Screening, Mapping, and Breeding for Flood Tolerance in Soybean

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Acknowledgements

Collaborators

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Flooding Factors



Excessive rain Rain after irrigation Zero grade fields Low tolerance Climate change

Flooding Damage



Reduced Nutrient Uptake

Reduced Nitrogen Fixation

Stunted Growth

Leaf Defoliation

Plant Death



Screening to identify flood tolerant sources:

Commercially available varieties Advanced Elite Lines Plant Introductions (PI)

Mapping QTL/genes for flood tolerance

Developing high-yielding adapted flood tolerant lines

Field Preparations



Plant Counting



Flooding Stages



V5



R1

Sensitive plants show foliar symptoms after 4-day flooding



V5



R1

Leaf Color Change



Visual Rating



Visual Score & Plant Death over Time







Flood Duration Experiment

- <u>40 lines:</u> 20 flood-tolerant & 20 sensitive; 3 reps
- <u>Flooded:</u> at V5 and R1 stage
- <u>Duration:</u> 3, 6, 9, 12, and 15-day flooding
- <u>Visual scoring:</u> 4 times (0, 2, 4, 6 day after flood removal) Visual score Plant survival rate

Plant Foliar Damage under Flooding for Different Durations



Plant Survival Rate under Flooding for Different Durations



Flood Duration Summary

T 4	EDC		Number of Varieties/Lines				
lest	FDS	PSK (%)	Tolerant	Moderately Tolerant	Sensitive		
D3V5	1.1	99.4	40	0	0		
D3R1	1.7	86.5	40	0	0		
D6V5	3.2	69.1	31	8	1		
D6R1	4.6	53.9	15	17	8		
D9V5	5.3	42.0	11	19	10		
D9R1	7.5	15.9	0	1	39		
D12V5	6.0	36.1	2	19	19		
D12R1	8.7	4.0	0	0	40		
D15V5	7.3	16.5	0	6	34		
D15R1	8.4	8.0	0	0	40		

D3V5 = 3-day flooding duration at V5 stage; D3R1 = 3-day flooding duration at R1 stage;

D6V5 = 6-day flooding duration at V5 stage; D6R1 = 6-day flooding duration at R1 stage;

D9V5 = 9-day flooding duration at V5 stage; D9R1 = 9-day flooding duration at R1 stage;

D12V5 = 12-day flooding duration at V5 stage; D12R1 = 12-day flooding duration at R1 stage;

D15V5 = 15-day flooding duration at V5 stage; D15R1 = 15-day flooding duration at R1 stage.

EDS - foliage damage score

Conclusions

- The longer flood duration at either V5 or R1, the more damage.
- Foliar damage scores are negatively correlated with plant survival rate.
- Most soybean plants will not survive after 12 days of flooding in the field.
- The optimum flooding duration for screening in the field is between 9 and 12 for V5 and between 6 and 9 days for R1.



Screening to identify flood tolerant sources:

Commercially available varieties Advanced Elite Lines Plant Introductions (PI)

AR Flood Screening

- Commercial varieties (MG-4 and MG-5)
- Arkansas released cultivars and germplasms
- High-yielding lines and potential releases
- Drought-tolerant and flood-tolerant lines
- Mapping populations

Screening of Commercial Varieties in 2016

•85 MG-4

- •57 MG-5
- •RCBD 2 reps

•Growth stage – R 1



85 MG-4 Commercial Cultivars Screened in 2016 (2 reps, 8-day flooding)

Name	Visual Score	% Plant Survival	Classification
CZ 4590 RY	3.5	67.6	Tolerant
CZ 4044 LL	3.8	62.1	Tolerant
16 Varieties	4.5 - 5.8	38.6 - 60.8	Moderately Tolerant
63 Varieties	6.0 - 7.5	20.6 - 44.0	Sensitive
4 Varieties	8.0 - 8.3	12.8 - 16.5	Highly Sensitive

57 MG-5 Commercial Cultivars Screened in 2016 (2 reps, 8-day flooding)

Name	Visual Score	% Plant Survival	Classification
CZ 5147 LL	3.0	69.7	Tolerant
S11-16653	3.0	72.5	Tolerant
CZ 5242 LL	3.3	71.7	Tolerant
R10-230	3.3	69.1	Tolerant
Dyna-Gro S52LL66	3.8	63.2	Tolerant
UAX 59013C	3.8	61.7	Tolerant
27 Varieties	4.3 - 5.3	39.2 - 57.7	Moderately Tolerant
21 Varieties	6.0 - 7.5	20.4 - 42.8	Sensitive
3 Varieties	8.0 - 8.3	11.1 – 15.6	Highly Sensitive

MO Delta Center Screening of Current Varieties in 2016

10 lines with <2.5

FTS	
Delta Grow DG4860RR2	
U of MO S12-3791	Progeny 4757
Syngenta 39-T3	Syngenta 45-R7
Armor 48D24	Morsoy LL4524
Bayer CZ5225LL	Dyna Gro S52RY75

Flood Tolerance of AR High-yielding Cultivars (2012 - 2016)

