

MOLECULAR RESPONSE OF DIPLOID WHEAT TO GRAIN APHIDS

Wenzhu Guan¹; Natalie Ferry¹; Howard A. Bell²; John A Gatehouse³; Angharad M. R. Gatehouse¹.

¹University of Newcastle upon Tyne, Newcastle upon Tyne, Tyne and Wear, NE1 7RU, United Kingdom; w.z.guan@newcastle.ac.uk

²The Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, United Kingdom;

³Department of Biological Sciences, University of Durham, Co. Durham, DH1 3HP.

The grain aphid (*Sitobion avenae*) is a major insect pest of cereal crops, acting as a virus vector as well as causing direct plant damage. The molecular responses of a commercial wheat variety (Claire) to infestation by *S. avenae* were investigated in order to identify defence response genes/products for a directed strategy for wheat breeding programmes (Ferry et al., 2011). The results showed that Claire, one of the most commonly grown varieties in the UK, lacks a specific insect defence response, although general response genes were shown to be present. The present study was carried out to investigate the potential of a diploid wheat line (ACC20 PGR#1755) exhibiting resistance to *S. avenae* to serve as a source of resistance genes, using a proteomic-based approach. Approximately 200 protein spots were reproducibly detected in leaf extracts from both the resistant and a susceptible (ACC5 PGR#1735) line using 2-dimensional gel electrophoresis and Progenesis SameSpots software. Twenty-four spots were significantly up-regulated (> two-fold) in the resistant line after 24h of aphid feeding (13 and 11 involved in local and systemic response, respectively). In the susceptible control, sixteen protein spots were significantly up-regulated after 24h aphid feeding, with 12 being involved in the local response and 4 involved in the systemic response. After 8 days, there was a further increase in the number of differentially expressed proteins in the resistant variety (43 spots were significantly up-regulated; 37 locally and 6 systemically), whereas in the susceptible line the number of differentially expressed protein spots decreased to 12 (8 locally and 4 systemically). Approximately 50% of all differentially expressed protein spots were identified by peptide mass fingerprinting, revealing that the majority of proteins up-regulated by aphid infestation were involved in metabolic processes (including photosynthesis) and transcriptional/translational regulation. However, in the resistant line several antioxidant and stress response proteins were identified as well as those involved in DNA synthesis/replication/repair. Interestingly, no antioxidant or stress response proteins were up-regulated in the susceptible line in response to aphid feeding. These data suggest that the antioxidant, stress response and DNA synthesis/replication/repair proteins play a role in conferring resistance to *S. avenae* in the diploid line studied.

Financial support: BBSRC