

The NABGMP/USBGP/RBGMP

States which have received NABGMP/USBGP/RGMP funding

1. Alabama
2. California
3. Colorado
4. Idaho
5. Iowa
6. Maryland
7. Michigan
8. Minnesota
9. Montana
10. New York
11. North Dakota
12. Oregon
13. South Carolina
14. Utah
15. Virginia
16. Washington
17. Wisconsin

Principal Investigators funded by the NABGMP/USBGP/RGMP

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3. Biyashev
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6. Bowman
7. Bregitzer
8. Budde
9. Carollo
10. Chen, T
11. Chen, X
12. Close
13. Cooper
14. Costa
15. Dahleen
16. Dietzer
17. Dill-Macky
18. Dofing
19. Duke
20. Dvorak
21. Effertz
22. Faris
23. Fischer
24. Frankowiak
25. Friesen

26. Froseth
27. Gallo-Meagher
28. Gao
29. Garcia
30. Gustafson
31. Han
32. Hang
33. Hayes
34. Hellewel
35. Henson
36. Hoffman
37. Hole
38. Horsley
39. Johnston
40. Jones
41. Kaeppler
42. Kaiser
43. Kilian
44. Kleinhofs
45. Kling
46. Knapp
47. Kudrna
48. Lapitan
49. Lawrence
50. Lemaux
51. Line
52. Liu
53. Louwerse
54. Ma
55. Maroof
56. Muehbauer
57. McElroy
58. Mesfin
59. Mickelson
60. Morhinweg
61. Newman
62. Pickering
63. Raboy
64. Rasmusson
65. Riera-Lizarazu
66. Roche
67. Schmitt
68. Schwartz
69. Skadsen
70. Smith
71. Somerville

72. Sorrells
73. Steffenson
74. Surber
75. Toubia-Rahme
76. Tsuchiya
77. Ullrich
78. Vales
79. Wesenberg
80. Wing
81. Wise
82. Whitman

Titles of NABGMP/USBGP/RGMP projects

1. Agronomic phenotyping
2. A genetic analysis of stripe rust (*Puccinia striiformis*) in the kold x colter cross
3. Assessment of linkage drag in a *Hordeum bulbosum* – *Hordeum vulgare* recombinant
4. An arrayed barley cDNA library and expressed sequence tagging sequencing
5. An integrated analysis of malting quality, winter hardiness, and agronomic performance traits in barley
6. Allelic & sequence variations in alpha amylase and alpha glucosidase and isoamylase genes: their characterization & contributions to diastatic power & fermentable sugar production
7. Analysis of barley samples for genome mapping
8. Approach validation for targeted sequencing of gene-rich regions
9. A physical map of the barley genome
10. An integrated database for barley genomics
11. Association mapping
12. Analysis of barley cap entries for tocopherol and tocotrienol composition
13. Barley genome analysis and disease resistance genes
14. Barley resistance gene analogs: isolation, mapping and sequencing
15. Barley genome analysis new knowledge a physical map of the barley genome
16. BAC library data
17. Cloning *rca5*
18. Construction of a barley microarray
19. Characterization of QTLs for Fusarium head blight resistance in barley
20. Cataloging leaf rust resistance genes in barley
21. Characterization and mapping of simple sequence repeat (SSR) and resistance gene analog (RGA) loci in North American barley genome mapping project germplasm.
22. Characterization of the determinants of quantitative adult plant stripe rust resistance pathway via the systematic introgression of multiple resistance genes into a six-row quality background
23. Construction and distribution of λ genomic libraries of NABGMP cross parents
24. Construction of rice/barley synteny maps and development of barley microsatellite DNA markers.

25. Collaborative efforts to locate and validate agronomic and malting quality QTLs
26. Disease phenotyping
27. Determination of genetic markers associated with digestibility of barley in beef cattle.
28. Development of DNA markers for marker-resisted breeding Fusarium head blight resistant six-rowed barley cultivars.
29. Development of markers closely linked to disease resistance and other target loci, synteny and anchor probes, other mapping and housekeeping.
30. Development and mapping of microsatellite DNA markers in barley.
31. Developing Fusarium resistant cultivars
32. Development of recombinant chromosome substitution lines (RCSLs)
33. Developing of single QTL near-isogenic lines from Zhedar 2.
34. Development of promoters for organ-specific expression of an anti-*Fusarium graminearum* hordothionin gene.
35. Development and characterization of multiple genetic stocks
36. Developing new SSR markers for barley derived from the EST database and wheat SSRs.
37. Development and characterization of germplasm resources
38. Development of a comprehensive set of *Hordeum vulgare* subsp. *spontaneum*: barley introgression lines
39. Determining the genetic basis of pre-harvest sprouting resistance and malt quality difference
40. Development and genetic characterization of the OrNe six-row winter malting barley germplasm
41. Enhancing mashing yield with better enzymes
42. Exploring *Hordeum vulgare* subsp. *spontaneum* germplasm for disease resistance
43. Evaluation of reduced phytic acid-p barley lines for non-ruminants and ruminants.
44. Exploiting *Hordeum vulgare* subsp. *spontaneum* germplasm for disease resistance.
45. Expanding the Oregon Wolfe Barley population genetic resources
46. Evaluation of barley populations for resistance to Fusarium head blight and the accumulation of deoxynivalenol
47. Evaluation and improvement of barley for food and feed / analysis of barley feed quality
48. Fine structure analysis of diastatic power QTLs.
49. Functionality of maize transposable elements in barley
50. Fusarium head blight: mapping genes conferring resistance to Fusarium head blight in barley
51. Functional genomics of malting
52. Functional analysis of genes controlling barley grain protein concentration.
53. Genetics of malting quality
54. Gene chips for mapping and gene expression
55. Genetics of stripe rust resistance
56. Gene chips for high throughput mapping
57. Gene expression patterns
58. Genetics of mapping of Septoria speckled leaf blotch resistance in barley.

