Evaluating Genetics of Soybean Host Plant Reaction to Soybean Gall Midge Infestation

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Evaluations 2020, 2021

Set of genetically diverse accessions from USDA Soybean Germplasm Collections

- 713 Accessions represent complete genetic diversity in the collection in MG I-IV
- Evaluated in 2 reps, 3 locs
- Larval presence/absence
- Injury score



Map of SGM plots on field edges

500 ft

Field Edge

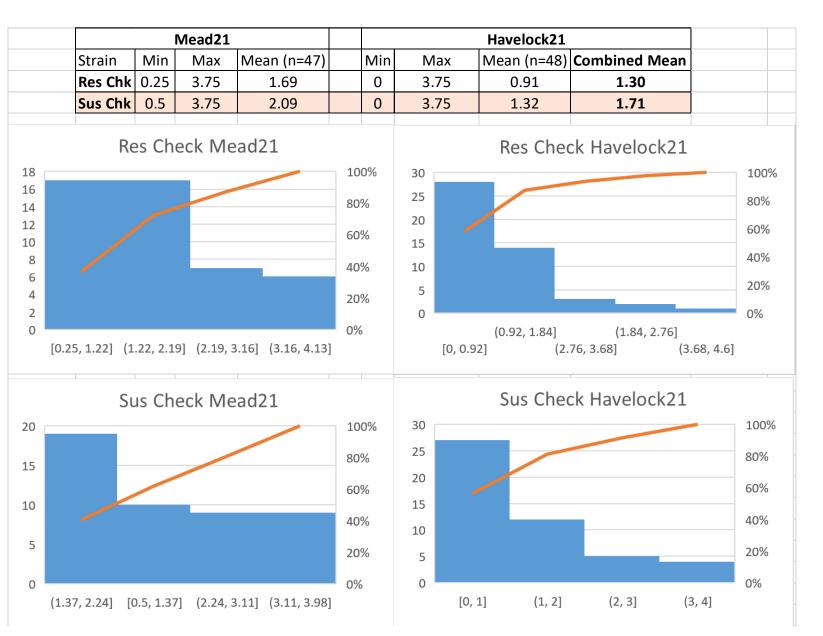
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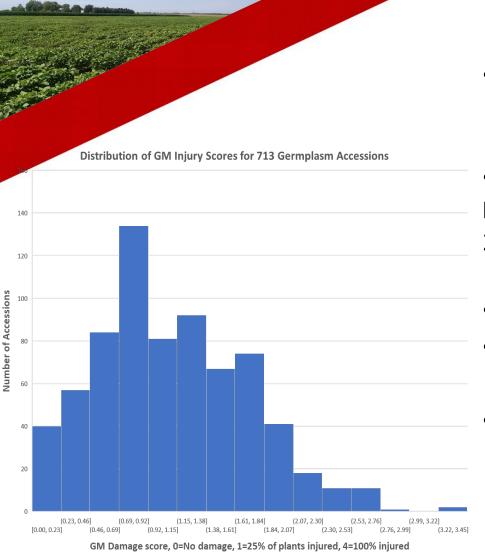


- Plots planted in long strips along field edge
- 500+ ft long, 50 ft into the field from edge

Field Experimental Design 2020-2021

- Augmented Incomplete Block
- 24 Blocks of 32 Entries
 - 30 new lines
 - 2 common checks





Soybean Resistance to Gall Midge

• Evaluation of **713 genetically diverse soybean accessions** from the USDA Soybean Germplasm Collection

• 3 Env, 2 Reps/Env

Environments are Mead, NE 2020, Mead, NE 2021, Havelock, NE 2021

• Injury Score 0=No injury, 1=25% injured, 4=100% injured

- Injury means dead or wilted plants due to GM infestation
- Distribution shows predominance of more resistant reactions = Good News
 - 40 accessions with mean injury score <0.25
 - 114 with mean score of 0.50 or less
 - 350 with mean score of 1.0 or less
 - 15 accessions with mean score of 2.50 or higher

