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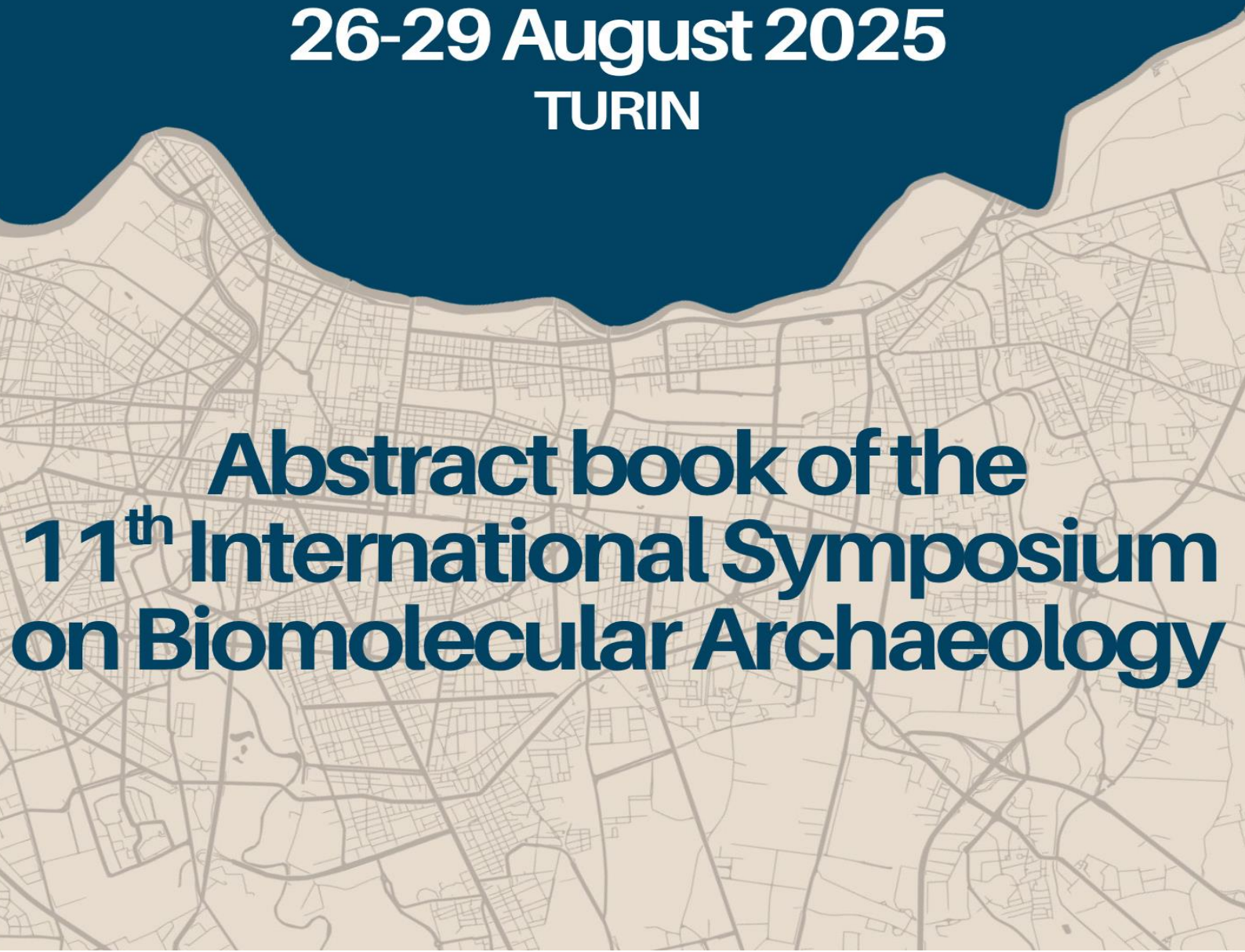
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Investigating Past Human Mobility and Interactions in the Southern Cone of the Americas using Phylogenomics of Ancient Commensal Microbes



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Dental calculus, the calcified biofilm that accumulates on teeth's surfaces during an individual's life, preserves an exceptional archaeogenetic record of hundreds of microbial species that are part of the human oral microbiome. However, most of what we know about oral microbiomes is based on modern samples, and little is known about how these human-microbe associations were established over large spatiotemporal scales. Previous metagenomics works –on modern and ancient samples– have found relatively low differences in the oral microbiome composition of populations from different periods and continents. Thus, we hypothesised that if oral microbial species are maintained within human populations over long periods, their genomes could reflect human population movements through time. To test this hypothesis, we sequenced and analysed ancient dental calculus samples from multiple individuals from the Southern Cone of the Americas, a region with a rich archaeological record, but underexplored using paleogenomic approaches. Phylogenomic methods were used to reconstruct the relationship between strains of oral microbial species

recovered from individuals across multiple spatiotemporal contexts. When combined with archaeological data, we revealed several species with strong spatiotemporal associations with their host populations. Together, our results bring not only unprecedented information about the oral microbial diversity associated with indigenous populations of South America but also novel insight into the long-term association between humans and their commensal microbes. We propose that this type of data and the implemented analytical approaches could be also used as a novel and complementary approach to investigate the mobility and interactions of ancient human populations.