CONFERENCE PROGRAMME

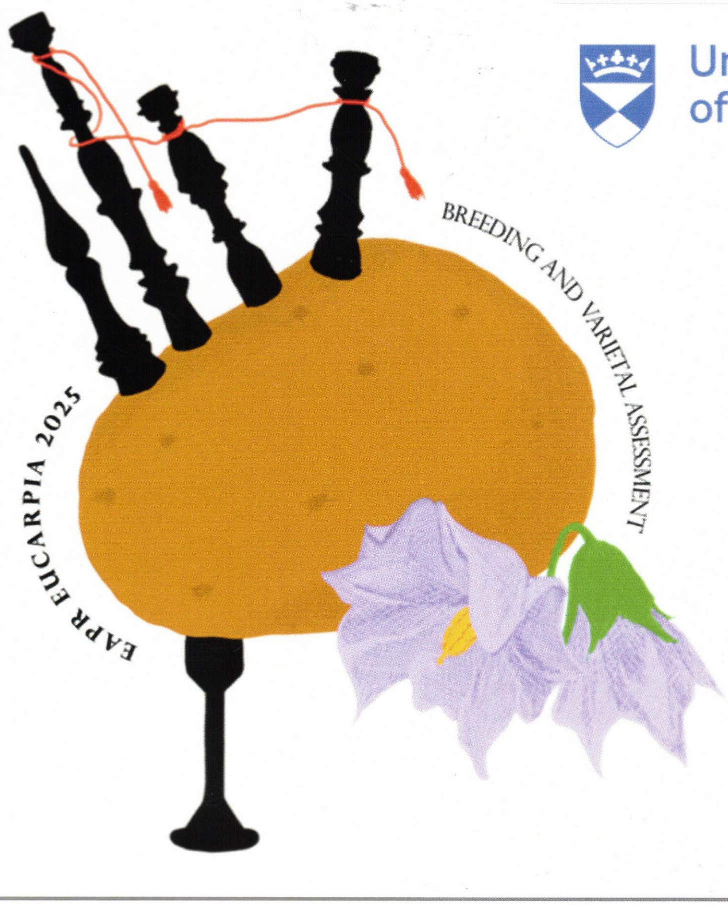
20^TH JOINT MEETING OF

EAPR SECTION "BREEDING & VARIETAL ASSESSMENT" AND

EUCARPIA SECTION "POTATOES"

ST ANDREWS

15 – 18 JUNE 2025



Poster 18

Bulked segregant RNA-seq reveals key genes associated with potato resistance to *Dickeya solani*

Authors: Anna Grupa-Urbańska[1], Katarzyna Szajko[1], Waldemar Marczewski[1], Renata Lebecka[1]
Affiliation: ***[1]Plant Breeding and Acclimatization Institute - National Research Institute, Poland***

Abstract: Potato resistance to pectinolytic bacteria, including *Dickeya solani*, is inherited polygenically. We selected phenotypically well-characterised diploid progeny from a mapping population obtained by crossing a highly resistant form with a susceptible form to *D. solani*. Pooled samples representing extreme phenotypes were collected at 8, 24, and 48 h post-inoculation (hpi) and subjected to transcriptome analysis. Principal component analysis showed that the 8 hpi time point was the most discriminative for identifying defence-related gene expression. Comparative DEG analysis between resistant and susceptible sets (BR vs. BS and WR vs. WS) revealed a significant up-regulation of genes involved in phenylpropanoid biosynthesis, suberisation, and early immune signalling. GO and KEGG enrichment confirmed the activation of PTI- and ETI-related pathways. qPCR validation of selected DEGs confirmed the RNA-seq results and revealed consistent expression patterns in individual genotypes. Three candidate genes related to suberin and lignin biosynthesis showed strong and early induction in resistant genotypes. The results of this work provide insight into the temporal regulation of defence responses and suggest that rapid suberinisation and early activation of immune pathways are key components of resistance. These results contribute to understanding potato *D. solani* interactions and provide molecular targets for resistance breeding.