Developing summer-dormant tall fescue for the southern Great Plains

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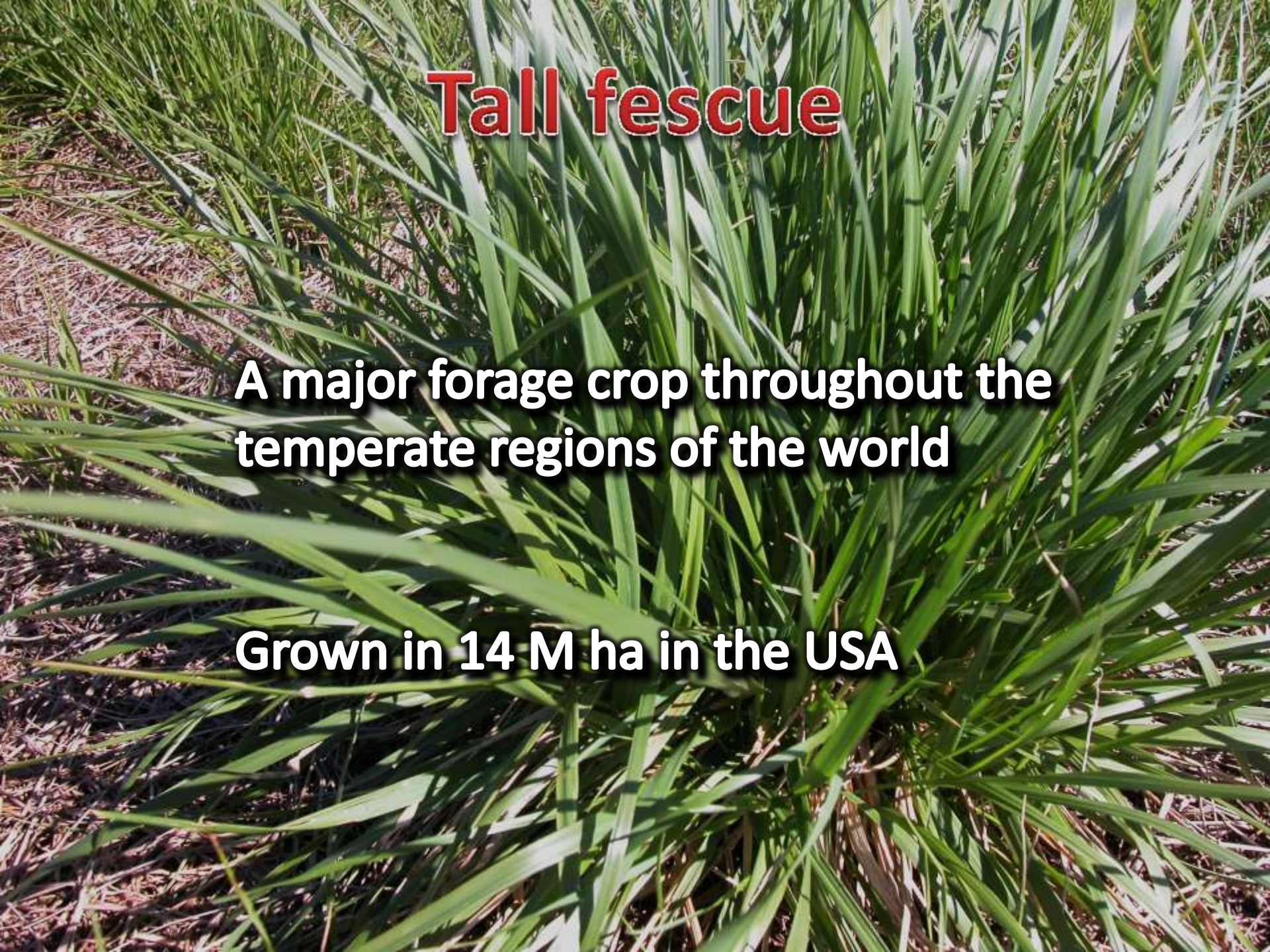

Tall fescue
A major forage crop throughout the temperate regions of the world
Grown in 14 M ha in the USA

Heat and Drought are characteristics of summer in south-central U.S.A.

