Detection of Quantitative Trait Loci Associated with Drought Tolerance in St. Augustinegrass

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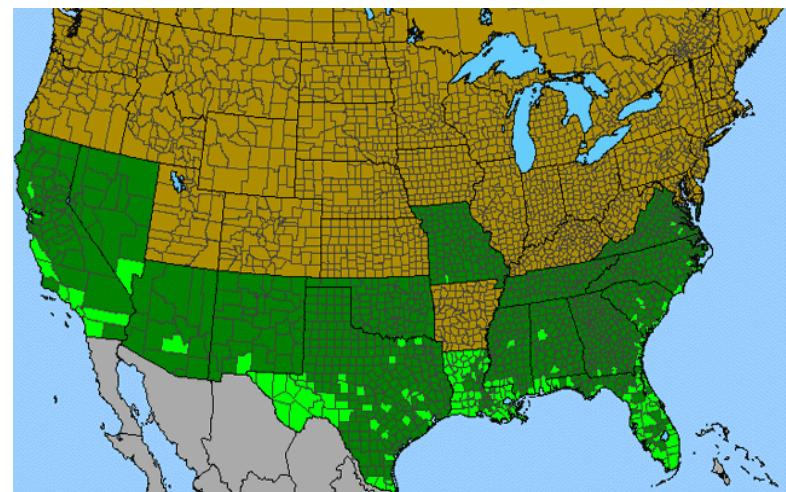Crop and Soil Sciences, North Carolina State University

NC STATE

TURFGRASS BREEDING & GENETICS

St. Augustinegrass breeding

NC STATE
TURFGRASS BREEDING
& GENETICS

Properties:

❖ Warm-season grass

❖ Widely used as lawn grass in southern US

❖ Creeping growth habit via stolon

❖ Fast growing, establishes rapidly

❖ Relatively low input

Breeding goals:

❖ Aesthetic performance

❖ Drought tolerance

❖ Cold tolerance

❖ Resistance to chinch bug

❖ Resistance to grey leaf spot

Molecular breeding in turfgrass

The areas of molecular breeding include:

❖ QTL mapping or gene discovery

❖ Marker assisted selection and genomic selection

❖ Genetic engineering and transformation

Application on turfgrass

❖ Conventional breeding methods still are the most applied and efficient methodologies

❖ Molecular breeding is becoming popular

❖ This is the time to equip turfgrass breeding programs with advanced genomic tools

Drought tolerance

Drought stress:

❖ One of the most important environmental factors limiting the growth of turfgrasses.

❖ The selection and development of species and cultivars of turfgrasses that resist drought stress and require minimal inputs of supplemental irrigation is a viable strategy to conserve water.

Drought tolerance evaluation:

Visual rating
Turf quality
Leaf wilting and firing   Morris and Shearman, 2006
                                 Kim et al., 1988

Morphological traits
Root depth
Root dry weight   Huang et al., 1997
                         Su et al., 2008

Physiological response
Chlorophyll content and fluorescence
Relative water content (RWC)   Huang et al., 1997

Digital image analysis
Green cover (%)   Steinke et al., 2010

Objectives

❖ **Develop high density SNP-based genetic map for St. Augustinegrass**

❖ **Evaluate drought tolerance related traits in St. Augustinegrass**

❖ **Identify QTL controlling drought traits in St. Augustinegrass**

Plant materials

❖ Population was derived from cross between St. Augustinegrass cultivars
‘Raleigh’ and ‘Seville’, both on diploid level (2n=2x=18).

cv. ‘Raleigh’   X   *cv*. ‘Seville’

115 F$_1$ hybrids

Segregating for drought tolerance

Drought tolerance evaluation

Experimental design:

Experiment	Greenhouse 2017 (GH17)	Greenhouse 2018 (GH18)	Sandhill field 2018 (F18)
Design	Three replicates at Randomized complete block design		
Drought	Withhold water until 5% soil water content		Annually recurring drought period in July and August
Traits	Leaf relative water content (RWC)	RWC	NDVI
	Green cover percent (GC)	GC	LF
	Leaf wilting (LW)	LW	
	Leaf firing (LF)	LF	
	ChlorophyII fluorescence (Fv/Fm)	Fv/Fm	

Traits measurement:

❖ RWC (%) = (Fresh weight – Dry weight)/(Turgid weight – Dry weight) *100.

