

Genome assembly of a new *Wolbachia pipientis* strain: a promising source for studying *Drosophila melanogaster* endosymbiosis

Klimenko A.I.^{1,2*}, Korenskaia A.E.^{2,3}, Shishkina O.D.^{1,3}, Andreenkova O.V.¹, Shatskaya N.V.¹, Vasiliev G.V.¹, Gruntenko N.E.¹

¹ Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

² Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

³ Novosibirsk State University, Novosibirsk, Russia

* klimenko@bionet.nsc.ru

Key words: wolbachia pipientis, genomics, microbiology, drosophila melanogaster endosymbionts

Motivation and Aim: One of the promising directions in searching the ways to control the number of both harmful and beneficial insects is the study of the possibilities of controlling the insect microbiome, which plays a very important role in the regulation of their vital activity. In this regard, the study of the intracellular symbiotic bacterium of the genus *Wolbachia*, found in more than half of existing insect species, and capable of controlling the reproductive function and physiology of the host insect, may be of particular interest. We had previously found a unique strain *Wolbachia pipientis* (wMelPlus), which provides an increase in stress resistance and fertility of its host, the model species *Drosophila melanogaster* [1].

Methods and Materials: Distinct samples containing *Wolbachia* cells of wMelPlus and wMelCS strains were sequenced using Illumina MiSeq platform and characterized using the following pipeline of bioinformatic analysis. We used SPAdes *de novo* assembler [4] and MinYS hybrid assembler [3] for a primary assembling of contigs. Subsequent scaffolding and polishing of the genome assembly have been performed using Pilon, Ragout and Gfinisher [2] employing two independent reference genomes of a wMelCS strain (see Figure 1), which is closely related to the strain of our interest. We assessed the quality of the interim and resulting assemblies using QUAST. The obtained genomes have been annotated using Prokka [5] annotation pipeline and compared with the already published genomes of *W. pipientis*.

Results: The genome assembly of a new *W. pipientis* strain has been obtained. Applying the methods of assembly correction and polishing allowed to significantly reduce the number of fragments, approach the expected GC-content, increase the number of identified genes and achieve the expected genome size. Using WMelCS_b (GCA_016584405.1) as a reference genome has demonstrated the best assembly quality for both wMelCS and wMelPlus strains, genome fraction ~96 %. However, the genome is still fragmented and there are some misassemblies to be resolved in future using long read sequencing and assembly. Nonetheless, the obtained genome assembly of wMelPlus *Wolbachia pipientis* strain exhibits enough quality for subsequent comparative genomics analysis and can be regarded as a promising source for studying different aspects of its endosymbiosis with *Drosophila melanogaster*.

Acknowledgements: The study is supported by RSF grant No. 21-14-00090.

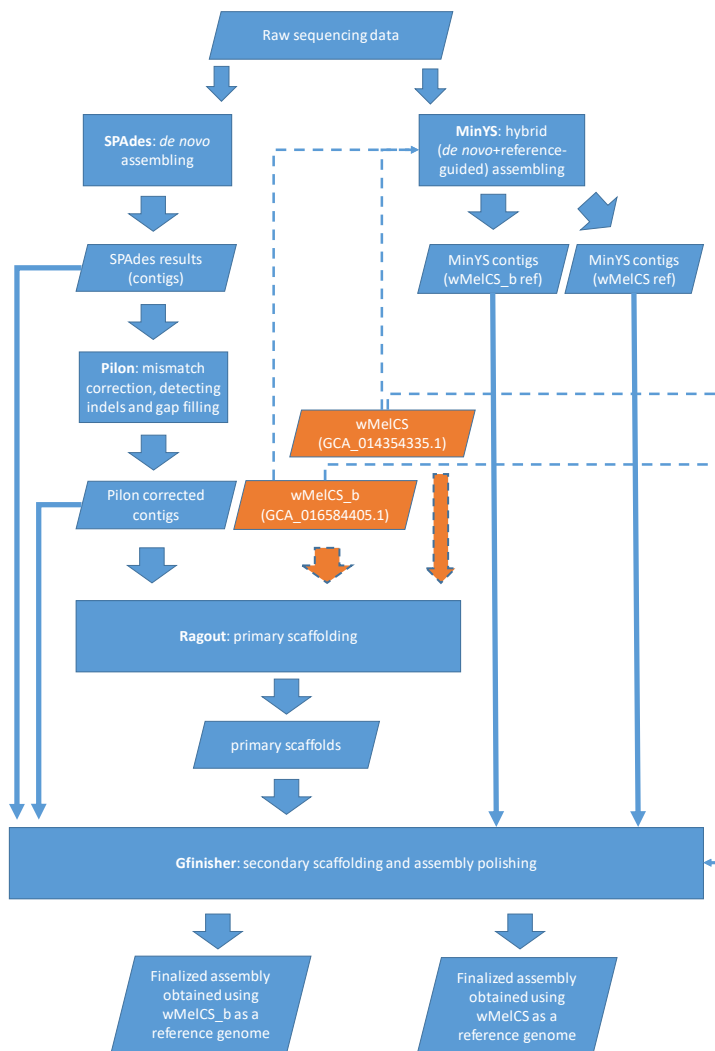


Fig. 1. The bioinformatic genome assembly, correction and polishing pipeline used in the current work. Solid lines illustrate the work- and data-flow. Dashed lines depict using as a reference genome

References

1. Burdina E.V., Bykov R.A., Menshanov P.N., Ilinsky Y.Y., Gruntenko N.E. Unique Wolbachia strain wMelPlus increases heat stress resistance in *Drosophila melanogaster*. *Arch Insect Biochem Physiol*. 2021;106(4):e21776. doi: 10.1002/arch.21776.
2. Guizelini D., Raittz R.T., Cruz L.M., Souza E.M., Steffens M.B.R., Pedrosa F.O. GFinisher: A new strategy to refine and finish bacterial genome assemblies. *Sci Rep*. 2016;6:34963. doi: 10.1038/srep34963.
3. Guyomar C., Delage W., Legeai F., Mougél C., Simon J.-C., Lemaître C. MinYS: mine your symbiont by targeted genome assembly in symbiotic communities. *NAR Genom Bioinform*. 2020;2(3):lqaa047. doi: 10.1093/nargab/lqaa047.
4. Prjibelski A., Antipov D., Meleshko D., Lapidus A., Korobeynikov A. Using SPAdes De Novo Assembler. *Curr Protoc Bioinform*. 2020;70(1):e102. doi: 10.1002/cpbi.102.
5. Seemann T. Prokka: Rapid prokaryotic genome annotation. *Bioinformatics*. 2014;30(14):2068-2069. doi: 10.1093/bioinformatics/btu153.