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Preliminary genome assembly of the *Wolbachia* endosymbiont of the South American fruit fly, *Anastrepha fraterculus* sp. 1.

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INTRODUCTION & AIMS

Wolbachia sp., an alpha-proteobacterium associated with reproductive phenotypes, has been described with a high prevalence in the South American fruit fly, *Anastrepha fraterculus* (Diptera: Tephritidae).

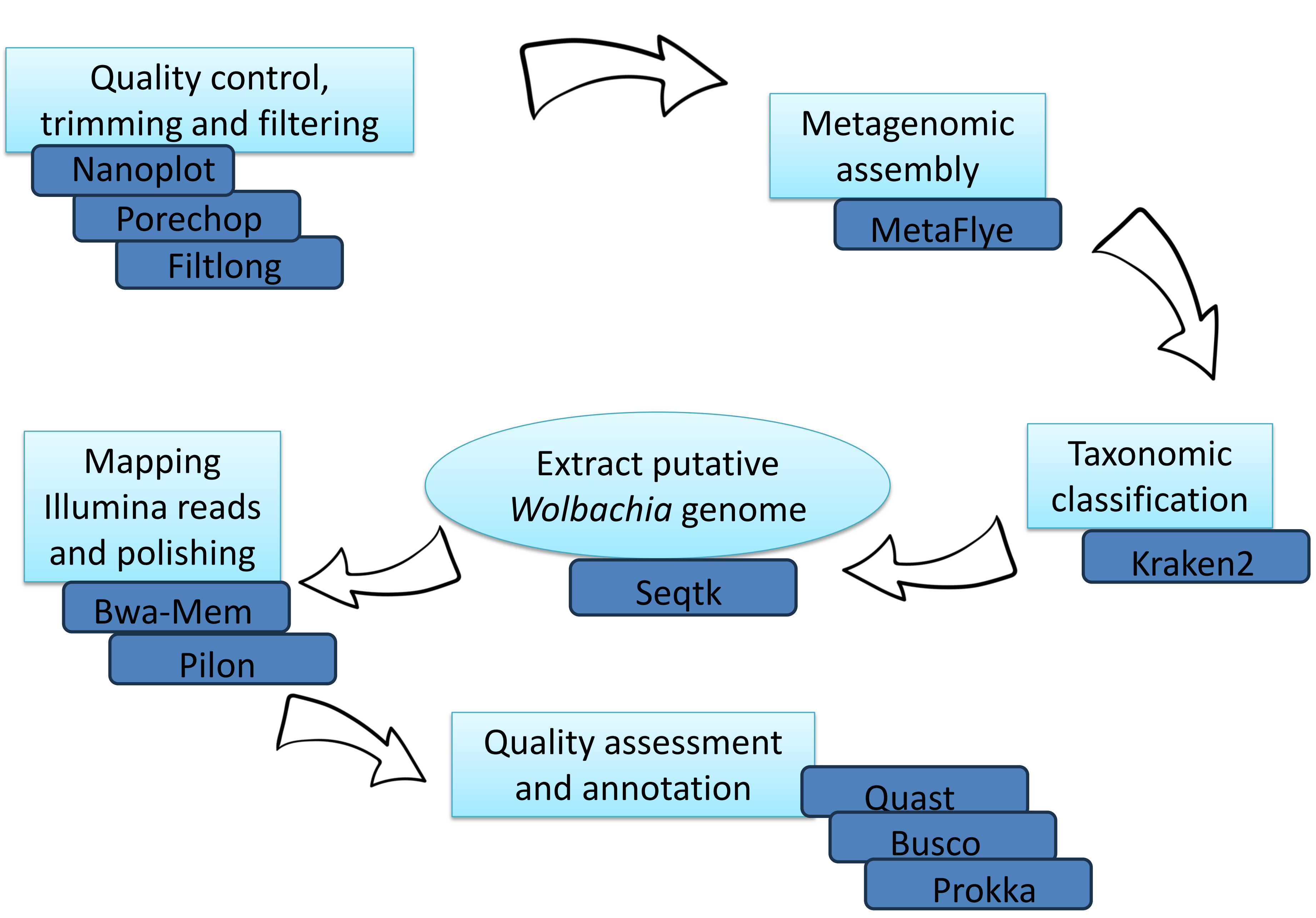
Two *Wolbachia* strains (*w*AfraCast1_A and *w*AfraCast2_A) have been identified in *A. fraterculus* by sequencing 15 loci. The phenotypes associated with the presence of *Wolbachia* in this fly were female-biased sex ratio in flies carrying *w*AfraCast1_A, and a protective effect against parasitoids in *A. fraterculus* larvae harboring wAfraCast2_A (Conte, 2021).