❖ ChlorophyII fluorescence (Fv/Fm): MultiSpeQ v 1.0.

❖ Green cover (GC): Fiji image analysis.

❖ Leaf wilting (LW) and firing (LF): visual rating score 1-5.

❖ NDVI: TCM 500 Turf Color Meter.

Genotyping and QTL detection

Genotyping platform:

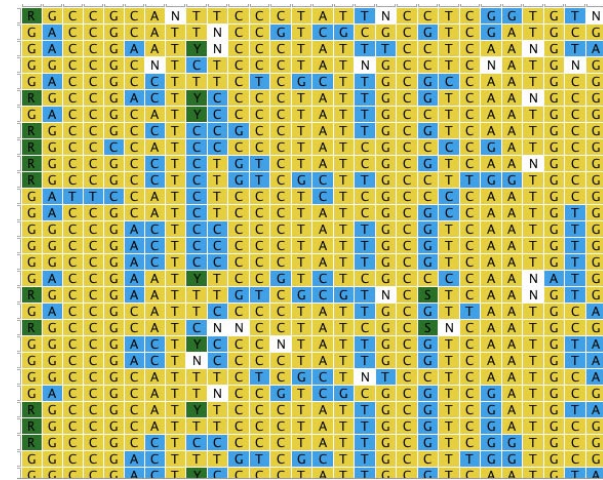❖ Genotyping-by-sequencing on Illumina HiSeq 2500

Linkage map:

❖ Joinmap 4.0

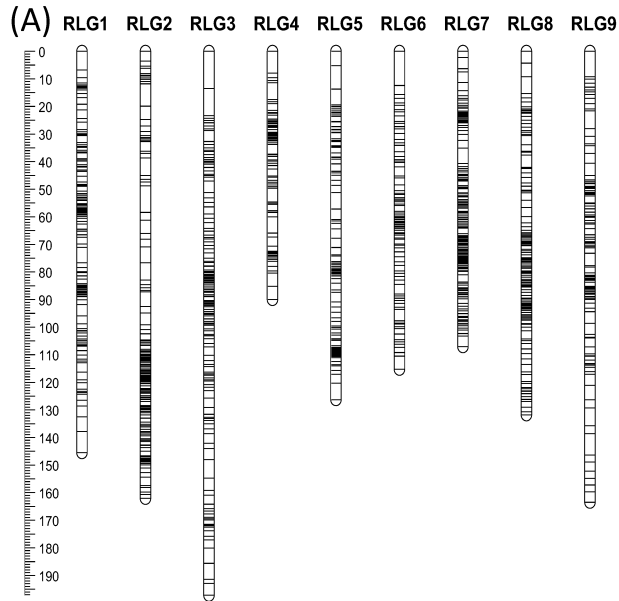**QTL detection:**

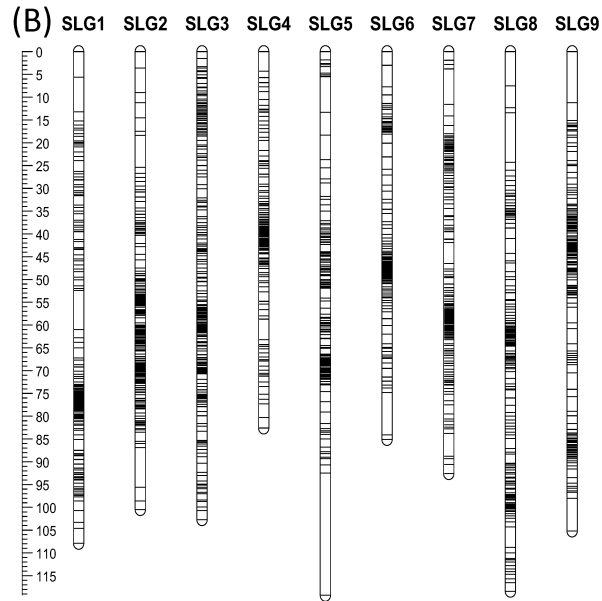❖ MQM composite interval mapping on MapQTL 6.0

