

**The genome of *Fusarium oxysporum* infecting *Camelina sativa***

Matias Pasquali<sup>1</sup>, Ali Farnian<sup>1</sup>, Li Ningxiao<sup>2</sup>, Paolo Cortesi<sup>1</sup>, Andrea Kunova<sup>1</sup>, Marco Saracchi<sup>1</sup>, Cristina Pizzatti<sup>1</sup>, Frank Martin<sup>2</sup> and David Geiser<sup>3</sup>

<sup>1</sup>University of Milan, Department of Food, Environment and Nutritional Sciences, via Celoria 2, 20133, Italy, <sup>2</sup>USDA, Crop Improvement and Protection Research, 1636 E. Alisal ST. Salinas, CA 93905, USA, <sup>3</sup>PennState University, Department of Plant Pathology and Environmental Microbiology, University Park, PA 16802, USA; matias.pasquali@unimi.it

*Fusarium* wilt, an important fungal disease worldwide, is caused by members of the *Fusarium oxysporum* species complex (FOSC). Host specificity in FOSC is given by differences in the effectors arsenal, including SIX (secreted in xylem) protein genes. *Camelina sativa* (L) Crantz, a member of *Brassicaceae* family has gained attention as a re-emerging oil-seed crop. *Fusarium* wilt symptoms reported on the crop in 2018 led to the isolation of *Fusarium oxysporum* strains from camelina seeds. Koch's postulates proved the ability of two *Fusarium oxysporum* isolates to cause *Fusarium* wilt on camelina. Genome analysis (genome size 57.3 Mb) showed a unique SIX gene profile of the strains that may explain the differential infection capacity of different *Brassicaceae* plants. The strains are therefore different from other FOSC infecting *Brassicaceae*, including *Fusarium oxysporum* f.sp. *raphani* and *conglutinans*, suggesting the existence of a further differentiation within formae speciales infecting this important plant family.