

Papadopoulou A., Psonis N., Vassou D., Tabakaki E., Koptekin D., Neuenschwander S., Rodríguez-Varela R., Anchieri L., Hübner L., Papadantonakis S., Nafplioti A., Koursioti S., Stravopodi E., Kontaxi C., Aravantinos L.V., Kyparissi-Apostolika N., Yilmaz Y., Yorulmaz S., Daskalaki E., Allentoft M., Götherström A., Özer F., Somel M., Pavlidis P., Stamatakis A., Malaspinas A.S., Poulakakis N. "The genetic history of Neolithic to Bronze Age Aegean at the crossroad between Anatolia and Europe". Annual Meeting of the Society for Molecular Biology and Evolution, Puerto Vallarta, Mexico, 7-11 July 2024 (poster presentation).

Papadopoulou A., Psonis N., Vassou D., Tabakaki E., Koptekin D., Neuenschwander S., Rodríguez-Varela R., Anchieri L., Hübner L., Papadantonakis S., Nafplioti A., Koursioti S., Stravopodi E., Kontaxi C., Aravantinos L.V., Kyparissi-Apostolika N., Yilmaz Y., Yorulmaz S., Daskalaki E., Allentoft M., Götherström A., Özer F., Somel M., Pavlidis P., Stamatakis A., Malaspinas A.S., Poulakakis N. "The genetic history of Neolithic to Bronze Age Aegean at the crossroad between Anatolia and Europe". EMBL Symposium - Reconstructing the human past: using ancient and modern genomics, Heidelberg, Germany, 17-20 September 2024 (poster presentation).

Abstract

The Neolithic and Bronze Age (BA) periods in the Aegean are characterized by genetic transitions, extensive population interactions, and migrations. Questions pertaining to the Neolithisation process, the contribution of local hunter-gatherer (HG) populations, and the extent as well as timing of a Steppe-like migration during the BA, are still unanswered. To characterize the population structure across time, we generated whole-genome sequence data for 14 Neolithic to Late BA individuals from the Aegean and Anatolia. We compared them with published ancient genomes from western Eurasia, and conducted population genetic analyses including admixture modeling and f-statistics using pseudo-haploid as well as imputed data. We further examined the levels of inbreeding in the Aegean populations through time by estimating the Runs of Homozygosity (ROH). Our results show that the Neolithic Aegean population was predominantly derived from Western Anatolian farmers, confirming previous studies and suggesting a genetic turnover from the Mesolithic. By the Late Neolithic and onwards there was an influx of a Caucasus HG/Iran Neolithic-like component, possibly introduced by migrants from the east. During the BA, population heterogeneity in the Aegean increased. An Eastern HG-related component already appeared during the Early BA, suggesting that a Steppe-like ancestry may have reached the Aegean earlier than previously described. The EHG-related component is maximized in Middle BA Aegean populations, but compared to other European BA populations its proportion remains low, suggesting that extensive Steppe-like ancestry reached Greece later than mainland Europe. Based on ROH, it seems that the Aegean population experienced an increase in the population size during Neolithic and BA, which can be related to the aforementioned migrations and gene flow events.