Statistics:

❖ SAS PROC MIX

Genetic maps

Raleigh map

Seville map

Linkage group	Number of markers	
	'Raleigh' map	'Seville' map
LG1	132	172
LG2	148	189
LG3	142	223
LG4	78	150
LG5	108	175
LG6	93	128
LG7	151	200
LG8	129	164
LG9	119	170
Total	1100	1571

Yu *et al*. *BMC Plant Biology* (2018) 18:346

Distribution of traits

❖ Distribution of each traits in *Raleigh x Seville* population


▼ Raleigh   ▽ Seville
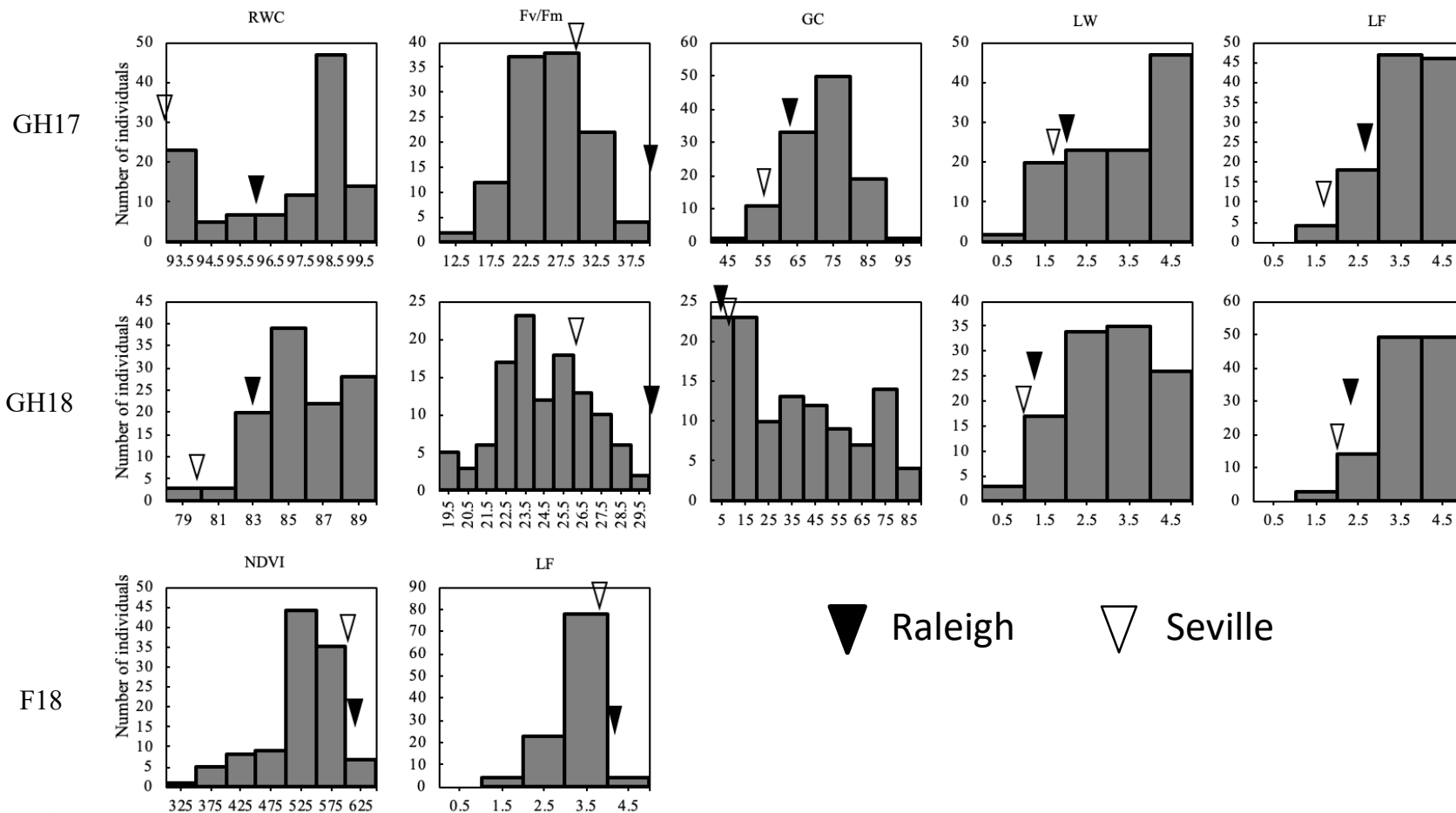
Traits variance

❖ Variance (genotype effect) of drought related traits in *Raleigh x Seville* population

	GH17					GH18					F18	
	Fv/Fm	GC	RWC	LW	LF	Fv/Fm	GC	RWC	LW	LF	NDVI	LF
