



79th



International
Scientific
Conference of
the University
of Latvia



Latvijas Biomedicīnas
pētījumu un studiju centrs
biomedicīnas pētījumi un izglītība no ģenēm līdz cilvēkam



Metagenome analysis of archaeological teeth samples from Latvian Iron Age, 8th–11th centuries AD

Ķīmsis Jānis, Kazarina Alisa, Gerhards Guntis, Ranka Renāte

Background

Ancient teeth and dental pulps are valuable sources of human DNA and ancient oral microbiomes.

Oral microbiome is the second most studied human microbiome subtype that includes over 700 species of bacteria.

Reconstructed microbiomes of pre-antibiotic lifestyles is highly valuable for understanding the evolution of human microbiome and its role in health and disease.



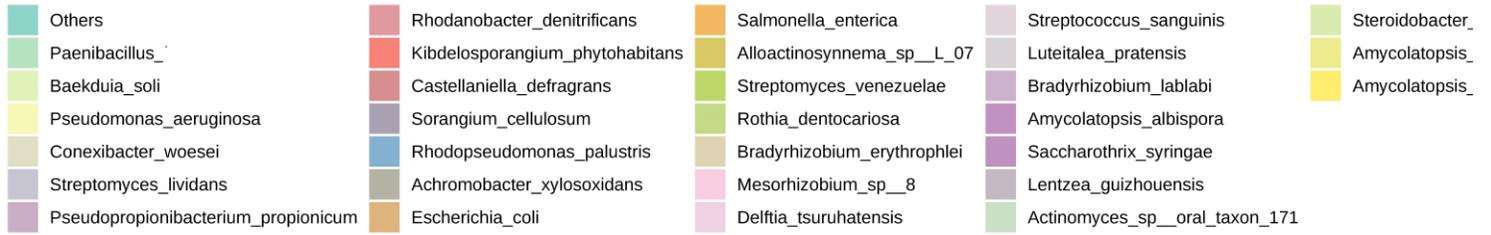
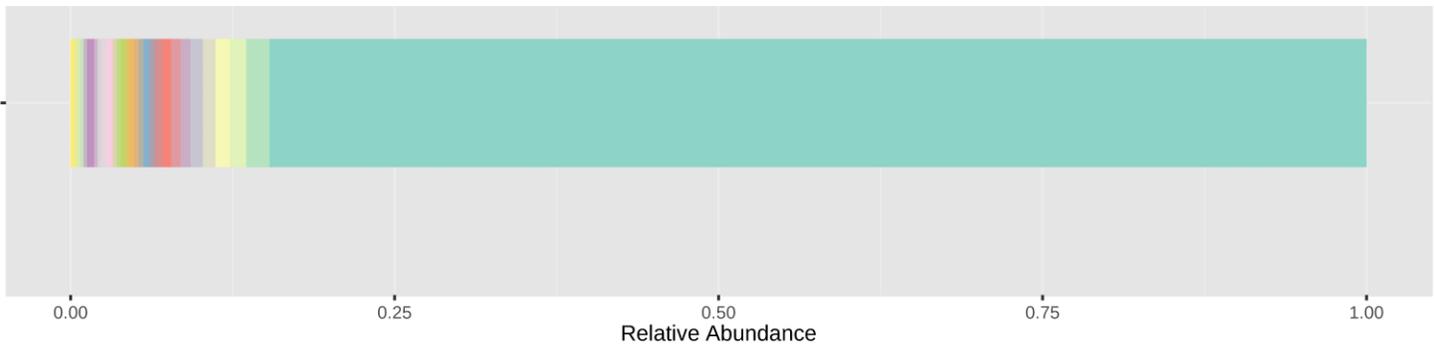
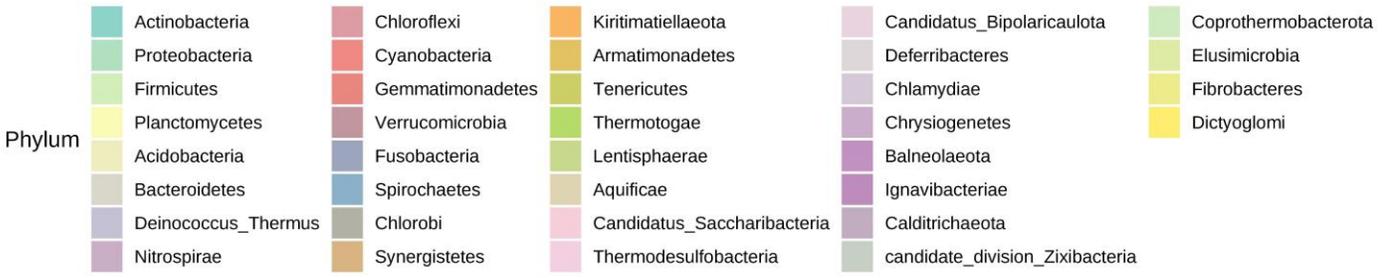
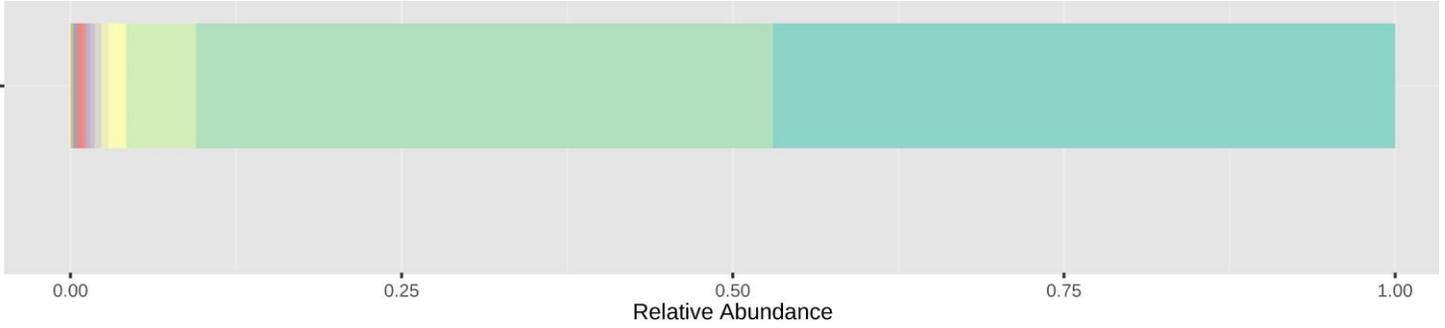
The aim of the study was to explore in detail the taxonomic composition of ancient dental samples dated to Iron Age Latvia (the 8th–11th centuries AD).