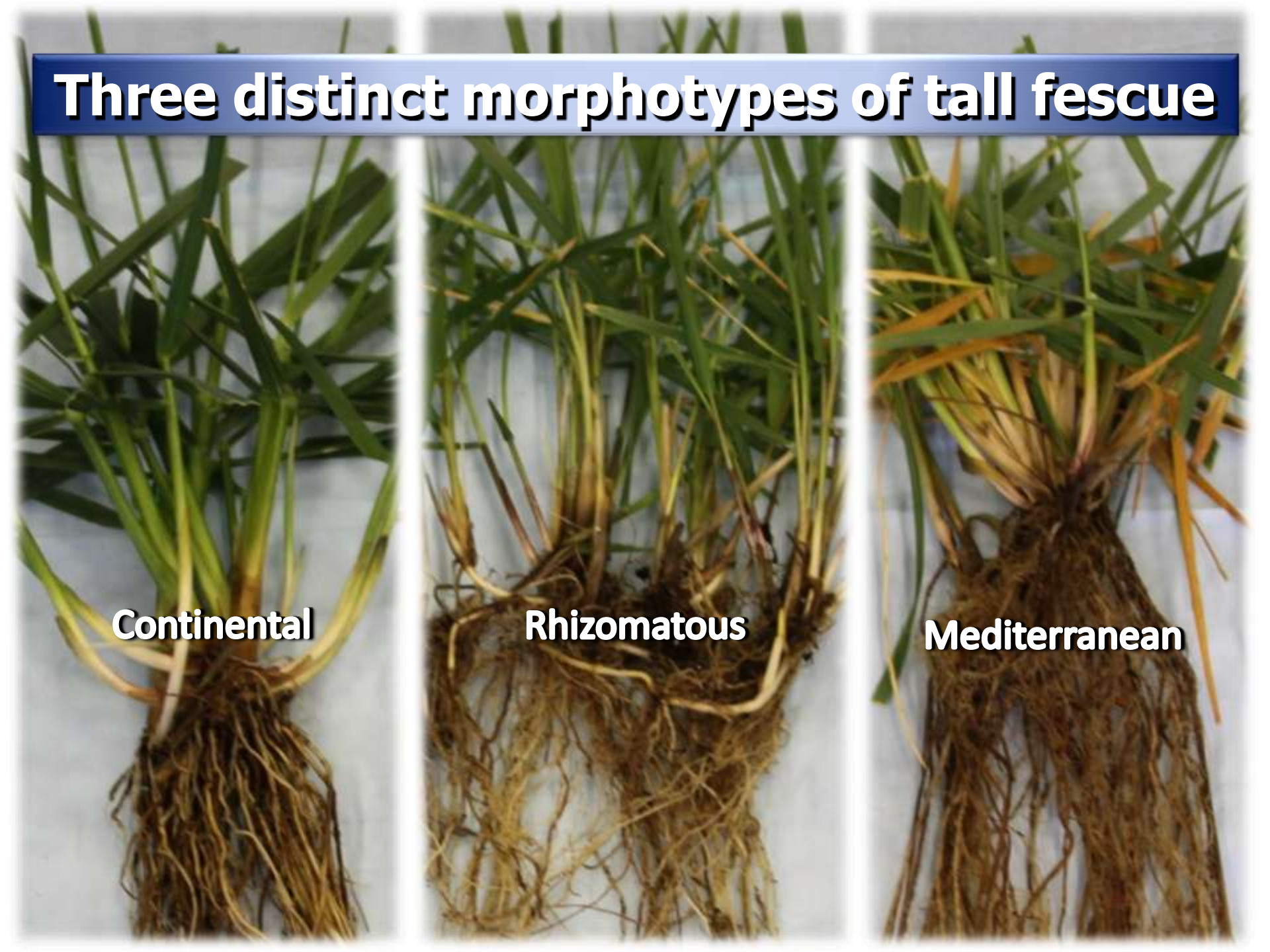
Persistence is the major constraint of growing tall fescue in south-central USA

40-60% stand loss in a year

Improve persistence

- **Drought tolerance**
- **Summer dormancy**

Three distinct morphotypes of tall fescue



Mediterranean Tall Fescue

Contains high levels of summer dormancy

Key environmental factors for Summer dormancy?

