Update on Genetics and Breeding Studies at USDA

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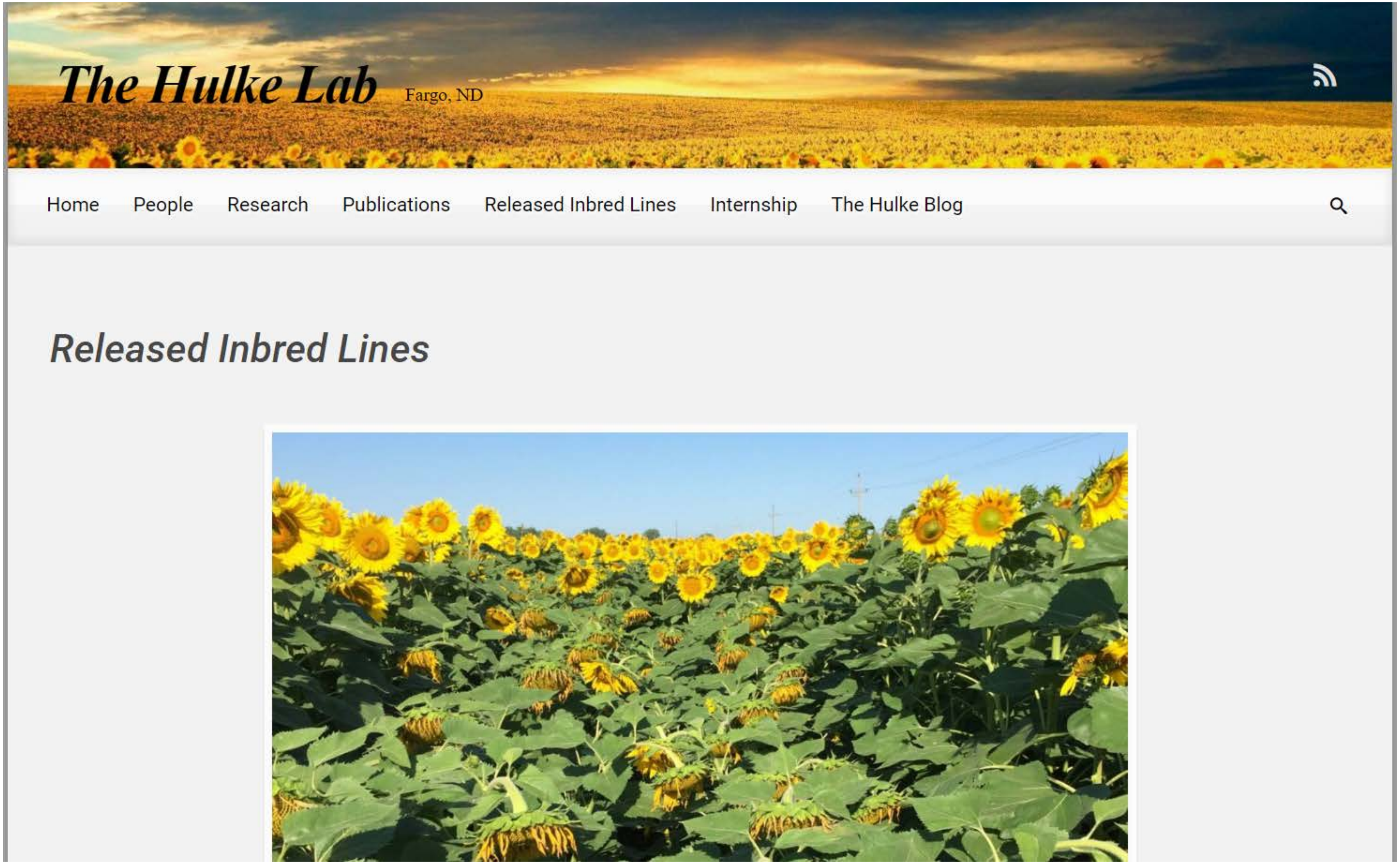
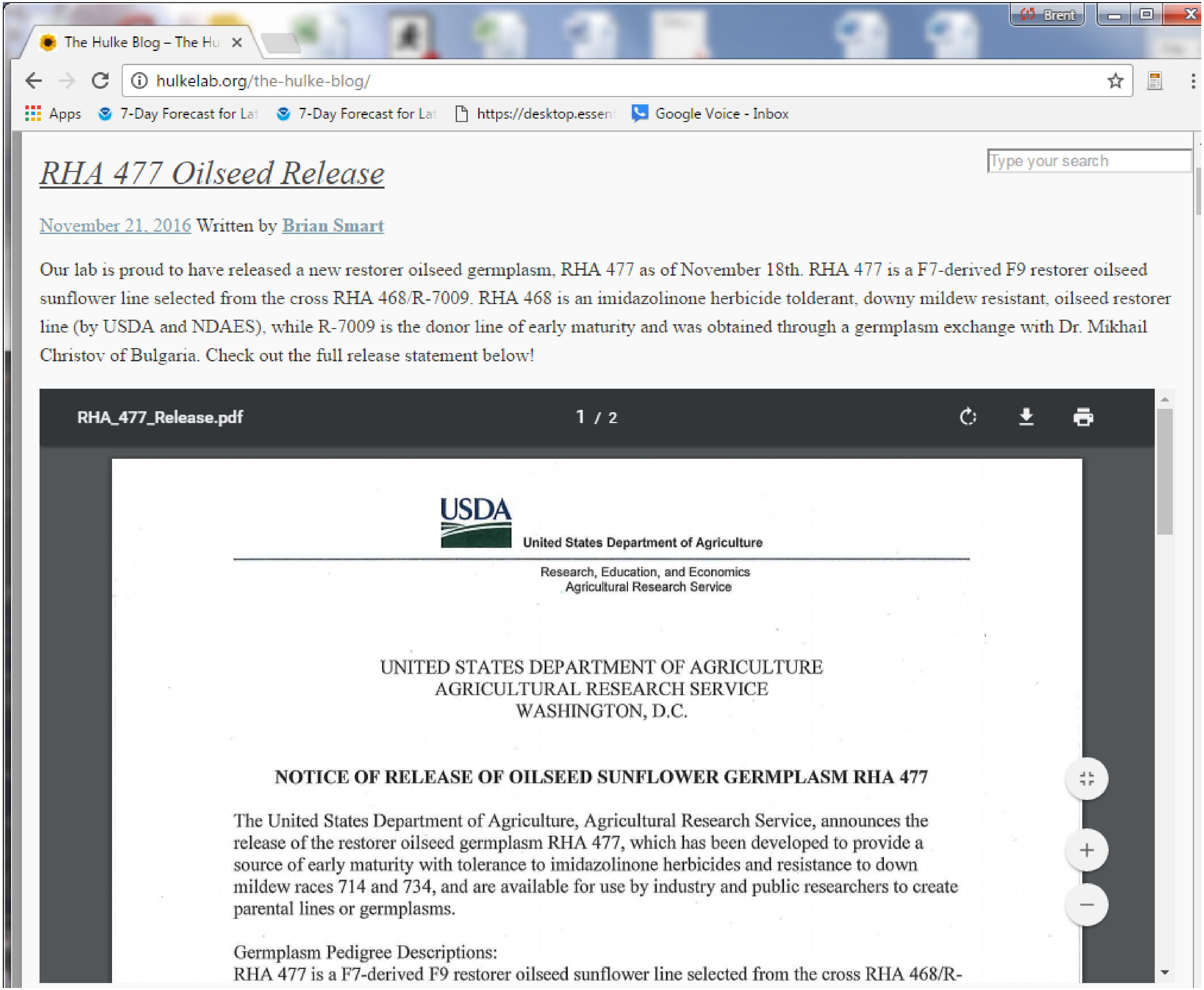
New releases

