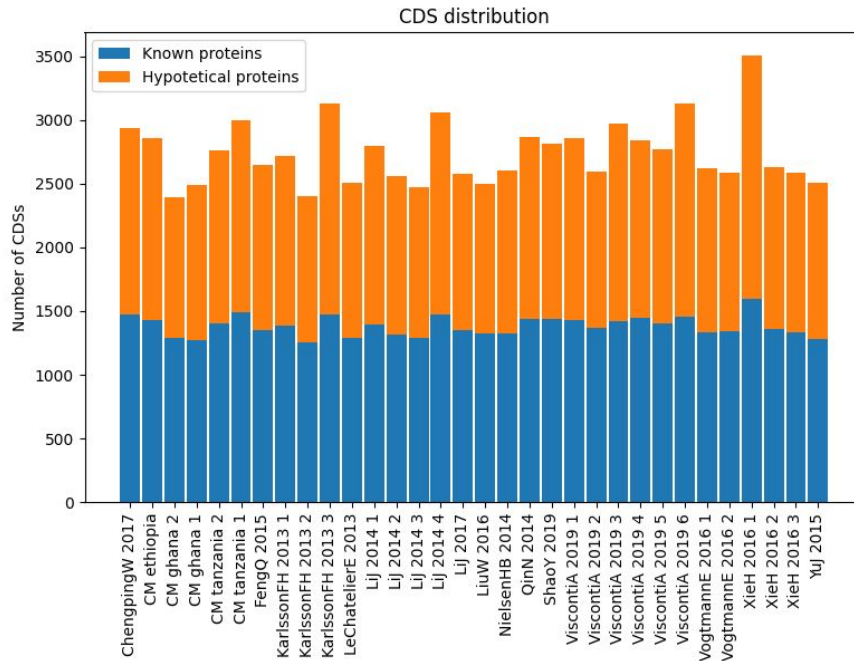


Analysis and characterization of a uSGB: SGB4894

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Master of Science in Quantitative and Computational
Biology - 2021/22
Computational Microbial Genomics

Genome annotation



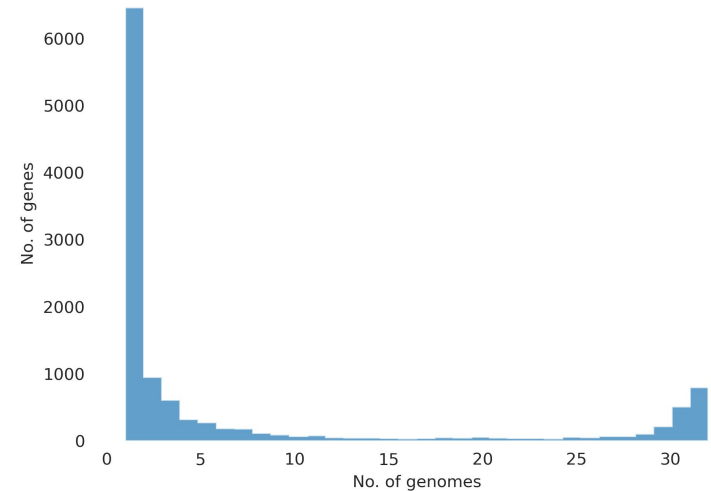
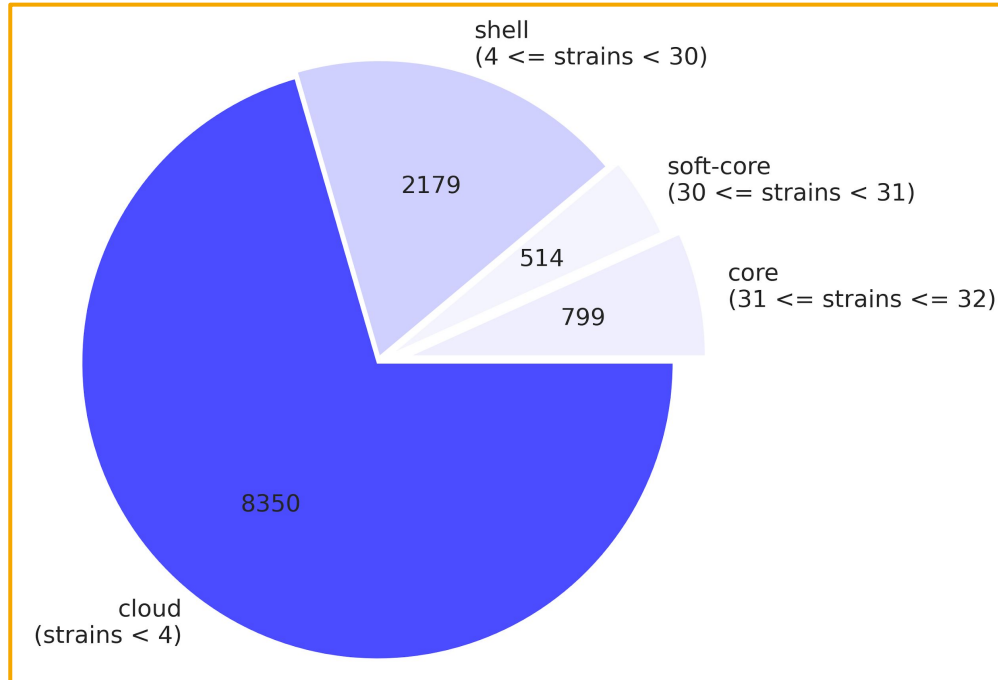
→ Performed using Prokka

