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Published in:

Abstracts : 14th International Cereal Rusts and Powdery Mildews Conference 2015

Publication date:

2015

Document Version

Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):

Chen, Y.-J., Vogt, J. K., Sørensen, C. K., Rodriguez-Algaba, J., Sicheritz-Pontén, T., Hovmøller, M. S., & Justesen, A. F. (2015). Identifying transcripts associated with aggressiveness in wheat yellow rust by transcriptomic sequencing. In Abstracts : 14th International Cereal Rusts and Powdery Mildews Conference 2015 (pp. 106-106). (ARO Abstracts).

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Identifying transcripts associated with aggressiveness in wheat yellow rust by transcriptomic sequencing

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Yellow rust (*Puccinia striiformis*) is currently one of the most prevalent and damaging disease on wheat, which may threaten global food security. This is emphasized by new strains adapted to warmer temperatures, and being more aggressive in general, which have spread rapidly in many wheat growing areas in recent years. More detailed knowledge is needed for understanding rust biology and epidemiology, e.g., the characteristics of aggressive isolates. Since 2011, the isolate DK09/11 of the “Warrior” race is considered ‘aggressive’ and spreading rapidly in Europe. In this study, progeny isolates arising from a selfing of the isolate DK09/11 on *Berberis vulgaris* (Rodriguez-Algaba J, et al., 2014) were selected for transcriptomic analysis. Four progeny isolates and the parent isolate DK09/11 showing different levels of aggressiveness were point inoculated on wheat leaves and harvested at three different time points (5, 7 and 9 dai) for RNA-sequencing. By using next-generation sequencing technologies, transcript expression profiles under different growth stages will be analyzed to reveal molecular mechanisms underlying aggressiveness.

Rodriguez-Algaba J, Walter S, Sørensen C K, Hovmøller MS & Justesen AF. 2014. Sexual structures and recombination of the wheat rust fungus *Puccinia striiformis* on *Berberis vulgaris*. *Fungal Genetics and Biology* 70, 77-85.