Genomic analysis of *Bacillus pumilus* phytopathogenic strain 11-1-1

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Key message. Pathogenicity studies with *Bacillus pumilus* bacteria showed that they could cause disease symptoms of the tested plants. Genome one of the most aggressive strains was sequenced for understanding on the pathogenesis.

Keywords: *Bacillus pumilus*, phytopathogen, PCR-based genotyping, genome sequencing

Environmental bacteria *Bacillus pumilus* have been occasionally identified as a pathogen of plant. A number of enzymes with the potential to harm plant cells have been found from this bacterium but the mechanism of pathogenesis of *B. pumilus* is currently unknown. The genomic information of pathogenic strains of *B. pumilus* will be important for understanding on the pathogenesis. Aim of this study is analysis of phytopathogenic *B. pumilus* strain genome to identify gene candidates with functions in the interaction between bacterial pathogens and plants.

Pathogenicity of strain was tested by inoculation with suspension of bacterium into the parenchyma of test plants at approximately 10⁸CFU/ml. PCR-based genotyping was done using the RAPD primer 1254 and REP primers ERIC1, BOX and GTG₅. Whole-genome sequencing *B. pumilus* was performed using Illumina MiSeq.

We investigated 34 strains of *B. pumilus* isolated in Belarus including 28 strains isolated from affected cucumber, tomato, potato tubers, flax plants, 5 soil strains and 1 strain from chicken feces. Preliminary pathogenicity studies demonstrated that many strains could cause plant infection symptoms after injection with bacterial suspension. Seven most aggressive strains induced rot of potato tubers (cultivars Zhuravinka and Briz) as well as necrosis of bean plant leaves. Surprisingly, BIM B-171 isolated from soil was among these strains. We used RAPD- and REP-PCR to study the genome diversity of *B. pumilus* strains. Results indicated that pathogenic strains 38.2, 39.2, T1, 11-1-1 have identical genomic fingerprint in all PCR-typing methods, the rest of pathogenic strains 61.2, 63-3-1, BIM B-171 have considerable genetic heterogeneity. The *B. pumilus* strain 11-1-1 isolated from Mogilev region of Belarus from rotten potato tuber was selected for whole-genome sequencing. Totaling 740 600 reads (2×300 bp) were obtained after quality trimming and filtering and used for *de novo* assembling with SPAdes 3.13. The final assembly was 3,85 Mbp in length and consisted of 51 contigs with maximum size 530 090 bp. Gene prediction and functional annotation are performed at this moment. Analysis result will be reported on conference.

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