



Metagenome-scale metabolic modelling for the characterization of cross-feeding interactions in Microcystis-associated microbial communities, in the context of freshwater cyanobacterial blooms

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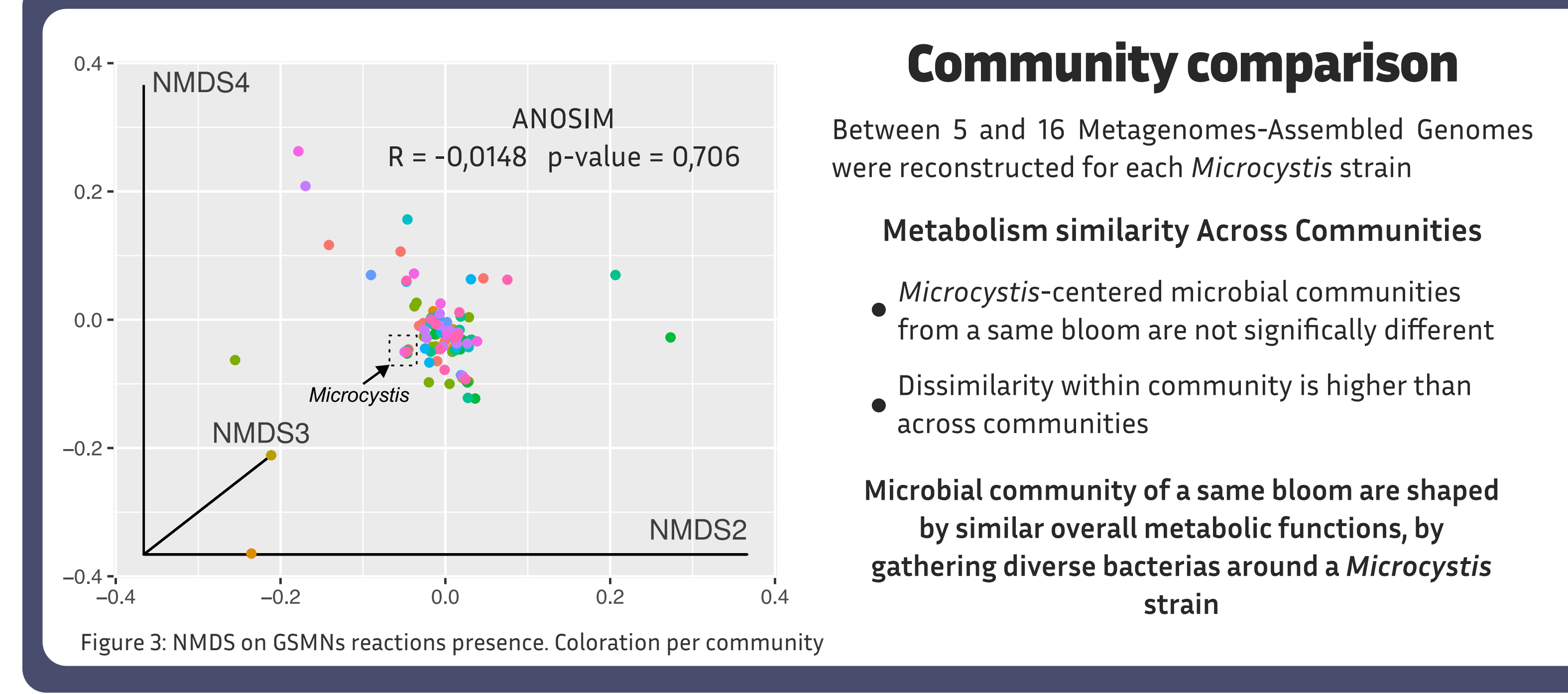
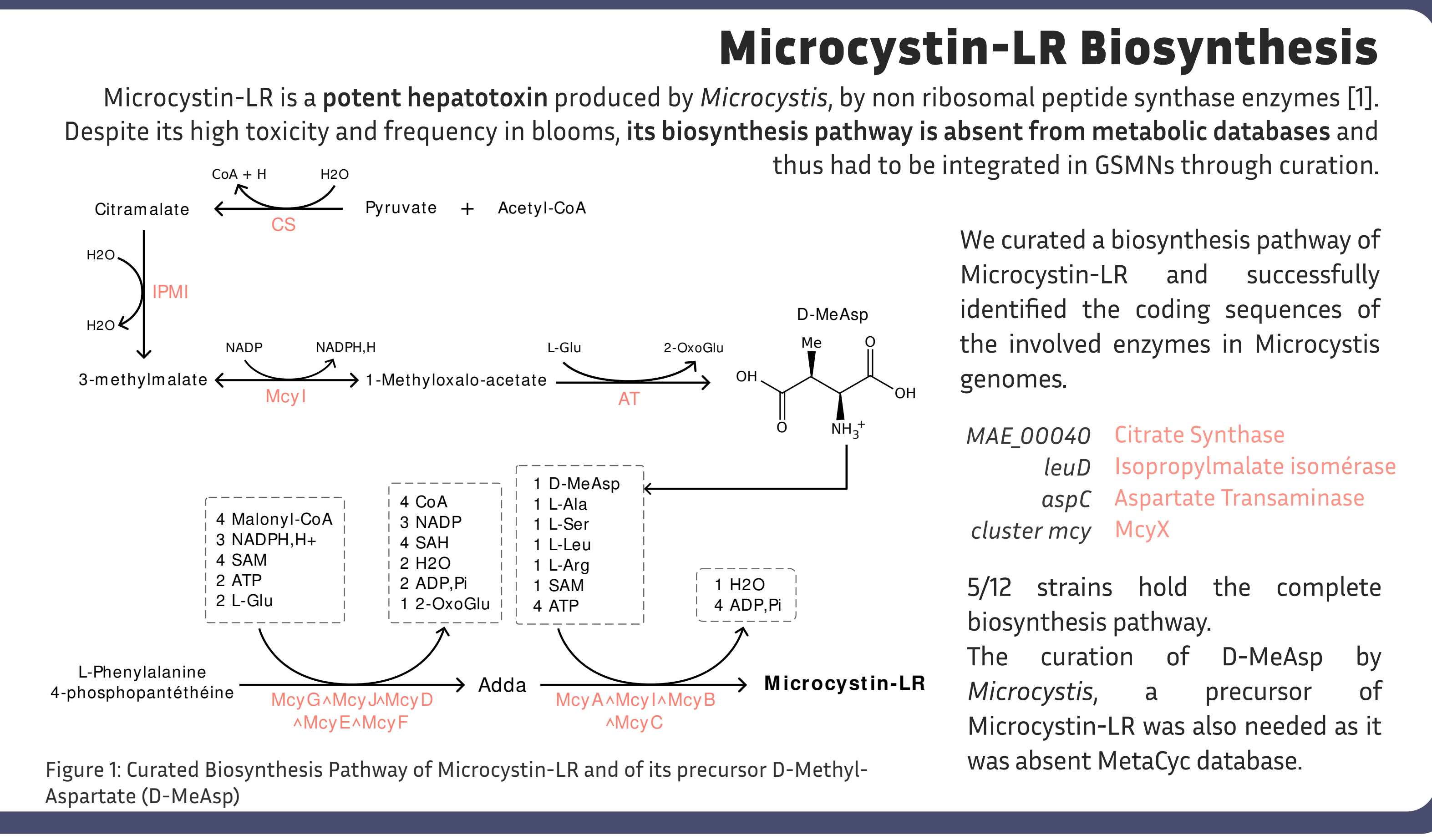
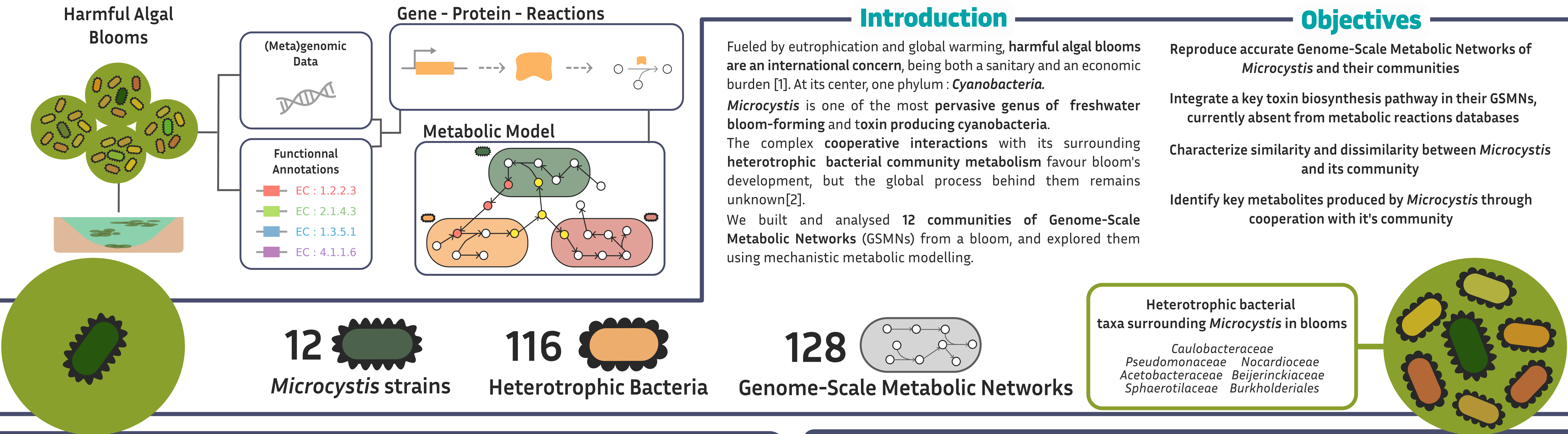