To enhance the genetic understanding of this bacteria, we assembled the *w*AfraCast2_A genome using sequence data from a whole-genome project of *A. fraterculus* morphotype 1 (Argentina).

METHODS

Total HMW DNA was extracted from a single *A. fraterculus* adult female → Oxford Nanopore and Illumina sequencing technologies

Rivarola *et al.* 2023.



Quality control, trimming and filtering
- Nanoplot
- Porechop
- Filtlong

Metagenomic assembly
- MetaFlye

Taxonomic classification
- Kraken2

Extract putative *Wolbachia* genome
- Seqtk

Mapping Illumina reads and polishing
- Bwa-Mem
- Pilon

Quality assessment and annotation
- Quast
- Busco
- Prokka

RESULTS

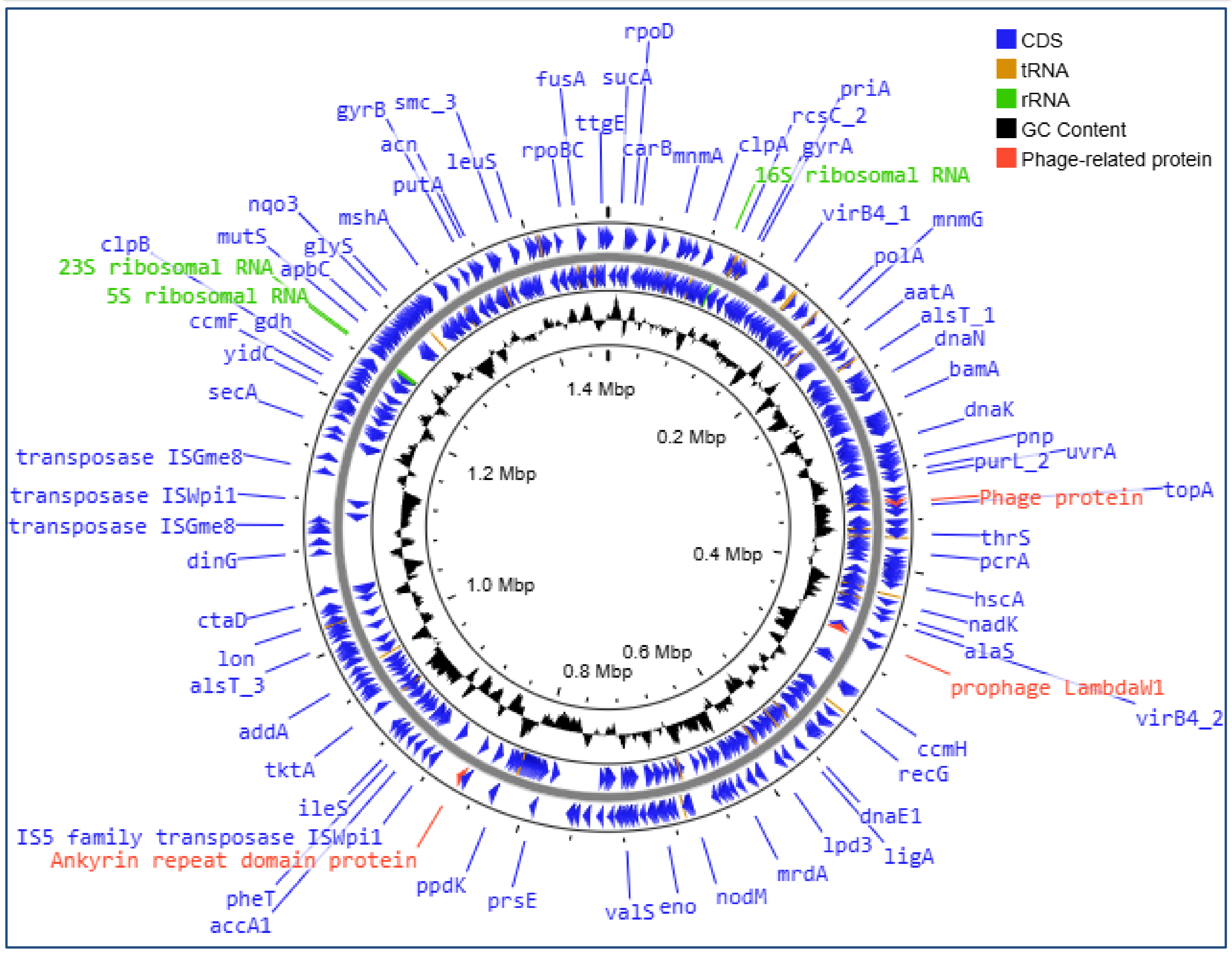
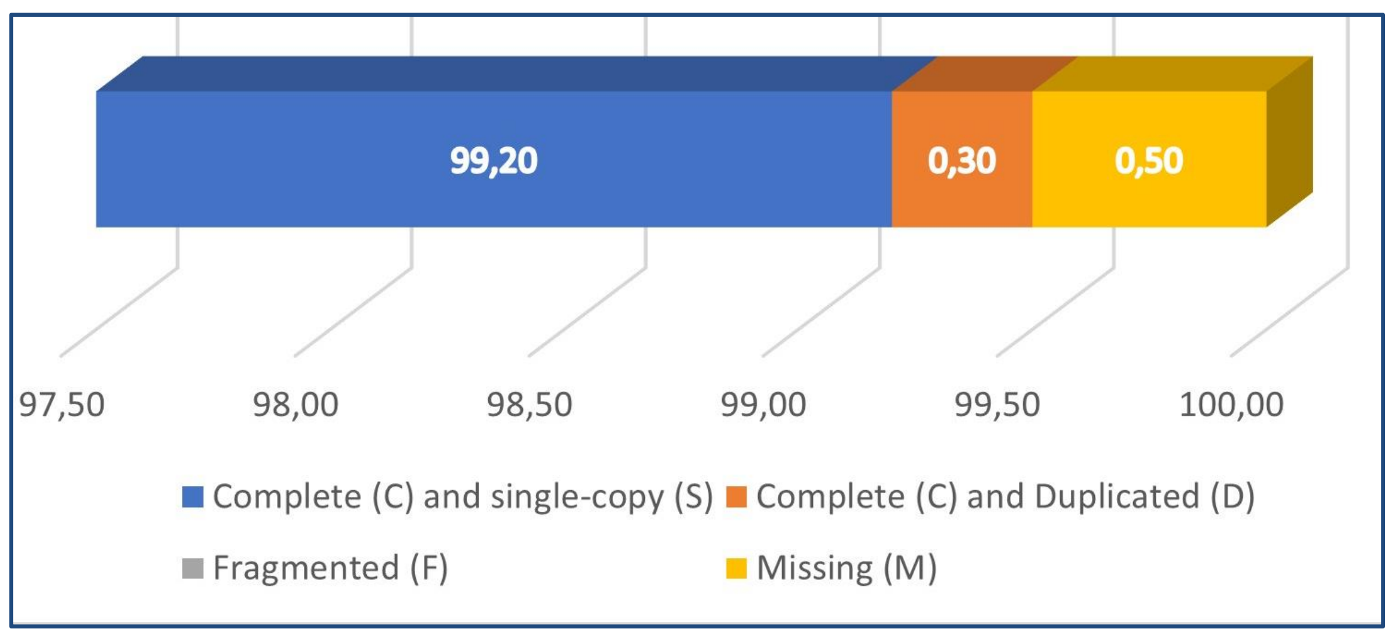


