Global features of the Alcanivorax borkumensis SK2 genome

The global feature of the completely sequenced Alcanivorax borkumensis SK2 type strain chromosome is its symmetry and homogeneity. The origin and terminus of replication are located opposite to each other in the chromosome and are discerned with high signal to noise ratios by maximal oligonucleotide usage biases on the leading and lagging strand. Genomic DNA structure is rather uniform throughout the chromosome with respect to intrinsic curvature, position preference or base stacking energy. The orthologs and paralogs of A. borkumensis genes with the highest sequence homology were found in most cases among gamma-Proteobacteria, with Acinetobacter and P. aeruginosa as closest relatives. A. borkumensis shares a similar oligonucleotide usage and promoter structure with the Pseudomonadales. A comparatively low number of only 18 genome islands with atypical oligonucleotide usage was detected in the A. borkumensis chromosome. The gene clusters that confer the assimilation of aliphatic hydrocarbons, are localized in two genome islands which were probably acquired from an ancestor of the Yersinia lineage, whereas the alk genes of Pseudomonas putida still exhibit the typical Alcanivorax oligonucleotide signature indicating a complex evolution of this major hydrocarbonoclastic trait.

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