

Fusarium pathogenesis: mechanisms of infection and disease progression in flax

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Key words: flax; Fusarium wilt; pangenome; virulence; resistance

Motivation and Aim: Fusarium wilt is one of the most economically damaging flax diseases caused by a specific type of *Fusarium oxysporum* Schlecht., a fungus in the Ascomycota phylum [1]. This special form (i. e., forma specialis, f. sp.) of *Fusarium oxysporum* is known to infect only flax [2]. The mechanisms of flax resistance to Fusarium wilt have never been fully understood, although resistance to the disease was developed by selection. Here we applied the analysis of genomics data, as well as innovative breeding methods (GWAS and bulk segregant analysis) to (1) perform chromosome-level assembly of the fungus genome and reveal its complex multi-compartmentalized organization, (2) construct the pangenome to assess the genomic diversity of *Fusarium oxysporum* f. sp. *lini* (Folini) strains and (3) map several resistance genes identified previously by classical genetics methods to reference flax genome.

Methods and Algorithms: Strain virulence was assessed under greenhouse conditions using reference cultivars with contrasting susceptibility to Fusarium wilt. LRS, Illumina and Hi-C technologies were used to sequence and assemble the genomes of 36 *Folini* strains with different virulence status. Protein orthogroups were identified with silix software (version 1.3.0). Candidate secreted proteins were identified in three steps as described in [4]. GWAS on flax collection of 306 lines was conducted with GAPIT [5] and 3VmrMLM [6] packages.

Results: The size of *Folini* genome is about 65 MBp, it contains 14,000 gene models. Most *Folini* strains have 20 chromosomes. There are at least 3 partitions in *Folini* genome, which differ in conservation, the density of genes, SNPs and repeats, speed of evolution. The pangenome of 36 *Folini* isolates is open. The *Folini* pansectorome, encompassing secreted proteins critical for fungal pathogenicity, primarily consists of three functional classes: effector proteins, CAZymes, and proteases. Each functional class within the pansectorome was meticulously annotated and characterized with respect to pangenome category distribution, PFAM domain frequency, and strain virulence assessment. Regions in plant genome associated with resistance were identified on 1, 8, 11 and 13 chromosomes.

Conclusion: Our results provide novel insights into plant-pathogen interactions and pinpoint potential candidate genes for further in-depth studies.

Funding: The study is supported by the RScF grant 23-16-00037.

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