Historic human teeth samples were obtained from two Iron Age burials in Latvia: Lejasbitēni (Vidzeme region), and Čunkāni–Dreņģeri (Zemgale region).

DNA was extracted from the teeth samples and sequenced using shotgun Next Generation sequencing approach (Illumina). Data on microbial composition were obtained using MALT, KRAKEN and bioinformatics pipelines dedicated to ancient DNA analysis.

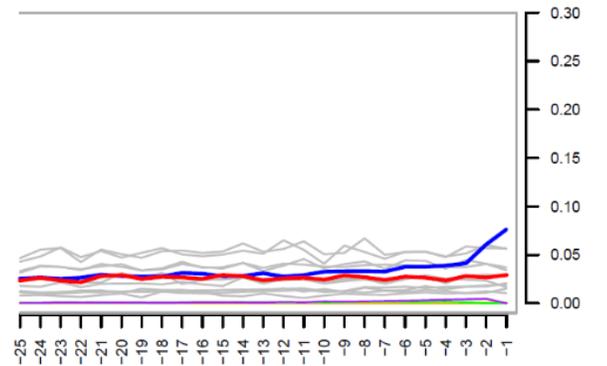
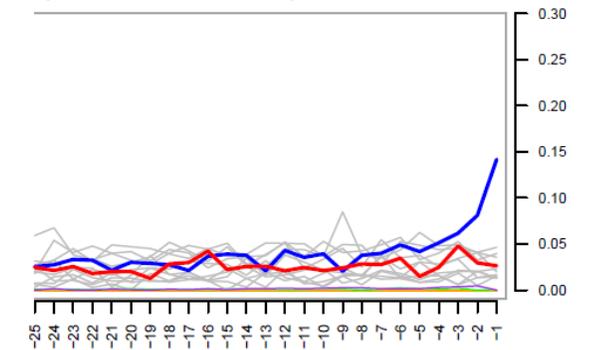
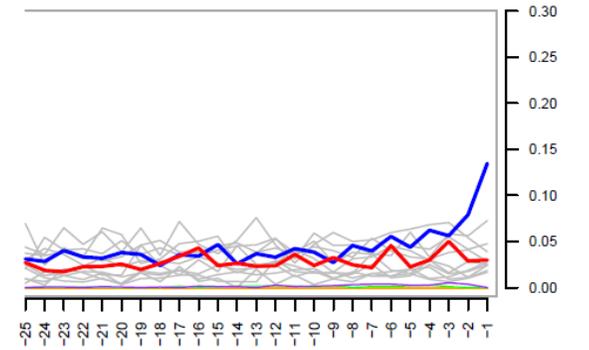
Results

- On average, 18.7 million reads per sample were obtained.
- 36 bacterial phyla were identified, and the most abundant phyla were Actinobacteria (47%) and Proteobacteria (43.5%).
- At the species level, based on low prevalence filter, a total of 2,158 features remained after data filtering.
- The most abundant bacterial species were typical soil and environmental bacteria.
- Oral microbiome signature was also present.



Results II

- For the authentication of oral microbiome preservation in historic dental calculus samples, the DNA damage pattern of the most prevalent oral microorganism, *Actinomyces* sp. oral taxon 171, was evaluated.
- The analysis revealed signs of cytosine to thymine substitutions at the ends of DNA fragments characteristic of aDNA.
- Apart from microbiome, human aDNA reads were present.
- Based on bioinformatics analysis, sex and mitochondrial DNA haplogroup of the human remains could be identified in several cases.



Conclusions

- The obtained results indicate that, although ancient dental samples were invaded by environmental bacteria after death, they also conserve a record of the microbial communities that are naturally present in the oral cavity.
- The availability of microbial and human aDNA data will be highly important for investigation of the composition of the oral microbiome and the demographic history in Iron-Age Latvia.

Acknowledgements

This research was supported by the Latvian Council of Science project No. Izp-2018/1-0395.