Updates on Genomics Assisted Breeding Resources for Sunflower

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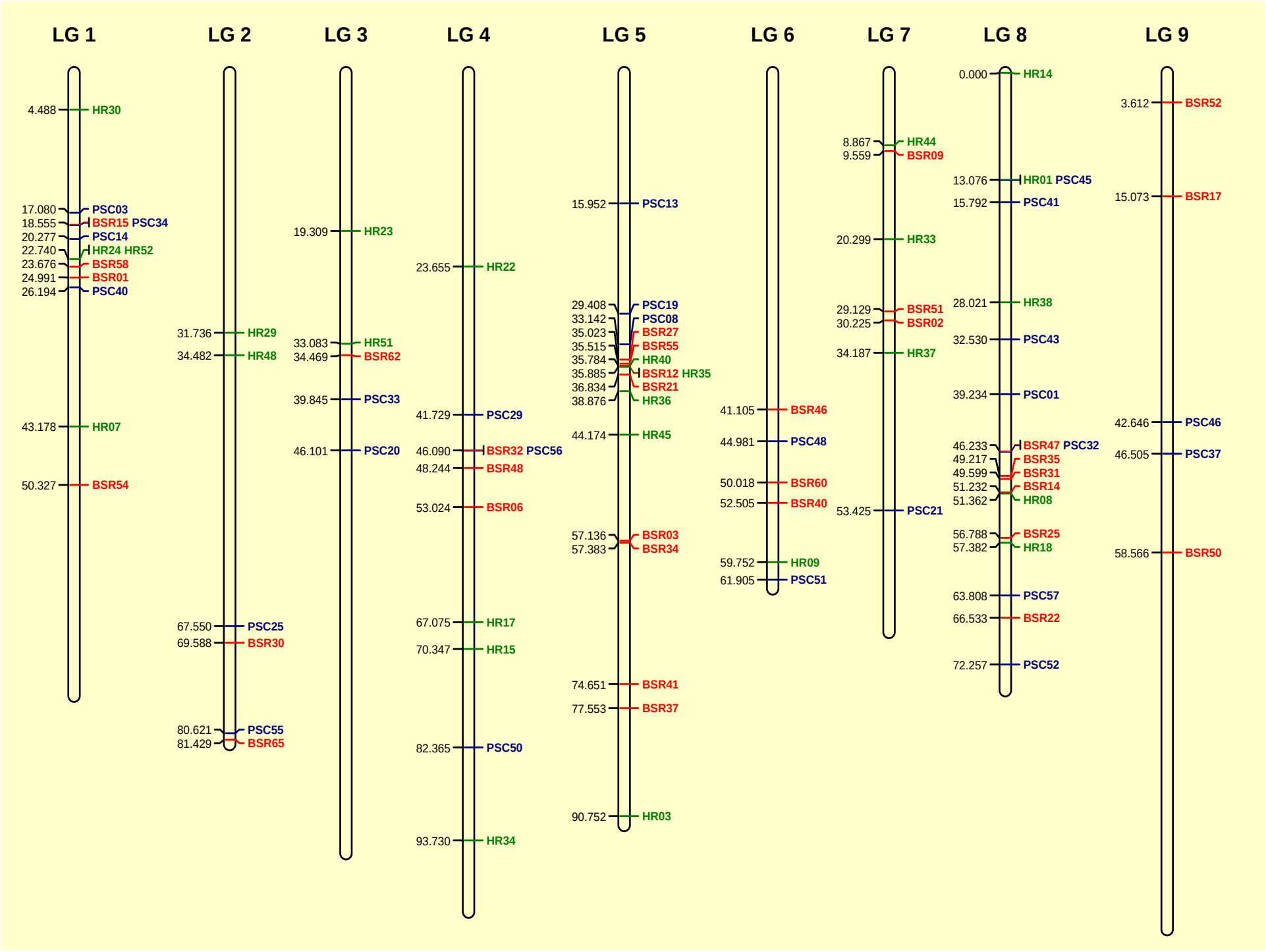
Update on Sclerotinia and Phomopsis resistance mapping

