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Gentic similarity patterns of conspecific microbial populations from abandoned mines

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Massive chemolithotrophic biofilms are common at water seepages in abandoned mines. These biofilms typically show low diversity and spotted distribution. These properties allow us to analyze genetic variability of prokaryotic populations with various degrees of geographical isolation. It enables us to address questions that have raised after the biological species concept was extended to prokaryotes [1]. We collected the stalactite-like biofilms formed by the iron-oxidizer *Ferrovum myxofaciens* in five abandoned mines in Czech republic and Slovakia. Metagenomes were sequenced by a combination of Illumina and Oxford nanopore. Complete metagenome-assembled genomes (MAGs) of *F. myxofaciens* representing all mines have been obtained without any binning step. Genetic content and sequence similarity of the MAGs followed neither geographic nor environmental distances. Conversely, the most distant genotypes were found at two water seepages in a single adit. Detailed analysis of the gene content revealed that almost entire variability within as well as between populations can be attributed to the mobile elements, „selfish“ DNA, and genes with unknown function and, frequently, low sequential complexity (i.e., probable pseudogenes). Contrary to the established theory, no signs of genetic fine-tuning to the specific local conditions were found. The variability can be better explained by random processes, since mines that host more *F. myxofaciens* populations can preserve more genomic variants.

The genomic content with adaptive function was surprisingly conserved even among geographically isolated populations. Genes with known biological function that were probably gained by horizontal gene transfer (HGT) from other microbial species frequently showed signs of advanced genetic erosion. It suggests that interspecific HGT is not excluded, but it has limited and temporary effect on the genome content of *F. myxofaciens*. Examination of the interspecific gene flow barrier is important since its mechanism remains elusive more than decade after the genetic isolation of sympatric prokaryotic populations have been observed [2].

References:

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