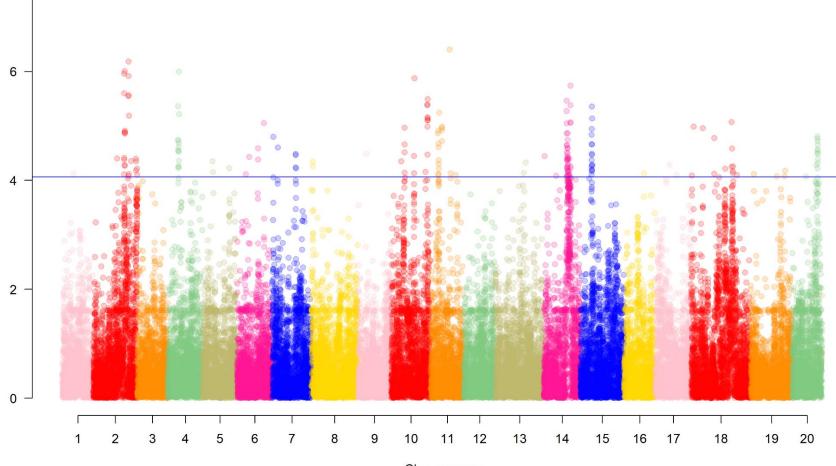
Soybean Gall Midge Genome-wide Association Mapping Preliminary analysis

GM All environments (3)

Manhattan plot from genome-wide association mapping of Gall Midge Injury Scores on 713 soybean accessions evaluated in 3 environments. 8

-log10(P-value)

Significant SNPs are identified on all chromosomes except 1, 3, and 12.

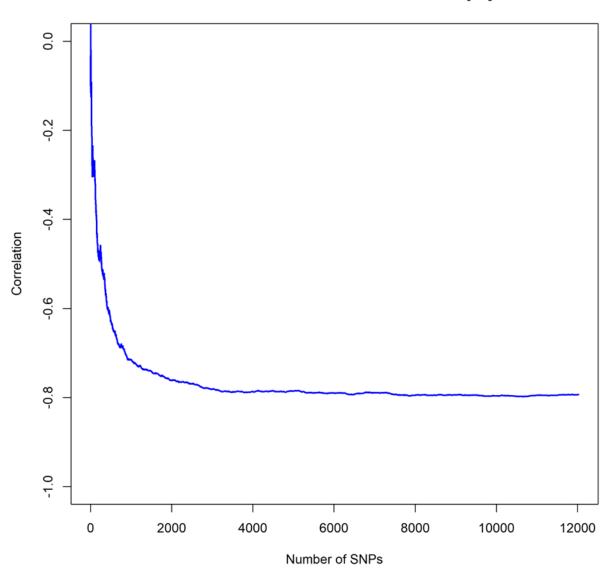




Chromosome

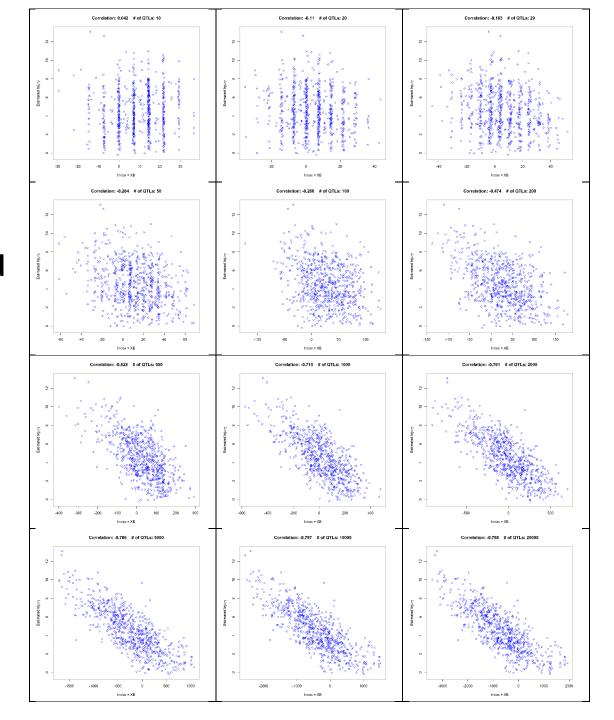
Correlation between the **Estimated Injury** and the **Index I=XB** computed as the *product between the selected SNPs and their corresponding effects*. In this case, the SNPs were selected based on the estimated marker effects derived from the GWAS (top 10, 20, 29, 50, etc.)