- Used a genome-wide association mapping approach
- Over 5000 NSA markers (now public)
- Multiple environments of data (locations and years) for Sclerotinia stalk and head rot, Phomopsis stalk canker
  - Talukder et al., Crop Science, 2014
- Used a Mixed Model-LASSO algorithm, as appropriate for moderate to small effect loci
  - Based on previous QTL mapping results
- Results in review currently, and available by MTA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4.488 HR30
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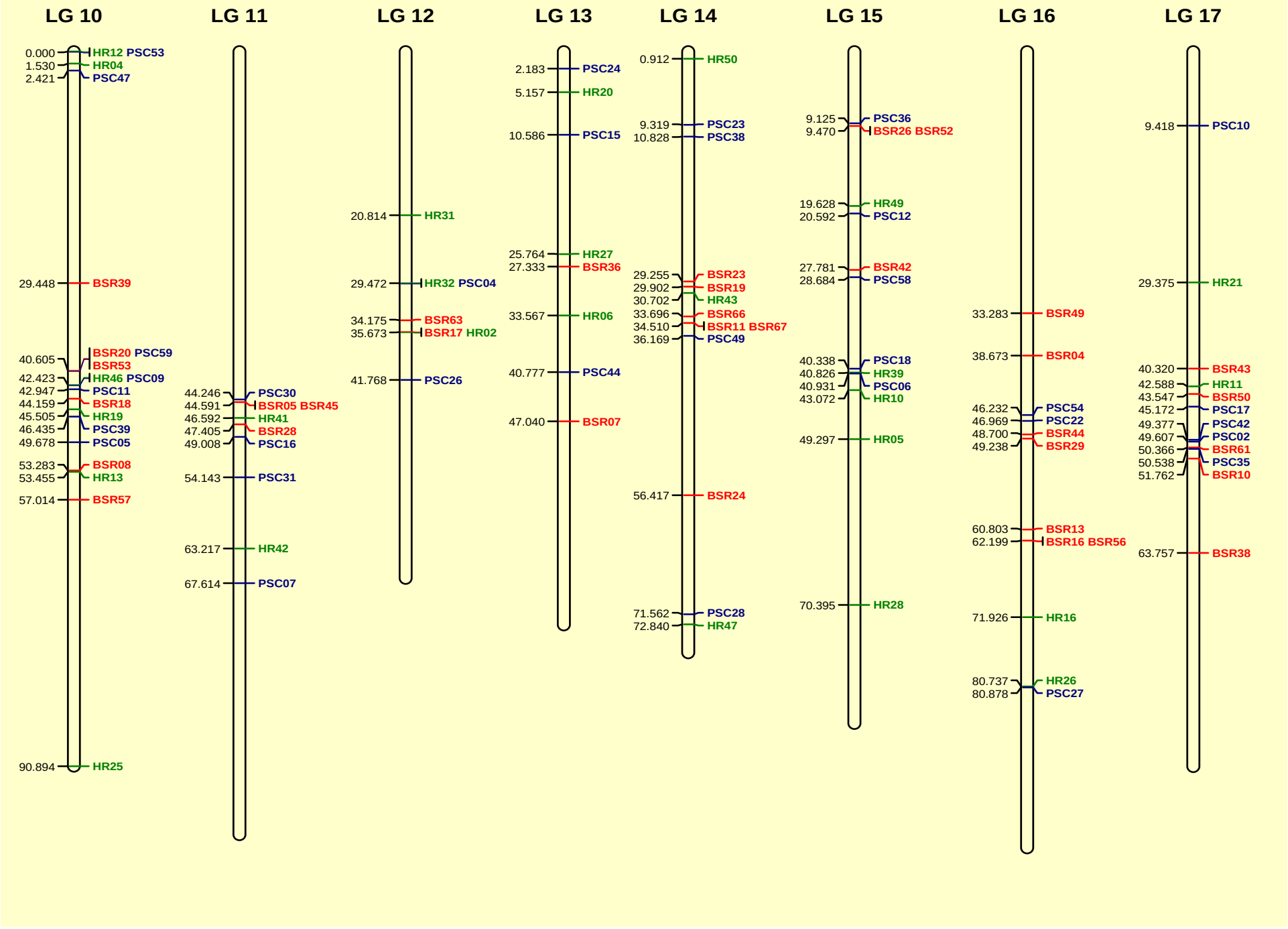
18.555 BSR15 PSC34
20.277 PSC14
22.740 HR24 HR52
23.676 BSR58
24.991 BSR01
26.194 PSC40
43.178 HR07
50.327 BSR54
LG 2
31.736 HR29
34.482 HR48
67.550 PSC25
69.588 BSR30
80.621 PSC55
81.429 BSR65
LG 3
19.309 HR23
33.083 HR51
34.469 BSR62
39.845 PSC33
46.101 PSC20
LG 4
23.655 HR22
41.729 PSC29
46.090 BSR32 PSC56
48.244 BSR48
53.024 BSR06
67.075 HR17
70.347 HR15
82.365 PSC50
93.730 HR34
LG 5
15.952 PSC13
29.408 PSC19
33.142 PSC08
35.023 BSR27
35.515 BSR55
35.784 HR40
35.885 BSR12 HR35
36.834 BSR21
38.876 HR36
44.174 HR45
57.136 BSR03
57.383 BSR34
74.651 BSR41
77.553 BSR37
90.752 HR03
LG 6
41.105 BSR46
44.981 PSC48
50.018 BSR60
52.505 BSR40
59.752 HR09
61.905 PSC51
LG 7
8.867 HR44
9.559 BSR09
20.299 HR33
29.129 BSR51
30.225 BSR02
34.187 HR37
53.425 PSC21
LG 8
0.000 HR14
13.076 HR01 PSC45
15.792 PSC41
28.021 HR38
32.530 PSC43
39.234 PSC01
