

Comparative whole-genome approach to identify traits underlying microbial interactions

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Research

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Abstract

Background

Interactions among microorganisms affect the structure and function of microbial communities, potentially affecting ecosystem health and biogeochemical cycles. The functional traits mediating microbial interactions are known for several model organisms, but the prevalence of these traits across microbial diversity is unknown.

Results

We developed a new genomic approach to systematically explore the occurrence of metabolic functions and specific interaction traits, and applied it to 473 sequenced genomes from marine bacteria. The bacteria could be divided into coherent genome functional clusters (GFCs), some of which are consistent with known bacterial ecotypes (e.g. within pico-Cyanobacteria and *Vibrio* taxa) while others suggest new ecological units (e.g. *Marinobacter*, *Alteromonas* and *Pseudoalteromonas*). Some traits important for microbial interactions, such as the production of and resistance towards antimicrobial compounds and the production of phytohormones, are widely distributed among the GFCs. Other traits, such as the production of siderophores and secretion systems, as well as the production and export of specific B vitamins, are less common. Linked Trait Clusters (LTCs) include traits that may have evolved together, for example chemotaxis, motility and adhesion are linked with regulatory systems involved in virulence and biofilm formation.

Conclusions

Our results highlight specific GFCs, such as those comprising Alpha- and Gammaproteobacteria, as particularly poised to interact both synergistically and antagonistically with co-occurring bacteria and phytoplankton. Similar efficient processing of multidimensional microbial information will be increasingly essential for translating genomes into ecosystem understanding across biomes, and identifying the fundamental rules that govern community dynamics and assembly.