Genotypes and conditions evaluated

Three genotypes with known phenotype:

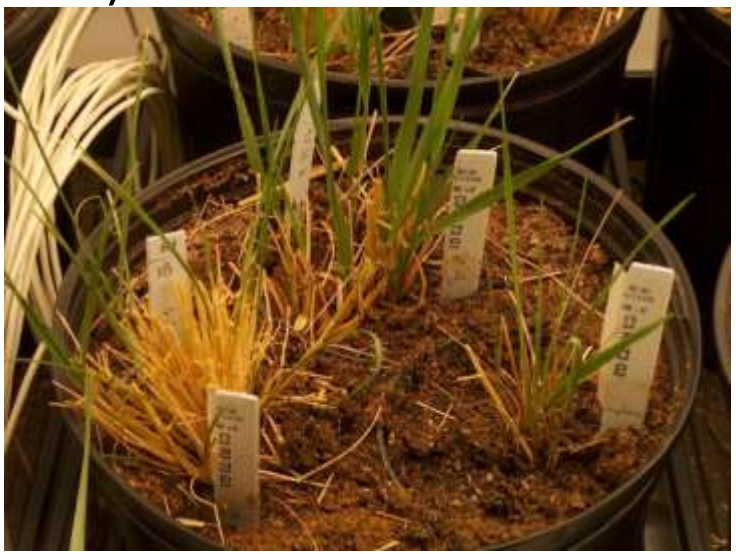
- Summer active (SA)
- Strongly summer dormant (SSD)
- Moderately summer dormant (MSD)

Daylength and temperature

- Short day (SD, 10 h)
- Long day (LD, 16 h)
- High temperature (HT, 34°C)
- Optimum temp. (OT, 24°C)

Moisture and vernalization

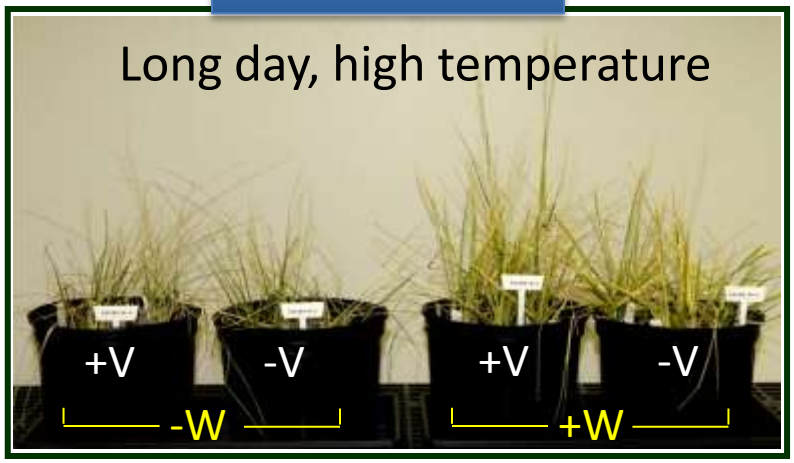
- Well watered (+W)
- Water stressed (-W)
- Vernalized (+V)
- Non-vernalized (-V)



