

Dr. Les Kuhlman

DUPONT PIONEER

SENIOR RESEARCH SCIENTIST







Commercial Soybean Breeding in a Changing World

Les Kuhlman, Ph.D. DuPont Pioneer

Personal Introduction

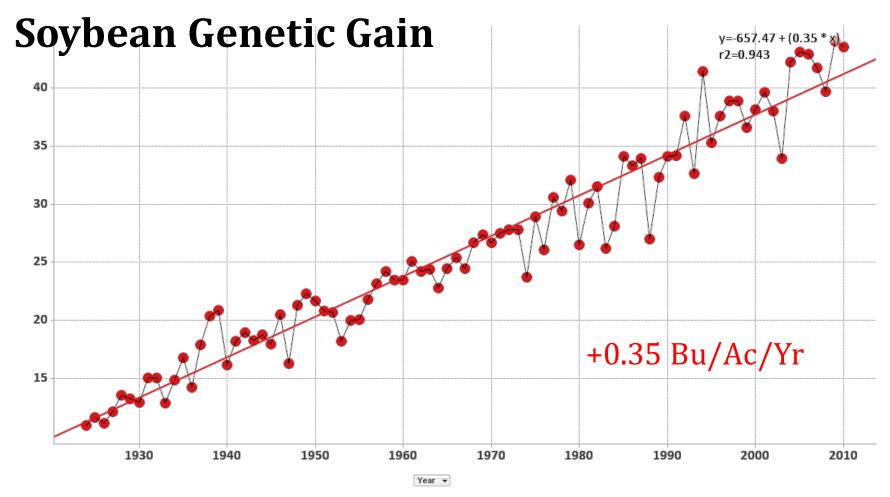
- Born and raised in Manhattan, KS (Go Cats!)
 One generation removed from the family farm
- B.S. in Agronomy, Kansas State Univ., 2001
- M.S. in Plant Breeding, Texas A&M Univ., 2005
- PhD in Plant Breeding, Texas A&M Univ., 2007
- Hired by DuPont Pioneer to start the Lawrence Soybean Research Center in 2007



Pace of Change Marker Assisted **Re-sequencing** Selection for 815 SSRs 4.5 million SNPs SCN 2012 1993 1995 20012003 2008 2011 Isozymes 3072 SNPs (Dawn of Time) 1536 SNPs 350 SSRs Initiated QTL mapping for SCN resistance

Today's challenge is to turn this data into information which can be used to create value.

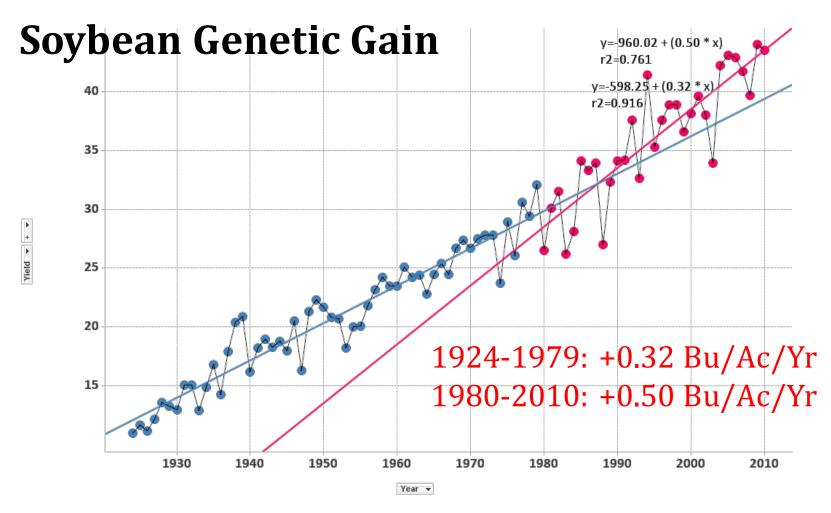




U.S. Soybean Yields 1924 - 2010



National Agricultural Statistics Service – February, 2011



U.S. Soybean Yields 1924 - 1979, 1980 - 2010



National Agricultural Statistics Service – February, 2011

Commercial Breeding

Highly focused on our customers

•Are your breeding targets capturing value?