46.233 BSR47 PSC32
49.217 BSR35
49.599 BSR31
51.232 BSR14
51.362 HR08
56.788 BSR25
57.382 HR18
63.808 PSC57
66.533 BSR22
72.257 PSC52
LG 9
3.612 BSR52
15.073 BSR17
42.646 PSC46
46.505 PSC37
58.566 BSR50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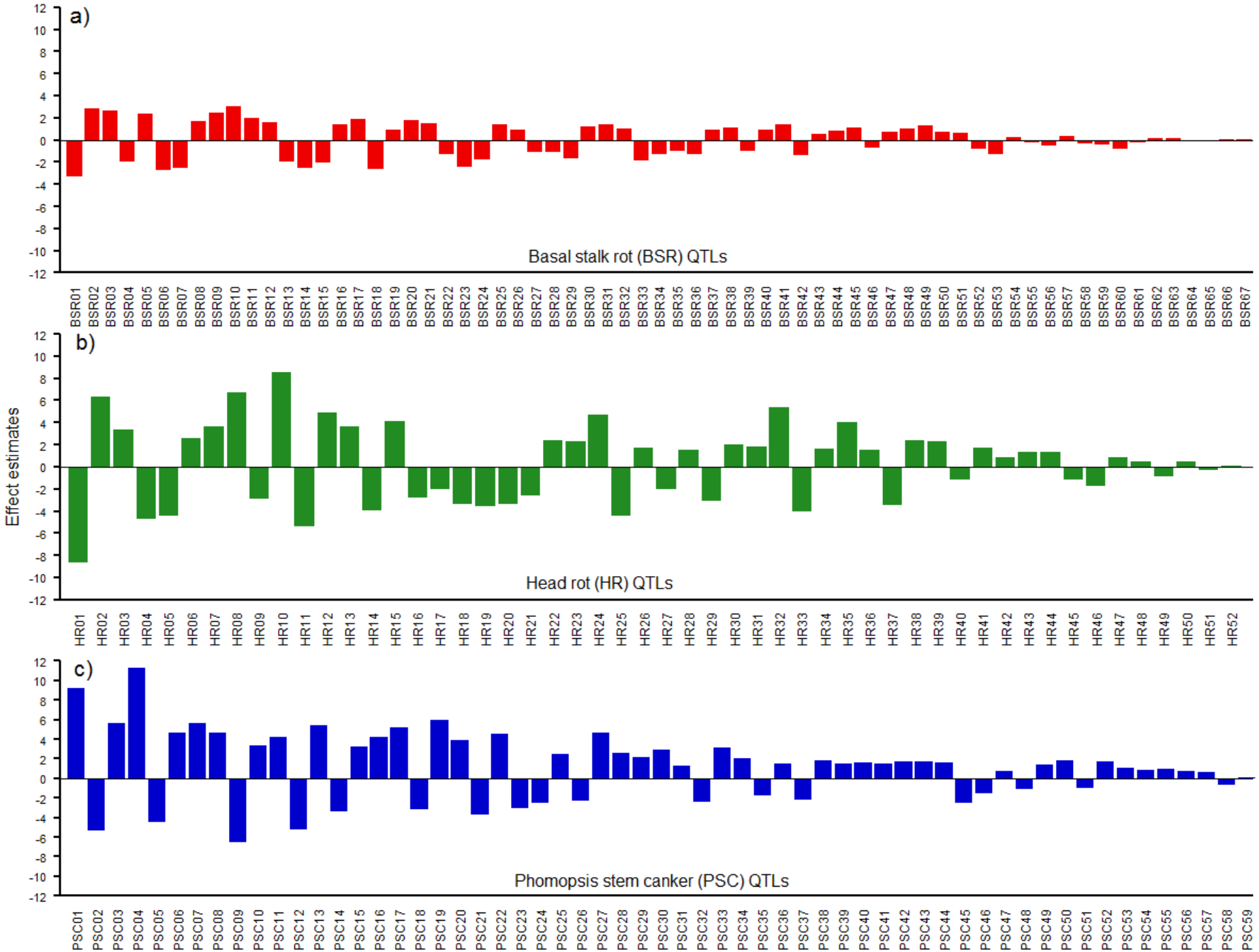
1.530 HR04
2.421 PSC47
29.448 BSR39
40.605 BSR20 PSC59
BSR53
42.423 HR46 PSC09
42.947 PSC11
44.159 BSR18
45.505 HR19
46.435 PSC39
49.678 PSC05
53.283 BSR08
53.455 HR13
57.014 BSR57
90.894 HR25
LG 11
44.246 PSC30
44.591 BSR05 BSR45
46.592 HR41
47.405 BSR28
49.008 PSC16
54.143 PSC31
63.217 HR42
67.614 PSC07
LG 12
20.814 HR31
29.472 HR32 PSC04
34.175 BSR63
35.673 BSR17 HR02
41.768 PSC26
LG 13
2.183 PSC24
5.157 HR20
10.586 PSC15
25.764 HR27
27.333 BSR36
33.567 HR06
40.777 PSC44
47.040 BSR07
LG 14
0.912 HR50
9.319 PSC23
10.828 PSC38
29.255 BSR23
29.902 BSR19
30.702 HR43
33.696 BSR66
34.510 BSR11 BSR67
36.169 PSC49
56.417 BSR24
71.562 PSC28
72.840 HR47
LG 15
9.125 PSC36
9.470 BSR26 BSR52
19.628 HR49
20.592 PSC12
27.781 BSR42
28.684 PSC58
40.338 PSC18
40.826 HR39
40.931 PSC06
43.072 HR10
49.297 HR05
70.395 HR28
LG 16
33.283 BSR49
38.673 BSR04
46.232 PSC54
46.969 PSC22
48.700 BSR44
49.238 BSR29
60.803 BSR13
62.199 BSR16 BSR56
71.926 HR16
80.737 HR26
80.878 PSC27
LG 17
9.418 PSC10
29.375 HR21
40.320 BSR43
42.588 HR11
43.547 BSR50
45.172 PSC17
49.377 PSC42
49.607 PSC02
50.366 BSR61
50.538 PSC35
51.762 BSR10
63.757 BSR38