- Reach plateau ~2000 most influential SNPs
- Indicates complexity of the trait

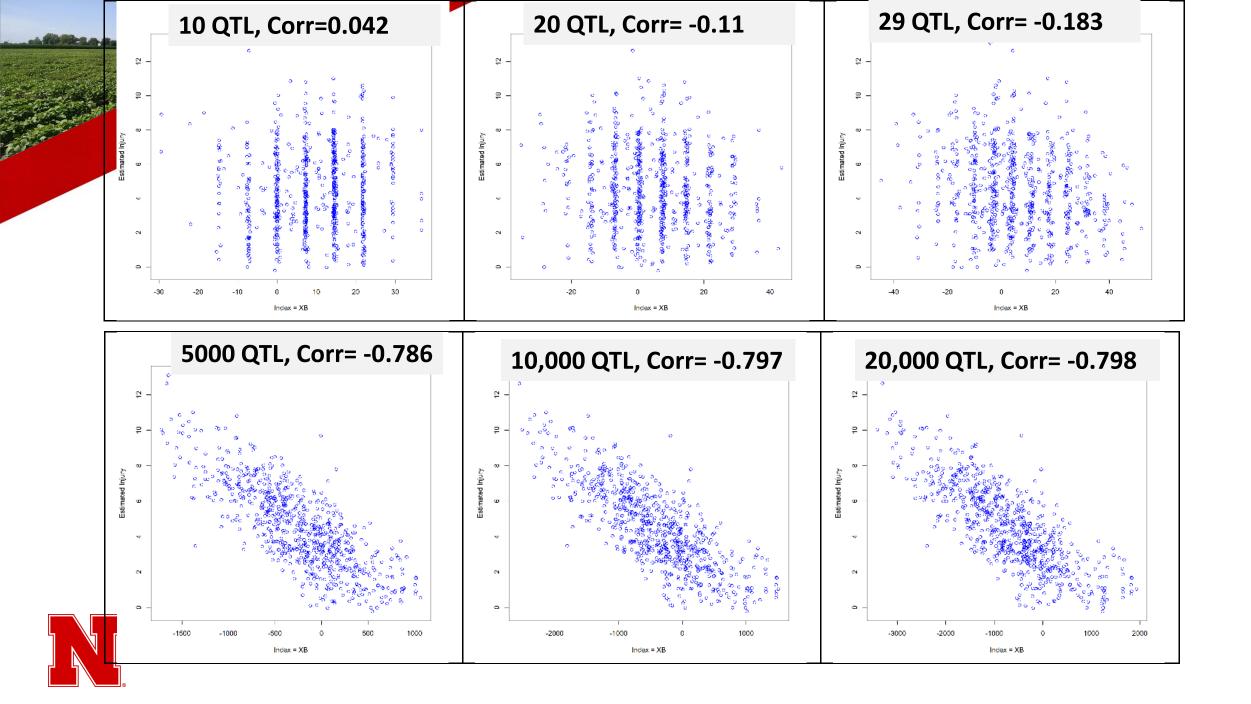




Scatter plot between the Estimated Injury and the Index I=XB computed as the product between the selected SNPs and their corresponding effects. In this case, the SNPs were selected based on the estimated marker effects derived from the GWAS (top 10, 20, 29, 50, etc.)







➢ Use 2020-2021 injury score data and genotype info to predict injury score of remaining ~7,000 accessions in MG 0, I, II, III, and IV in the USDA Soybean Germplasm Collection

