Food-borne bacteria undercover: MAG reconstruction can reveal the biases in cultured food bacterial isolates and help identifying new species and strains

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Food-Borne Bacteria Undercover

MAGs (metagenome-assembled genomes) can reveal biases in cultured food bacterial isolates and help identifying new species and strains.

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HYPOTHESIS

Food-borne bacteria are considered non-recalcitrant to isolation on culture medium. However, recent studies on food microbiota using 16S amplicon sequencing has revealed that this paradigm deserves to be re-evaluated scientifically. The most obvious bias concerns the search for subdominant species (or even strains), the most part of which pass under the detection filter of isolation practices (requirement for non-canonical growth conditions, or less competitive than dominant strains), although these taxa may represent an important functional role, or participate in certain processes in a transient manner (dynamic succession of populations).

MODELS & DATASET

The dataset is composed of ~80 food metagenomes of raw sausages[A] and fermented vegetables[B]. To verify the hypothesis, 3 Target species were studied as models:

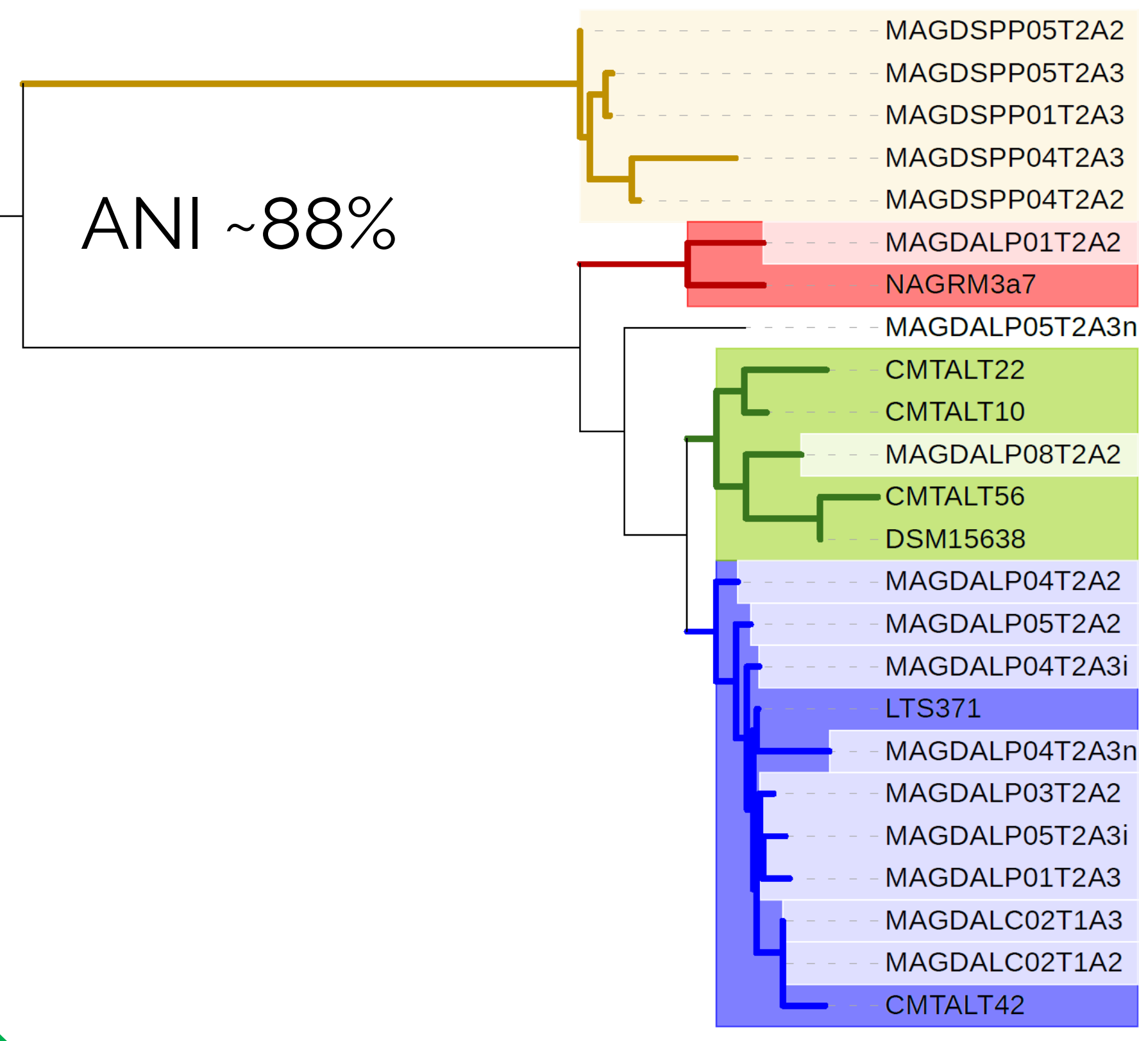
1. ***Latilactobacillus sakei*** (60 genomes available, high diversity of strains)
2. ***Brochothrix thermopshacta*** (25 genomes available, low diversity of strains)
3. ***Dellaglioa algida*** (4 genomes available, hard to cultivate)