a)
Basal stalk rot (BSR) QTLs
b)
Head rot (HR) QTLs
c)
Phomopsis stem canker (PSC) QTLs
Effect estimates

Update on NSA markers/map

- NSA map and markers publicly released this year (Talukder et al., PLoS One, 2014)
- Additional effort was put to combining the NSA map with the other existing public map from Steve Knapp and John Burke's labs.
  - Hulke et al., Crop Science, in review
  - 17,043 markers placed on the common RHA 801 x RHA 280 map
  - Expect it to be accepted soon

Other efforts

- Mapping of commonly selected traits
  - Pl6, Pl8, PlArg, Rf1, IMISUN, recessive branching, etc.
  - Using variation across a large number of inbred lines, clear signals of association were found for these, with LOD values above 10 for some traits
  - Mapping complete, data available by MTA
  - Manuscript in draft

Future efforts

- Genomic Selection
  - Funded by National Sclerotinia Initiative, USDA headquarters, and NSA
  - Recruiting of postdoc nearly complete
  - Will use a Genotype by Sequencing (GBS) approach for genotyping data, leveraging whole genome sequence data for USDA parental lines (Thanks to Loren Rieseberg!)
  - Will train a model from 5 years of past data for which we also have DNA

Future Efforts

- Expected timeline for Genomic Selection
  - By next January, may have cross-validation data suggesting the use of genomic data on selection of all traits, including yield, lodging, disease, etc.
  - Plan to publish results and begin using the method immediately in breeding program
- Will also integrate mapping of minor fatty acid loci with this work as well
  - Goal: find markers that could explain very high oleic content (~95 %)

- Thanks to NSA and Sclerotinia Initiative, for funding
- Thanks to students and technicians at USDA for help, especially Trent Neisen, Brady Koehler, Chris Misar, and Michelle Gilley

- Questions?