Selected 100 accessions: 90 most resistant, 10 most susceptible

➢Grew seed increase during 2022 for evaluation in 2023 field plots



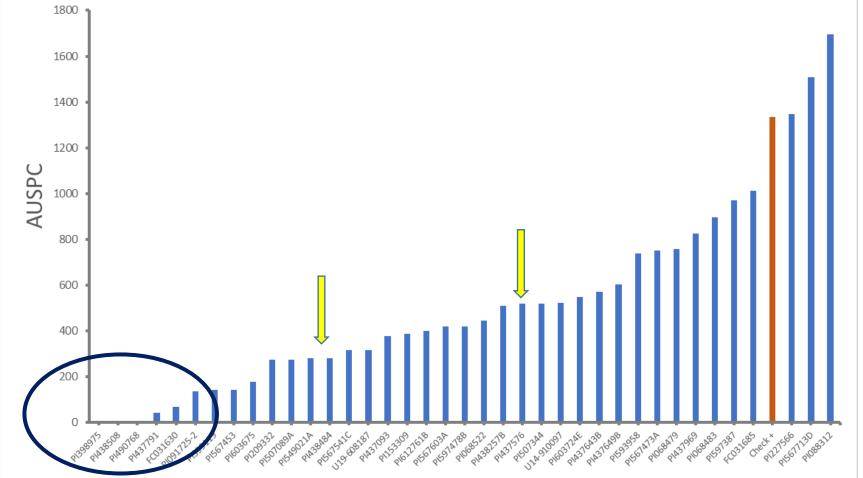
2022 Tests

120 selected lines from 2020-21 evaluation of 713 lines
Yield test plots 4 locs – 2 NE, 1 IA, 1 SD

- Larval counts on yield test plot border rows at NE locs
- Damage scores on yield test plots
 - Included multiple ratings at NE locs, 5 dates, to generate severity progress curves (AUSPC)

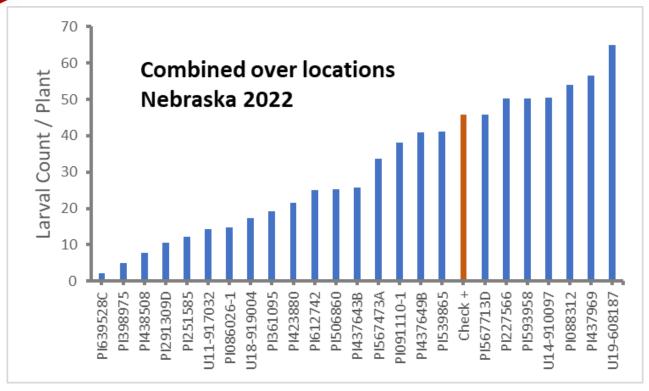


Area Under the Severity Progress Curve Syracuse, NE 2022

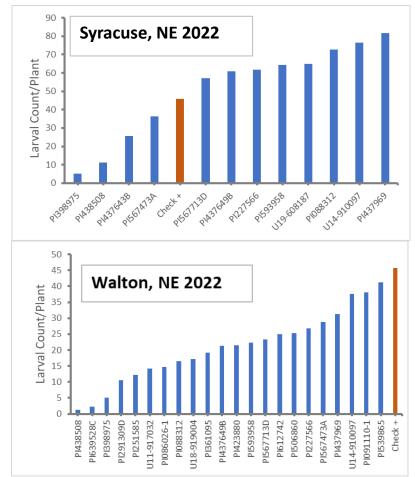


- Damage severity scores made on
 - July 14, 26
 - Aug 5, 14, 24
- 3 PI lines with virtually zero damage
- 9 PI lines with minimal damage
- 2 elite Nebraska lines with lower damage vs. commercial susc. check

Larval count per plant at two Nebraska locations in 2022



- Significant differences in # of larvae per plant
- Illustrates differences in plant response to larval infestation
- Important information, along with damage scores, to ID target lines for next phase of research



•2023 Field Evaluations

- Validation set: 100 PI Accessions
 - o 90 Resistant, 10 Susceptible
 - 3 Locations (2 NE, 1 IA; 3 reps/loc)
 - Plant injury score. Plant injury scale (use 0.25 increments to fine-tune injury score)
 - 0 0% of plants wilting or dead
 - 0.25 designated when any wilting or dead plants are found
 - 0.5 12.5 % wilting or dead plants
 - 1 25% wilting or dead plants
 - 2 50% wilting or dead plants
 - 3 75% wilting or dead plants
 - 4 100% wilting or dead plants
 - \circ Score ~ every 10-14 days to R6