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Metagenome-scale metabolic modelling for the characterization of cross-feeding interactions in *Microcystis*-associated microbial communities, in the context of freshwater cyanobacterial blooms

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Microcystis	Complete metabolic pathway	Reactions		Genes	Metabolites
		amount	with genes association (%)		
PMC1366.22	340	1776	68.1	4483	1882
PMC1367.22	329	1772	68.0	4729	1903
PMC1354.22	342	1845	67.3	4600	1968
PMC1371.22	343	1783	67.9	4859	1891
PMC1364.22	342	1793	68.5	4623	1911
PMC1372.22	343	1782	67.9	4856	1890
PMC1374.22	329	1772	68.0	4764	1903
PMC1369.22	333	1787	68.7	4956	1913
PMC1375.22	344	1788	67.7	4815	1906
PMC1356.22	344	1788	67.7	4811	1906
PMC1365.22	339	1791	68.5	4226	1897
PMC1358.22	340	1779	68.2	4460	1884

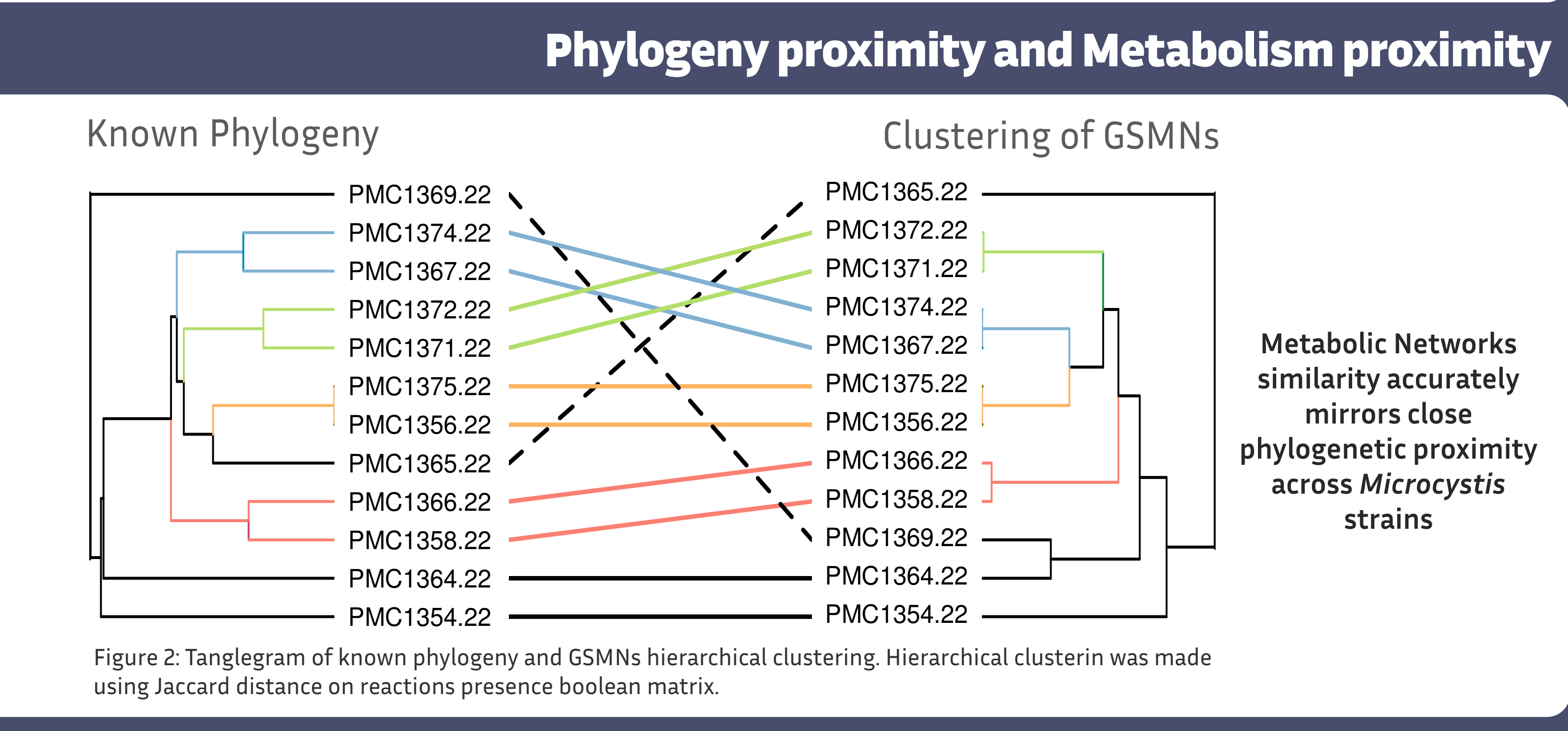
Automatic GSMNs Reconstruction

PathwayTools mpwt

MetaCyc

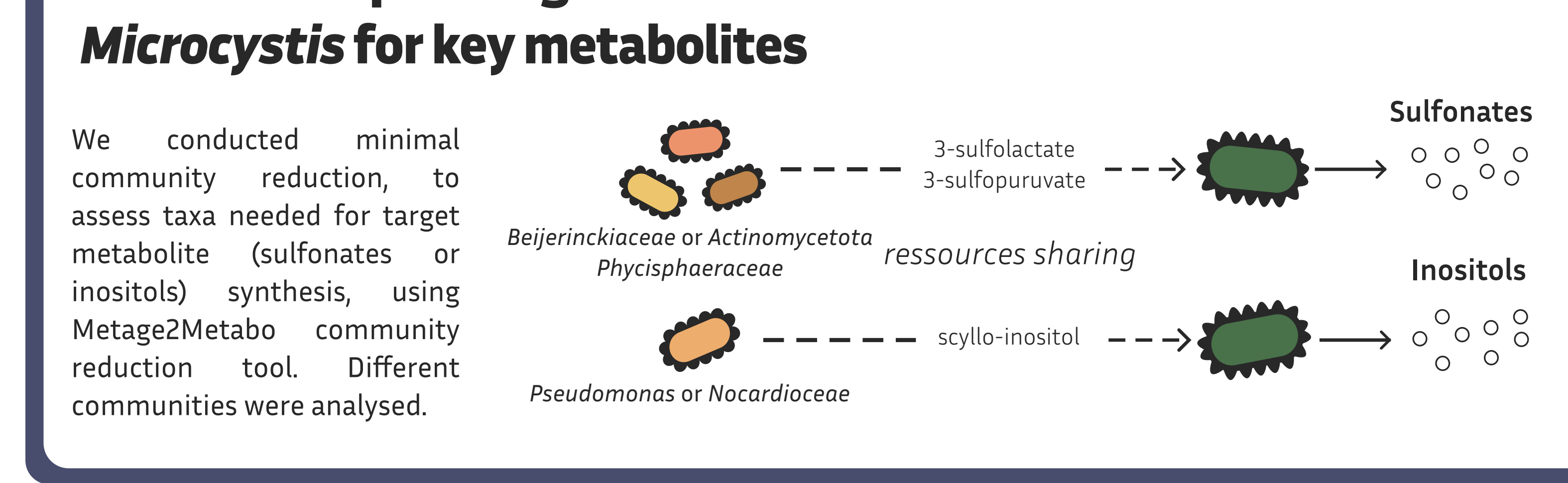
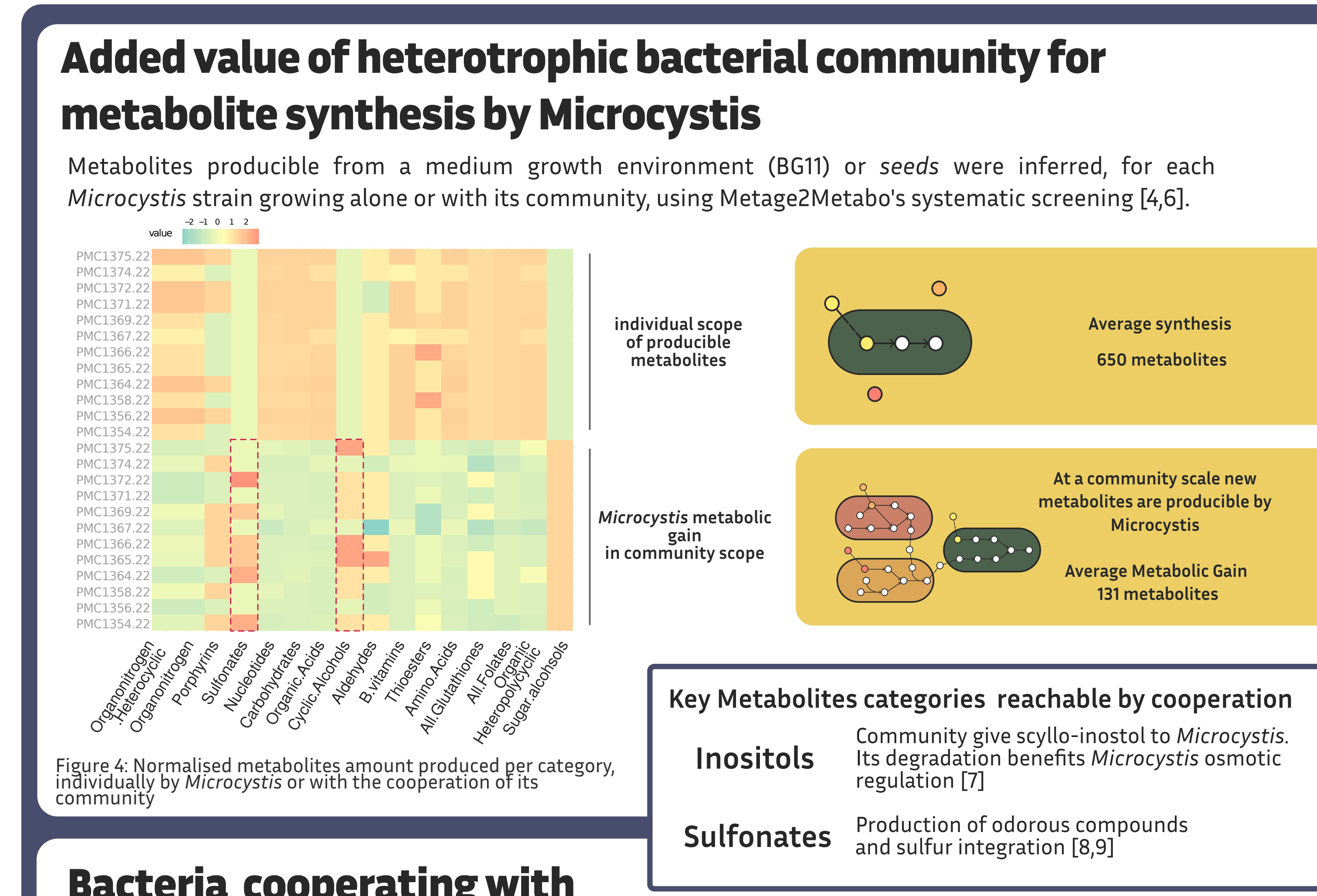
Metabolic Pathway Genome Database [5]

PathwayTools is a gene to reactions software for metabolic network reconstruction [3]. The process is automatised with the mpwt package [4].



Conclusion

We curated a Microcystin-LR toxin biosynthesis pathway in a collection of 12 *Microcystis* GSMNs. Out of the 12, 5 hold the full pathway. Our reconstructions of GSMNs are consistent with the phylogeny of *Microcystis*, which suggests accurate reconstruction of its metabolism. We assessed the metabolic functions carried by the heterophic community of *Microcystis* and identified categories of metabolites that are only producible through cooperation with the community and are expected to benefit the metabolism of *Microcystis*. For those categories, we identified essential taxa enabling target molecules synthesis by *Microcystis*.



Perspectives

We expect new (meta)genomic data from long-read sequencing, which may better capture the genomes of the heterotrophic community and its complementarity with *Microcystis*. Parallel to this work, metabolomic analysis on those same communities are conducted and results will furtherly be integrated into our analysis.

Funding

COMIC Project

Metaprogramme HOLOFLUX

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