

USWBSI Barley CP Milestone Matrix FYs 2016–2017

CP Objectives 2 and 3. Map novel QTL for resistance to FHB in barley; Validate and fine map FHB resistance QTL CP

PI(s)	Months	Milestones	Progress	Outputs/Linkages
RB	12	Phenotype F ₂ derived F ₇ RILs from CGN00483 X Harrington and genotype for 4H and 7H DON accumulation QTL regions to delimit these QTLs and enable ID additional markers		Improved markers for 4H and 7H QTL from CGN00483
CG	12	Phenotype two Eve-derived mapping populations and Nomini population; produce DH lines from Nomini/Violetta		Data and germplasm to enable QTL ID
GM, KS	12	Fine mapping of 6H 7H QTLs, field testing, and selection of recombinants		Improved markers and recombinants with low protein
BS	12	Evaluate BC2 doubled haploid lines for FHB reaction; genotype; and upload data to T3		Markers for potentially novel QTL
JS	12	Mapping of resistance in NAM lines and data uploaded to T3		Markers for potentially novel QTL
RB	24	ID of additional markers from CGN00483		New markers useful for MAS
CG	24	Phenotype Nomini populations		Data to enable QTL ID
BS	24	Evaluate BC2 doubled haploid lines for FHB reaction; distribute useful lines to breeders; and upload data to T3		Validation of prior data; new useful germplasm for variety development

CP Objectives 1 and 4: screen available *Hordeum* germplasm for novel sources of resistance; Develop new barley varieties with enhanced resistance to FHB and lower DON

PI(s)	Months	Milestones	Progress	Outputs/Linkages
RB	12	Create, increase BC ₄ populations from CGN00483 to ND Genesis and Conlon with selection for 4H and 7H QTLs		Elite populations for testing and selection
CG	12	100 new crosses; 100 lines evaluated for FHB		Creation and ID of potentially improved germplasm
RH	12	200–300 new crosses; 3500 early generation lines genotyped for 2H and 6H QTL, phenotyped for quality		Creation and ID of potentially improved germplasm
RH	12	8 FHB resistant lines submitted to AMBA		Potential new varieties
RB, GH	12	Screen 100 Aberdeen elite lines for FHB; data uploaded to T3		ID of potentially novel sources of resistance in elite germplasm
KS	12	Mapping of minor effect QTL from Rasmusson/PI383933 cross completed		ID of potentially novel QTL
JS	12	Crosses made to FHB-resistant parents; Montana germplasm screened		Creation and ID of potentially useful germplasm
KS	12	Evaluation of breeding lines; selection of new parents; data uploaded to T3		Creation and ID of potentially improved germplasm
KS	12	4 resistant lines submitted to AMBA		Potential new varieties
KS, GH, JS, MS	12	For genomic selection: grow training populations at multiple locations; assemble standardized datasets for prediction models; evaluate various parameters for effects on prediction accuracy; initiate stream 1 crosses; upload data to T3		Generation of basic data, models, and materials for evaluating and optimizing genomic selection models
BS	12	Upload all data to T3 from past screening of exotic barley accessions		Data identifying resistant accessions widely available.
RB	24	Field evaluation of CGN00483 introgression lines		CGN00483 resistance QTL in elite backgrounds
CG	24	100 new crosses made to FHB resistant parents; 100 breeding lines evaluated for FHB reaction		Creation and ID of potentially improved germplasm
RH	24	200–300 new crosses; 3500 early generation lines genotyped for 2H and 6H QTL, phenotyped for quality		Creation and ID of potentially improved germplasm
RH	24	8 FHB resistant lines submitted to AMBA		Potential new varieties
RB, GH	24	Screen 100 Aberdeen elite lines for FHB; data uploaded to T3		ID of potentially novel sources of resistance in elite germplasm
GH	24	Make crosses to FHB resistant lines		Creation and ID of potentially improved germplasm
GM, KS	24	Field phenotyping of recombinants for grain protein, FHB.		ID of potentially useful, unique germplasm
JS, RB	24	New crosses made; evaluation of resistant lines in regional trials; data uploaded to T3		Creation and ID of potentially useful germplasm