Fig. 1: Preliminary genome of *Wolbachia* endosymbiont of Argentinean *A. fraterculus* sp1.

- ✓ From filtered 15,810,325 ONT reads, 1,360 contigs were assembled.
- ✓ One circularized contig of 1,463,312 bp was assigned to *Wolbachia* sp. (872X coverage).
- ✓ Final assembly, after polishing, was of 1,463,854 bp and GC% 35.07.

Fig 2.: BUSCO assessment for *Wolbachia* infecting *A. fraterculus* sp.1.
Total rickettsiales database: 364 core genes



- ✓ 633 genes, 907 hypothetical proteins, 3 rRNAs and 34 tRNAs were annotated (Fig. 1).
- ✓ Insertion Sequences (ISs) and prophage genes were identified throughout the genome (Fig. 1).
- ✓ The BUSCO analysis showed a 99.5% completeness (Fig. 2).
- ✓ 99.1% Average Nucleotide Identity (ANI) were obtained in comparison with *Wolbachia* from *Drosophila melanogaster*.

CONCLUSION

The whole genome of the *Wolbachia* sp. infecting Argentinean *A. fraterculus* sp. 1 was successfully assembled and annotated. The obtained results are in accordance with *Wolbachia* from *D. melanogaster*.

FUTURE WORK

Genomic structure and prophage genes analysis will be carried out to understand the mechanisms influencing host behavior and physiology, thereby supporting novel pest management strategies.

REFERENCES: Conte, 2021: PhD Thesis, UBA. Rivarola *et al*. 2023: RedBio, Buenos Aires (Arg).