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PROJECT 2 ABSTRACT

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Efforts to make significant improvement in the resistance of wheat to Fusarium head blight (FHB) require understanding the mechanism(s) of the naturally occurring FHB resistance pathways. Quantitative Trait Loci (QTL) conferring varying degrees of FHB resistance are known and these are being used by breeders to generate useful FHB resistant wheat and barley varieties. However, none of the actual gene sequences that underlie these QTL and determine the mechanism of FHB resistance are known. Until the molecular mechanism of FHB resistance is better understood, efforts to engineer improved FHB resistance will be futile.

The process of identifying the genes that are functionally essential to FHB resistance has been greatly hindered by the genetic complexities of wheat. In previous work funded by the USWBSI our group has developed a virus-induced gene silencing (VIGS) system that overcomes many of the obstacles for functional identification of genes involved in FHB resistance.

Previous work has shown that wheat and barley plants that are resistant to FHB initiate complex defense responses when challenged by *Fusarium graminearum*. Understanding how these responses are initiated is a key question to address. Very recent results in our VIGS analyses have implicated a receptor-like protein, TaBAK1, as playing a key role in FHB resistance. In model plants systems this proteins functions in the perception of conserved pathogen-associated molecular patterns (PAMPs), leading to PAMP-triggered immunity (PTI).

The discovery of a receptor-kinase protein that may play a key role in activating FHB resistance offers an excellent opportunity to engineer improved FHB resistance, and thereby directly serves the primary objective of the USWBSI Gene Discovery and Engineering Resistance research area.

Objectives:

1. Generate transgenic wheat plants that overexpress TaBAK1.
2. Begin the evaluation of these transgenics for increased FHB resistance.
3. Conduct VIGS experiments to evaluate the possible functions of three other TaBAK1-related sequences in FHB resistance, TaBAK2, 3, 4 and 5.
4. Generate cDNA clones for transformation if any of the TaBAK1-related sequences prove to make significant contributions to FHB resistance.
5. Continue the characterization of transgenic wheat overexpressing ethylene-signaling genes