P008 Exploiting numerous *Triticum monococcum* L.–pathogen interactions to identify critical defence signalling components for hexaploid wheat

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In plants, basal and *R* gene-mediated resistance are the prominent mechanisms against pathogen attacks. *RAR1*, *SGT1* and *NPR1* are some of the key players in defence signalling. The critical signalling components involved in wheat disease resistance are essentially unknown. We examined the resistance of a representative collection of *T. monococcum* accessions by challenging the plants with either *Soil-borne cereal mosaic virus* (SBCMV) transmitted by the vector *Polymyxa graminis,* or the fungal pathogens *Mycosphaerella graminocola* (*Septoria* leaf blotch), *Oculimacula yallundae / O. acuformis* (cereal eyespot disease), or *Fusarium culmorum* and *F. graminearum* (ear blight). The data sets generated revealed that most of the accessions exhibited resistance to certain pathogens but susceptibility to others. However, several accessions displayed resistance to most pathogens, while others were susceptible to most pathogens. To correlate the resistance phenotypes with specific defence signalling gene sequences among the accessions, the presence and sequence variation of the *TmRAR1, TmSGT1* and *TmNPR1* genes were examined by PCR, DNA sequencing and DNA gel blot analyses. *TmRAR1* and *TmSGT1* appeared to be single-copy genes, but *TmNPR1* has at least two copies. *TmRAR1, TmSGT1* and *TmNPR1* share high similarities with the known genes in the literature. TILLING (Targeting Induced Local Lesions IN Genomes) as a new technique to explore the relationship between novel pathogen-resistance phenotypes and variant alleles of these key signalling components in wheat will be discussed.