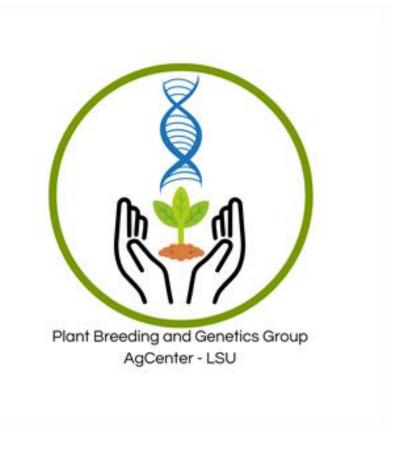
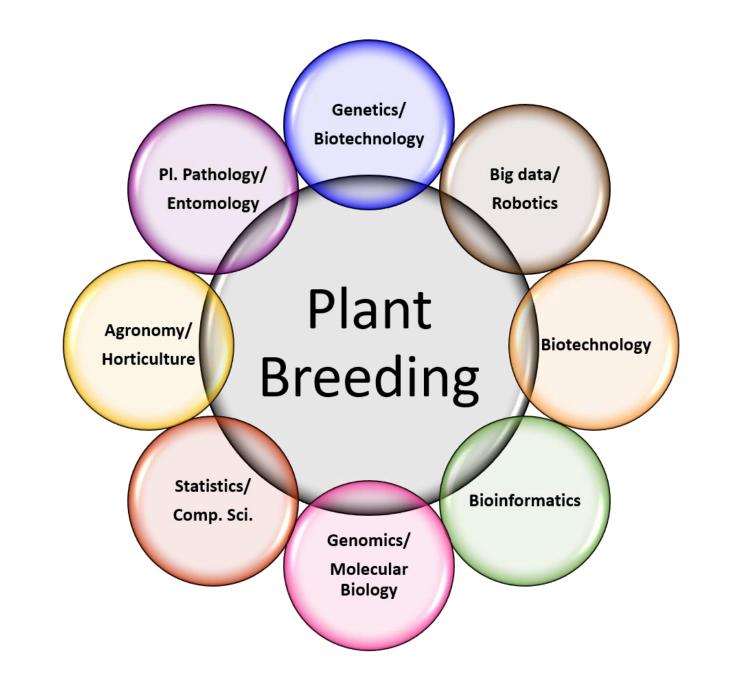
Flavia Furlan













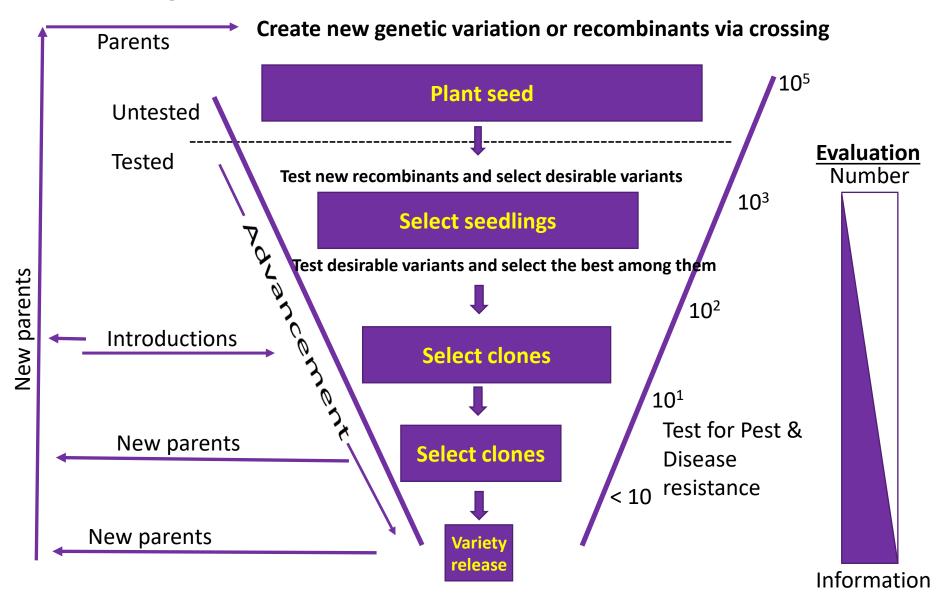






Crossing

# Selection (sugarcane)



## Selection Strategies

- Phenotypic data collection and statistical analysis
  - Trait observations (yield, disease, quality, vigor, etc.)
  - In-field instruments, drones, harvester monitors

