U.S. Wheat and Barley Scab Initiative
FY02 Final Performance Report (approx. May 02 – April 03)
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Cover Page

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Year:	**FY2002 (approx. May 02– April 03)**
Grant Number:	**NA**
Grant Title:	**Fusarium Head Blight Research**
FY02 ARS Award Amount:	**$ 33,780**

Project

Program Area	Project Title	USWBSI Recommended Amount
BIO	Spike-Specific Promoter Isolation from Bowman and Near-Isogenic Marker Lines.	$34,624
	Total Amount Recommended	**$34,624**

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Principal Investigator Date

Project 1: Spike-Specific Promoter Isolation from Bowman and Near-Isogenic Marker Lines.

1. What major problem or issue is being resolved and how are you resolving it?

Barley transformation has the potential to help combat Fusarium head blight by introducing anti-fungal and anti-toxin genes. Promoters currently in use for barley transformation give transgene expression in all plant tissue throughout development, which is not an efficient use of plant resources when FHB only attacks at heading. This project will isolate spike-specific promoters to target gene expression to the spike tissues that are attacked by Fusarium head blight. RNA differential display technology is being used to identify genes that are expressed in spike tissues of Bowman and ten near-isogenic lines with morphological mutations in spike tissues. Regulatory regions, i.e. promoters, of these genes will be identified by DNA sequencing. Candidate spike-specific promoters will be inserted into marker gene constructs and tested for transgene expression patterns. Differential display comparisons include Bowman spike tissue vs. non-spike tissue, expressing vs. non-expressing tissue of the morphological marker lines, and morphological line tissue expressing the trait vs. the comparable normal tissue in Bowman.

2. What were the most significant accomplishments?

Differentially expressed sequences have been identified by comparisons of near-isogenic lines expressing spike mutations with Bowman. These sequences were expressed in tissues showing the morphological trait but not in normal tissues, or were found in spike tissues but not in leaf tissues. All sequences were single copy on Southern blots. Internal primers were designed and used with random 10-mer primers for gene walking PCR to amplify regions upstream of the original differential display sequence. The longer amplification products are being sequenced Three-fourths of the sequences matched barley ESTs, most with more than 95% sequence similarity. The remaining sequences either showed similarity to rice ESTs or did not show any match with the EST database. Because of problems using the PCR-amplified sequences to probe the BAC blots, the homologous ESTs will be used to select the BACs containing full-length sequences. The longer sequences from the gene walking PCR that do not match any barley ESTs will be cloned and used for BAC screening. As promoters are identified and tested, they will be made available to other labs doing wheat and barley transformation.

Include below a list of the publications, presentations, peer-reviewed articles, and non-peer reviewed articles written about your work that resulted from all of the projects included in the grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

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