CDS: 2741 ± 250

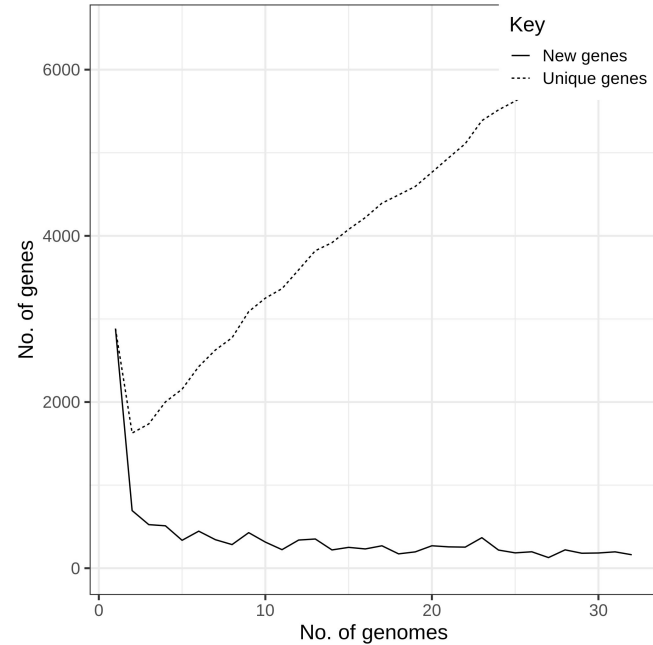
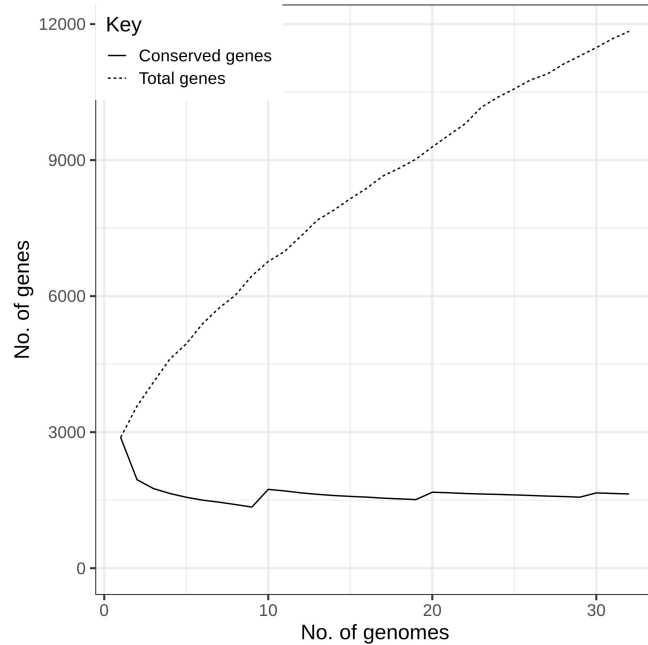
Known proteins: 1382 ± 78
Ratio over total CDSs: 49%