Full Text

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Figures

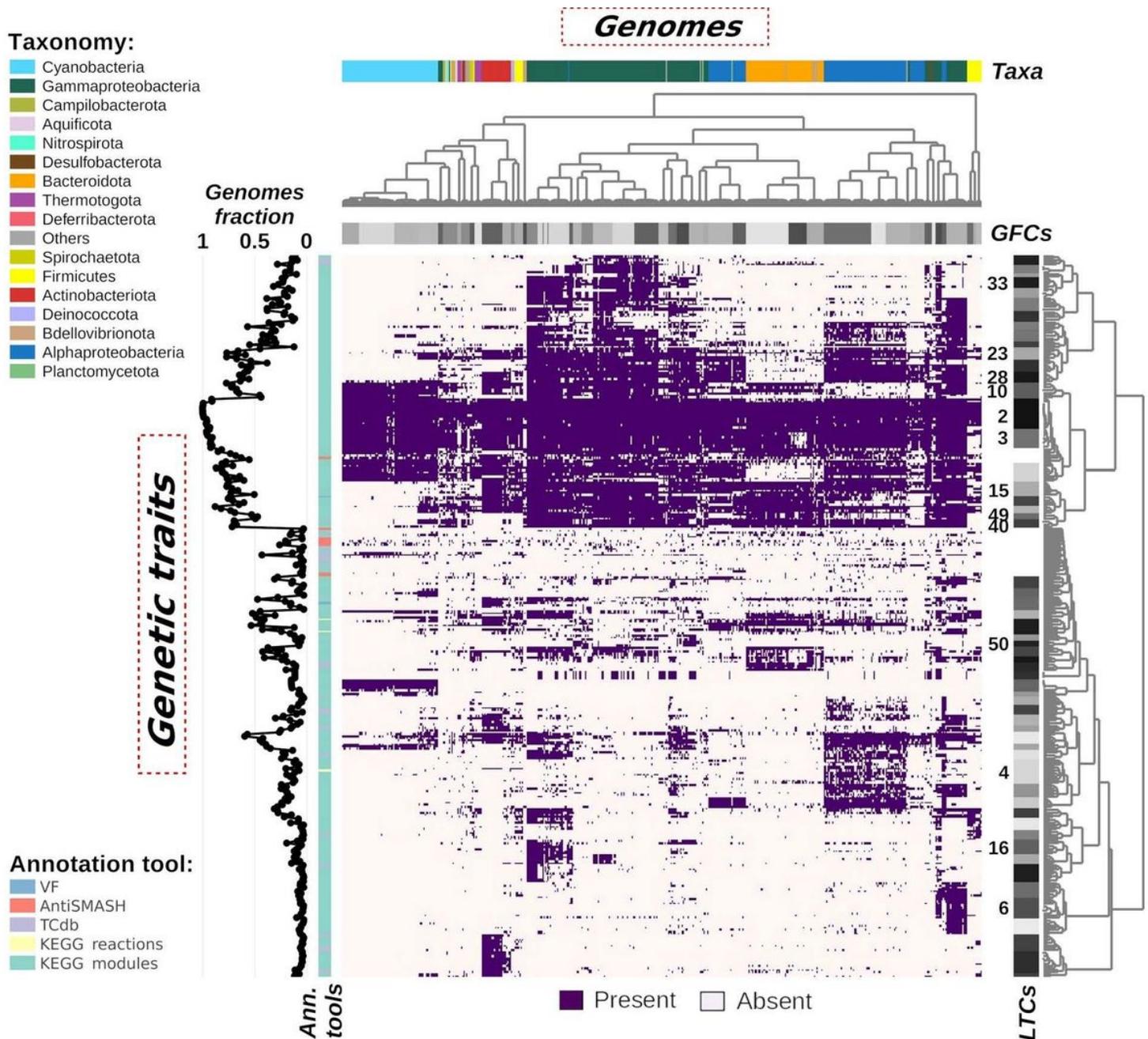


Figure 1

Atlas of Marine Microbial Functional Traits showing presence/absence of genetic traits across all analyzed genomes. Each column represents a genome and these are hierarchically clustered. The horizontal color bar represents the taxonomic affiliations of the genomes (mainly phyla, with the exception of Proteobacteria that are represented at the class level) and the horizontal grey bar delineates specific genome functional clusters (GFCs). Rows are the genetic traits clustered using the coefficient of disequilibrium into linked trait clusters (LTCs) (vertical grey bar); relevant LTCs are marked. Left-side row annotations show the average abundance for the genetic traits and the annotation tool (color coded bar) with which they have been annotated. An interactive version of this figure is available as Supplementary file 1.