- RHA 477: early maturity, IMI, DM resistant
- RHA 478: high yield, HO, IMI, Phomopsis, Sclerotinia resistance
- RHA 479: excellent Phomopsis, Sclerotinia resistance
- RHA 480: excellent yield and Phomopsis resistance, IMI resistant
- CMS/HA 481: HO, IMI, Phompsis*, Sclerotinia*



Released Inbred Lines

Visit us at: www.hulkelab.org



RHA 477 Oilseed Release

November 21, 2016 Written by **Brian Smart**

Our lab is proud to have released a new restorer oilseed germplasm, RHA 477 as of November 18th. RHA 477 is a F7-derived F9 restorer oilseed sunflower line selected from the cross RHA 468/R-7009. RHA 468 is an imidazolinone herbicide tolderant, downy mildew resistant, oilseed restorer line (by USDA and NDAES), while R-7009 is the donor line of early maturity and was obtained through a germplasm exchange with Dr. Mikhail Christov of Bulgaria. Check out the full release statement below!

USDA
United States Department of Agriculture

Research, Education, and Economics
Agricultural Research Service

UNITED STATES DEPARTMENT OF AGRICULTURE
AGRICULTURAL RESEARCH SERVICE
WASHINGTON, D.C.

NOTICE OF RELEASE OF OILSEED SUNFLOWER GERMPLASM RHA 477

The United States Department of Agriculture, Agricultural Research Service, announces the release of the restorer oilseed germplasm RHA 477, which has been developed to provide a source of early maturity with tolerance to imidazolinone herbicides and resistance to down mildew races 714 and 734, and are available for use by industry and public researchers to create parental lines or germplasms.

Germplasm Pedigree Descriptions:
RHA 477 is a F7-derived F9 restorer oilseed sunflower line selected from the cross RHA 468/R-

Genomic Selection / Trait mapping

- Genomic Selection: use of genome-wide markers to model effects of parts of the genome on all the traits we measure
- Traits being mapped: glandular trichome abundance, Seed Weevil resistance, fatty acids
- Using GBS data with trio imputation from parents to fill gaps in GBS data

