Fusarium Head Blight (FHB), caused primarily by *Fusarium graminearum*, has caused serious yield and quality losses to barley in the Upper Midwest region of the United States during the past decade (1993-2002). This disease also has raised public concerns regarding food safety due to contamination of grain by deoxynivalenol (DON), a mycotoxin produced by *F. graminearum*. The development of resistant cultivars is considered one of the best approaches for combating this disease. Evaluation of the entire of six-rowed spring barley collection from the USDA National Small Grains Collection (NSGC) (>8,100 accessions in total) revealed very few sources of FHB resistance. To broaden the genetic base of FHB resistance in barley, additional sources of resistance need to be identified and exploited. Thus, we propose to continue the systematic evaluation of cultivated barley (*Hordeum vulgare*) and its primary gene pool (*Hordeum vulgare* subsp. *spontaneum*) for FHB reaction and DON concentration. The germplasm to be tested in FY03 includes: 1) 89 putative resistance sources identified from germplasm screening efforts in 2001-2002; 2) 400 additional diverse accessions of six-rowed winter and wild barley germplasm from the NSGC; 3) 150 lines from the ICARDA/CIMMYT barley breeding program based in Mexico; and 4) 50 landrace barleys from Switzerland. This germplasm will be evaluated in an initial FHB screening test in Hangzhou, China. Spring and winter type accessions exhibiting high levels of resistance in the preliminary screening test will be re-evaluated in replicated FHB nurseries in Minnesota (St. Paul and Crookston) and Virginia (Blacksburg), respectively. Accessions exhibiting high levels of FHB resistance and low concentrations of DON will be distributed to barley breeders for crossing. The information obtained from this study will have immediate practical applications for developing FHB resistant barley cultivars, thereby minimizing the devastating effects of this disease.