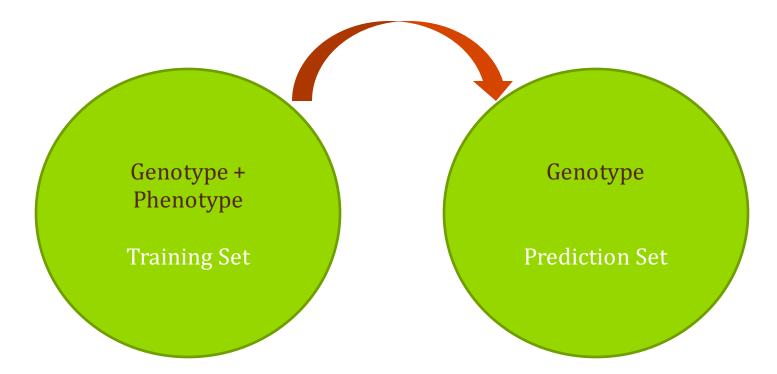
Resourced to win

Always looking for that edge to increase genetic gain
If you aren't...your competitors are.

Highly collaborative



Whole Genome Predictions



Train your model using genotype <u>and</u> phenotype and then apply it to genotypes

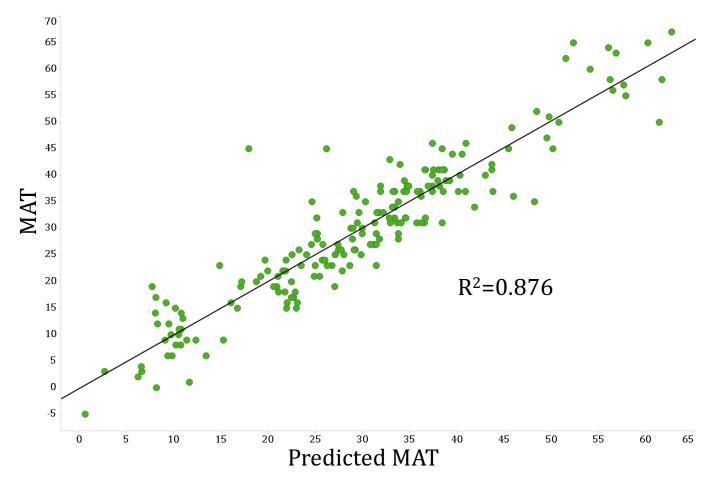






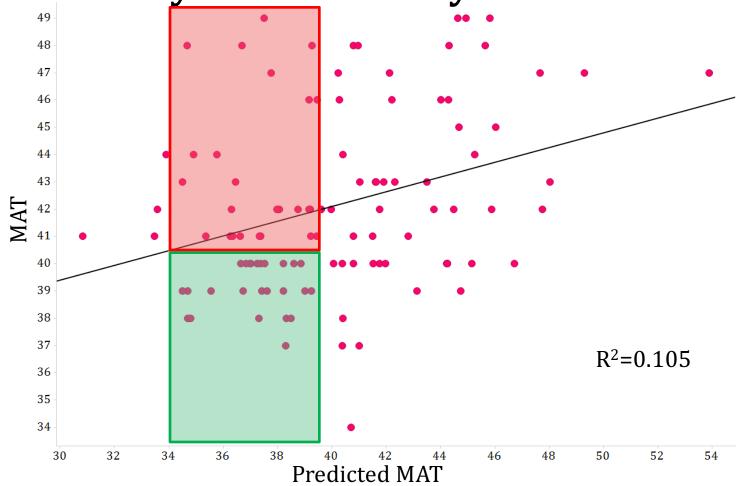
WGP for Soybean Maturity

B PIONEER



Regression showing phenotypic maturity vs cross-validated WGP predictions. The estimation set includes 191 individuals representing soybean parents important to the germplasm pool.

