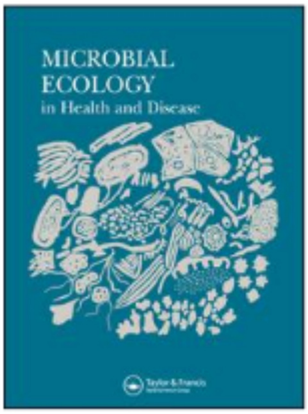

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Ancient permafrost staphylococci carr resistance genes

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contigs were assembled. The first strain was assigned to *Staphylococcus warneri* species (designated MMP1) and the second one to *Staphylococcus hominis* species (designated MMP2), based on the classification of 16S ribosomal RNA genes and genomic sequences.

Results: Genomic sequence analysis revealed the close relation of the isolated ancient bacteria to the modern bacteria of this species. Moreover, several genes associated with resistance to different groups of antibiotics were found in the *S. hominis* MMP2 genome.

Conclusions: These findings supports a hypothesis that antibiotic resistance has an ancient origin. The enrichment of cultivated bacterial communities with ancient permafrost strains is essential for the analysis of bacterial evolution and antibiotic resistance.

KEYWORDS: Permafrost, genome sequence, evolution, antibiotic resistance, microbial physiology, biofilm, *Staphylococcus*

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EK, GG, VK, UR, and AB conceived and designed the work; EK, SMK, OM, GG, VK, and AB performed the experiments; EK, AD, OM, IE, SMK, UR, and VK analyzed the data; and EK and AD drafted the work. All authors revised the work critically for important intellectual content, approved the version to be published, and agreed to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

OM, GG, VK, and AB performed the experiments; EK, AD, OM, IE, SMK, UR, and VK analyzed the data; and EK and AD drafted the work. All authors revised the work critically for important intellectual content, approved the version to be published, and agreed to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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