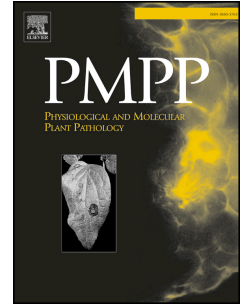


Accepted Manuscript

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PII: S0885-5765(16)30178-3

DOI: [10.1016/j.pmpp.2017.03.007](https://doi.org/10.1016/j.pmpp.2017.03.007)

Reference: YPMPP 1247

To appear in: *Physiological and Molecular Plant Pathology*

Received Date: 16 November 2016

Revised Date: 31 January 2017

Accepted Date: 17 March 2017

Please cite this article as: Ismail IA, Able AJ, Gene expression profiling of virulence-associated proteins *in planta* during net blotch disease of barley, *Physiological and Molecular Plant Pathology* (2017), doi: 10.1016/j.pmpp.2017.03.007.

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Gene expression profiling of virulence-associated proteins *in planta* during net blotch disease of barley

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Abstract

The proteinaceous extracts of culture filtrates from *Pyrenophora teres* f. *teres* (*Ptt*) have been previously shown to induce symptoms on susceptible barley cultivars suggesting these fungal proteins are likely to contribute to net form net blotch (NFNB) disease. This research primarily aimed to study the *in planta* gene expression of 222 proteins, previously identified in culture filtrates of virulent *Ptt* isolates, using qPCR. Genes classified by InterPro as virulence factors, proteolytic, contributing to oxidation-reduction processes, or carbohydrate metabolic processes (CMP) including the cell wall degrading enzymes (CWDEs) had very high to extremely high expression levels. The most common temporal co-expression pattern, for 41 of the genes, was an upregulation from 24 hours post inoculation (hpi) peaking at 96 hpi when necrotic symptoms became visible. The next most common pattern, for 27 of the genes, was also an upregulation from 24 hpi but peaking at 48 hpi. Genes categorised as encoding for CMP/CWDEs and involved in other metabolic processes were enriched in these

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