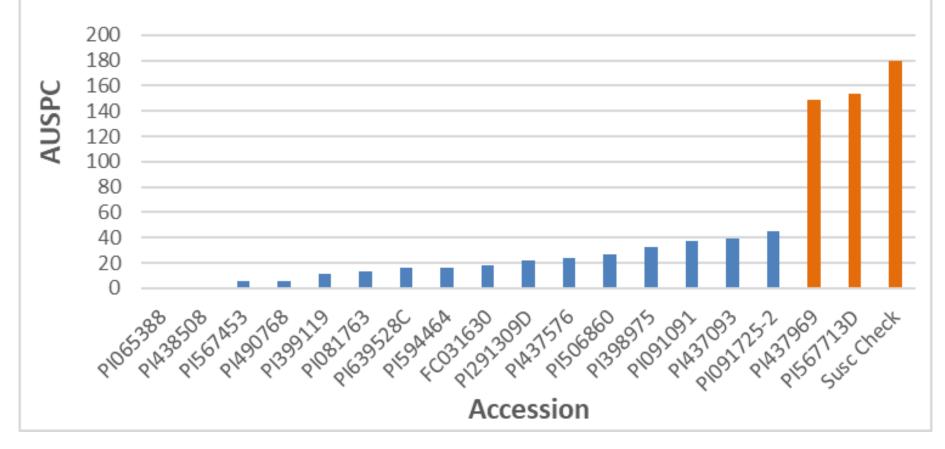


2023 Field Evaluations

- Selected accessions from previous years for more detailed study
 - 18 accessions 16 more resistant, 2 most susceptible. Plus common susc commercial check
 - 4-row plots, 3 reps, 3 locations (2 NE, 1 IA)
 - Damage scores as above, AUSPC
 - Larval presence
 - Larval counts
 - Fissure +/-, fissure type
 - Surface, deep, above ground, below ground



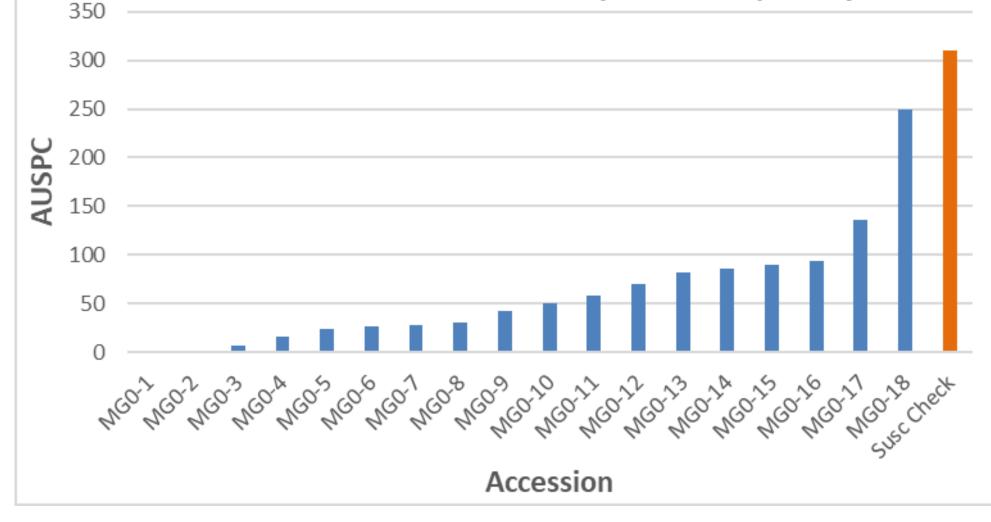
AUSPC for 18 PI accessions & 1 elite susc check 2023 Field, 3 locs (2 NE, 1 IA), 9 reps



