ancient genomes (colored points, see key) projected onto PC space created using modern-day genomes (gray dots). The individual cay008, inferred to be of migrant descent, is marked, along with a Çayönü individual with too few SNPs to reliably infer population genetic affinity from the plot.