

Arcobacteraceae: genome adaptation and genome size reduction in species isolated from animals and human demonstrated by comparative genome analysis



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Introduction: the *Arcobacteraceae* bacterial family includes species considered **foodborne pathogens**, present on different foods and animals (Ramees et al. 2017). *Arcobacter butzleri* and *Arcobacter cryaerophilus* are the two most isolated species from human clinical samples and have been isolated from food of animal origin. The different abilities of the *Arcobacteraceae* to survive in various hosts and environmental conditions suggest an evolutionary pressure linked to genome adaptation.

Aims: study of *Arcobacteraceae* pangenome to characterize possible relationships between **20** validly described species (Fig. 1).

Methods: the analyses have been conducted on type strains **whole genomes sequencing (WGS; Illumina sequencing)**. The species were included in different groups (Pérez-Cataluña et al. 2018) considering the isolation sources and information present in literature (Fig. 1, 2C-D). Several **bioinformatics tools** enabled the obtainment of **pangenome** information (Roary, Panaroo, PPanGGOLiN) and **gene classes** (EggNOG/e-mapper).

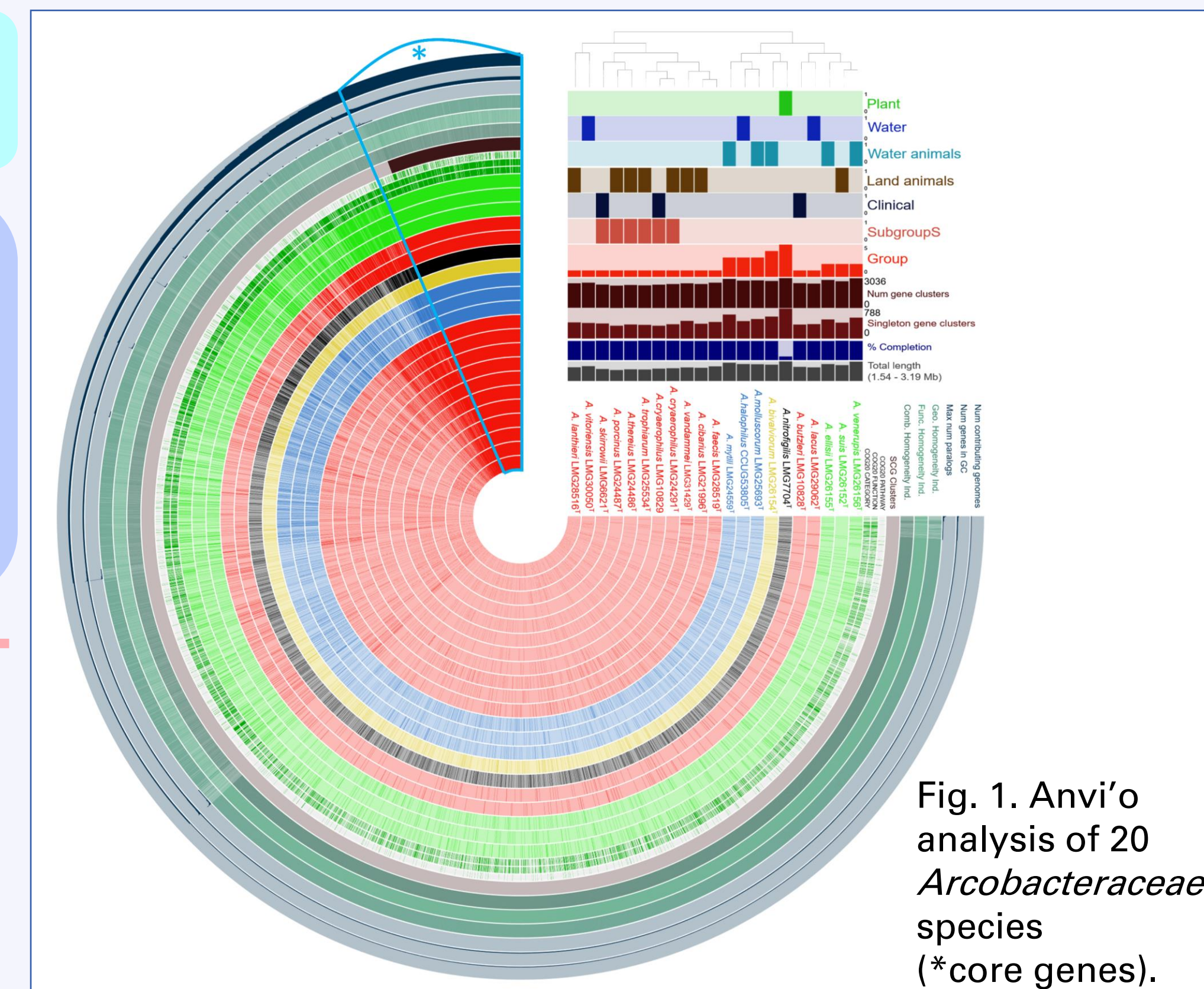


Fig. 1. Anvi'o analysis of 20 *Arcobacteraceae* species (*core genes).

