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In the Great Plains, FHB can be found in most hard winter wheat (HWW) fields in the U.S. Great Plains including Nebraska, South and North Dakota and Kansas. Recent severe FHB epidemics in these areas caused about 10-15% of yield losses in the years with severe epidemics. Most commercial HWW cultivars currently used in these regions are still highly susceptible. In previous USWBSI-funded projects, we have successfully transferred *Fhb1* from Sumai3 into 16 HWW cultivars, and the derived *Fhb1* lines are being used in HWW breeding programs. However, *Fhb1* alone cannot provide adequate protection in severe epidemics, identification of resistance quantitative trait loci (QTLs) for a different type of resistance and pyramiding *Fhb1* with QTLs from different sources are critical to further improvement of FHB resistance and to diversify sources of FHB resistance in HWW germplasm. Although several QTLs have been reported to have a major effect on FHB resistance, they are not deployed in HWW. *Fhb7* has been identified for a long time, but useful markers are not available for marker-assisted selection. In this proposal, we will 1) map QTLs for type I resistance to FHB from the source of Everest by genotyping two recombinant inbred line (RIL) populations [Everest*Fhb1*(R)xGarrison*Fhb1*(S) and Everest*Fhb1*(R)xKS061406LN-47*Fhb1*-244(S)] using genotyping-by-sequencing (GBS) and phenotyping the populations for type I FHB resistance in both greenhouses and field; 2) pyramid *Fhb1* with *Fhb7* and 3) with a major QTL from 2DL in US HWW Everest by marker-assisted backcross (MAB); and 4) develop functional markers for *Fhb7* for marker-assisted breeding. The proposed research will provide new breeding technologies and germplasm to facilitate quick release of FHB resistant HWW.