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A comparative analysis of the structural diversity of biosynthetic gene clusters in the phylum *Planctomycetota*

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Abstract

Background: *Planctomycetota* are bacteria with a unique cell biology known to possess important potential for the production of new molecules with biological activities. This potential has only recently started to be unveiled, motivated by reported antimicrobial and anticancer activities [1-3]. Three novel secondary metabolites have already been characterized [4,5]. Enzymes involved in the synthesis of bioactive compounds are often encoded in biosynthetic gene clusters (BGCs), which harbor biosynthetic genes and genes encoding transporter and regulator proteins [6]. Previous studies reported high numbers of up to 13 BGCs present in their genomes, with little to no similarity to characterized clusters in other phyla that belong to known compounds [7]. However, no information regarding the genomic structure of these BGCs is currently available. The discovery of new drugs can be arduous, costly and time-consuming. Bioinformatics analysis can address some of these problems, particularly in underexplored bacterial phyla such as *Planctomycetota*. In that regard, *in silico* analyses can accelerate the identification of putative novel clusters and compounds [8]. **Objective:** This study aimed to compare the presence and genomic organization of BGCs in *Planctomycetota* using bioinformatics tools**. Methods:** 129 planctomycetotal reference genomes were analyzed in a genome mining approach using antiSMASH. Similarity networks of the 987 detected BGCs were constructed using Biosynthetic Gene Similarity Clustering and Prospecting Engine, and Clinker was then used to visualize the similarities between BGCs and the genomic structure of the clusters. **Results:** Our data indicate that the predicted BGCs can vary between and within genera. The genomic organization of BGCs appears to be more conserved within certain genera of the class *Planctomycetia*: *Gimesia*, *Blastopirellula* and *Paludisphaera*, which seem to have more conserved BGC structures. The presence of similar organized BGCs in more distantly related taxonomic groups may point towards horizontal gene transfer events followed by the preservation of these genes within the groups. **Conclusions:** Our results provide one of the first insights into the structure of BGCs of *Planctomycetota*, which can be a key factor for the identification and production of novel compounds. The data also showed that members from the same genera may produce similar compounds, as the genomic structure of BGCs seems to be more conserved within genera.

Keywords: *Planctomycetia*; biotechnological potential; genomic structure

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