RESULTS AND DISCUSSION:

Gene Partitions	% Genomes	Roary	Panaroo	PPanGGOLiN
Core	99 - 100	296	505	269
Soft core	95 - 99	43	90	326
Shell genes	15 - 95	1839	1965	366
Cloud genes	0 - 15	21237	13629	23178

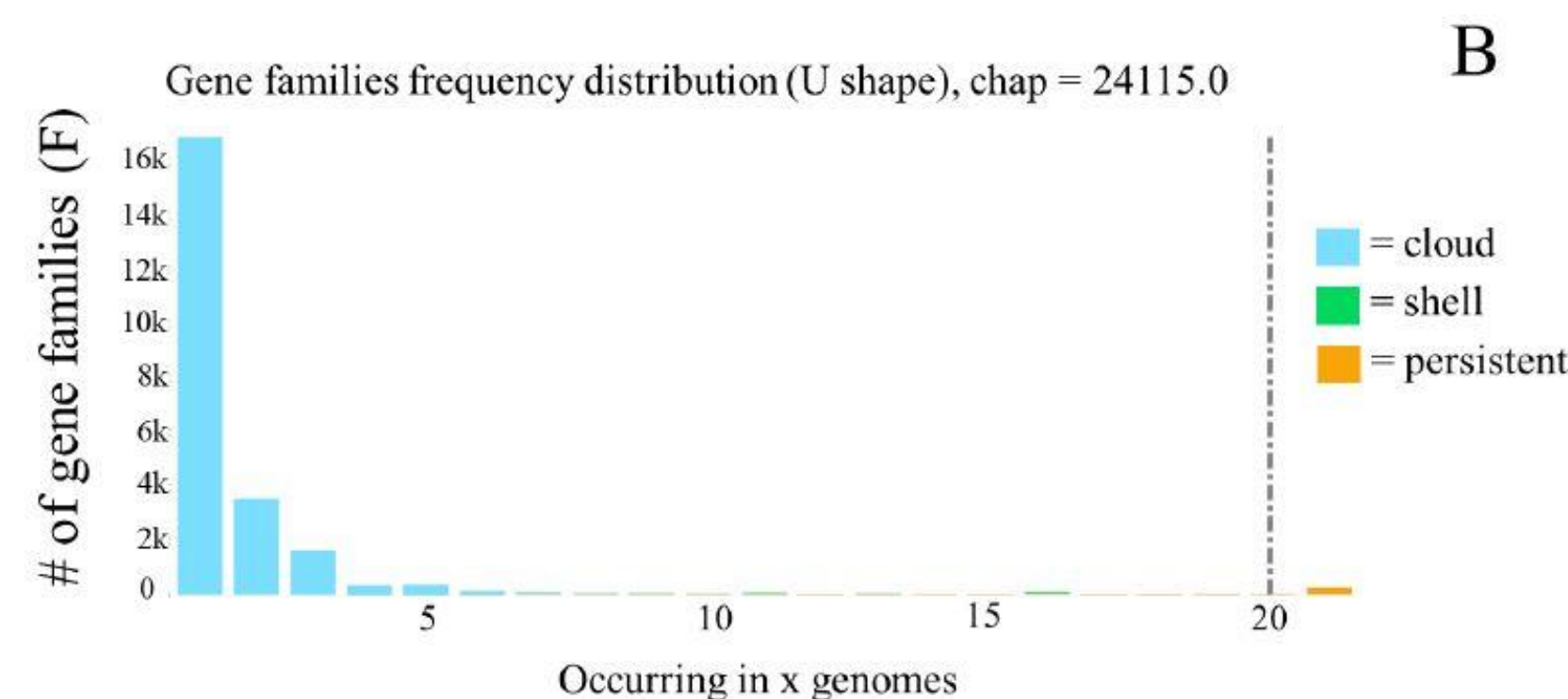
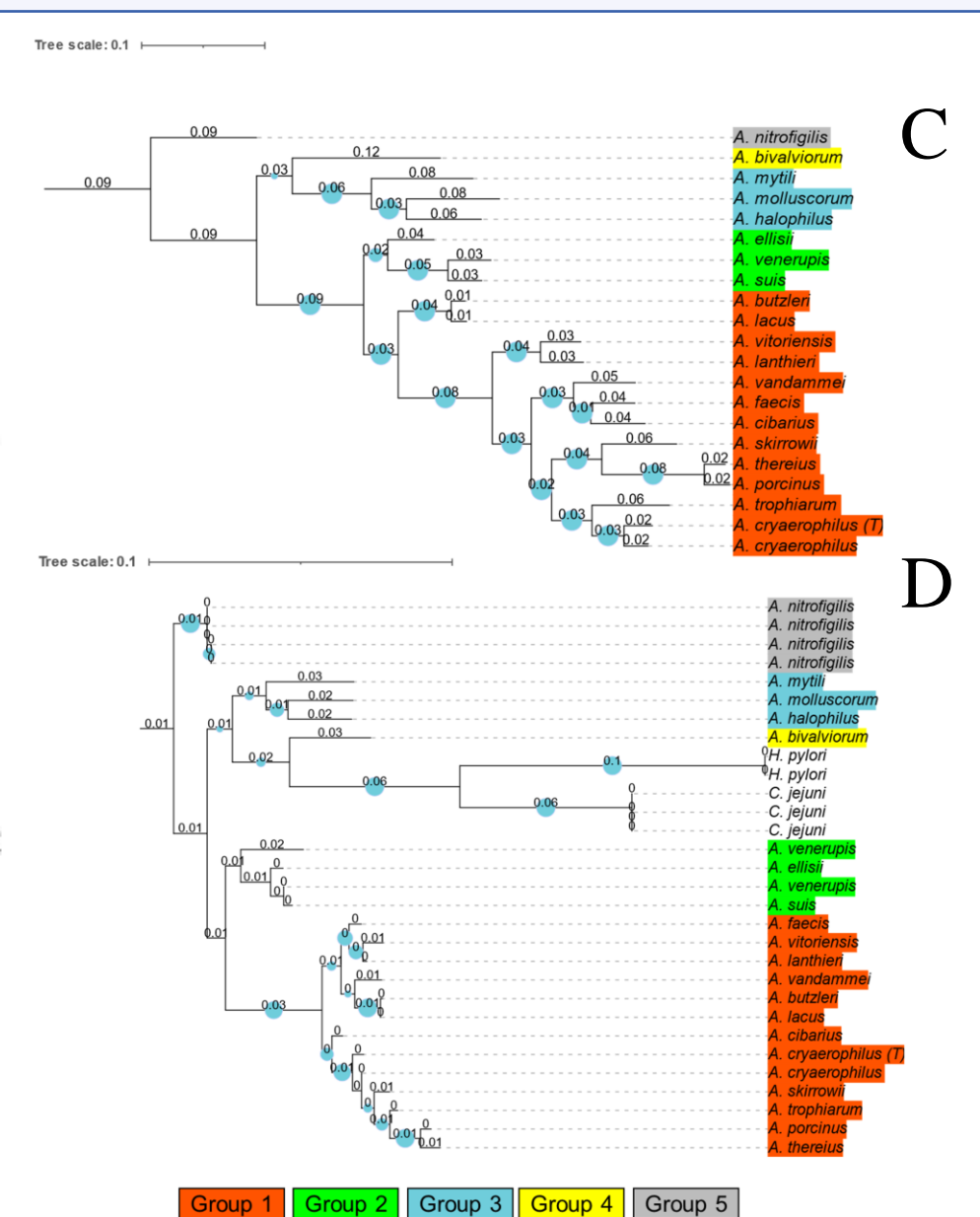