Raleigh	40.14	62.03	95.60	2.00	2.67	30.55	5.11	82.99	1.33	2.33	606.83	4.08
Seville	28.46	54.76	86.87	1.67	1.67	26.31	7.61	79.64	1.00	2.00	600.67	3.83
Progeny Mean	25.67	71.43	95.85	3.55	3.86	24.46	35.02	85.66	3.28	3.95	525.22	3.19
Progeny Min	12.33	46.10	77.72	1.00	1.33	19.00	2.15	79.01	1.00	1.67	310.00	1.25
Progeny Max	38.80	91.80	99.49	5.00	5.00	29.97	86.29	89.31	5.00	5.00	638.17	4.38
Variance (genotype)	*	***	**	***	***	*	***	**	***	***	***	***

*, **, *** Significance at *p-value < 0.05, 0.01, 0.001*, respectively.

Identification of top hybrids
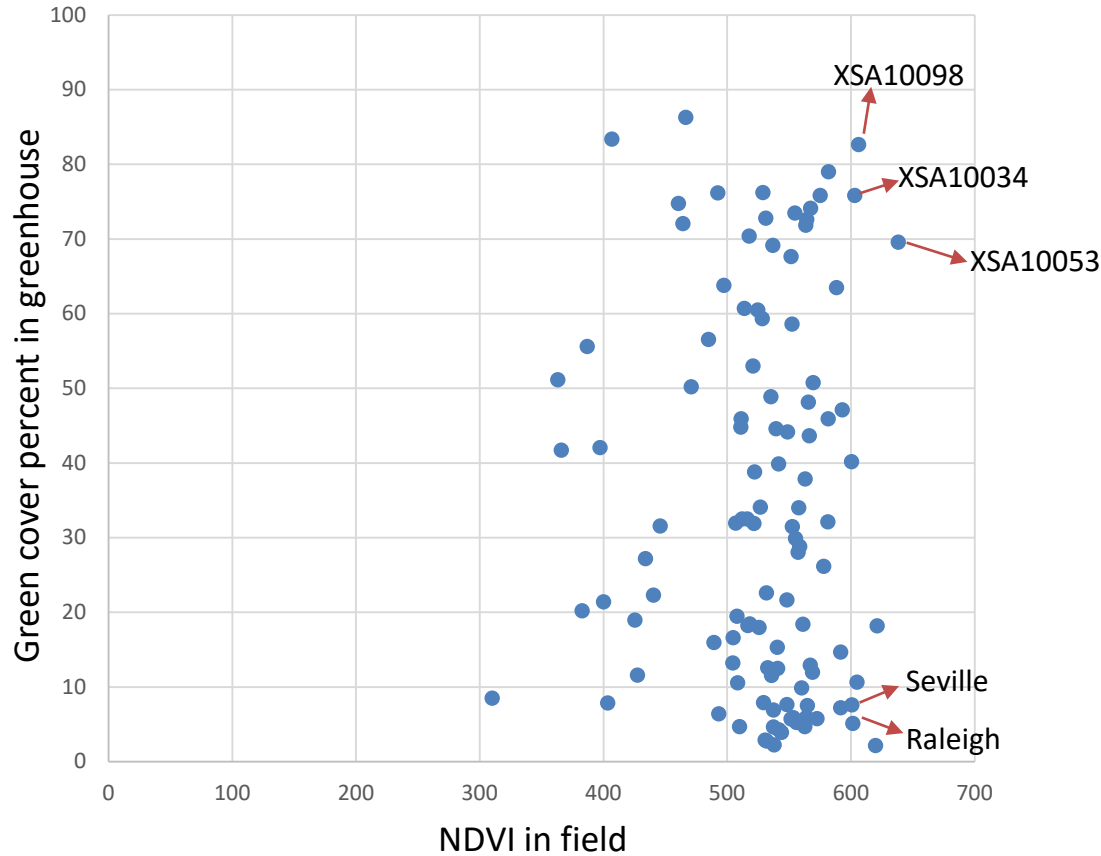
QTL detection