WGP for Soybean Maturity

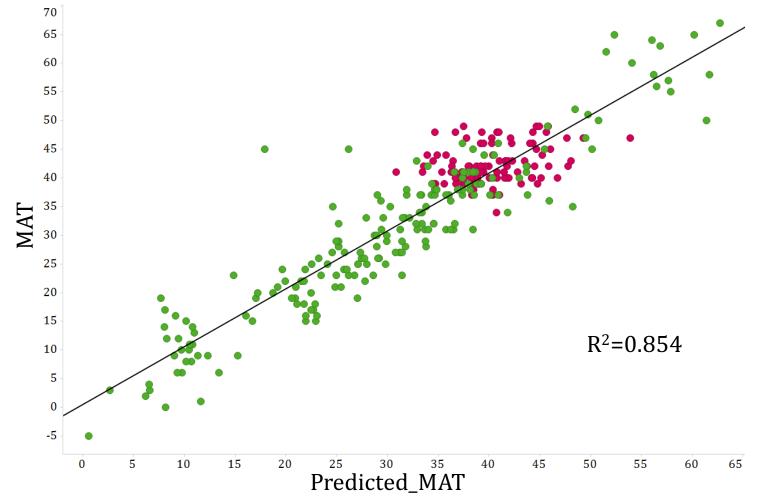


Regression showing the maturity predictions, using the same estimation set, onto a group of 108 experimental varieties in my breeding program.

QUPONT



WGP for Soybean Maturity



Both prediction sets together. This isn't a problem with the predictions, but a problem of our perspective.

A PIONEER.

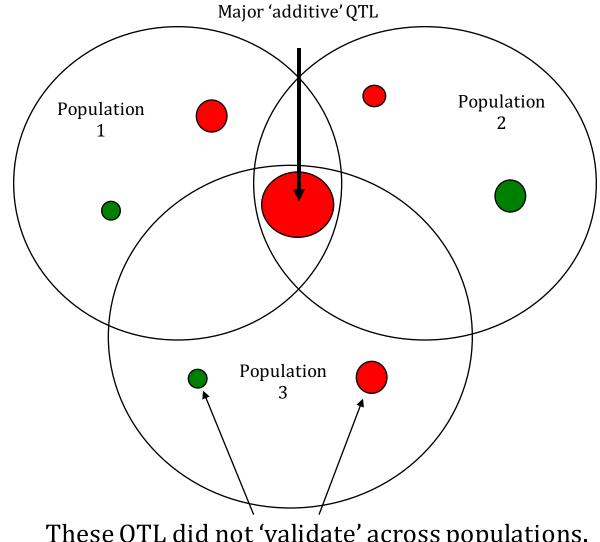
Whole Genome Predictions

Key learnings:

- Perspectives of a breeder are often different from other scientists conducting research
- •Breeders must be capable and willing to ask really good questions
- •Its all about...communication
- Plant breeding lesson #1: Understand your data.



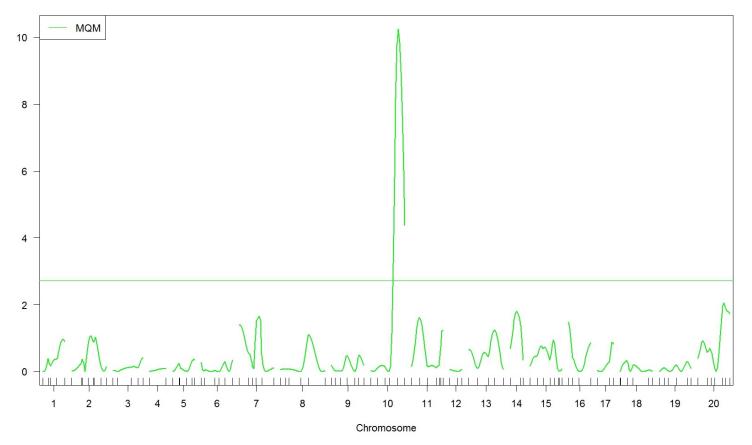
Quantitative Traits





These QTL did not 'validate' across populations.