RESULTS

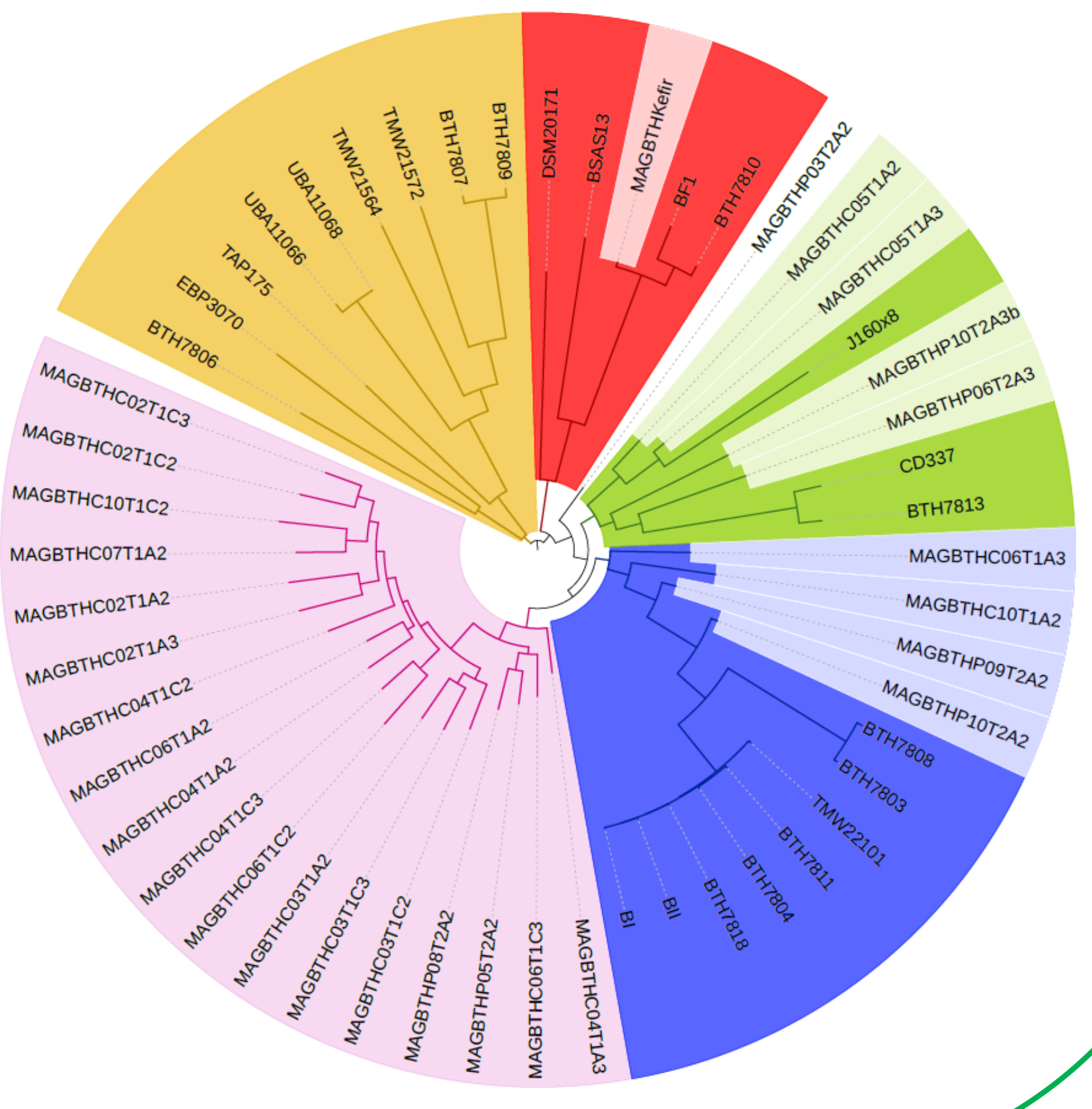
1. *Latilactobacillus sakei*

Phylogenomic trees of core genomes for the three target species. Isolates are shown in colored background whereas MAGs are shown in lighter colored background. Colors indicate main phylogenetic clades. New clades can clearly be detected for each species (yellow for *L. sakei* and purple for *B. thermophacta*). For *D. aligida* (tree N°2), average Nucleotide index revealed that some MAGs (i.e; MAGDSP in yellow background) are representing a new candidate *Dellaglioa* species.

