the bone marrow, followed by the infiltration of immature myeloblasts into the peripheral blood. Clinically and molecularly heterogeneous, AML remains one of the most widely studied malignancies. A spectrum of somatic mutations has been identified in genes relevant for AML pathogenesis, e.g. encoding multifunctional protein NPM1, transcription factors (CEBPA, RUNX1, WT1), signaling proteins (KIT, FLT3, JAK2, NRAS, KRAS, PTPN11) epigenetic regulators (DNMT3A, TET2, IDH1, IDH2) or spliceosome components (U2AF1, ZRSR2). The aim of the study was to identify mutations in a group of Polish patients with AML M1 and M2 FAB types, whose proteomes and transcriptomes were previously investigated. DNA was isolated from frozen blood or bone marrow cells collected from 37 patients and subjected to exome-enrichment procedure followed by high-throughput sequencing with Illumina platform. The data were mapped to the human genome GRCh38, genotyped with GATK (Genome Analysis Toolkit, Broad Institute) and filtrated with VQSR (Variant Quality Score Recalibration) method. Results were analyzed with VEP (Variant Effect Predictor, Ensemble). In total, over 800 thousand mutations (SNPs and small indels) were identified, including 66% existing and 34% novel variants. More than 187 thousand mutations were detected within transcripts, and close to 70 thousands within regulatory regions. About 40% variants were localized within introns whereas 2% were missense mutations. Potentially pathogenic mutations were detected in 37 out of 40 genes recurrently mutated in AML. On average, 4 genes were mutated per patient and the most frequently mutated genes were *KIT*, *NPM1*, *DNMT3A*, *NRAS* and *WT1*. Although the number is low, it corresponds with the literature data reporting AML has fewer mutations than other adult cancers.

P-02-030
Long-read sequencing of *Bacillus thuringiensis* strains reveals genome rearrangements affecting their virulence effectiveness

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Bacillus thuringiensis (*Bt*) is a spore-forming soil bacterium producing highly specific insecticidal toxins widely used as biopesticides. The unique feature of this bacterium is the ability to form so-called parasporal bodies or crystals during sporulation. These bodies contain proteinaceous toxins active against different organisms within Arthropoda, Nematoda and Mollusca phyla. Though *Bt* and their toxins are studied for more than 50 years, still very little is known about the molecular mechanisms controlling the parasporal bodies assembly. In this work, we perform comparative genomic analysis of 17 *Bt* strains obtained from the ARRIAM collection. These strains exhibit specific action against insects belonging to the Lepidoptera, Coleoptera and Diptera orders and are different in their ability to form crystals. Genome sequencing for the strains was performed via both Illumina and Oxford Nanopore platforms. The assemblies of their genomes reached the complete replicon level for most strains. We classified the strains with FastANI v1.1 as belonging to the *thuringiensis, darmstadiensis* and *israelensis* serovars. Further assembly comparison via Mummer v4.0.0 revealed several genome rearrangements mostly related to plasmid loss events to distinguish close strains. These plasmid vanishing acts appeared to be closely connected with virulence loss. However, genes forfeit this way encode not only canonical toxins, but also proteins responsible for cell wall biogenesis, stress response and sporulation as well several transcriptional regulators and RNA polymerase components. These genome rearrangements data suggest expansion of the repertoire of proteins governing virulence and parasporal bodies assembly in *Bt*. This work is supported by the Russian Science Foundation (Grant No 18-76-00028).

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Genetic control of lipid biosynthesis in a collection of flax (*Linum usitatissimum* L.) cultivars and lines

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Fatty acid composition influences the quality of seed lipids, which are the major source of vegetable oil. The proportion of fatty acids determines the end use of oil, with the ratio of the unsaturated fatty acids, like oleic acid (C18:1), linoleic acid (C18:2), and linolenic acid (C18:3), playing a key role. For human nutrition, flaxseed (*Linum usitatissimum* L.) plays an important role as a major source of essential ω-3 fatty acids. Despite the nutritional importance of fatty acid composition in seed storage lipids, the molecular mechanisms underlying the proportion of fatty acids in seed oil are still not fully established. Fatty acid biosynthesis involves several gene families, with some of them having already been identified, like *FAD* (fatty acid desaturase) and *SAD* (stearoyl-ACP desaturase) gene families. The purpose of our study was to analyze the role of these genes in the level of different fatty acids in seed oil. *SAD* and *FAD* genes were sequenced in 288 flax genotypes with different proportion of fatty acids, obtained from the Institute for Flax (Torzhok, Russia). DNA sequences with an average coverage of 100x for an individual sample were obtained on the Illumina platform and used to identify gene polymorphism among the genotypes. The correlation analysis between identified polymorphism of *SAD* and *FAD* genes and fatty acid composition in flax allows the determination of genetic variation leading to different proportion of fatty acids. These newly identified polymorphisms of flax genes, controlling the levels of fatty acids, will be a useful resource for marker development and marker-assisted selection of flaxseed cultivars with targeted fatty acid composition. This work was performed within the framework of the Program of fundamental research for state academies for 2013–2020 years (No. 01201363824) and was funded by RFBR according to the research project 17-29-08036.

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Comparative chromosomal microarray analysis of doxorubicin-resistant MCF7 cells

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Drug resistance is the resistance of tumor cells to various functionally unrelated chemotherapeutics and is the major reason of unsuccessful chemotherapy. Since drug resistance drastically