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Comparative genomics of the insecticidal bacterium *Bacillus thuringiensis* using Oxford Nanopore sequencing

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Bacillus thuringiensis (*Bt*) is a Gram-positive bacterium renowned for production of insecticidal toxins mostly of proteinaceous nature widely used as biopesticides. More than 700 different toxins are known and fall into at least five major groups. These toxins exhibit high specificity against particular orders within **Arthropoda**, **Nematoda** and **Mollusca** phyla as well as against several types of human malignant cells. At the same time, little is known about the mechanisms determining such specificity, and new strains of *Bt* and new forms of toxins continue to be discovered. In this work, we perform comparative genomic analysis of strains comprising the collection of All-Russia Research Institute for Agricultural Microbiology (ARRIAM). These strains exhibit specific action against insects of **Lepidoptera**, **Coleoptera** and **Diptera** orders, while some of the strains show multiple host affinity. Notably, for some of the strains avirulent derivatives were achieved so that comparison of virulent and avirulent variants was possible. Initial genome sequencing for 8 strains was performed with Oxford Nanopore platform. All reads went through base calling with Albacore v2.5.11 and trimming with Porechop v0.2.3. All genomes were assembled via Flye 2.3.6b with N50 more than 200kb and less than 70 contigs per genome. These assemblies allowed us to identify closest known strains *Bt* by FastANI and classify the strains of ARRIAM collection as belonging to the *thuringiensis*, *darmstadensis* and *israeliensis* serovars. Furthermore, strain-specific genomic regions responsible for toxins production were identified by comparison of the genomes of virulent and avirulent strains. Taking together, the data might shed light on the mechanism of specificity and efficiency of the *B. thuringiensis* strains. This work is supported by the Russian Science Foundation (Grant No 18-76-00028).