Name	Visual score							
	2012	2013	2014	2015	2016	Mean	Classification	
UA 5615C	-	2.8	4.0	3.5	4.5	3.7	Tolerant	
UA 5612	5.2	4.7	3.8	4.0	4.5	4.4	Moderately Tolerant	
UA 5115C	4.6	4.8	5.6	3.8	4.8	4.6	Moderately Tolerant	
Osage	5.0	4.2	5.2	4.5	4.8	4.8	Moderately Tolerant	
UA 5213C	5.8	4.6	4.4	4.7	5.3	5.1	Moderately Tolerant	
UA 5414RR	5.0	6.3	5.1	4.5	6.8	6.0	Sensitive	
UA 5715GT	-	5.8	6.4	4.3	6.9	6.2	Sensitive	

AR Flood Tolerant Lines (2012 - 2016)

Nama	Visual score					% Plant Survival						
Iname	12	13	14	15	16	Mean	12	13	14	15	16	Mean
R10-4892	3.1	3.3	3.2	3.0	4.3	3.4	83.6	67.6	79. 7	82.7	59.4	68.9
R11-6870	-	3.3	4.0	2.7	3.3	3.3	-	65.1	79.6	86.1	67.7	72.3
R10-230	-	2.8	4.0	3.5	4.5	3.7	-	72.4	77.5	84.2	57.1	67.6
R07-6669	3.8	3.1	3.9	3.7	3.8	3.7	82.3	83.7	75.8	69.2	61.6	68.3
R04-342	4.2	3.9	4.0	3.6	4.0	3.9	56.5	62.8	65.7	67.3	63.4	64.0
AG 5606	7.6	7.0	-	-	-	7.3	26.3	24.5	-	-	-	25.4
AG 5335	-	-	-	6.0	6.3	6.2	-	-	-	39.2	29.6	34.4
UA 5014C	8.3	7.7	8.1	8.0	8.0	8.0	6.7	11.5	9.5	9.9	14.9	12.2



Yield comparison of PI 408105A derived lines vs. check under flooding

Line (1st cycle breedin	(g)	BU/A under flood		
S11-25108 (S99-2281 x 408105A)	23.5			
S11-25615 (S99-2281 x 408105A)	PI	26.8		
Asgrow check AG 483	sgrow check AG 483: Line (2nd cy			BU/A under flood
	S15-19625 (S11-25108 x S05-114	482)	37.1
	S15-19719 (S	S11-25108 x S05-114	182)	35.7
	Asgrow chee	ck AG4835		5.9
				Shannon/Chen group



Shannon/Chen group

Comparison of *max* and *soja* PIs for flood Tolerance

Line	Cultivated (max) or wild (soja)	Flood score 1= no damage	Notes
Jake check	Cultivated	4.0	Adapted variety
PI 603910B	Cultivated	2.7	Selected for tolerance
PI 408105A	Cultivated	3.7	Selected for tolerance
UA 5612 check	Cultivated	2.7	Tolerant variety
PI 407729	Wild	1.5	Excellent tolerance
PI 407195	Wild	1.3	Excellent tolerance
PI 424116	Wild	1.0	Excellent tolerance
			Shannon/Chen group

Conclusions

There are flood tolerant commercial varieties, advanced elite lines, and PIs

MO PI-derived lines show yield improvement under flooding conditions compared to check cultivar

Wild soybean (*soja*) can be used as a new flood tolerance source





Germination Rate under Flooding Durations



Conclusions

- •Fungicide (Apron Maxx RTA) treatment increases soybean seed germination about 5% regardless of flooding duration.
- •Longer flood durations cause lower germination rate.
- •One day flooding causes 50% less germination rate compared to non-flooding .
- •We did not find significant difference on seed germination rate between tolerant and susceptible groups.



Mapping QTL/genes for flood tolerance





RIL segregating for flood tolerance (S99-2281 x PI 408105 A)

QTL Identification S99-2281 x PI 408105A (exotic)

Chr. 11 (B1) Chr. 13(F) - BE806308 - Sat_297 0 14 Sat_234 -Sat 272 19 26 BARC-024569-04982 32 Sat 270 33 Sat 154 34 Sct 033 45 Satt509 56 - Sat_375 60 BARC-042837-08435 68 -Satt197 77 BARC-025561-06521 79 BARC-016279-02316 Satt519 84 BARC-046144-10286 87 BARC-054421-12081 Satt657 90 88 Sat_156 BARC-061571-17276 105 BARC-041167-07925 BARC-050205-09457 AW756935 99 106 Sat 090 106 107 Satt332 BARC-018741-02997 109 108 Satt444 Sat 417 BARC-035379-07181 BARC-042299-08241 123 115 Satt656 124 123 Sat 074 Sat_123 BARC-027720-06642 125 Satt359 127 Satt665 FTS-DC-08 FYI-DC-08 FTS-WO-07 FYI-WO-08 BARC-054037-12260 150 **Major OTL with**

Gm13

Gm11

donor from exotic PI

- *qFT_Gm11* with donor from the elite line.
- *qFT_Gm13* is the major one with donor from exotic PI.
- Near isogenic lines have been developed for *qFT_Gm13* and QTL validation is ongoing.
- DNA markers flanking the QTL have been developed for MAS.



