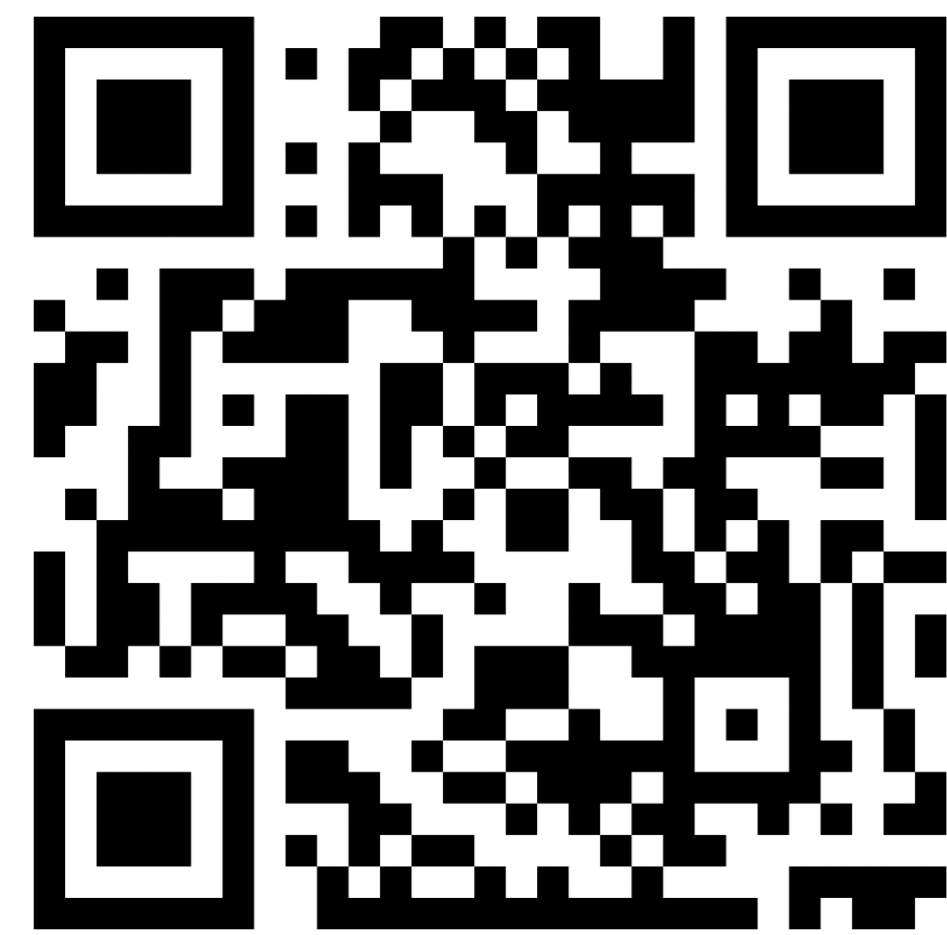


Whole Genome Sequencing of ancient bacteria

Draft Genome Sequences of Eight Bacilli Isolated from an Ancient Roman Amphora from IV-V century AD



- Paleomicrobiology
- Genome-sequencing
- Antibiotic-resistance
- Ancient Roman amphora
- Bacilli

The amphora and its content



AIMS:

The various paleomicrobiological discoveries of recent years have made it possible to study important microbiological subjects, providing valuable informations. In this regard, the genetic characteristics of 8 bacterial strains isolated from a Roman amphora of the 4th-5th century AD, found intact and still sealed during excavations conducted in Aquileia were studied in this work. After being taxonomically identified, a comparison was then made with current genomes of the same species to identify the evolutionary differences.

APPLICATIONS:

Through the compared study of these ancient genomes in respect to the modern species, it was possible to highlight the effects of evolutionary pressure on specific genetic features, for example the analysis the diffusion of antibiotic resistance traits.

RESULTS:

Bacillus spp. spores were found at a concentration of 7.26 LogCFU/g. Following characterization by genetic fingerprint, 8 representative strains were chosen for whole-genome sequencing. Strains were then identified comparing ANI and dDDH values with the reference strains available in the literature, but three strains showed no genetic correlation with currently deposited sequences and could be considered new species. Following the search for resistance factors through specific databases, it was possible to identify resistance factors related to vancomycin, azaleucine, phosphomycin and arsinothricin in 5 out of the 8 strains considered. These results suggest a widespread presence of factors related to resistance to antibiotic substances already in an era in which their use was not widespread.

