

Fusarium Head Blight (FHB), caused primarily by *Fusarium graminearum*, has caused serious yield and quality losses to barley in the Upper Midwest during the past nine years (1993-2001). 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 the best approach for combating this disease. Evaluation of the six-rowed spring barley collection from the USDA National Small Grains Collection (NSGC) 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 (*Hordeum vulgare* subsp. *spontaneum*) and secondary (*H. bulbosum*) gene pools for FHB reaction and DON concentration. The germplasm to be tested in FY02 includes: 1) 82 putative resistance sources of winter and wild barley identified from germplasm screening efforts in 2001; 2) 500 additional diverse accessions of six-rowed winter and wild barley germplasm from the NSGC; and 3) 44 *H. vulgare* x *H. bulbosum* recombinant lines. FHB evaluations of winter type germplasm will be made in Hangzhou, China where the vernalization requirement can be fulfilled. Spring type germplasm will be tested at two locations in Minnesota (St. Paul and Crookston). 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.