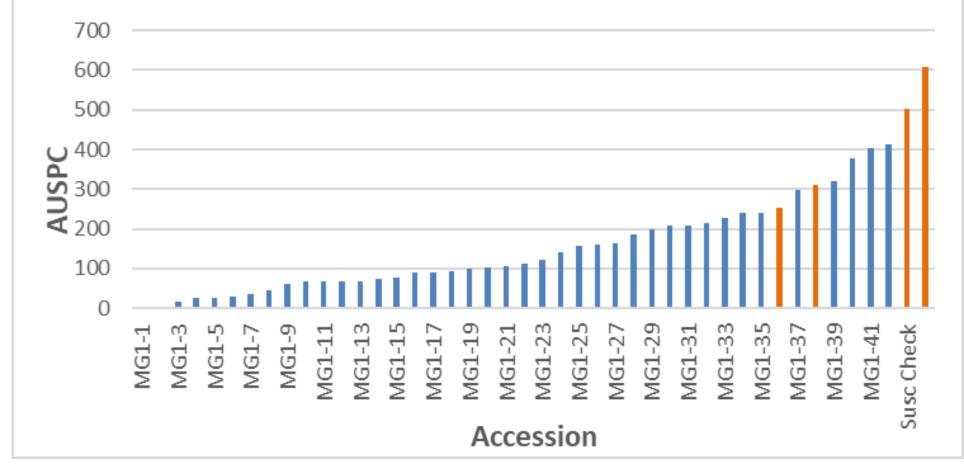


Luis Posadas

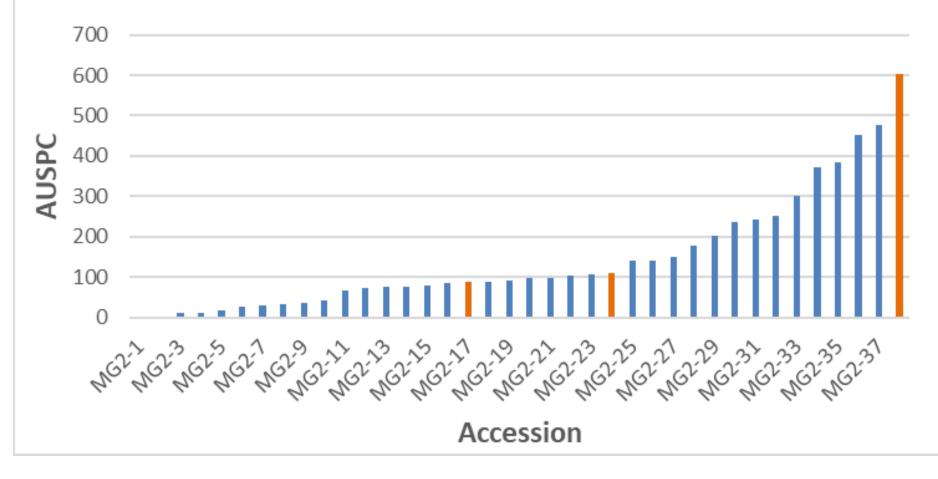
AUSPC for MG0 accessions in the Validation Set 2023 Field Evaluations, 3 locs (2 NE, 1 IA), 9 reps



AUSPC for MG I Accessions in the Validation Set 2023 Field Evaluations, 3 locs (2 NE, 1 IA), 9 reps

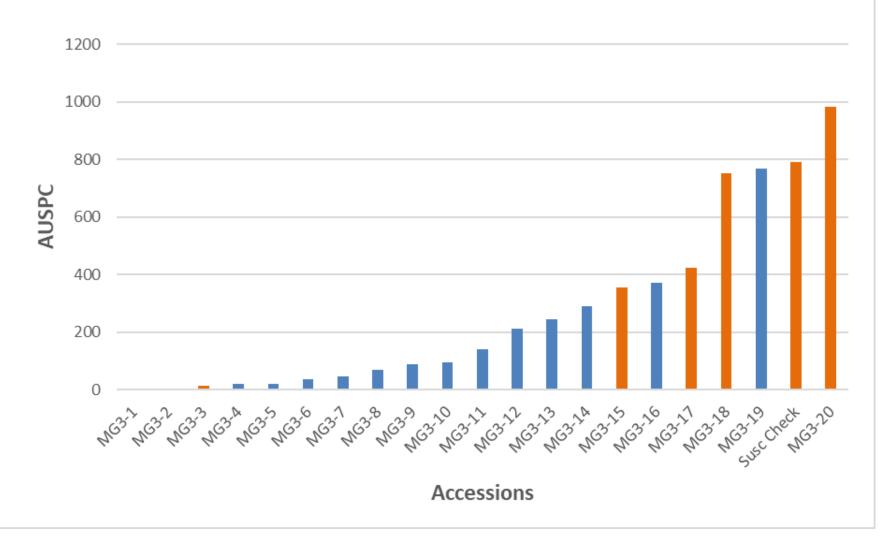


AUSPC for MG II Accessions in the Validation Set 2023 Field Evaluations, 3 Locs (2 NE, 1 IA), 9 reps





