**PI: Baenziger, Stephen** PI's E-mail: pbaenziger1@unl.edu Project ID: FY07-BA-043 **Research Area: VDUN** 

FY06 ARS Agreement #: 59-0790-4-092

**Duration of Award: 1 Year** 

Project Title: To Enhance Variety Development of Scab Resistant Hard Winter Wheat Varieties.

## **PROJECT 1 ABSTRACT** (1 Page Limit)

The long-term goals of this project are to: 1. develop elite hard winter wheat cultivars that are resistant to Fusarium head blight (FHB, scab) and 2. to screen experimental lines in regional FHB nurseries and hard winter wheat regional nurseries to identify the level of FHB resistance within the existing elite winter germplasm of the Great Plains The specific objectives in our varietal development effort are: A) Use known, elite FHB resistant germplasm, preferably with tagged QTLs, or rarely with exceptional tolerance from wild species as parents through crossing, B) use molecular markers to enrich populations for known OTLs in single and three way crosses, as well as, genotype later generation lines for known QTLs, C) continue our greenhouse and field screening efforts for native resistance in those lines and populations with FHB tolerance, but without known FHB QTLs, D) work cooperatively with winter wheat breeding and plant pathology programs in South Dakota State and Kansas State Universities to ensure broad testing and accurate measurement of FHB tolerance or lack thereof in adapted experimental and released cultivars. This year's proposal marks a transition from relying mainly on phenotypic breeding using diverse sources of FHB tolerance to a more focused approach that increases our reliance on molecular markers. There are two hypotheses/questions that we are asking: 1. that the incorporation of FHB tolerance QTLs/genes is best done in the hard winter wheat region by using fewer parents that have known FHB QTLs that also have known molecular markers (Van Sanford et al, 2001), and that 2. phenotypic evaluation is important for integration of native sources of FHB tolerance that do not have markers and is critical for evaluating lines that may be grown by producers. We are making this transition by haplotyping all of our parents, using molecular markers to track known OTLs, and using greenhouse and field phenotypic assays to identify lines with superior native resistance. Our expected results are: 1. elite germplasm and cultivars with enhanced FHB tolerance that is adapted to the northern and central Great Plains where FHB is potentially most damaging to HWW, 2. accurate information on current and future cultivars that may be grown in the northern and central Great Plains so that our producers will know the relative risk of growing each line to this potentially devastating disease.