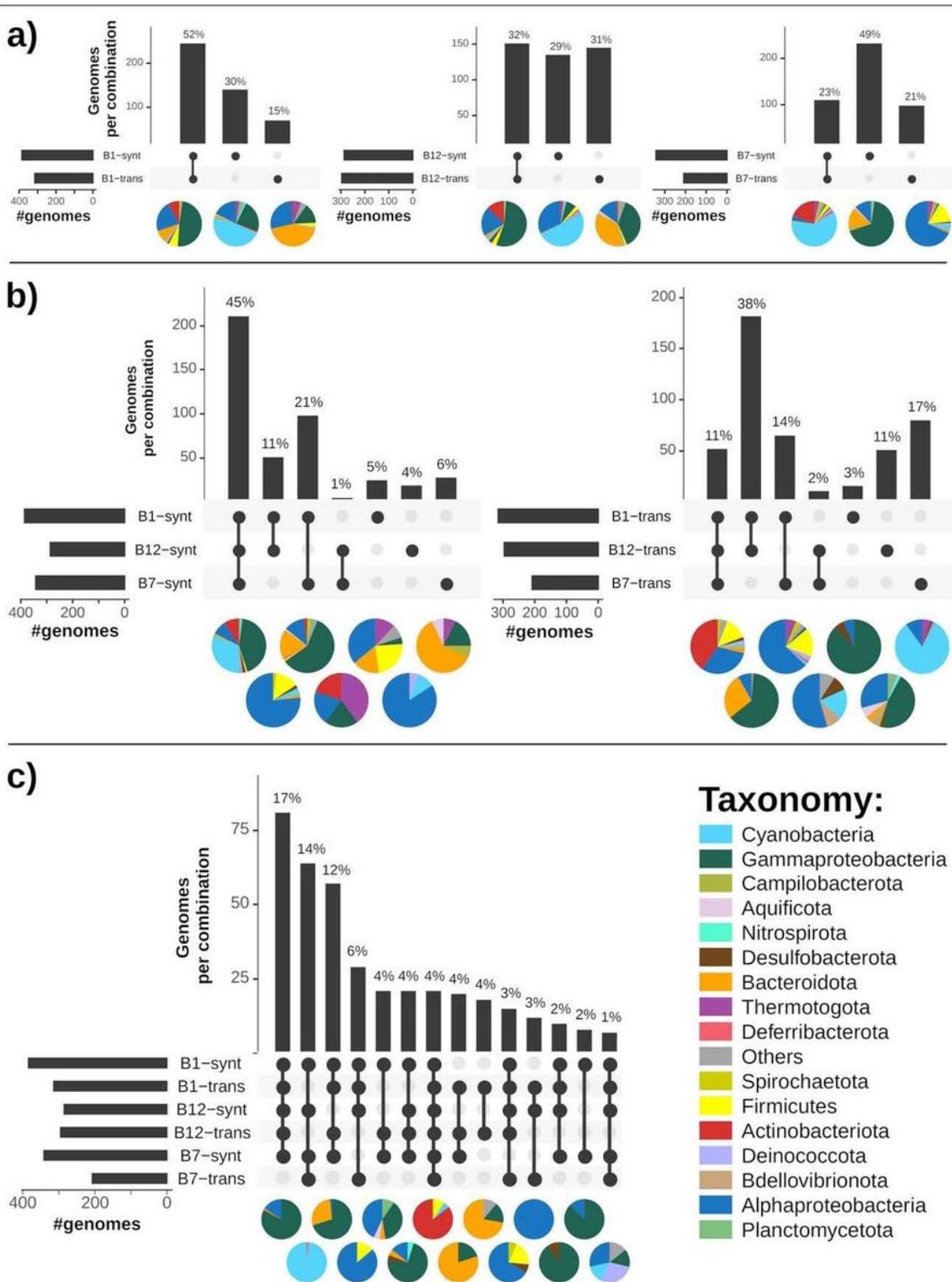


Figure 2

UpSet plots exploring the different genomic configurations of traits involved in the biosynthesis and transport of vitamins B1, B12, and B7. (a) Different strategy of acquisition of B vitamins among genomes in relation to their ability to produce or/and transport a certain vitamin. (b) Genome partitioning in relation to either production or transport of all selected B vitamins. (c) Most abundant combinations of all these traits across genomes; the remaining combinations are shown in Supplementary Fig. 6a. Overall, the left

bar chart indicates the total number of genomes for each trait, the dark connected dots indicate the different configurations of traits and the upper bar chart indicates the number of genomes provided with such configuration. Pie charts show the relative abundance of the different taxa represented in each configuration.

Taxonomy:

- Cyanobacteria
- Gammaproteobacteria
- Campilobacterota
- Aquificota
- Nitrospirota
- Desulfobacterota
- Bacteroidota
- Thermotogota
- Deferribacterota
- Others
- Spirochaetota
- Firmicutes
- Actinobacteriota
- Deinococcota
- Bdellovibrionota
- Alphaproteobacteria
- Planctomycetota

Interaction-traits:

- Vitamin B1 biosynthesis
- Vitamin B7 biosynthesis
- Vitamin B12 biosynthesis
- Vitamin B1 transport
- Vitamin B7 transport
- Vitamin B12 transport
- Fe-Siderophore
- Fe-Siderophore transporter
- Auxin: Indole-3-pyruvate pathway
- Auxin: Tryptamine pathway
- Auxin: Indole-3-acetonitrile pathway
- Auxin: Indole-3-acetamide pathway
- Quorum sensing
- Chemotactic behavior
- Motility and adhesion apparatus
- Type III secretion system
- Type IV secretion system
- Type VI secretion system
- Antimicrobial compounds biosynthesis
- Antimicrobial compounds resistance

