

Transcriptional profiling of fusarium wilt in flax

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Introduction

Fusarium wilt of flax (*Linum usitatissimum*) is an aggressive disease caused by soil-born fungal pathogen *Fusarium oxysporum* f. sp. *lini* (*Foli*) posing a major threat to flax production worldwide. Recently, we reported chromosome-level assemblies of 8 pathogenic *Foli* strains with different virulence, thus providing a background for detailed genomic studies of host-pathogen interaction mechanisms on multiple levels [ссылки].

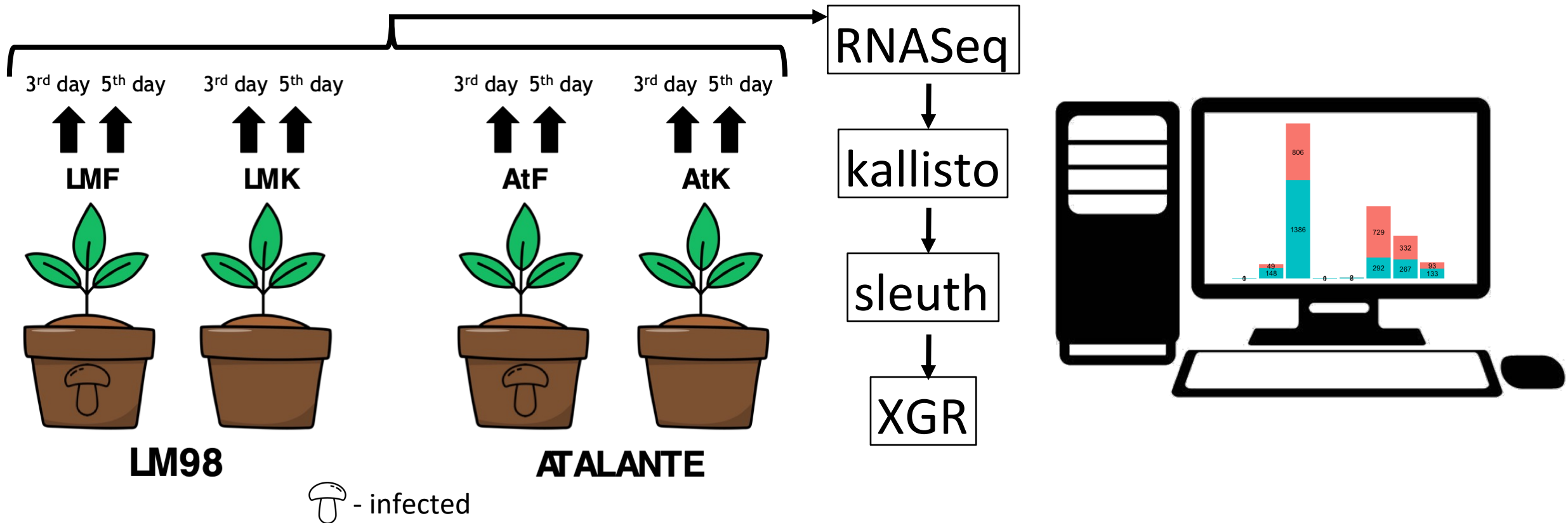
Here, we present a first insight into molecular mechanisms involved in response of flax to fusarium infection. We also report about changing of genes expression pattern in *Fusarium* during plant tissues colonization compare to mycelial culture. Such data may be of use when integrated with the infection resistance markers emerging from GWAS studies, thus opening up new possibilities for disease control and prevention.



