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The *rpg4*/*Rpg5* integrated decoy resistance to wheat stem rust race *TTKSK* in barley: Towards effector identification

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The barley *rpg4*/*Rpg5* locus confers resistance against wheat stem rust caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*) including race *TTKSK* (A.K.A. *Ug99*). The 70 kb region harbors two NLR R-genes, *Rpg5* and *HvRga1* that are required together for resistance. *HvRga1* and *Rpg5* contain typical NLR resistance-protein structure; however, *Rpg5* has an additional C-terminal serine threonine protein kinase (STPK) domain. The transcription factor, *HvVOZ1* was identified by yeast-two-hybrid of a library constructed from RNA of the *rpg4*/*Rpg5*+ line Q21861; 48 hours post inoculation, utilizing the Rpg5-STPK domain as bait. We hypothesize that the Rpg5-STPK acts as an integrated decoy that HvVOZ1 binds to negatively regulate defense activation or binds after activation as part of a signaling complex. The second NLR, HvRga1, may guard theHvVOZ1-Rpg5 interaction or surveil the *Rpg5*-STPK domain for *Pgtrpg4*/*Rpg5*-Avr (*r45-Avr*) effector manipulation. Thus, *HvRga1* is possibly the guard that detects manipulation of the *Rpg5* STPK or possibly HvVOZ1 by the *r45-Avr* effector eliciting a strong effector triggered immunity defense response. The *r45-Avr* needs to be identified to thoroughly investigate these mechanisms and test our hypothesis. To accomplish this a panel of 37 wheat stem rust isolates collected in North Dakota, many with differential race typing on the wheat differentials and differential reactions on *rpg4*/*Rpg5* and *Rpg1* in barley were genotyped using restriction site associated DNA-genotyping-by-sequencing (RAD-GBS). This RAD-GBS produced 4,919 informative SNPs and this initial genotyping was used to select 24 diverse isolates (16 *avrRpg4*/*rpg5* and 8 *Avrrpg4*/*Rpg5*+) that were used to conduct in planta RNA-seq analysis during *Pgt* colonization 5 days post inoculation on the susceptible barley cultivar Harrington. The RNA-seq data was utilized to identify ~181,000 variant calls (SNPs and indels) within these *Puccinia graminis* transcriptomes during the infection process. The robust genotyping and phenotyping on these diverse differential isolates should allow us to identify candidate *r45-Avr* genes utilizing association mapping.

Biography

Robert Saxon Brueggeman has completed his PhD in 2009 from Washington State University and Postdoctoral studies also from Washington State University Department of Crop and Soil Science. He is currently an Associate Professor at North Dakota State University as the Barley Pathologist/Molecular Geneticist. He has published more than 32 papers in reputed journals covering the topics of the cloning and characterization of barley disease resistance genes and fungal effectors.

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