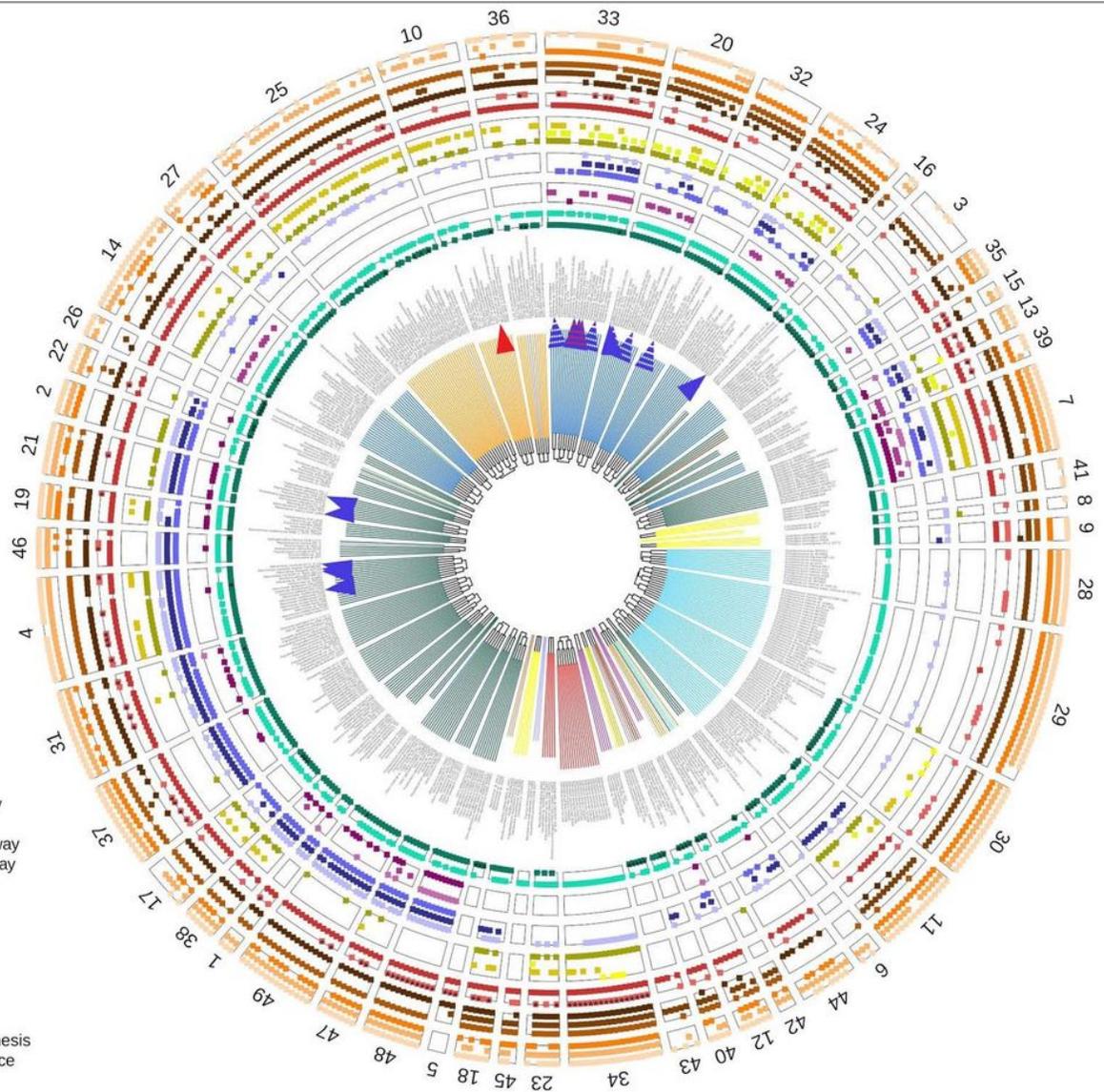


Figure 3

Overview on interaction-traits across genome functional clusters (GFCs). Each slice shows the interaction traits present in a GFC and, as dendrogram, the functional similarity of genetic traits of the grouped genomes. Known interactions (described in the referenced literature) between bacteria and phytoplankton are marked with arrows; a blue arrow indicates a positive interaction (an enhancing effect on phytoplankton growth), a red arrow a negative interaction, and a blue-red arrow a positive interaction that eventually becomes negative. A dashed arrow indicates a known interaction involving a bacterial genotype with a high similarity to one of the genomes included in the analysis. Asterisks in siderophores annotation indicate the presence of the specific vibrioferrin synthetic pathway along with the secondary

metabolite pathway, while asterisks in the antimicrobial resistance annotation indicate that only generic resistance traits were annotated for that genome.