Methods

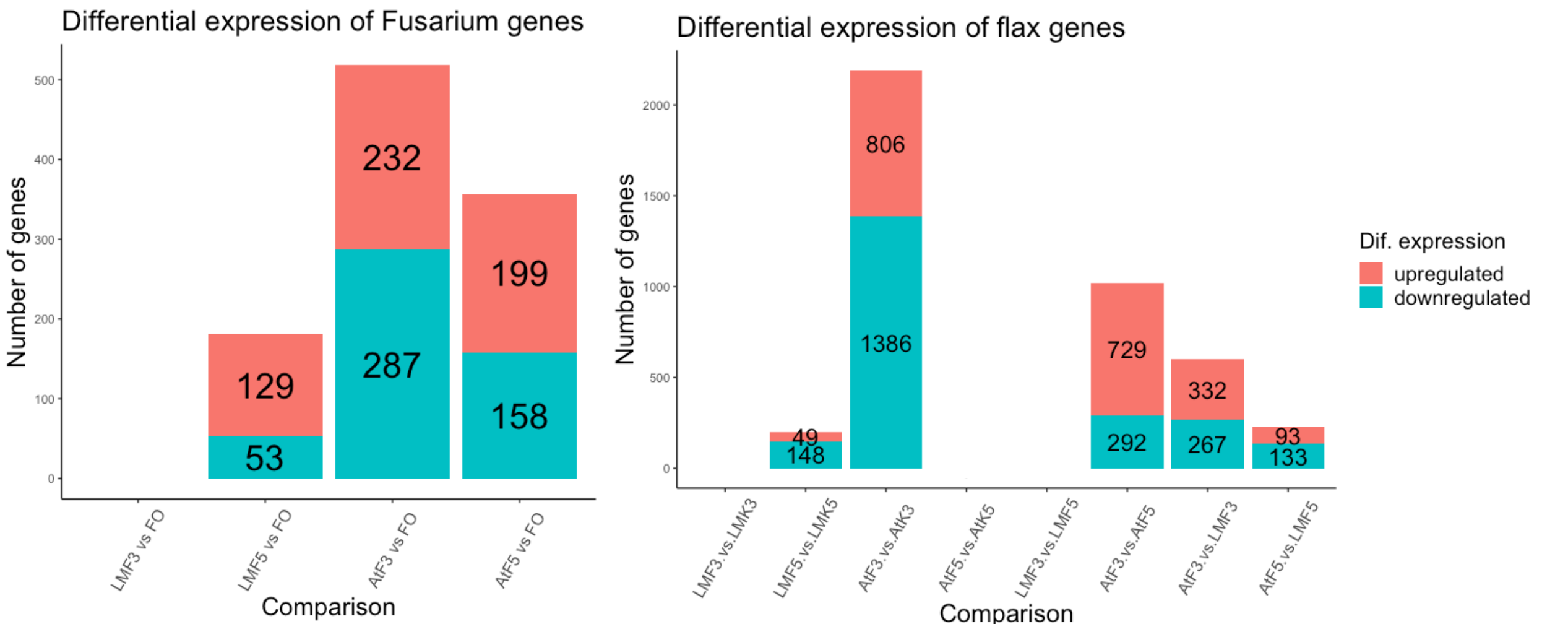
In this study we examined susceptible and resistant flax cultivars (cv.), namely, LM98 (LM) and Atalante (At), infected by highly virulent MI39 *Foli* isolate. Uninfected plants (AtK and LMK) and pure culture of the fungus (FO) served as controls. Flax samples were harvested on the third and the fifth day post inoculation (dpi).

A total RNA mixture (i.e., flax and fungus) was extracted from infected plant roots and sequenced. The RNASeq data was processed in parallel with kallisto/sleuth suite using flax and *Fusarium* gene models. The functional annotation and GO enrichment analyses of resulting sets of differentially expressed genes was done with XGR package.



Results

Fusarium infection produces a diverse spectrum of transcriptional states of the host that depends on resistance level of cultivars and virulence of the fungus strain. The resistant plants (cv. At) exhibited a sharp, prolonged response to the infection as early as the 3 dpi. We observed the upregulation of flax cytochrome-related genes in response to fusarium infection. Furthermore, an activation of Germin-like genes provides indication of flax response to the biotic stress associated with disease progression. In contrast, the susceptible plants (cv. LM) provided no sign of significant transcriptional response on the 3 dpi.



Results

The delayed changes in transcriptional profiles were visible on the 5 dpi, manifesting activity of cytochrome-related genes and glycoproteins associated with plant resistance to diseases. Upon invasion the fungus exhibits upregulation of genes associated with protein expression, pathogen penetration through the host’s cell walls and further progression irrespective of the host’s resistance status.

Three of the most significant upregulated GO annotations in each comparison

Flax

LMF3 vs LMK3	LMF5 vs LMK5	AtF3 vs AtK3	AtF5 vs AtK5	LMF3 vs LMF5	AtF3 vs AtF5	LMF3 vs AtF3	LMF3 vs AtF3
-	heme binding	endopeptidase inhibitor activity	-	-	endopeptidase inhibitor activity	DNA-templated transcription	-
	protein kinase activity	peroxidase activity			oxidoreductase activity	oxidoreductase activity	
	response to oxidative stress	Germin-like proteins subfamily			Germin-like proteins subfamily	response to oxidative stress	

Fusarium

LM3 vs FO	LMF5 vs FO	AtF3 vs FO	AtF5 vs FO
-	hydrolase activity	oxidation-reduction process	oxidation-reduction process
	transmembrane transport	membrane	integral component of membrane
	translation	translation	translation

Conclusion

- The results obtained in our research suggest different speed of response to infection in susceptible (LM98) and resistant (Atalante) flax cultivars. Atalante's response was rapid and strong, unlike LM98, where on the 3rd dpi the fungus' genes as well as the flax' did not changed expression in comparison to control samples. Moreover, it means that *Foli* probably change its genes expression in response to protection metabolites of flax.
- Flax is protected by regulating genes related to cytochrome and Germin-like proteins.
- While infection, MI39 *Foli* increases expression of genes that responsible for proteins translation and membrane penetration
- We discovered possible existence of specific model of response to fusarium infestation by resistant variety of flax. This hypothesis is confirmed by the decrease in expression of some of protective genes (FANCM-MHF complex, defense response, chitinase activity) while Atalante's infection

Acknowledgements

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Literature

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