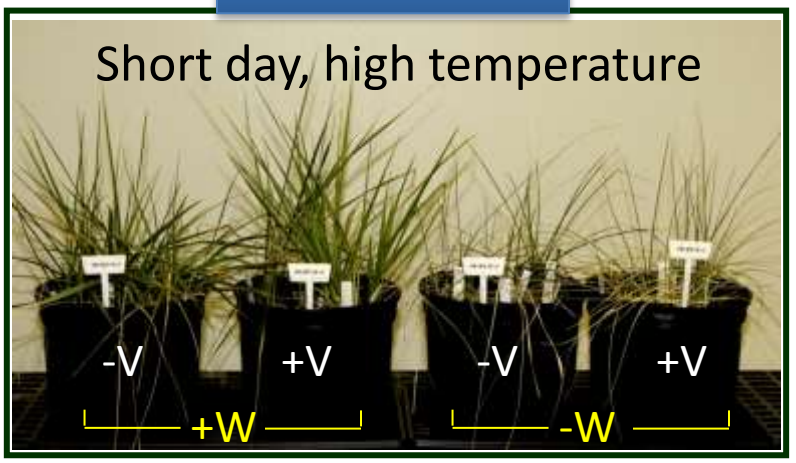
Three genotypes in same pot

Growth chamber conditions

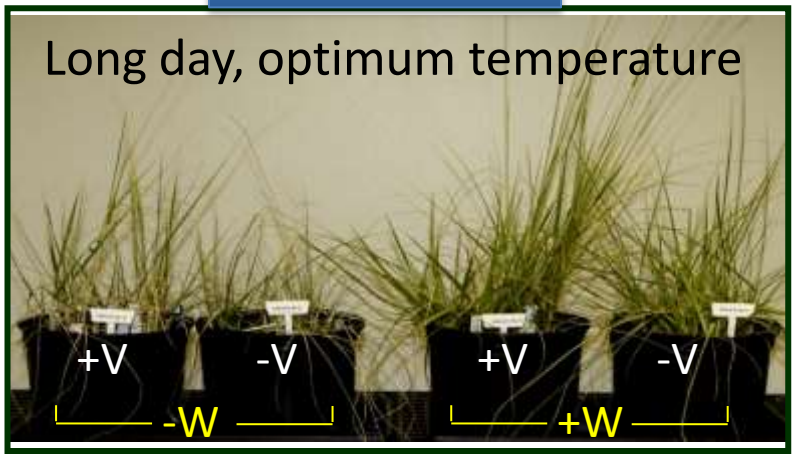
Chamber 1



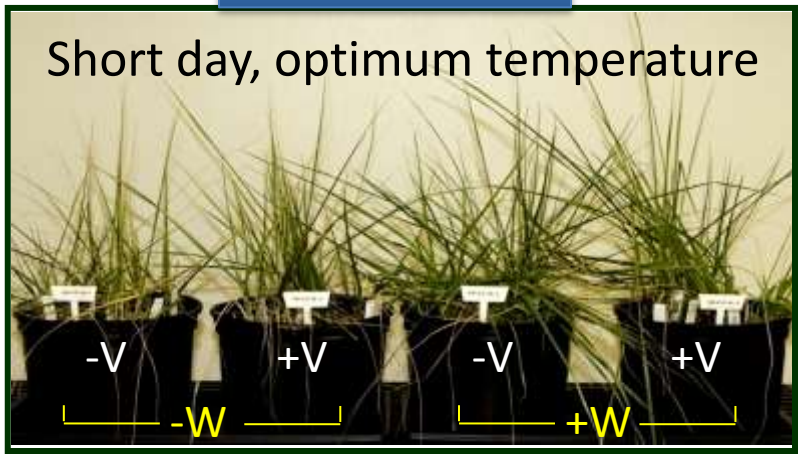
Chamber 2