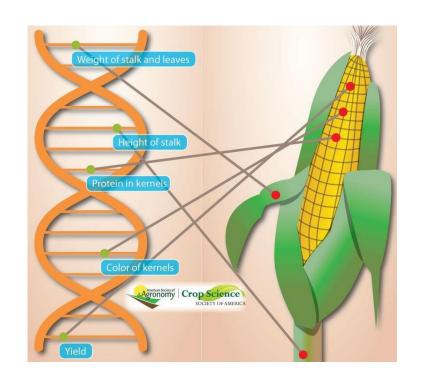


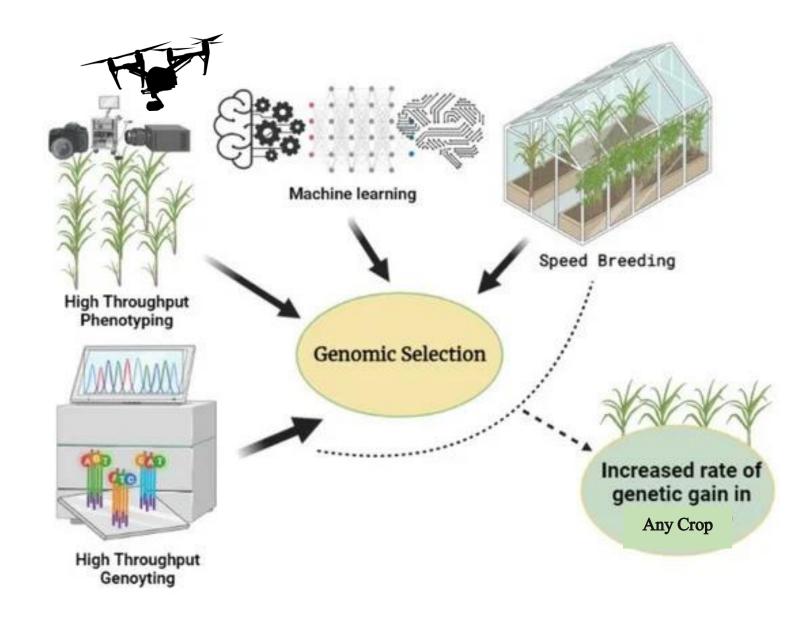




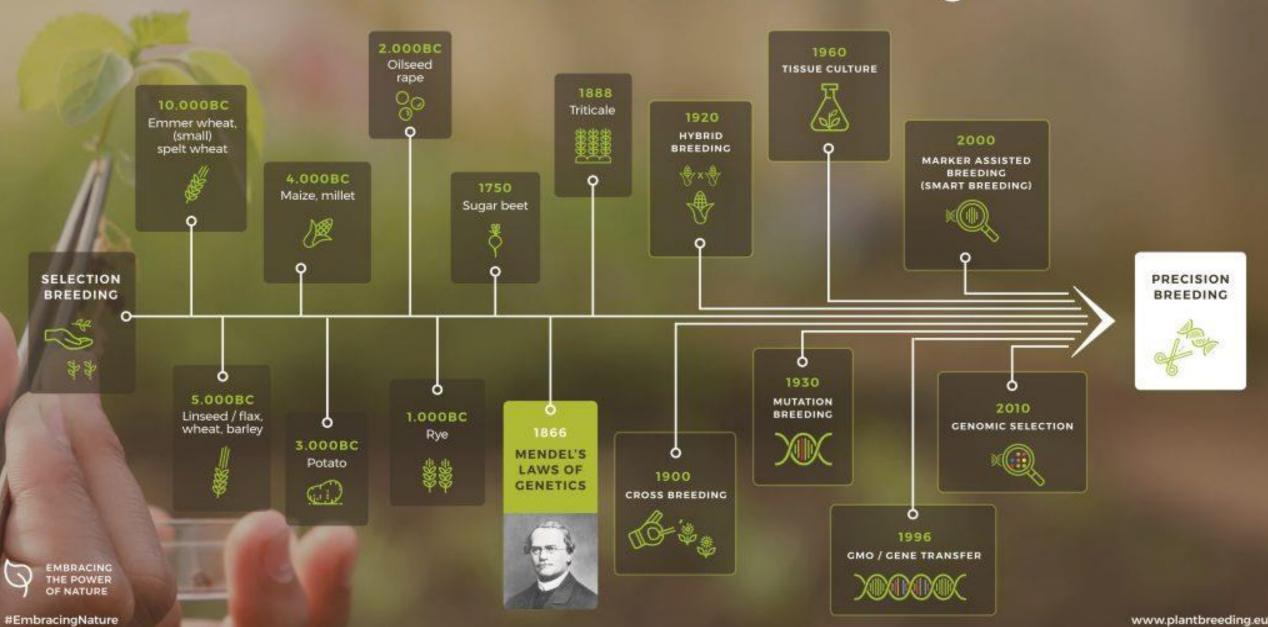
### Selection Strategies

 Genomic Selection, Genome-wide Association, Marker Assisted Selection





# Milestones in Plant Breeding



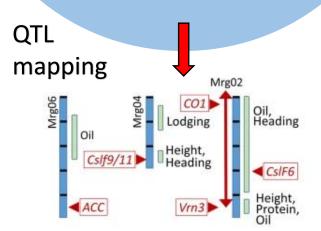




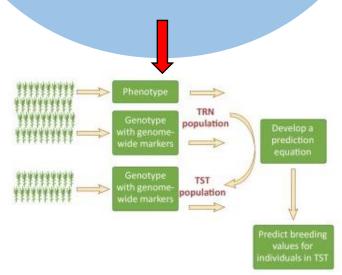
# **OAT BREEDING**

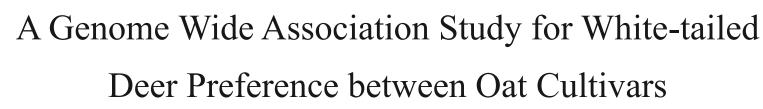
Disease resistance:

Puccinia coronata f. sp.
avenae (Pca), a
biotrophic parasite, is
the causal agent of
crown rust, the most
important and harmful
foliar disease in
cultivated and wild oats



Genomic Selection:
 genotypic and
phenotypic data in a
training population to
estimate genotypic
breeding values
(GEBV) forof the
genotypes





Masters Thesis by: Steven Abernathy

This study aims to compare white-tailed deer's forage preference between 234 different oat cultivars using genomic data to find any association between loci on the genome and deer preference.

Hunting is big business in Louisiana and many hunters plant food plots to attract deer. Oats are commonly planted species because they are highly palatable to deer.