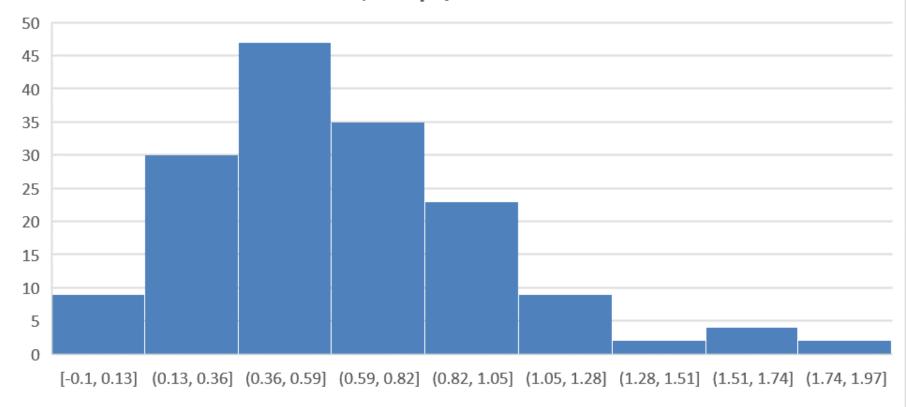
AUSPC for MG 3 Accessions in Validation Set 2023 Field Evaluations, 3 Locs (2 NE, 1 IA), 9 reps





What about elite lines & cultivars? Is there "resistance"?

Distribution of average GM Injury Score for 163 elite soybean lines from University of Nebraska Soybean Breeding Program 2-3 Env, 2 reps/Env 2020-2021

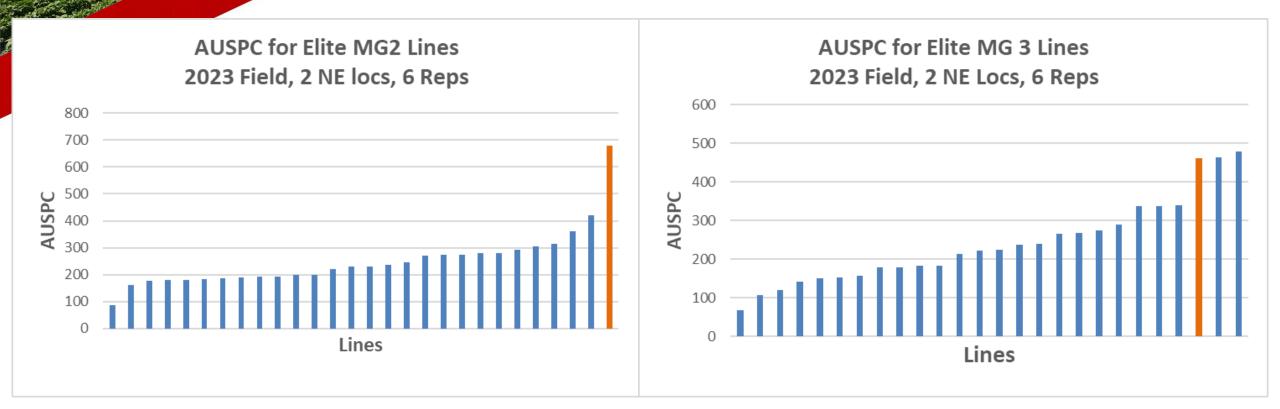


- Injury scores are skewed to the low end in elite germplasm.
- Good news

Injury Score

0=no injury, 1= 25% injured to 4= 100% of plants injured

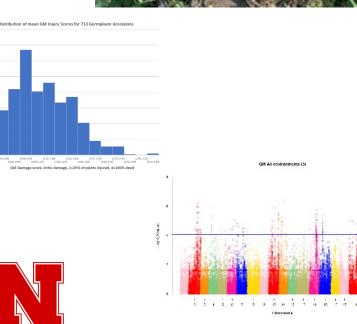




Elite MG2 & MG3 lines from the University of Nebraska soybean breeding program

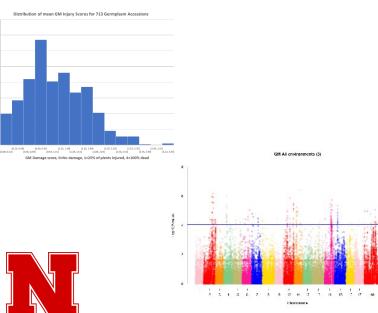






- Soybean lines show differential response to GM infestation
- There are genotype differences
- Identified significant SNPs
- Good results from Validation Set selected based on GEBVs for injury score
- ID'd several accessions with zero or very low AUSPC in both the initial set and validation set