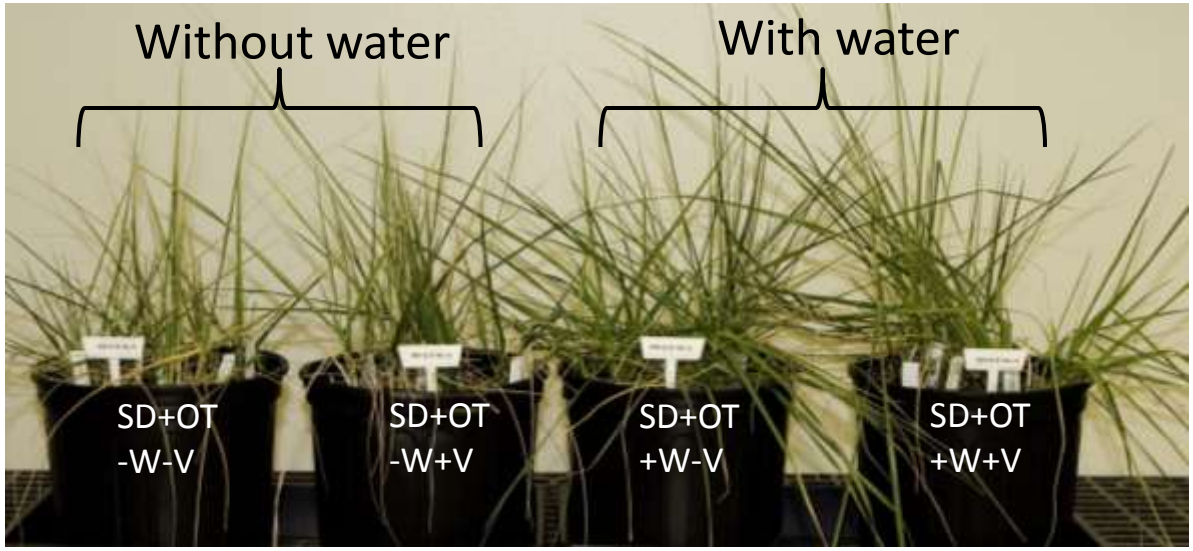
Chamber 3



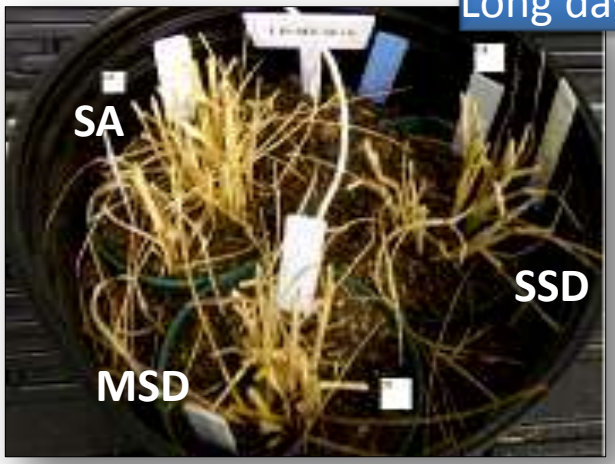
Chamber 4



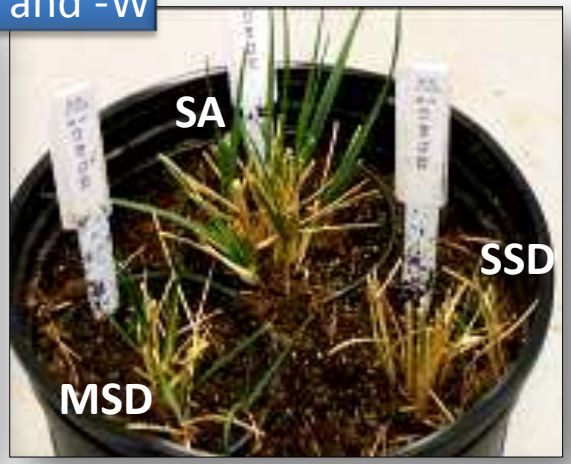
Water stress in optimum temperature conditions



