Genomic prediction of salinity stress tolerance in Maize (Zea mays L.)

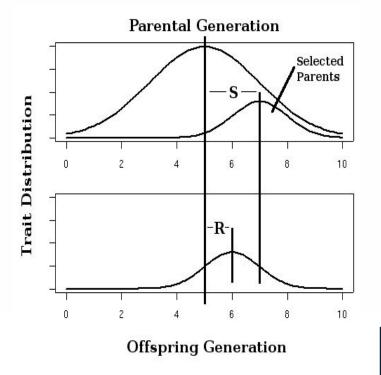
Vishal Singh, Amita Kaundal

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Selection in plant breeding

Selection has been a key method in plant breeding to improve plant traits

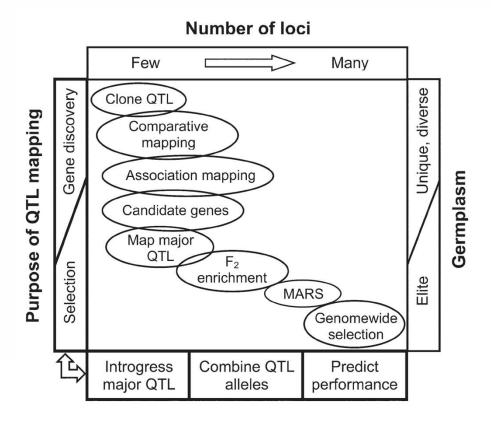
Practised for a long time



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Molecular techniques in trait improvement



Bernardo, 2008



Inclusion of DNA information in selection

- Selection (traditionally): phenotypic records of individuals and its relatives.
- ❖BLUP (Henderson, 1950): Estimation of breeding values based on phenotypic data
- Fernando and Grossman (1989): Inclusion of marker information into BLUP breeding values



Maize salinity tolerance

	MAIZE		
	1997 Demand	2020 Demand	Change (%)
Global	586	852	266 (45)
Industrial Countries	291	344	53 (18)
Developing Countries	295	508	213 (72)



(IFPRI, 2003) (Data in million metric tonnes)

Tolerant	Barley, Sugar Beet, Wildrye, Asparagus	
Moderately Tolerant	Wheat, Wheat Grass, Zucchini, Beet (red)	
Moderately Sensitive Tomato, Cucumber, Alfalfa, Clover, Corn, Muskmellon, Potato		
Sensitive	Onion, Carrot, Bean, Apple, Cherry, Raspberry, Strawberry	

Hill and Koenig, 1999

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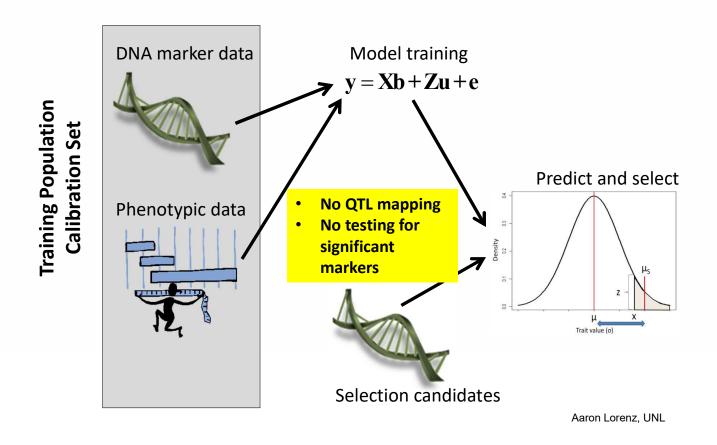








Genomic Selection scheme



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Material and methods

- Screening for salinity stress tolerance: Sandhu et. al., 2019
- Inbred lines:
 - 399, A subset of the maize diversity panel (Mazaheri et al. 2019)
- Traits measured: shoot length, shoot weight
 - BLUP estimates were used for further analysis
- Molecular data: 10,000 SNPs (random subset of a full dataset)



Modelling approach

- Ridge Regression: rrBLUP package in R (Endelman, 2011)
- Data cleaning and processing:
 - Removal of SNPs with <0.05 MAF
 - Training and Testing set (80:20)
- Model prediction accuracy





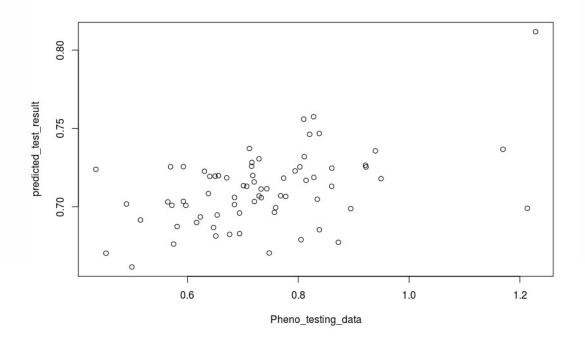






Results

• Prediction accuracy of the model: 0.47





Future direction

- Model building using full SNPs data
- Cross validation
- Additional models
- Screening of inbred lines for salt tolerance for true validation set



THANK YOU