Troubleshooting GBS data

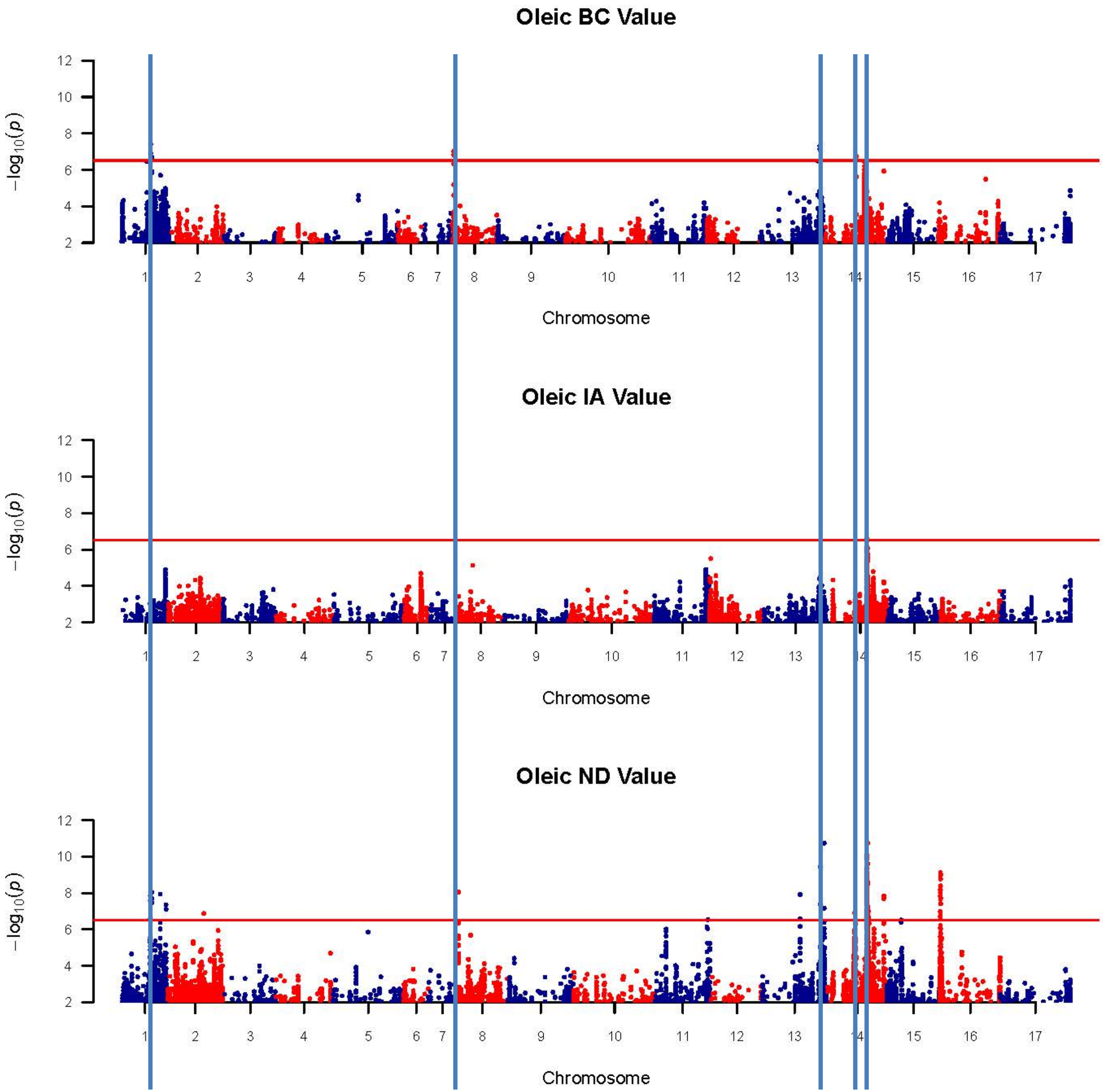
- Sunflower genomics is complicated by ancient genome duplication and large amount of redundant DNA from transposable elements
- All marker assays suffer from errors to some extent, but GBS data requires multiple filtration and haplotype identification steps
- Good news is that the data is dense enough to allow us to see haplotypes, we need to develop a tool that uses that information to correct errors

Fatty acid association mapping

- NSA funded project
  - SAM association population + 49 other released inbred lines
  - Evaluated at 6 environments with a range of different temperatures at bloom
  - Analyzed using association mapping analyses, controlled for population structure and kinship
  - Opportunities to study minor effect QTL and their interaction with the environment