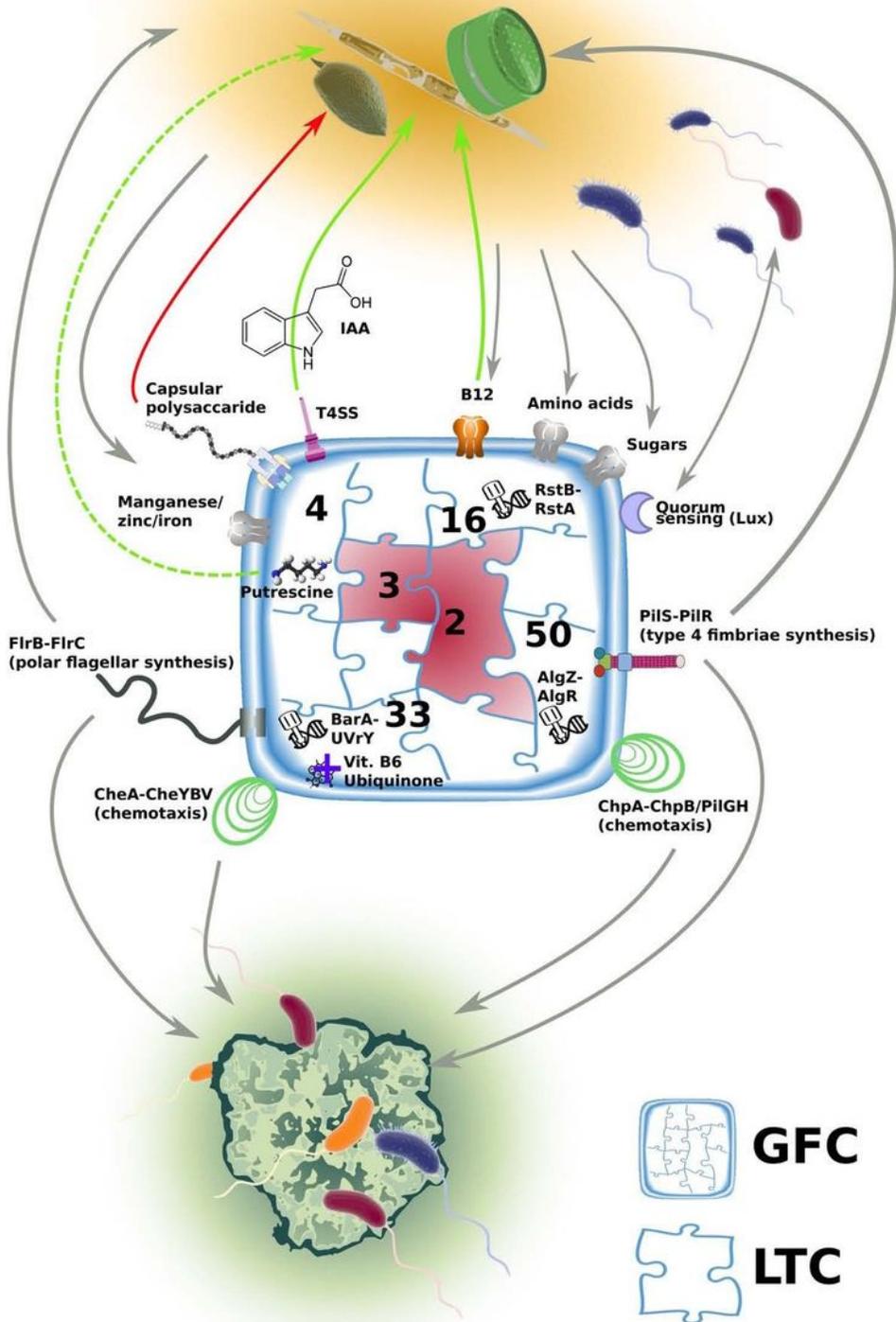


Figure 4

Conceptual representation of a hypothetical bacterial cell characterized by the presence of the core linked trait clusters (LTCs) 2 and 3 (marked in red) and different common/ancillary LTCs mediating interactions with phytoplankton, other bacteria and particles. Green arrows indicate positive effects (e.g. enhancing

growth), grey arrows are for metabolites/chemical exchange, movement or attachment, and red arrows for negative effects (e.g. pathogenicity). LTCs 4 and 16 could be mainly involved in interactions with phytoplankton, while LTCs 33 and 50 in interactions with organic matter particles.

Supplementary Files

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