Genome assembly of *Fusarium oxysporum* f. sp. *lini* using a combination of Oxford Nanopore and Illumina reads

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Fusarium oxysporum f. sp. *lini* is claimed to be one of the most harmful flax pathogens. The pathogen causes flax wilt







The results of thorough investigation of
F. oxysporum at molecular and genetic levels can
be of great help for those fighting against it

• Our work was focused on achieving the first high-quality assembly of *F. oxysporum* f. sp. *lini* genome

• One of the modern approaches for obtaining high-quality *de novo* assemblies implies using a combination of long and high-accuracy reads

illumin

Methods and Algorithms Preparation of material and DNA sequencing



Methods and Algorithms Data processing and analysis



According to QUAST and BUSCO statistics and the presence of possible misassemblies, Canu assembly polished with Racon, Medaka and POLCA seems to be the most full and accurate

Results

99,5

No.

5

Assembly statistics

QUAST BUSCO

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150.

No

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• The combination of data received from the two sequencing platforms allowed us to obtain the first high-quality assembly of *F. oxysporum* f. sp. *lini* genome

- This knowledge will support further investigations of *F. oxysporum* and flax-pathogen interaction
- The assembled genome can be accessed at DDBJ/ENA/GenBank (accession – WHMS00000000, BioProject accession – PRJNA578147)

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Oxdord Nanopore

•+ Illumina reads