Genome wide association studies (GWAS) use broadly distributed genetic markers to statistically find associations between specific markers and phenotypic traits. Any significant markers can then be used to find causal genes. They can also be used in marker assisted selection to help more efficiently select varieties with the desired trait.

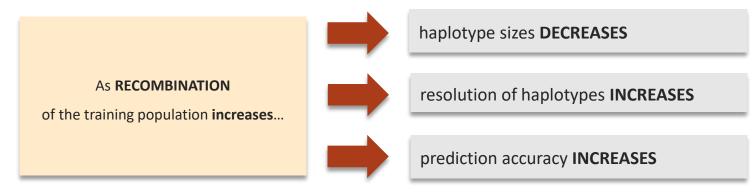
Field trials have been completed. Deer were discriminating in their selection with some varieties eaten to the ground, others completely untouched. Data analysis for associating preference with DNA markers is ongoing.

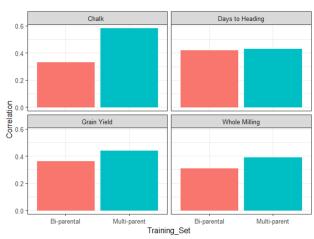


# The Effect of Haplotype Size and Linkage Disequilibrium on Genomic Selection Accuracy in Rice (*Oryza sativa* L.)

PhD Thesis Research, Maria G. Montiel

The objective of this study is to demonstrate how haplotype resolution in the training population impacts prediction accuracy of genomic selection in rice.





- Genomic Selection relies on the RELATEDNESS between training and prediction sets of individuals.
- LD decay is faster as Recombination increases.
- Recombination decreases haplotype sizes, which increases the resolution for genomic predictions.
- For highly quantitative traits, smaller haplotype sizes in the training population, increase the prediction accuracy.
- The use of Multi-parent populations to predict simple crosses constitute a very efficient way to predict complex traits.