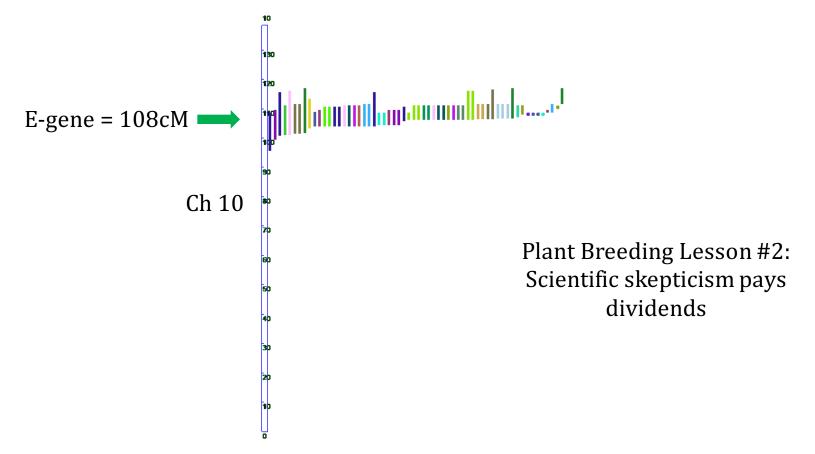
Ex. 1: Quantitative Traits



QTL mapping yield in an elite population



Ex. 1: Quantitative Traits



Multiple populations confirm a yield gene on Ch 10 between 100-110cM

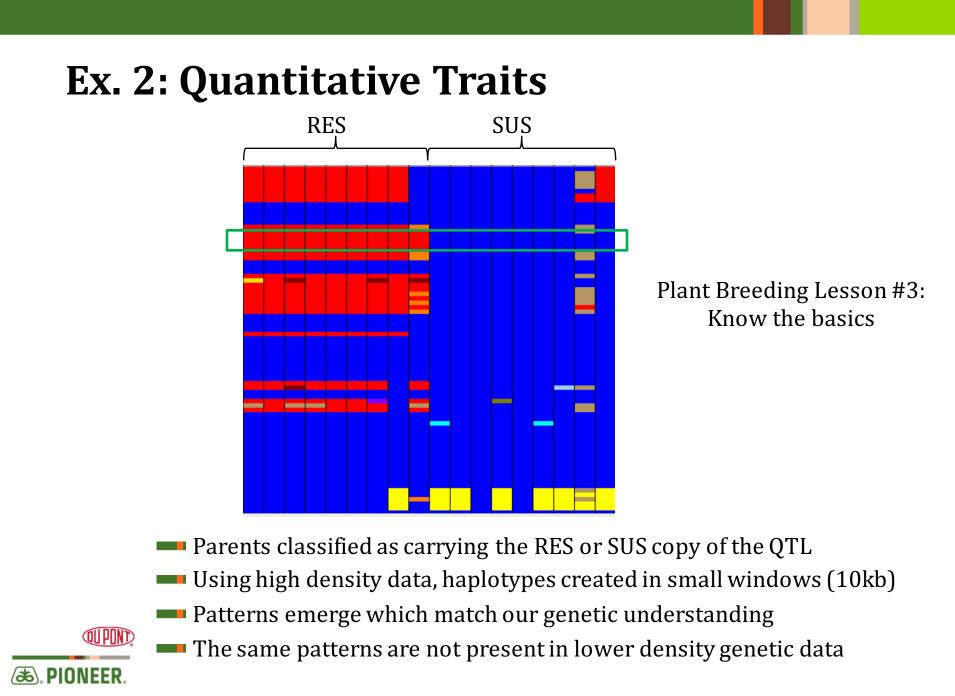
Major maturity gene sits at 108cM; yield and maturity are strongly correlated