❖ Number of QTL distributed on each linkage group for each trait.

		GC	LF	LW	NDVI	RWC	Fv/Fm	Total
Raleigh map	R1	2		5				7
	R2		1	1		1		3
	R3	2	2			3		7
	R4	1	2				2	5
	R5	2		1				3
	R6	1	4	2		1		8
	R7	1	1		4			6
	R8	2	1			1		4
	R9	2				1		3
Seville map	S1		2					2
	S2	4	3		2			9
	S3	1		1		1		3
	S4	1						1
	S5		2	3				5
	S6							
	S7							
	S8	2		1				3
	S9				1			1
	Total	21	18	14	7	8	2	**70**

QTL detection

❖ Loc   ation

| GH17 | LW-R1.2 | R1 | 11.85 | 11.45 - 12.56 | SNP5027 | 8.17 | 6.2 | 0.54 |
GH18	LW-R1.2	R1	12.26	11.65 - 12.56	SNP5027	5.57	6.0	0.59
GH18	LW-R6.1	R6	104.50	103.38 - 105.30	SNP43183	5.36	5.8	-0.30
GH17	LW-R6.2	R6	105.44	104.50 - 106.24	SNP50810	14.52	12.9	-0.53
GH17	Fv/Fm-R4.2	R4	39.39	39.09 - 39.69	SNP47984	3.82	8.8	1.78
GH18	Fv/Fm-R4.2	R4	39.39	39.29 - 39.45	SNP47984	3.62	9.3	0.83
GH17	GC-S3.1	S3	33.00	32.69 - 33.10	SNP13076	4.40	5.9	-2.73	F18	NDVI-R7.2	R7	76.29	76.28 - 76.39	SNP45148	49.19	7.6	-237.47
									F18	NDVI-R7.3	R7	77.73	77.73 - 78.26	SNP53130	47.80	7.1	233.17
GH17	LW-R1.4	R1	47.58	45.80 - 48.28	SNP16248	12.99	11.0	-0.97
GH17	GC-R1.1	R1	47.38	46.20 - 48.28	SNP16248	4.67	6.3	-2.89
GH18	LW-R5.1	R5	67.84	61.45 - 69.14	SNP2879	13.63	17.6	1.00
GH17	GC-R5.2	R5	62.42	61.45 - 64.32	SNP24133	5.00	6.8	-2.50
GH17	GC-S2.2	S2	48.20	47.48 - 48.40	SNP32244	6.17	8.6	2.99
GH17	LF-S2.2	S2	47.40	46.50 - 48.18	SNP28455	19.55	20.4	0.64