#### Sweet Potato Variety Program

Variety development is a major effort in the Louisiana sweet potato production program in LSU. A few examples of impactful cultivars are

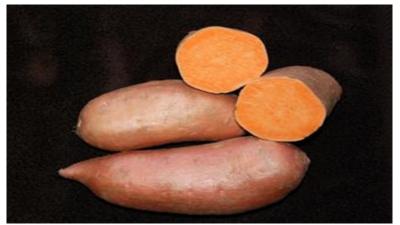
1. Beauregard - a classic Louisiana sweet potato variety that was released by the Louisiana Agricultural Experiment Station in 1987. It is consider one of the best variety of sweet potato in USA. Developed by L.H. Rolston

2. Murasaki-29 - Developed by the LSU AgCenter in 2008 by Dr. Don Labonte.

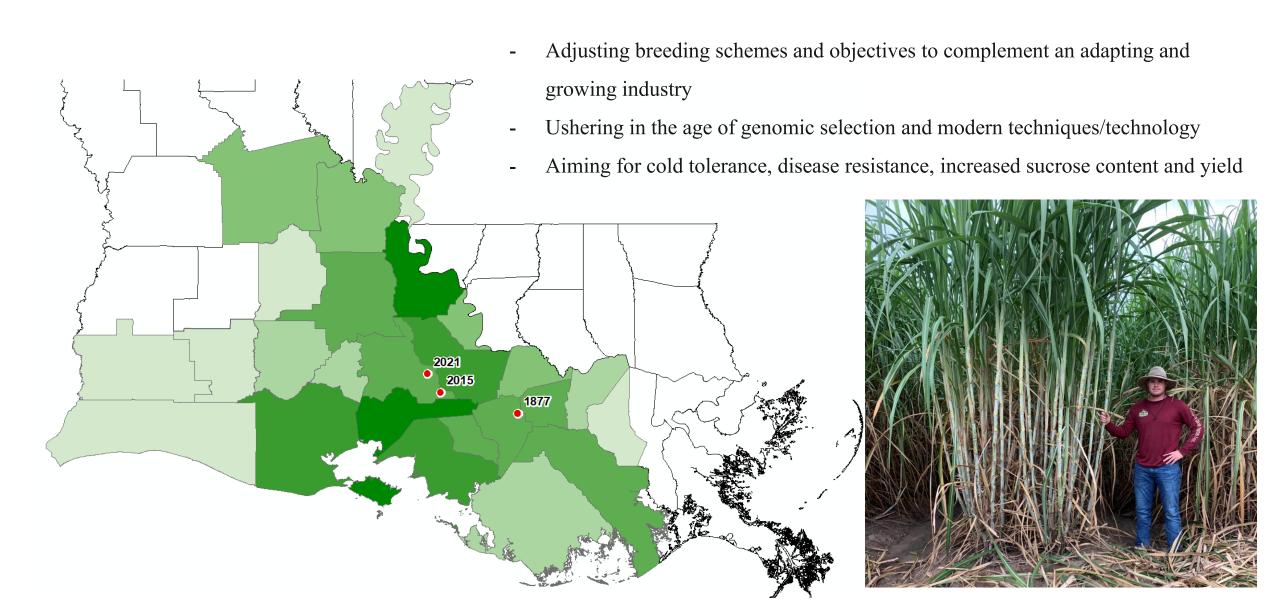
3. New Orleans - Developed in LSU AgCenter in 2012 by Dr. Don Labonte.



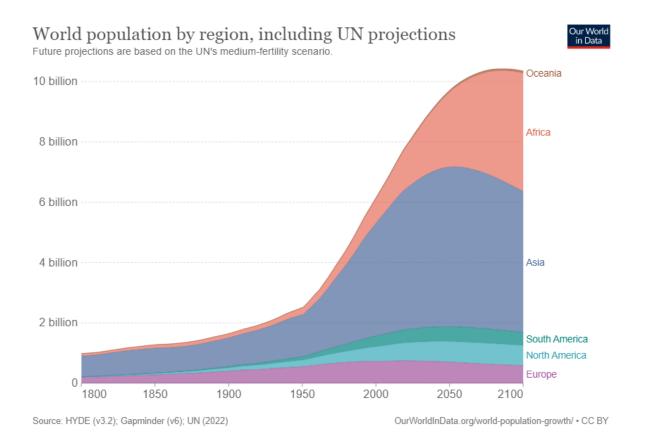




### Research Areas of Sugarcane



### Why Plant Breeding?







## Why Plant Breeding? Careers

- MS and PhD programs of major commodity crops at LSU
- Substantial and direct impact
- Diverse industries and regions
  - specialty crops to large commodities
  - local private industry to federal government or large international corporations
- Data science skills are highly marketable and widely transferable
- Connection to community (wherever that is)





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