

BACKGROUND AND QUESTIONS

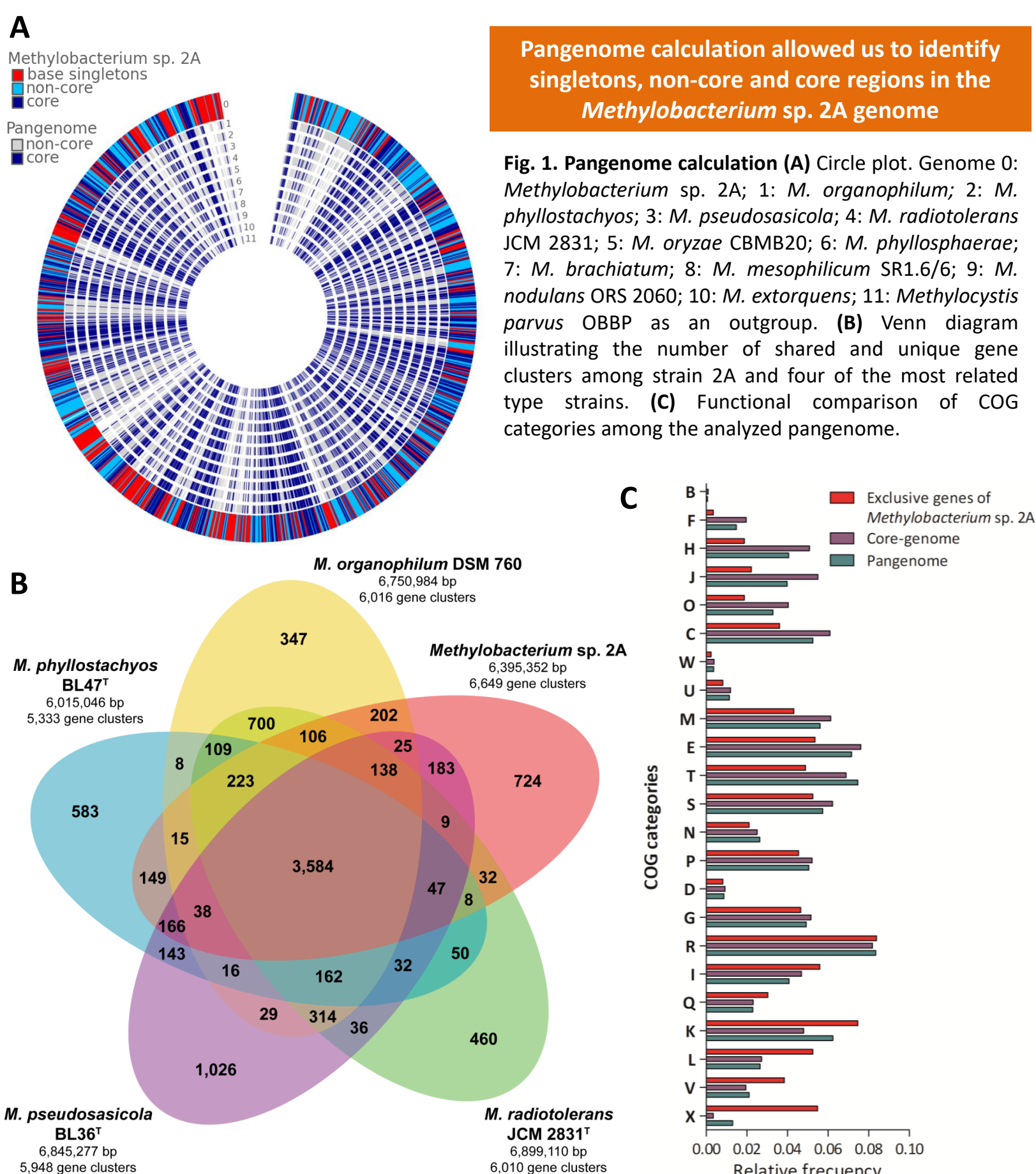
Genomic analysis has become an established tool in the characterization of plant-beneficial microbes since it offers the opportunity to study the full arsenal of a strain [1]. In this work, we analyzed the genome of *Methylobacterium* sp. 2A, a plant growth-promoting rhizobacteria (PGPR) isolated from roots of potato plants that has important biotechnological features such as plant growth promotion and biocontrol activities [2].