2. *Dellaglioa algida*

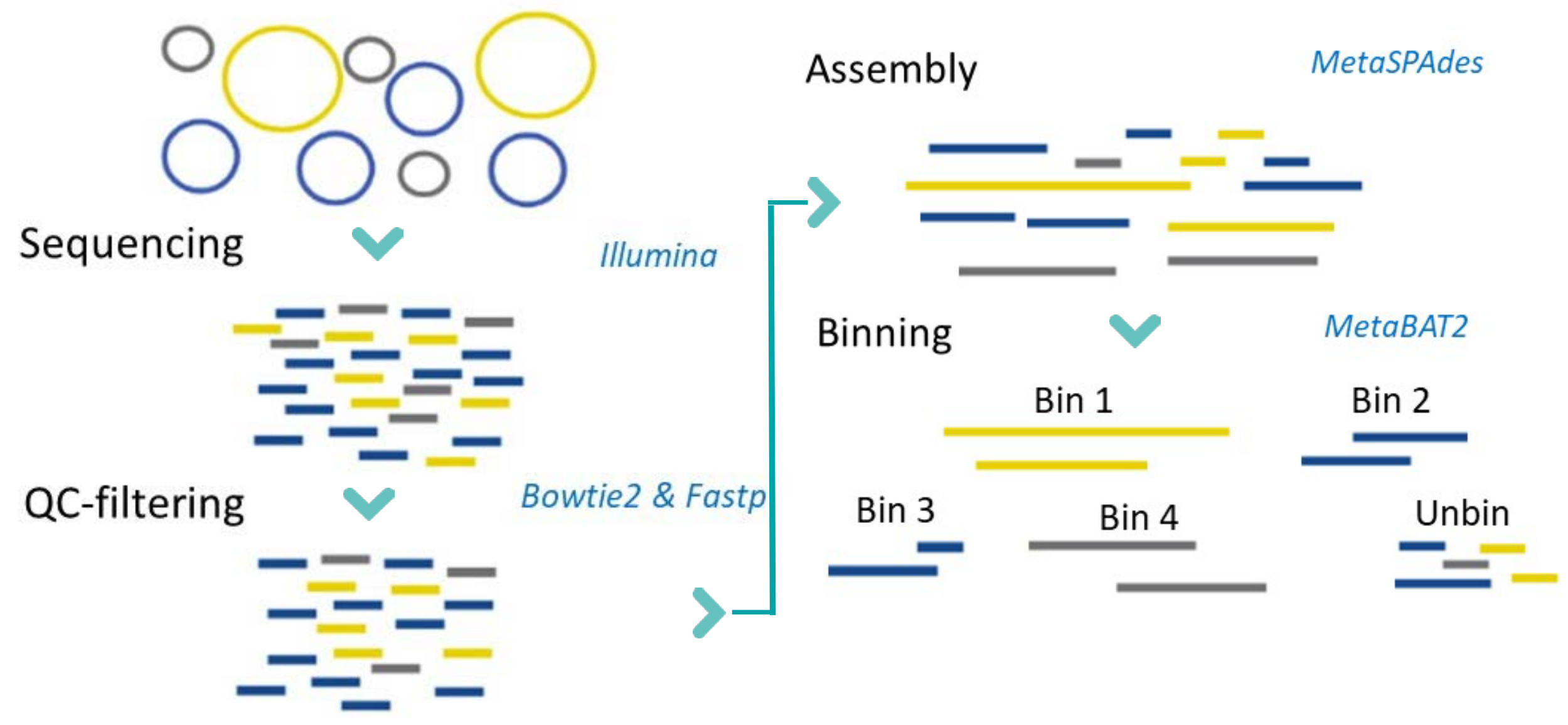


3. *Brochothrix thermosphacta*

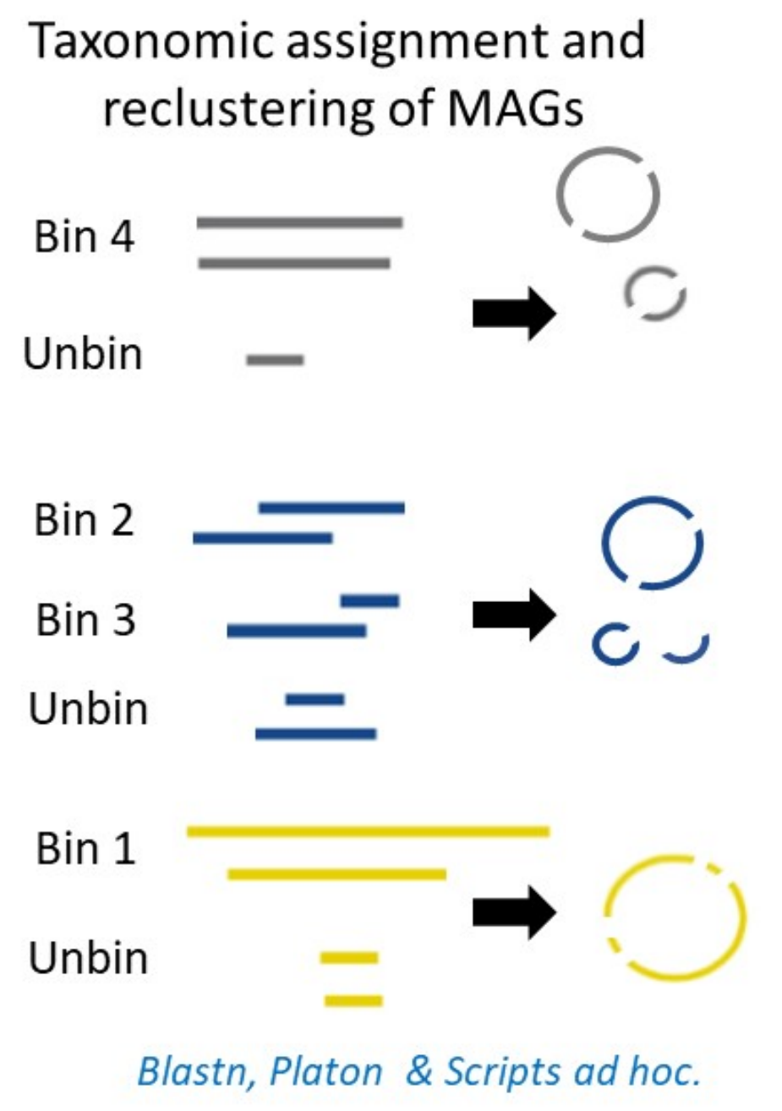


METHODS

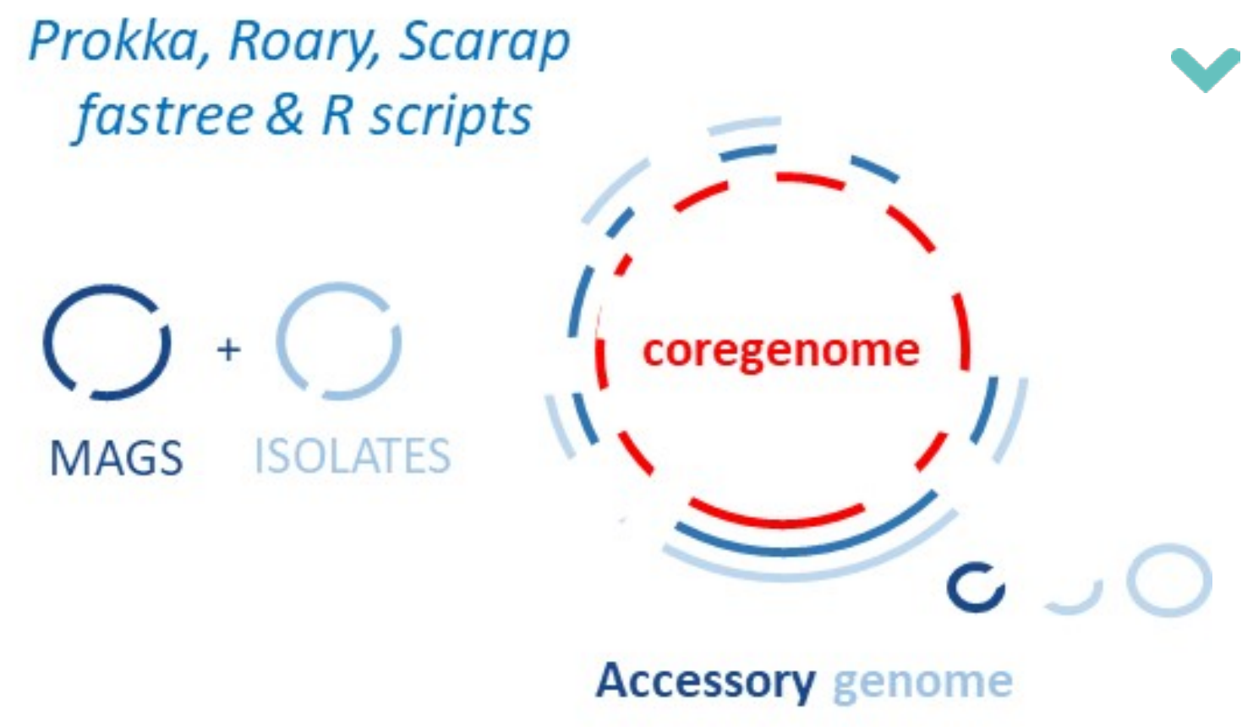
1. Assembly and binning of MAGs from metagenomic data



2. Refining the MAGs by clustering several bins and unbinned contigs using taxonomic assignment = better recovery of genomic islands and plasmids



3. Comparative phylogenomic analysis of core and accesory genomes between MAGs and published genomes of isolates



CONCLUSIONS

- ➢ With only few metagenomes and few target species, our results clearly demonstrate the existence of strong biases in the diversity of cultured food-borne bacterial isolates.
- ➢ The potential of identifying new strains, clades or even species in food metagenomes is very high.

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References

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