Fig. 2. Gene (A) and gene families (B) pangenome partitions; 107 core amino acid sequences (C) and 16S rDNA (D) dendrograms.



Separation of *A. butzleri* and *Arcobacter lacus* from their group

(g1; Gene presence/absence; Fig. 1).

The pangenome partitions support the presence of a **single genus** in *Arcobacteraceae* family (core genes; Fig 2A-B).

Dendrograms distance dissimilar between proposed groups (Fig. 2C-D).

Smaller genome size of the animal related species was observed suggesting an **evolutionary adaptation to hosts** (Fig. 1).

The gene class compositions in **animal and human-associated species** showed a **higher percentage of virulence-related** gene classes, among them cell motility genes (Fig 3).

Some **orthologues** like MotA/TolQ/ExbB proton channel family (TonB-related; virulence functions), were positively **correlated to** the animals related species suggesting a **specific function** of different orthologues while a strong correlation between pathogenic species and ten putative virulence genes was not observed.

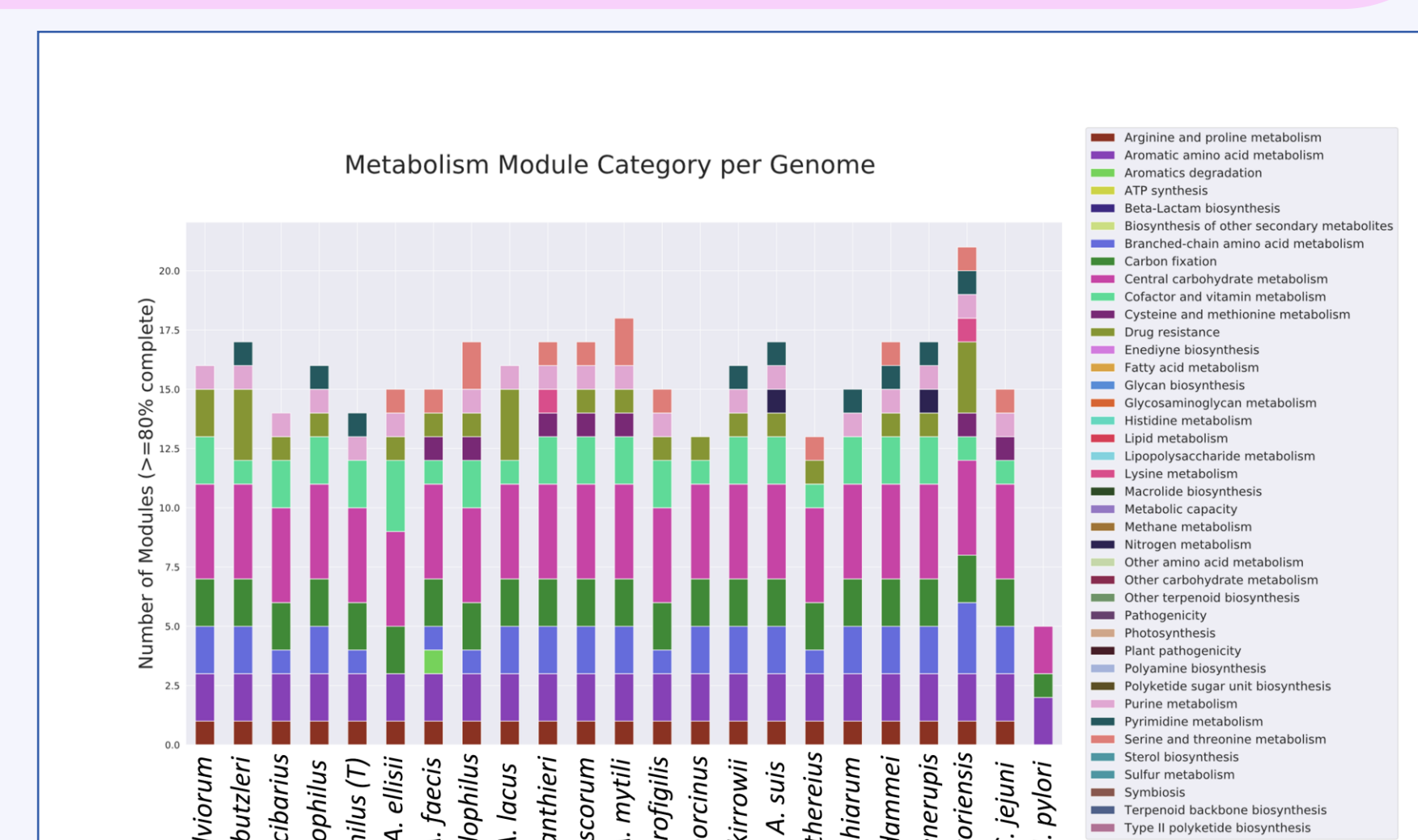


Fig. 3. Metabolism Module categories per genome annotated with MicrobeAnnotator.

Conclusions:

- The genome analysis identified the presence of specific **genes linked to different species groups**.
- A **division into pathogenic and non-pathogenic species** is suggested, supporting future research on food safety and public health.
- The division in **several genera of *Arcobacteraceae*** is **not supported** by WGS data as stated by other authors (On et al. 2020).

Literature:

- Buzzanca, D., Kerkhof, P., et al. (2023) '*Arcobacteraceae* comparative genome analysis demonstrates genome heterogeneity and reduction in species isolated from animals and associated with human illness', *Heliyon*, 9(7), p. e17652.
- On, S.L.W. et al. (2020) 'A critical rebuttal of the proposed division of the genus *Arcobacter* into six genera using comparative genomic, phylogenetic, and phenotypic criteria', *Systematic and Applied Microbiology*, 43(5), p. 126108.
- Pérez-Cataluña, A. et al. (2018) 'Revisiting the taxonomy of the Genus *Arcobacter*: Getting Order From the Chaos', *Frontiers in Microbiology*, 9(2077), p. 2077.
- Ramees, T.P. et al. (2017) '*Arcobacter*: An emerging food-borne zoonotic pathogen, its public health concerns and advances in diagnosis and control - A comprehensive review', *Veterinary Quarterly*, 37(1), pp. 136-161.