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Fusarium head blight (FHB) resistance in barley is controlled by many minor effect QTL which are affected by environmental conditions. Some of the QTL are associated with various agronomic and morphological trait as an escape mechanism which also complicates breeding efforts. Although considerable progress in the search for host resistance in barley and its wild relatives has been made, the mycotoxin deoxynivalenol (DON) content in the most resistant sources still exceeds the acceptable levels for the brewing industry. *FHB1*, a QTL in the Chinese wheat variety Sumai3, confers durable and broad-spectrum resistance to *Fusarium* species, and it has been extensively used as the best source of FHB resistance in wheat. The recent breakthrough on FHB research is that the *FHB1* gene has been successfully cloned and functionally characterized in wheat. It was revealed that the *FHB1* is probably required for disease susceptibility, and a deletion spanning the start codon in the 'Sumai 3' allele disrupts pathogen colonization. Isolation of this major QTL provides novel perspective to control this devastating disease, and FHB immunity may be achieved by manipulation of the *FHB1* orthologs in other species. BLAST search revealed that *FHB1* and its orthologs are well conserved in monocots susceptible to FHB, such as barley, rice, oat and maize, but not in dicots. The barley ortholog is a single copy gene and resides within the genomic region syntenic to the wheat *FHB1* locus. Knocking out of the ortholog of *FHB1* may enable barley plants resistant to FHB. Here, I am proposing to characterize the *Fhb1* ortholog and to determine if this gene is also required for FHB susceptibility in barley. We will use the CRISPR technology and investigate disease levels in the derived knockout mutants. Efforts in this direction will offer an efficient gene editing platform in barley and a potential target for breeders to generate FHB-resistant resources. Therefore, the outputs of this project meet the overall goal of the USWBSI.