Long day and -W



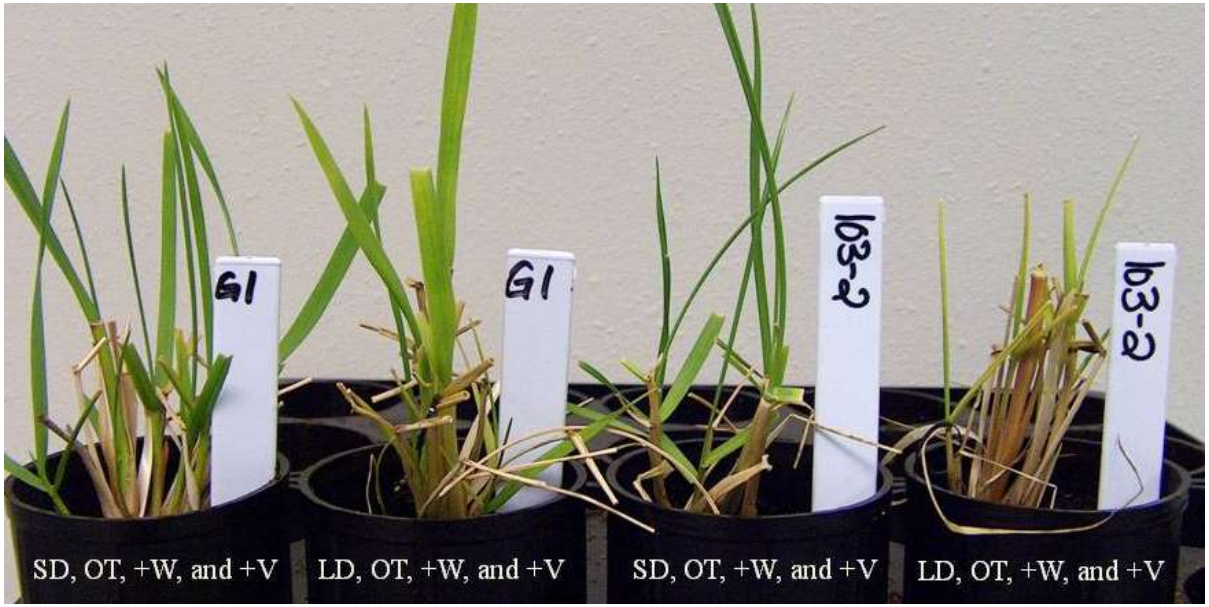
Before top watering



After top watering

Water is not a critical factor for summer dormancy

Key factor for dormancy induction



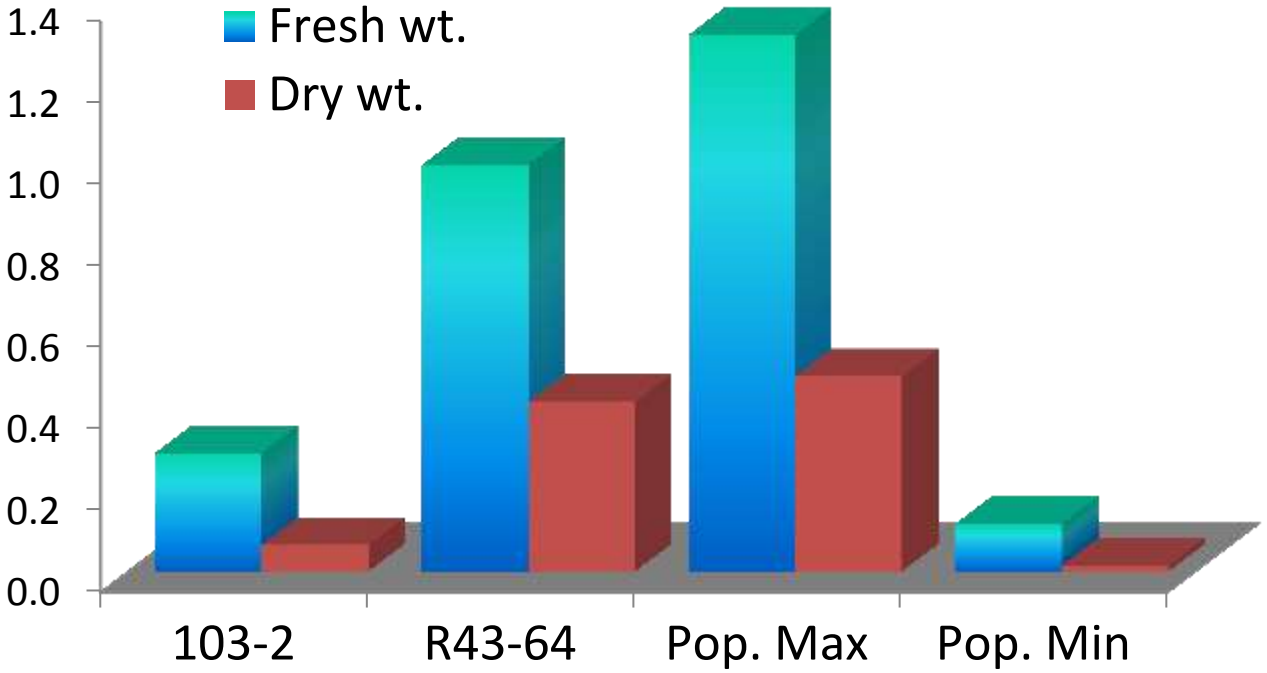
Dormancy response could be phenotyped by comparing growth of plants under optimal (SD, OT,+W, and +V) versus dormancy inducing (LD, OT, +W, and +V) conditions