- There is significant resistance observed in elite soybean germplasm (based on evaluation of Nebraska breeding program elite lines)
- Good news for soybean farmers & companies => can screen current elite germplasm
 phenotypically and genotypically to ID best lines
 for SGM infested areas, breeding programs

2024 tests and beyond

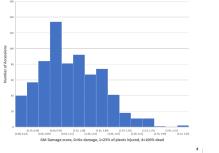
- •Yield tests of elite lines in infested fields, with hilling or other treatments?
- •Evaluate USDA Uniform Test entries using genotype information, ID and evaluate selected lines for reaction in infested fields
- Use selected most resistant lines in more detailed and controlled environment studies to help elucidate insect/plant interactions and genetics
- •Develop cross populations for further genetic study

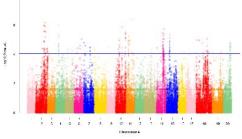






Distribution of mean GM Injury Scores for 713 Germplasm Accession





Thank you



The North Central Soybean Research Program, a collaboration of 12 state soybean associations, invests soybean checkoff funds to improve yields and profitability via university research and extension.





Agricultural Research Service



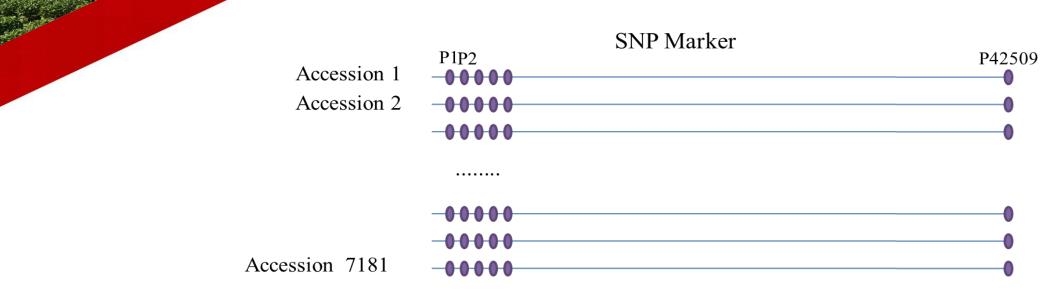
UNIVERSITY of NEBRASKA



Additional slides for possible inclusion or for questions



Data set for accessions & SNPs



- n= 7181 accessions MGI to MGIV
- **p**= 42509 SNP (single-nucleotide polymorphism) markers.
- Each of genotypes in the collection has a 1xp vector of genotypic binary marker information.
- Reduced total SNPs to 19,356
- m=200 << P selected from total accessions</p>

Distribution of accessions across maturity group & sample method

Representation of soybean accessions by sampling method across Maturity Group 100% 80% 60% 40% 20% 0% Ш Ш IV

Maturity Group

RAN

SSD

CLU



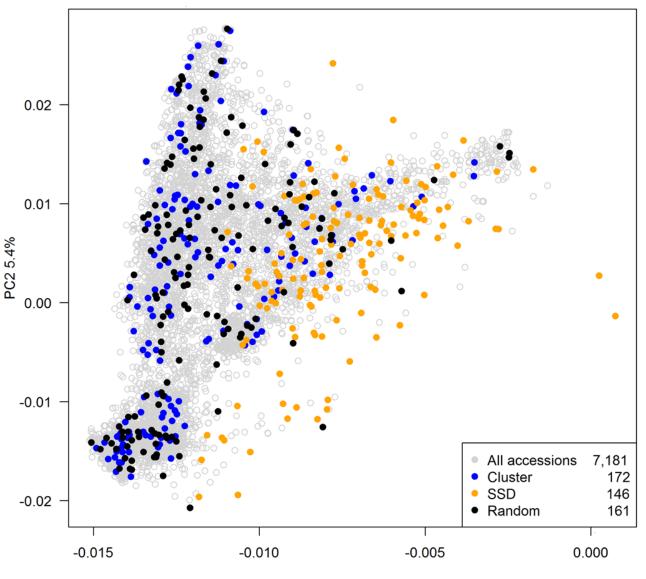
Percent

Graef et al. NCSRP

Distribution of accessions sampled by each sample type CLU(Blue) SSD (Orange) Random (Black)

Compare with Entire collection (Light Gray)

*Our sample represents the total genetic diversity in the USDA Soybean Germplasm Collection in MG I to IV





PC plot – D. Jarquin

PC1 30%