Justification

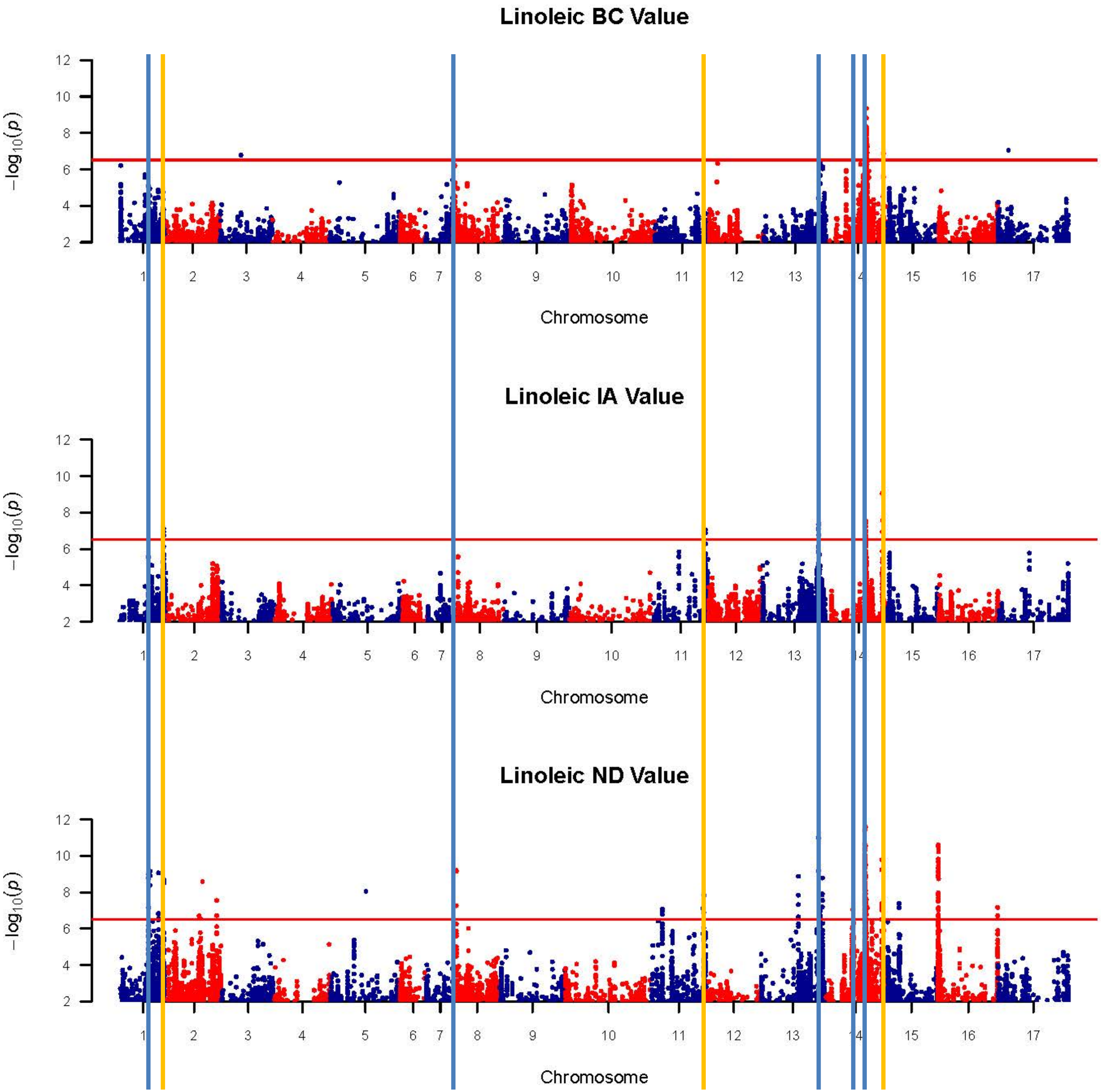
- Phenotyping fatty acids is expensive in resources and time
- Marker-based prediction methods are increasingly being employed in sunflower, so fatty acids could be a cheap addition
- Precision in engineering oil profiles may be needed in the near future
- Better understanding of GxE is needed