Dormant genotypes grew significantly less than the active for:

- number of tillers (5.6 vs. 15.8)
- leaf elongation (44.3 vs. 52.1 days)
- fresh weight (6.0 vs. 16.0 g)
- dry weight (3.1 vs. 8.8 g)

under long day, optimum temperature, +W, and +V conditions

Validation of the concept in a segregating population

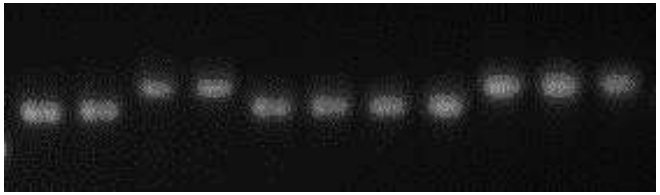


- Distinct parental growth (reduced growth of dormant parent under LD, OT, +W, and +V)
- Transgressive segregation in the population

Marker development

Similar plant characteristics
Difficult to distinguish morphologically

Nuclear and chloroplast genome specific markers used for identification



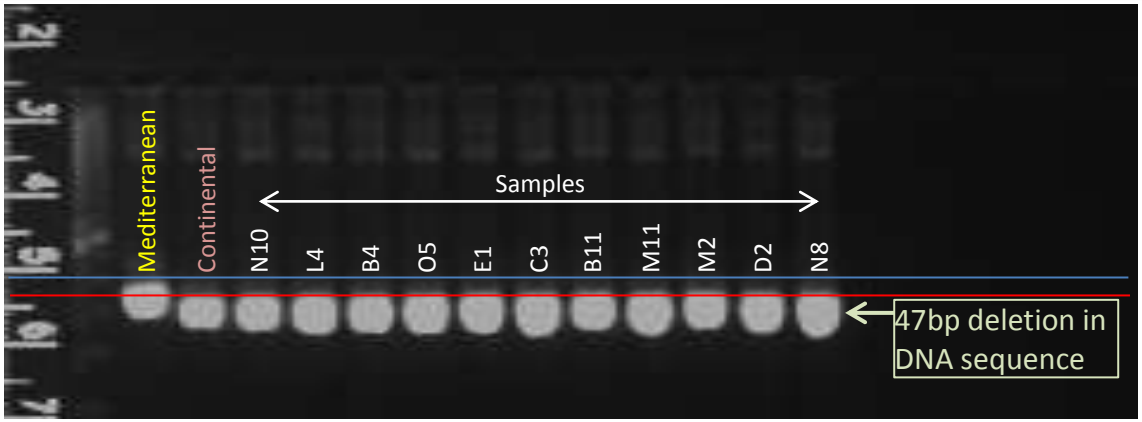
Sequences of chloroplast specific markers showed additions, deletions and substitutions

Primer	P-48	P-48	P-48	P-48	P-48	P-48	P-30	P-30	P-30	P-45
NT position	47095	47282	47286	47295	47299	47447	47298	47299	47411	85684
Ref. KY31	A	A	T	G	TTATT	C	G	A	C	-
Torpedo	A	A	T	G	TTATT	C	G	A	C	-
KY-31	A	A	T	G	TTATT	C	G	A	C	-
PDF584	A	A	T	G	TTATT	C	G	A	C	-
Flecha MaX Q	G	T	-	G	-	A	T	C	C	AGAAGATAGAGGAGAGCGCCAGGCGCAGATTTTCGGAATACTTCTAC
Prosper	G	T	-	G	-	A	T	C	C	AGAAGATAGAGGAGAGCGCCAGGCGCAGATTTTCGGAATACTTCTAC
Resoulte	G	T	-	G	-	A	T	C	C	AGAAGATAGAGGAGAGCGCCAGGCGCAGATTTTCGGAATACTTCTAC

Morphotype specific chloroplast primers

- Four primer pairs identified which can clearly distinguish the Continental and Mediterranean morphotypes
- Primer NFTCHL045 has a 47 bp deletion in the Continental materials and can be differentiated in agarose gel