Co-localization of QTL
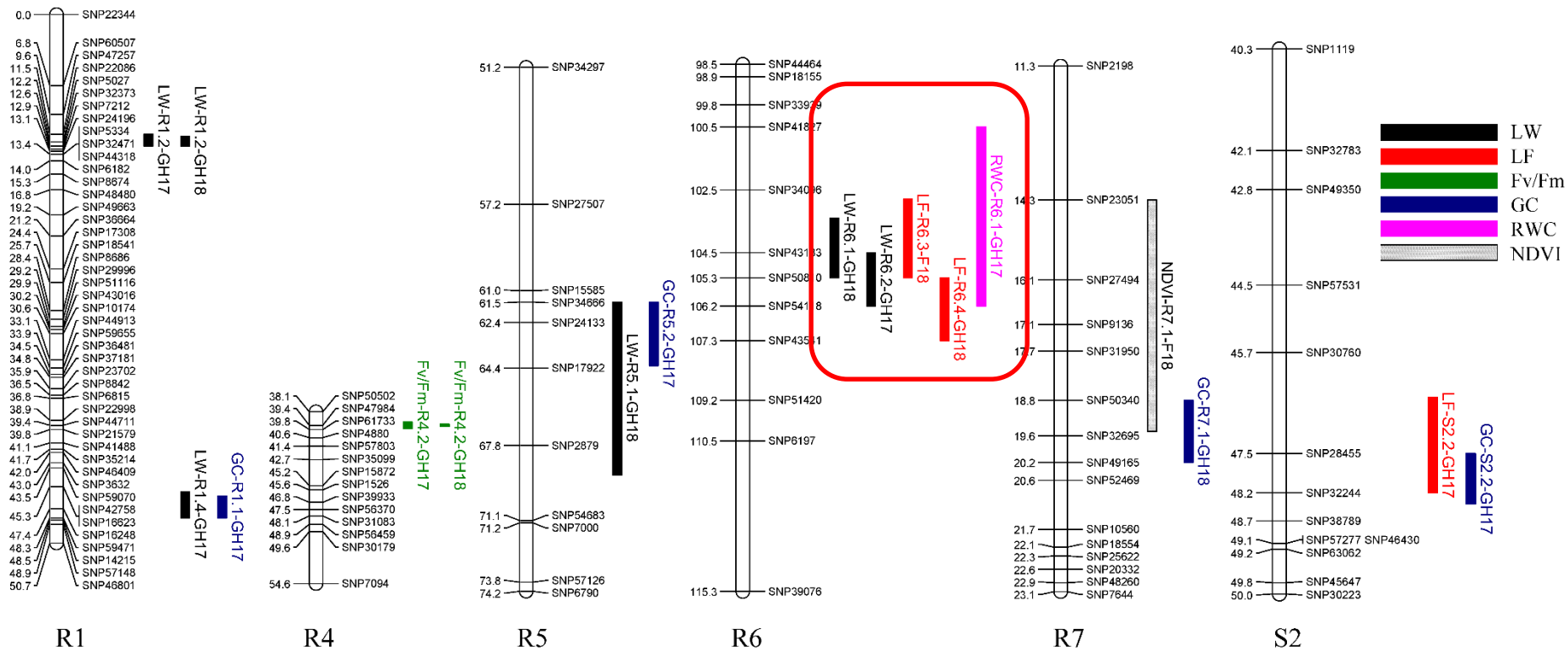
Conclusions

Population containing 115 hybrids

Develop high density genetic maps

Evaluate drought traits in greenhouse and field

Detect 70 drought associated QTL

1. Understand the molecular basis and genetic control of drought tolerance in St. Augustinegrass.

2. Improve drought tolerance breeding through marker assisted breeding.

Ongoing works

❖ **Mining candidate genes and allelic variation with drought tolerance in putative QTL.**

❖ **Developing new mapping population using identified hybrids with different drought tolerance level to validate QTL.**

❖ **Conducting RNA-Seq analysis to illustrate gene expression profile under drought stress.**

Acknowledgements

United States Department of Agriculture
National Institute of Food and Agriculture