59. Genetic analysis of barley low phytic acid mutants.
60. Genetic transformation of barley with the gene for hordeothionin protein which is toxic to *Fusarium graminearum*.
61. Genome map assisted plant breeding and germplasm enhancement.
62. Generating a novel barley germplasm group by STS/QTL analysis and pedigree advancement.
63. Harrington x Morex population analysis
64. High resolution and physical mapping around *Rph5*, a barley leaf rust resistance gene.
65. High density mapping of genes controlling winter hardiness-related traits in order to develop winter malting varieties.
66. Identification and isolation of markers closely linked to disease resistance genes and markers for malting quality in elite, closely related, malting cultivars.
67. Identification and mapping of disease resistance-related DNA sequences in barley
68. Identification of carbohydrases with novel/enhanced enzymatic capabilities
69. Identification of genes conferring low protein in barley.
70. Identification of genes conferring low protein in spring barley
71. Identification of genetic markers associated with forage quality in Lewis x Karl barley lines for beef cattle.
72. Identification of molecular markers linked to grain protein, kernel color, and associated malt quality traits in barley
73. Implementing marker assisted selection for malting quality in Midwest 6-rowed breeding germplasm.
74. Improving Barley (*Hordeum vulgare*) yield under drought using HAP transcription factors
75. Integrating information on quantitative and qualitative stripe rust resistance genes.
76. Interval Mapping of PCR-RAPD loci in barley and genotyping of W166 barley cultivars.
77. Isolation and tagging of leaf rust resistance genes.
78. Lewis/Baronesse RIL development
79. Karl protein gene mapping
80. Low phytic acid genetics
81. Low protein genetics
82. Maintenance and map improvement
83. Malt analysis
84. Malting gene signatures
85. Malting Quality QTL mapping
86. Malting quality sample analysis
87. Map Based Cloning of Rcs5
88. Map construction
89. Mapping
90. Mapping and marker assisted selection of multiple disease resistance genes in barley.
91. Mapping and marker assisted selection of net blotch and spot blotch resistance genes in barley
92. Mapping genes conferring resistance to barley stripe rust, race 24.

93. Mapping genes conferring resistance to Fusarium head blight
94. Mapping genes conferring resistance to Fusarium head blight in barley
95. Mapping of Fusarium head blight resistance in barley
96. Mapping of genes involved in the photoperiodic induction of flowering in barley
97. Mapping of leaf rust resistance genes in barley.
98. Mapping of Septoria speckled leaf blotch resistance in barley.
99. Mapping rph5
100. Mapping spot blotch resistance
101. MAS for malting quality
102. Micromalting
103. Mining *Hordeum spontaneum* germplasm
104. Molecular breeding and genetic analysis of improved 2-row and 6-row malting barley germplasm and cultivars.
105. Molecular breeding and genetics of pre-harvest sprouting
106. Molecular breeding of 2 and 6-row germplasm.
107. Molecular maps for Fusarium Quantitative Trait Loci
108. New SSR Markers and association mapping
109. Nutritional analysis
110. Phenotypic and marker assisted selection for low grain protein QTL utilizing a Lewis x Karl RIL population.
111. Pre-harvest sprouting genetics
112. Project coordination
113. Proteinase activity and malting quality in Harrington x *H. spontaneum* RCSLs
114. QTL analysis
115. QTL analysis of progeny from biparental matings
116. QTL curation workbook
117. Regulatory genes in GA signaling pathway
118. Resolution and manipulation of QTL for malting quality.
119. Resolution and manipulation of QTL for malting quality.
120. Resolution of QTL for malting quality in the Steptoe/Morex Cross
121. Restriction fragment differential display & bulked segregant analysis to study epistasis in the Oregon Wolfe barley population.
122. Russian wheat aphid resistance mapping
123. Saturate the barley molecular marker map with disease resistance-like loci
124. Saturation mapping of a barley chromosome 6h locus containing multiple net blotch resistance
125. Seed proteomics using RCSLs
126. Seedling and adult plant stripe rust resistance in barley
127. SNP analysis of malting genotypes
128. Spike-specific gene promoter isolation from Bowman barley and near-isogenic morphological marker lines
129. Spot blotch disease resistance genes
130. Stripe rust resistance and microsatellite diversity in barley
131. Temperature challenges in malting barley.
132. The barley QTL community curation workbook

133. The enhancement of western six-rowed malting barley with marker-assisted and phenotypic selection
134. Transcript profiling of drought
135. Transposon tagging
136. Trap mapping
137. USBGP genetic stocks management
138. Utilization of Morex-based QTLs for selection of agronomic and malting quality traits in the malting barley germplasm pool.
139. Wild barley allele mining
140. Wild barley gene networks