Since its genome sequence was obtained we wanted to answer these questions:

- ① How many genes are shared between this isolate and other related members of the genus?
- ② Does it have any genomic islands (GI) or genes recently acquired through horizontal gene transfer (HGT) that could be involved in the environmental adaptability of this isolate?

RESULTS AND CONCLUSIONS

① Comparative genomics of *Methylobacterium* sp. 2A and closest relatives through the pangenomic approach



Pangenome calculation allowed us to identify singletons, non-core and core regions in the *Methylobacterium* sp. 2A genome

Fig. 1. Pangenome calculation (A) Circle plot. Genome 0: *Methylobacterium* sp. 2A; 1: *M. organophilum*; 2: *M. phyllostachyos*; 3: *M. pseudosasicola*; 4: *M. radiotolerans* JCM 2831; 5: *M. oryzae* CBMB20; 6: *M. phyllosphaerae*; 7: *M. brachiatum*; 8: *M. mesophilicum* SR1.6/6; 9: *M. nodulans* ORS 2060; 10: *M. extorquens*; 11: *Methylocystis parvus* OBBP as an outgroup. **(B)** Venn diagram illustrating the number of shared and unique gene clusters among strain 2A and four of the most related type strains. **(C)** Functional comparison of COG categories among the analyzed pangenome.

A core-genome of 3,584 gene clusters was identified; 724 gene clusters are exclusive of this isolate

Mobilome (X), Defense mechanisms (V) and Secondary metabolites biosynthesis (Q) COG categories are overrepresented in *Methylobacterium* sp. 2A

② GI analysis, the nodulation protein case, and the search for genes involved in the environmental adaptability of this isolate

