

# Clustered Gene Strand Bias on Gemmatimonadota Chromosomes

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## **Background:**

On most bacterial chromosomes, the majority of genes is coded on the leading strand. The extent of this gene orientation bias ranges from up to 85% in some Firmicutes to little more than 50% in some Proteobacteria. The understudied phylum Gemmatimonadota has currently only four closed genomes available that share a unique chromosome architecture: A conserved 600 kb region around the terminus of replication shows a pronounced gene orientation bias while the rest of the chromosome does not.

## **Objective:**

Here, we asked which genome properties can explain the clustered gene orientation bias in Gemmatimonadota and if its origin can be traced back to earlier branching, or is conserved in later branching phyla.

## **Methods:**

We determined the location of conserved genes and possible sources of instability such as transposons and repetitive DNA in the genomes of Gemmatimonadota and neighboring phyla. We also analyzed transcriptomes of two Gemmatimonas strains in order to test if this unusual genome architecture has an impact on gene expression.

## **Results:**

In Gemmatimonadota, the region of interest is poor in repetitive elements compared to the rest of the chromosome and harbors mostly core genes of this phylum. These genes show a consistently high expression level, while gene expression outside this region is more variable. Despite 'unusual' chromosome architectures in some representatives, neither earlier nor later branching phyla show a clustered gene orientation bias as found for Gemmatimonadota. This suggests a unique evolution of chromosome architecture in this phylum.