New QTL Identification S99-2281 x PI 561271 (exotic)

QTL	Year	Nearest marker	а	R2 (%)	Donor
	2013	Gm03_3087237	-0.27	18.1	PI 561271
qFT_Gm 03	2014	Gm03_3087237	-0.39	33.1	PI 561271
	2015	Gm03_3225968	-0.28	16.8	PI 561271
qFT_Gm	2013	Gm10_4384037 6	0.26	15.4	S99-2281
10	2014	Gm10_4310796 1	0.20	8.5	S99-2281

- 2 QTL were mapped: *qFT_Gm03* and *qFT_Gm10*.
- The effect of *qFT_Gm10* is relatively minor; mapped in 2013 and 2014.
- *qFT_Gm03* is the major QTL and with the donor source from exotic PI.
- DNA markers flanking the QTL regions have been developed for MAS.
- Effects of the major QTL have validated at the near-isogenic background at both early Nguyen lab. Unpublished data vegetative and reproductive stages.



Mapped across all 3 years in DC; donor from PI.

Map-based Cloning of the Major Gene



- Identified NILs from HIFs (F8) that still is segregating the *qFT_Gm03*
- Screen recombinants
- Developed high-resolution map
- Progeny tests of the recombinants
- Key recombinants Rec#01, 05, 08
 - Gene was delimited between markers m07 and m09



Gene's Function at NIL Background



Developing high-yielding adapted flood tolerant lines

2016 AR Flood Project Overview

Advanced Test	35 lines		
Preliminary Test	43 lines		
Progeny Rows	341 rows (15 populations)		
	\rightarrow 27 selected		
F4	10 populations		
F3	13 populations		
F2	22 populations		
F1	25 populations		
New Crosses	18 combinations		

Twenty populations from crosses to improve soybeans for flooding tolerance MO Delta Center

Cross	Generation	Current status
S10-11227 x PI479740	F6	Advance in CR - gene mapping
S10-11227 x PI603155	F6	Advance in CR - gene mapping
S10-11227 x PI603910B	F6	Advance in CR - gene mapping
S13-15826 x S13-13342	F4	Advance in CR - variety dev
S12-25615 x S13-13342	F4	Advance in CR - variety dev
S13-15826 x S12-1362	F4	Advance in CR - variety dev
S13-15826 x S12-25615	F4	Advance in CR - variety dev
S12-25615 x S12-1362	F4	Advance in CR - variety dev
S12-25108 x Summit	F6	Advance in CR - variety dev
S12-25108 x Lorian	F6	Advance in CR - variety dev
S12-25108 x M09-W105	F6	Advance in CR - variety dev
S12-25108 x M11-HO31	F6	Advance in CR - variety dev
S12-3782 x S12-25615	F1	Advance in CR - variety dev
S13-10590 x S12-25615	F1	Advance in CR - variety dev
S13-11061 x S12-25615	F1	Advance in CR - variety dev
	E1	

Current USB Flooding Tolerance Project (2017-2019)

Collaborators

- MO Dr. Nguyen
- MO Drs. Chen & Shannon
- NC Dr. Carter
- MS Dr. Orlowskii
- LA Dr. Buckley

Current USB Flooding Tolerance Project (2017-19)

Obj 1. Characterize germplasm and identify genes for flooding tolerance.

- Screen germplasm (~500 exotic and wild) to identify additional promising lines in field (reproductive stage) and greenhouse (vegetative stage).
- Characterize environmental factors affecting stability of flooding tolerance.
- Test 70 selected lines in multiple states for $G \times E$ study: MO, AR, NC, MS. LA.
- Soil profiling: pH, nutrients and *Phytophthora*.
- Identify flooding tolerant genes in RIL populations.
- Perform QTL mapping in 4 new mapping populations.
- Fine-map and clone significant QTLs for allele mining and gene-based markers.
- Develop new populations (elite × wild) and NILs for tolerance mechanisms.
- Conduct GWAS in diverse lines using high density SNP markers.
- Flooding tolerance at vegetative stage in greenhouse (~500 lines).
- Flooding tolerance at early reproductive stage in field (~500 lines MGs III-V).

Current USB Flooding Tolerance Project (2017-19)

Obj 2. Improve germplasm for flooding tolerance.

- Develop functional markers associated with flooding tolerance QTLs and genes.
- Improve germplasm by pyramiding and stacking flooding tolerance QTLs into elite lines (MGs III to V) utilizing MAS (4 mapped QTL).
- Conduct field evaluation of yield and flooding tolerance in the new germplasm.

Obj 3. Develop high yielding and flooding tolerant varieties.

- Develop breeding populations using new germplasm and select new varieties based on field performance and marker-assisted selection.
- Release varieties with improved flooding tolerance and high yield.

Thank you!