Hypothetical proteins: 1359 ± 177
Ratio over total CDSs: 51%

Pangenome analysis

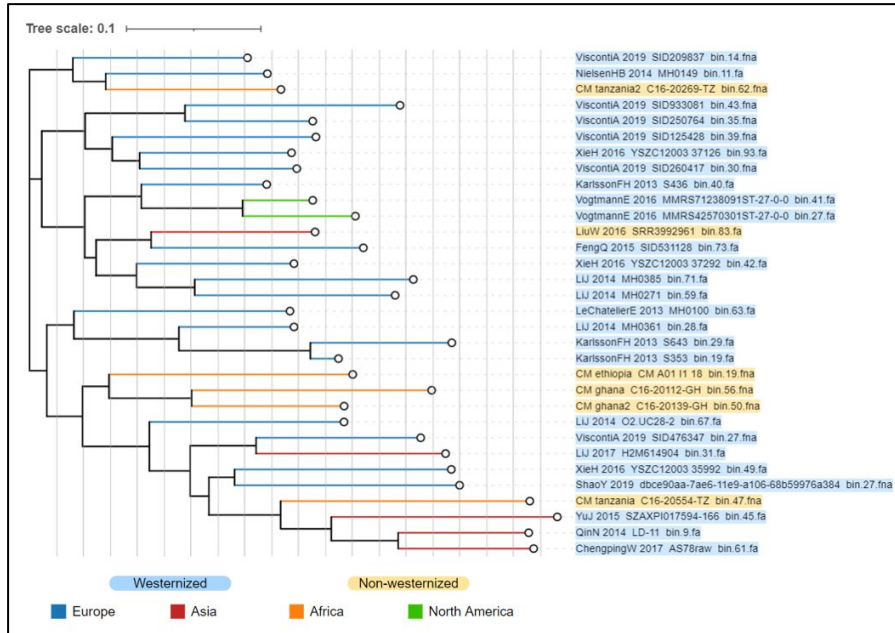


Open pangenome

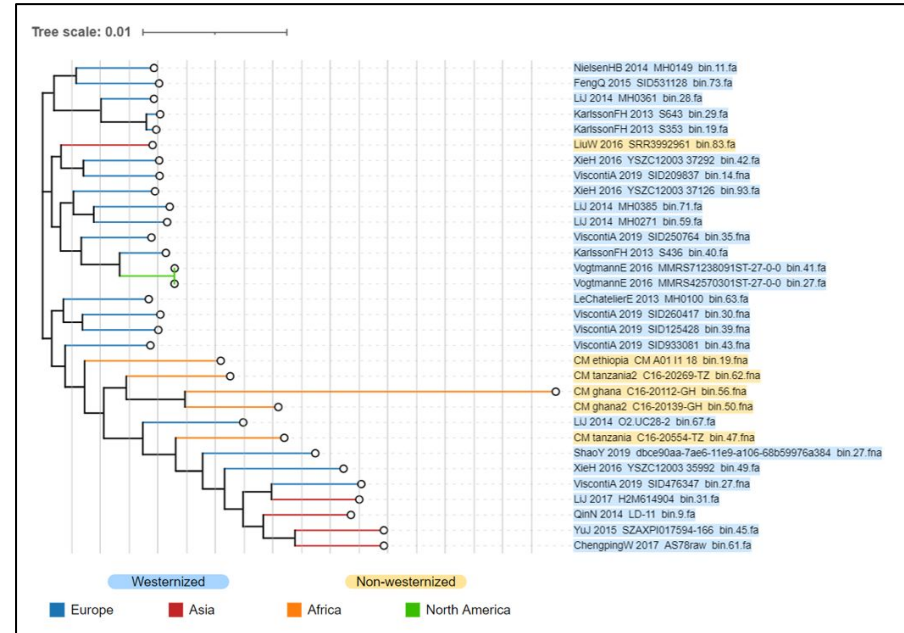


Phylogenetic analysis

Accessory genes presence/absence



Core genes alignment



Conclusion

WHAT WE KNOW:

- Bacterium from *Lachnospiraceae* family
- Individual genome of about 2700 genes (half of which unknown)
- Open pangenome
- Potentially three strains, one of which mostly associated with Africa and Asia

WHAT IS NEXT:

- Consolidating geographical correlation
- In depth protein functional characterization
- Retrieve new samples with more heterogeneous metadata