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Metabolo-proteomics approach to identify candidate genes for resistance in plants against biotic stress

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Abstract

Plants are subjected to several abiotic and biotic stresses. The resistance to pathogen stress can be qualitative or quantitative. The former, because of monogenic inheritance, has been successfully used in plant improvement. However, the latter, because of polygenic inheritance, has not been well exploited. Hundreds of quantitative trait loci (QTLs) for resistance have been identified but these contain several genes, including undesirable traits due to linkage drags. Integrated non-target metabolomics and proteomics, using high resolution mass spectrometry, were applied to identify the mechanisms of resistance in wheat against *Fusarium graminearum*. Near isogenic lines, with contrasting alleles at QTL-*Fhb1*, were pathogen or mock-inoculated, metabolites and proteins were analyzed using high resolution mass spectrometry. Mass spectral outputs were processed using MZmine for metabolites and MASCOT for proteins. The abundances were used to identify resistance-related metabolites and proteins, and mapped to metabolic pathways. Metabolites of the shunt phenylpropanoid pathway such as hydroxycinnamic acid amides, phenolic glucosides and flavonoids were significantly induced in the resistant NIL. Concurrently, the enzymes of phenylpropanoid biosynthesis such as cinnamyl alcohol dehydrogenase, caffeoyl-CoA O-methyltransferase, caffeic acid O-methyltransferase, flavonoid O-methyltransferase, agmatine coumaroyltransferase and peroxidase were also up-regulated. A protein coding gene (GENBANK No: CBH32656.1) near the *Fhb1* locus was putatively annotated as hydroxycinnamoyl transferase that catalyzes the conjugation of hydroxycinnamic acid amides, whose high expression in resistant NIL was confirmed by quantitative RT-PCR using the sequence of wheat agmatine coumaroyltransferase. This demonstrates the potential of metabolo-proteomics approach to identify biotic stress resistance candidate genes. This gene can be used in plant improvement following further validation.

Biography

Ajjamada C. Kushalappa is an Associate Professor at the McGill University. He has published 80 papers in refereed scientific journals. Current focus of his research is the application of non-target metabolomics and proteomics technologies to identify candidate genes for resistance against biotic stress. He was an invited speaker at several international and national conferences on metabolomics application to plant stress. He is a recipient of Dr. and Mrs. Bailey award by the Canadian Phytopathological Society for his exceptional and distinguished contribution to plant pathology.