Oleic BC Value

Oleic IA Value

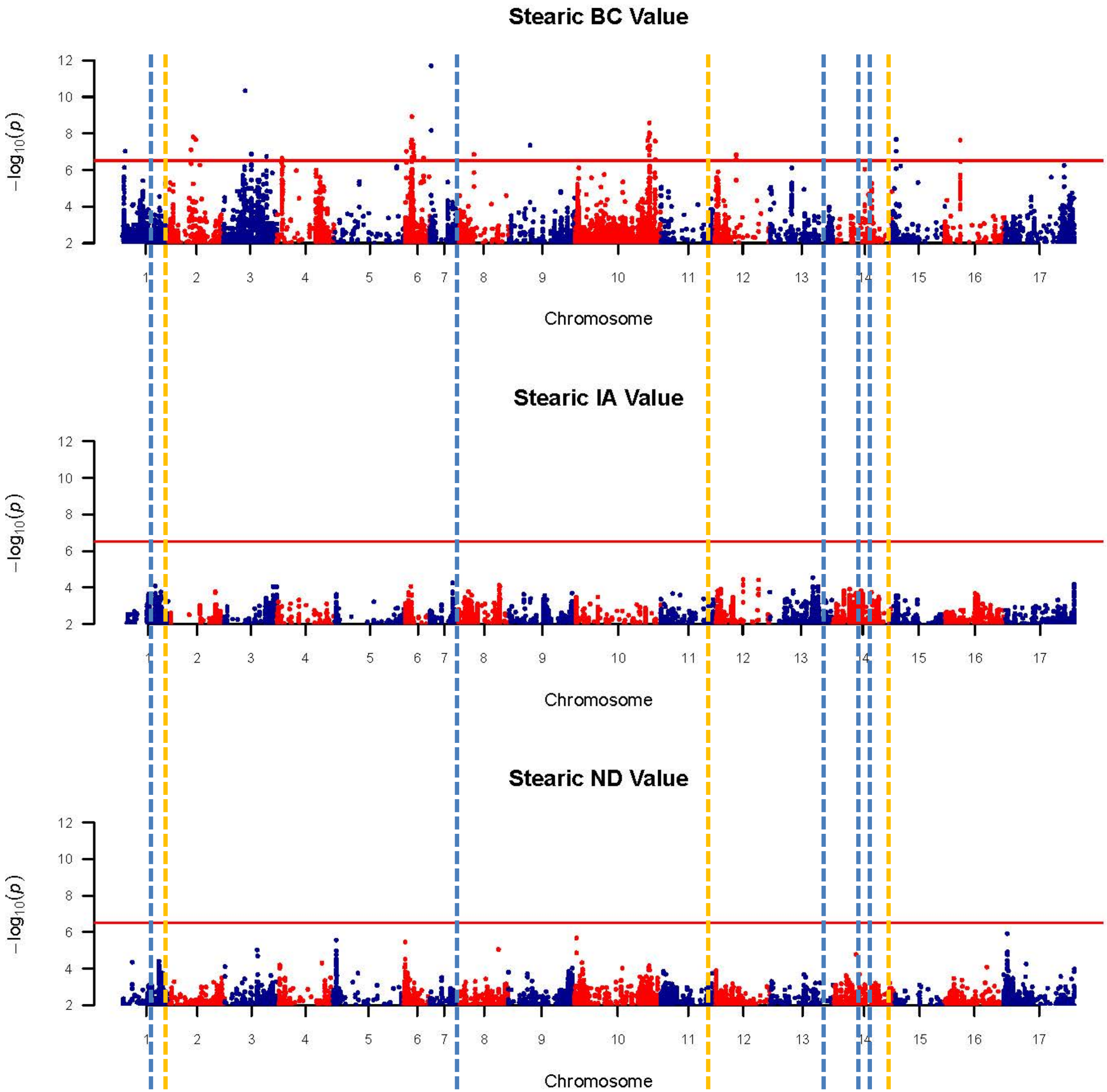
Oleic ND Value

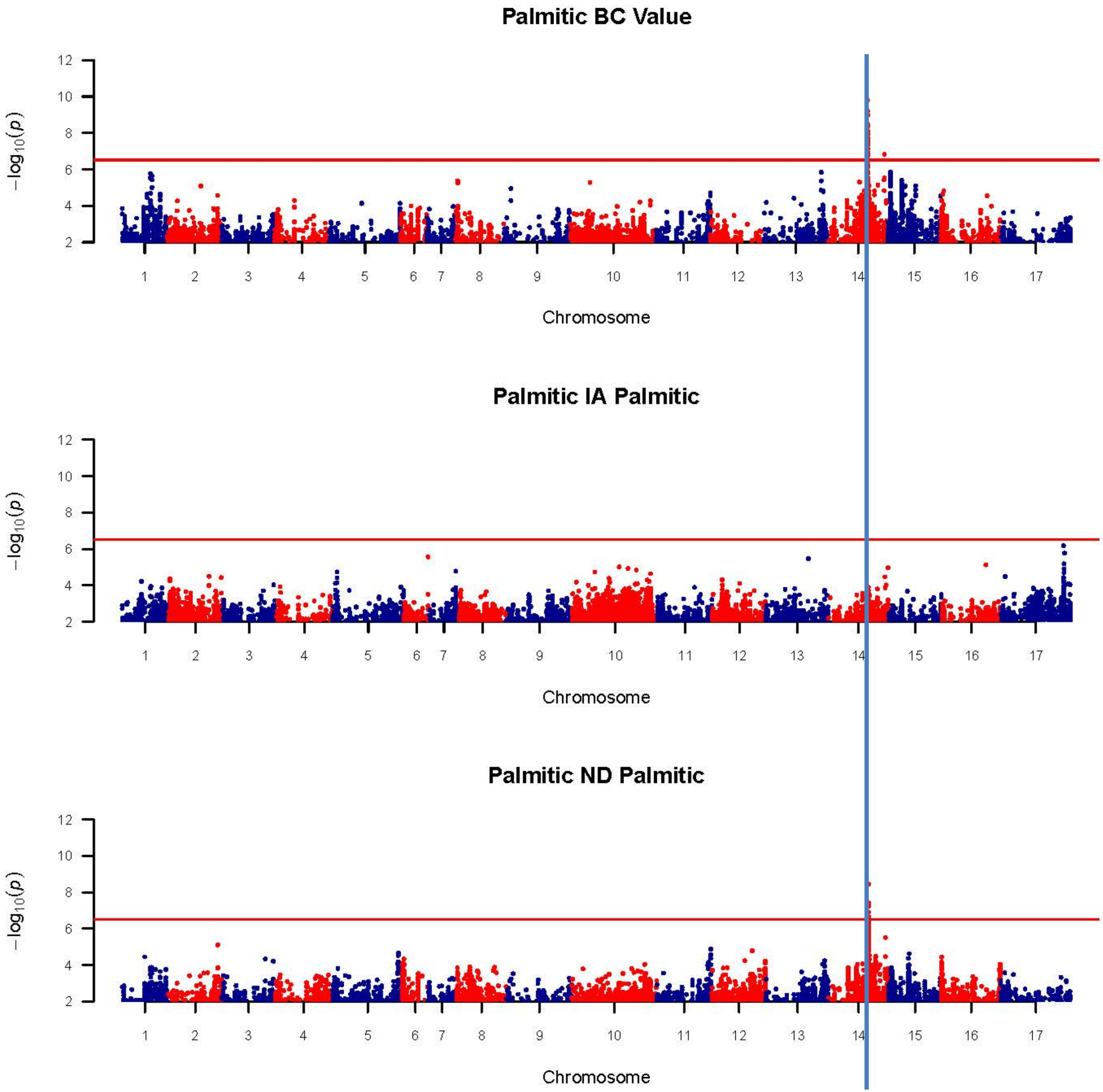


Linoleic BC Value

Linoleic IA Value

Linoleic ND Value


Stearic BC Value
Stearic IA Value
Stearic ND Value
−log10(p)
12
10
8
6
4
2
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
Chromosome