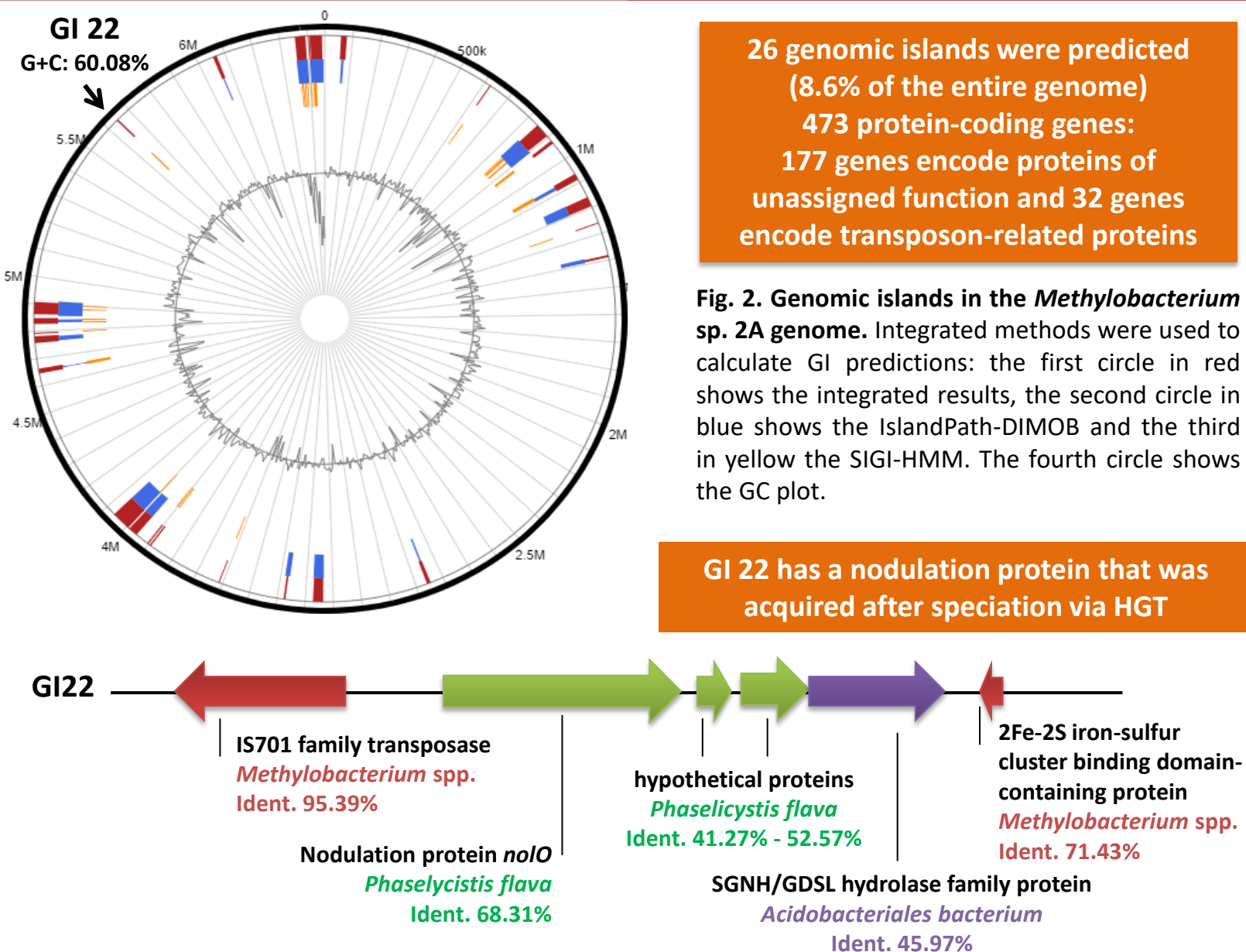


Fig. 3. Diagram of the GI 22. Relative position and putative origin of each gene is shown.

GI 15 and GI 24 have genes involved in the environmental adaptability of this isolate

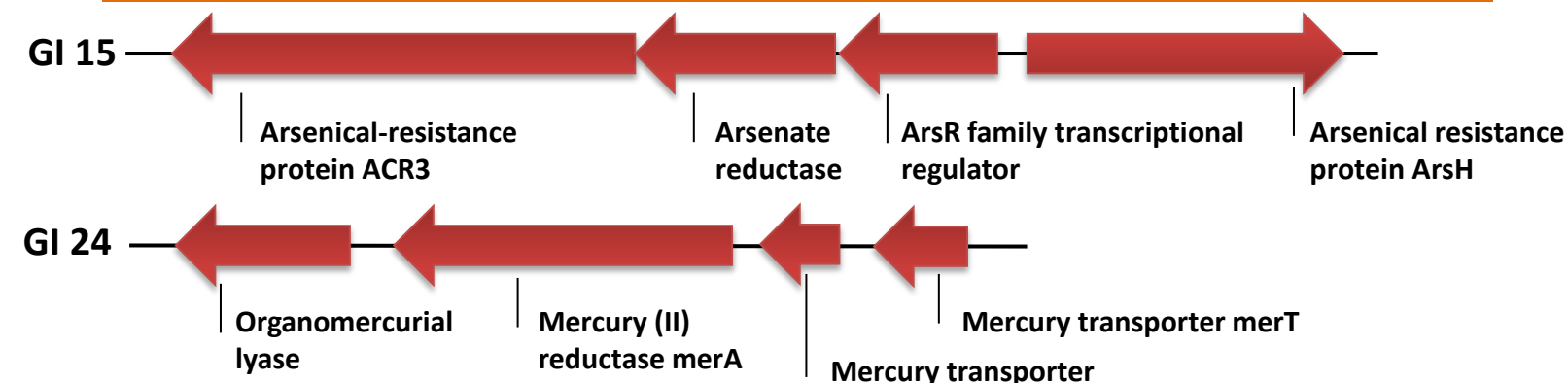


Fig. 4. Diagram showing the resistance gene clusters for arsenic and mercury in GI 15 and GI 24, respectively.

Other genes involved in heavy metal resistance are not located in GI

- Cobalt/zinc/cadmium resistance:** Cobalt-zinc-cadmium resistance protein czcA; Cobalt-zinc-cadmium efflux system protein czcD
- Copper resistance:** copper resistance protein B copB
- Chromate resistance:** chromate transporter chrA

METHODS

Pangenome was obtained through OrthoMCL and data was analyzed by R Studio. COG categories were assigned through COGNITOR. HGT were inferred with IslandViewer followed by manual adjustments.

REFERENCES

- [1] Paterson et al. (2017) The contribution of genome mining strategies to the understanding of active principles of PGPR strains. FEMS Microbiol Ecol 93:1–12. [2] Grossi et al. (2020) *Methylobacterium* sp. 2A is a Plant Growth-Promoting Rhizobacteria That Has the Potential to Improve Potato Crop Yield Under Adverse Conditions. Front Plant Sci 11:1–15.