Ex. 2: Quantitative Traits

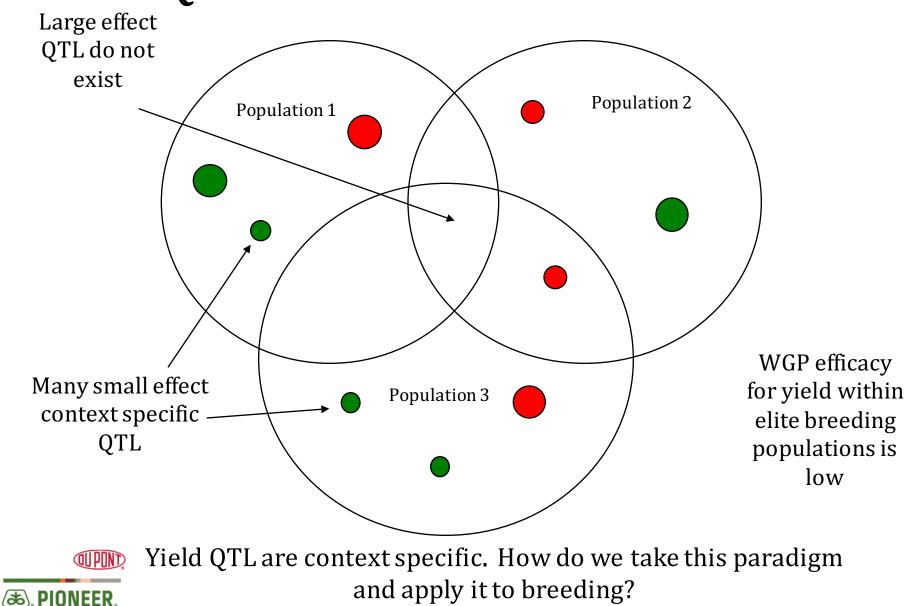
For an important soybean fungal trait:

- •2 significant medium effect QTL have been identified in a mapping population
- •2 different medium effect QTL were identified in a different population
- •Heritability of the phenotype >0.7
- •WGP has shown low predictive power
- As a breeder my instinct says this is an additive trait with many medium effect QTL





Ex. 3: Quantitative Traits



Ex. 3: Quantitative Traits

AYT-Context Specific Mapping (CSM)

- •Each bi-parental population is genotyped and phenotyped (estimation set = prediction set)
- Populations must be large enough to estimate genetic effects
- •No effort is made to apply predictions from one family to another everyone is independent
- Predicted yield is better than the phenotype



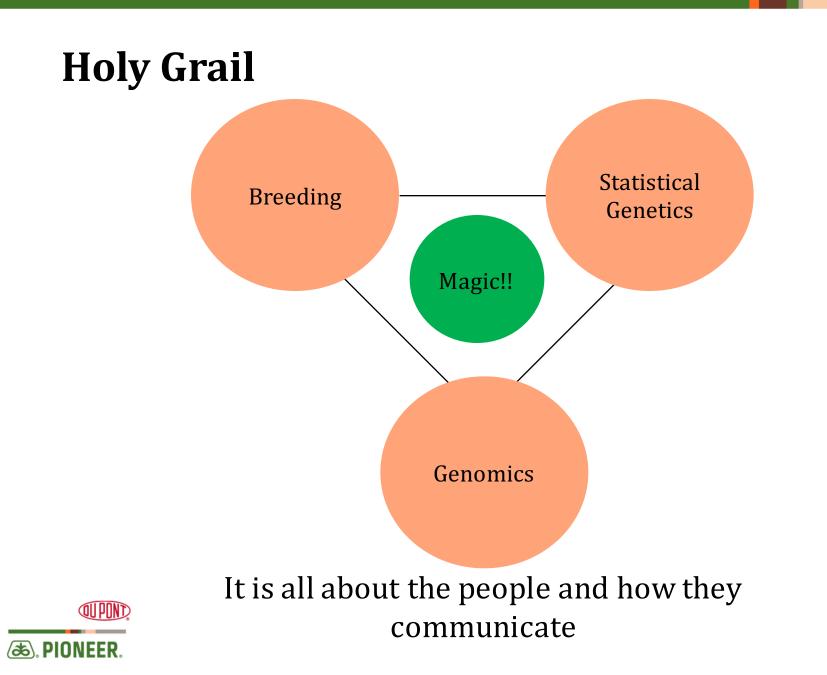
Plant Breeding Lesson #4: Be science driven

Select winners by Target Genotype

AA bb DD ...

Selection leverages ALL of the data simultaneously

AYT respects the contextspecific nature of yield QTL



Conclusions

Plant breeding is all about the basics

- •Understand your data
- •Be skeptical
- •Apply the basics
- •Be science driven
- What is the most important lesson I learned?

You must see the process through from beginning to end. – Norman Borlaug



Questions?

Thank you to my excellent collaborators:

- Jon Massman
- John Woodward
- Jordan Spear
- •Don Kyle

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