Genetic Architecture of Salinity Tolerance

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Introduction

Goal: Improve sunflower tolerance to high soil salinity using association mapping



Soil Salinity

- Assign plots to "High" or "Low" soil salinity
- Problem: Need salinity estimates for each plot but few soil samples



Soil Salinity

Danie G. Krige

Objective: Obtain plot level estimates of soil salinity using soil samples.



Michiel Van der Meulen Figure 5 https://www.researchgate.net/profile/Michiel-Van-Der-Meulen-2

Kriging



Sunflower Association Mapping Population





Genome-Wide Association Study (GWAS)

• Iteratively tests association between a SNP and trait value



Results



Yield



Results: Summary

	Trait	t Salinity Chr.		Position	
I	DTA	Slope	9	4,152,597	
-	Height	Low	8	13,593,081	
-	Leaf Area	Low	5	32,886,022	
	Leaf Area	High	13	18,054,346	
_	Leaf Area	Slope	12	61,311,476	
-	Leaf Weight	High	13	18,054,346	
	Leaf Weight	High	16	202,396,981	
	Oil %	Low	15	145,002,138	
	Oil %	High	10	18,009,713	
_	Oil %	Slope	17	170,676,936	
	Yield	High	13	165,654,686	
	Yield	Slope	11	4,726,109	
	Yield	Slope	11	153,189,931	
	Yield	Slope	15	26,889,266	

Results: Candidate Gene Analysis

Key Traits and Genes Associate with Salinity Tolerance Independent from Vigor in Cultivated Sunflower^{1[OPEN]}

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Trait	Salinity	Chr.	Position	<u>Temme et al. 2020</u>
Leaf Area	Slope	12	61,311,476	• Height & plant mass
Leaf Weight (suggestive)	High	10	20,541,564	• Leaf & plant mass

Results: Candidate Gene Analysis

Trait	Salinity	Chr.	Position	Species	Gene
Leaf Area	Slope	12	61,311,476	Arabidopsis	MYB53
			-	Maize	GDSL esterase/lipase CPRD49
			-	Cotton	cationic amino acid transporter 1
Leaf Weight	High	16	202,396,981	Flax	F-box/FBD/LRR-repeat
			_	Pearl Millet Sugar Beet	V-type proton ATPase subunit C
Yield	High	13	165,654,686	Alfalfa Barley Sorghum	FBD-associated F-box protein F-box/LRR-repeat

Future Objectives

- Salinity Lethality Greenhouse Study
 - Planting soon
 - Evaluate the same population in the greenhouse environment with a high soil salinity

To Predict

- Develop genetic markers based on results
 - Marker Assisted Selection (MAS)
 - Identify prospective parents containing desirable alleles for salinity tolerance
 - Cross and identify progeny having genetic markers associated with salt tolerance
 - Genomic Prediction
 - Use genetic markers for salinity tolerance in a statistical model (as fixed effect) to predict performance of new/untested progeny or hybrids

To Explain

• Identify and characterize the causative gene underlying the QTL

Questions!

Authors

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