(Continued) CP Objective 4. Develop new barley varieties with enhanced resistance to FHB and lower DON

PI(s)	Months	Milestones	Progress	Outputs/Linkages
KS	24	Evaluation of breeding lines; selection of new parents; data uploaded to T3		Creation and ID of potentially improved germplasm
KS	24	4 resistant lines submitted to AMBA		Potential new varieties
KS	24	Evaluate stream 1 crosses		Data necessary to validate, optimize genomic selection model
KS, GH, JS, MS	24	For genomic selection: grow training populations at multiple locations; assemble standardized datasets for prediction models; upload data to T3		Generation of basic data, models, and materials for evaluating and optimizing genomic selection models
MS, KS	24	Use prediction models to design crosses for NY breeding lines; initiate crosses		ID and creation of potentially useful germplasm

CP Objectives 9 and 10: Develop and evaluate chemical/biological management strategies that reduce FHB and/or DON in barley/Develop and promote best management strategies through integrated disease management.

PI(s)	Months	Milestones	Progress	Outputs/Linkages
RB, RH	12	2016 NABSEN evaluated and data uploaded to T3/Datafarm		Data useful for FHB management
CG	12	2015/16 uniform winter malt barley nursery evaluated and data uploaded to T3/DataFarm		Data useful for FHB management
MS, RH	12	Evaluate Uniform Eastern Spring Malting Barley nursery and upload data to T3/DataFarm		Data useful for FHB management
RB, RH	24	2017 NABSEN evaluated and data uploaded to T3/Datafarm		Data useful for FHB management
CG	24	2015/16 uniform winter malt barley nursery evaluated and data uploaded to T3/DataFarm		Data useful for FHB management
MS, RH	12	Evaluate Uniform Eastern Spring Malting Barley nursery and upload data to T3/DataFarm		Data useful for FHB management

CP Objective 8. Elucidate the epidemiology of colonization and survival of *Fusarium graminearum* on host tissue, disease development, and toxin accumulation.

PI(s)	Months	Milestones	Progress	Outputs/Linkages
FT	12	Determine whether the resistance response in two-row barley trichomes is correlated with cessation of fungal penetration		Basic data on host-pathogen interaction
FT	24	Determine whether the resistance response differs between classes of barley		Elucidation of a component of observed differential response between major market classes of barley
FT	24	Determine whether MLO and ROR2 alter the observed resistance response associated with barley trichomes.		Elucidation of possible interactions between genetic responses to multiple diseases

CP Objectives 5 and 6: Evaluate promising transgenes in adapted genetic backgrounds in regional nurseries; Identify barley genes conferring (?) resistance to *Fusarium*.

PI(s)	Months	Milestones	Progress	Outputs/Linkages
PB	12	Create and demonstrate HR vector; analyze effect of insertions at two site		Vectors for testing RNAi construct at locations that will not result in confounding vector effects and position effects
PB	12	Create knockouts of FDB2 and OAH to determine if they are candidates for RNAi-based suppression of Fg virulence; Determine sRNA profiles for Fg transformed with RNAi constructs targeting TRI5 TRI6 LAEA and (if found to be appropriate targets) FDB2 and OAH.		Prediction of effects of RNAi directed against specific <i>Fusarium</i> genes; basic data on dsRNA processing; and creation of basic information that will be used to design barley transformation vectors for producing FHB-resistant germplasm.
GM	12	Field trials of HvUGT lines		Data on HvUGT overexpression effect on DON accumulation
PB	24	Determine sRNA profiles for Fg transformed with RNAi constructs; determine effects on Fg growth and virulence		basic data on dsRNA processing; and creation of basic information that will be used to design barley transformation vectors for producing FHB-resistant germplasm.
GM	24	Field trials of HvUGT lines		Complete dataset on HvUGT overexpression effect on DON accumulation