

An integrated approach to understanding adult plant resistance: histology and molecular features of stem rust on wheat

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Commercially implemented single gene resistance in wheat may be overcome by fungal pathogens such as *Puccinia graminis* f. sp. *tritici*. The emergence of Ug99, and variants within this race group, highlighted the necessity of durable stem rust resistance. Adult plant resistance (APR) has the potential to remain durable in the presence of new rust variants. Two entries, JIC218 and JIC542, were selected from the John Innes Centre collection for African wheat to possess APR against stem rust. Stem rust development and wheat defense responses were monitored in stems of the two JIC lines in comparison with a susceptible control (Line 37-07) under greenhouse conditions. Histological techniques such as scanning electron microscopy and fluorescence microscopy provided insight into the colonization of adult wheat plants by stem rust. Molecular techniques included quantifying fungal biomass by WGA-TITC binding fluorescence and RT-qPCR. Expression of a fungal haustorium-associated gene was also tracked by RT-qPCR. Microscopic observations and the molecular based infection timeline allowed the APR lines to be clearly distinguished from the susceptible check at 120 hours post infection. RNA sequencing was used to investigate transcriptional changes observed in the JIC lines and stem rust race PTKST after infection. A total of 3134 genes were differentially expressed during the plant pathogen interaction. Integration of these various methods allows a better understanding of APR as well as the relationship between different resistance loci and cellular responses.