Palmitic BC Value

Palmitic IA Palmitic

Palmitic ND Palmitic

Summary

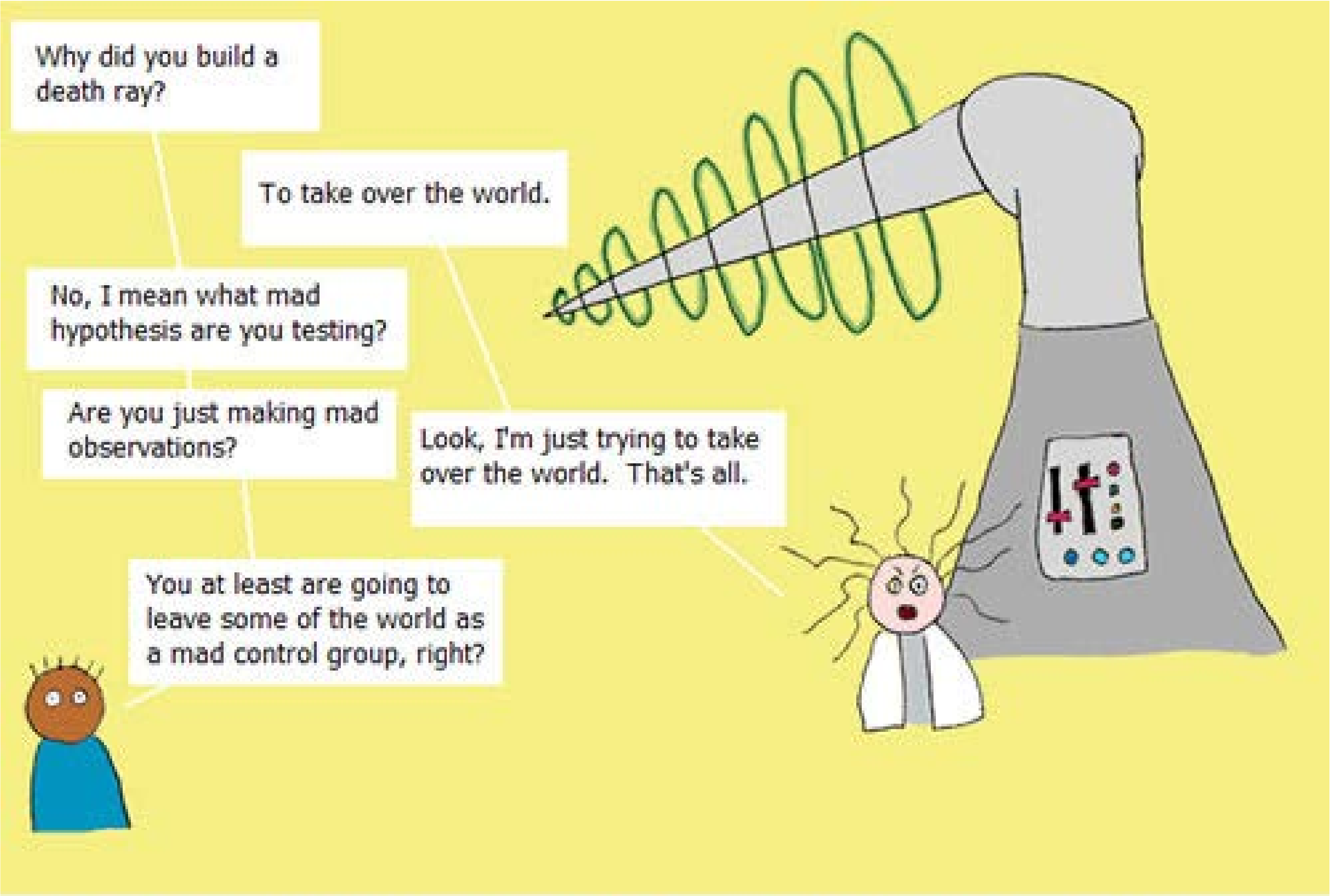
- Detected 8 loci that appear to be important for fatty acid concentration among environments
  - Includes Pervenents mutation of FAD2-1
- Potentially an additional 15 loci which we only see signficance in one environment
  - Mirrors known importance of GxE in fatty acid metabolism

Future Steps

- Complete gas chromatography analysis of another three environments
- Subject fatty acid data to complexity reduction methods
  - Principle components on the correlated phenotypes
  - MMM analysis with exploratory factor analysis on the multienvironment data to establish environmental continuum and correlate with loci

Thanks to our research sponsors!

- -Genome Canada/Genome British Columbia
- -USDA Sclerotinia Initiative
- -National Sunflower Association
- -Saskatchewan Ministry of Ag.



Sad truth: Most "mad scientists" are actually just mad engineers