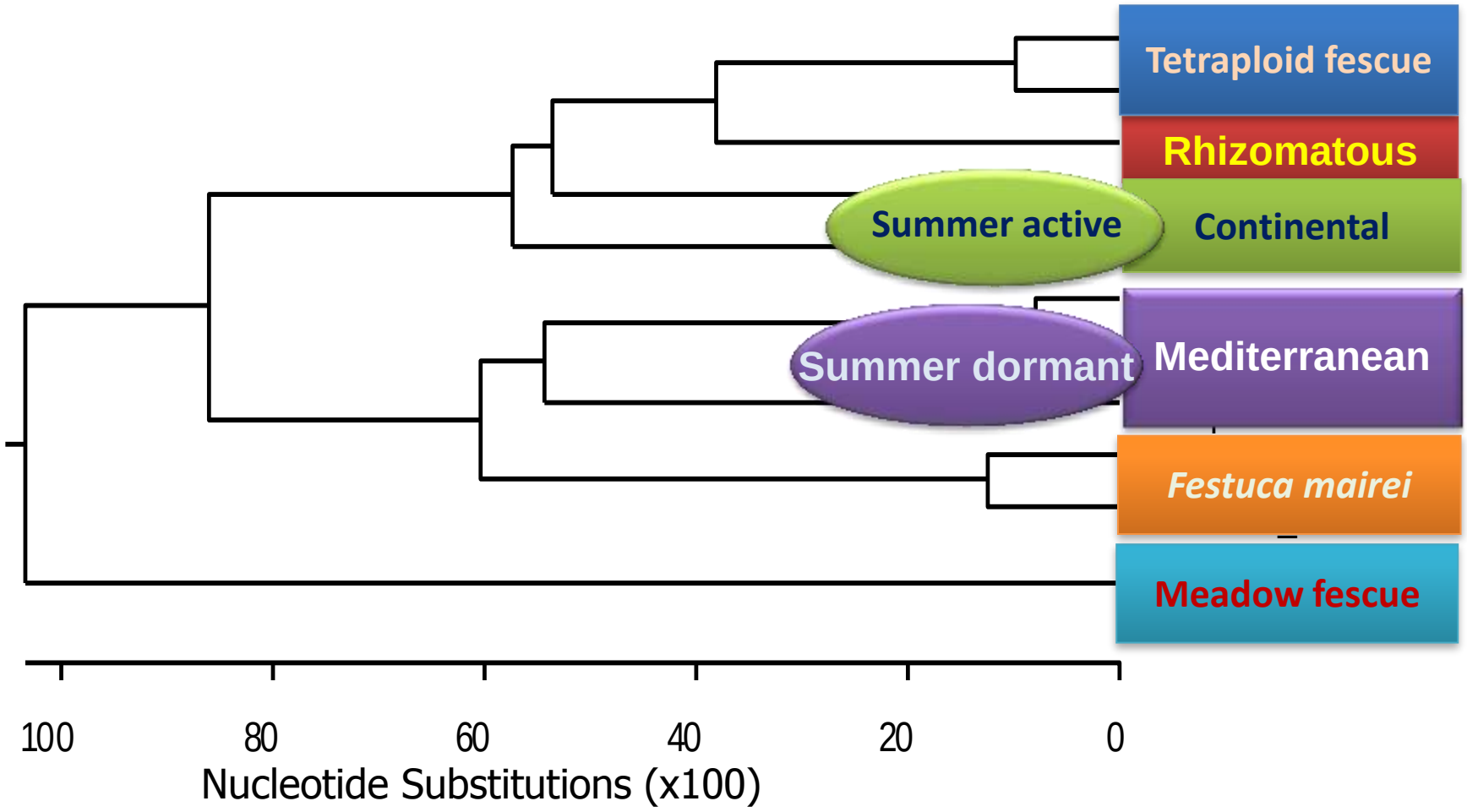
NFTCHL045 was used to classify tall fescue collection



DNA from all tall fescue plants collected from a field at Ardmore, OK posses the 47 bp deletion fragment correspond to Continental morphotype

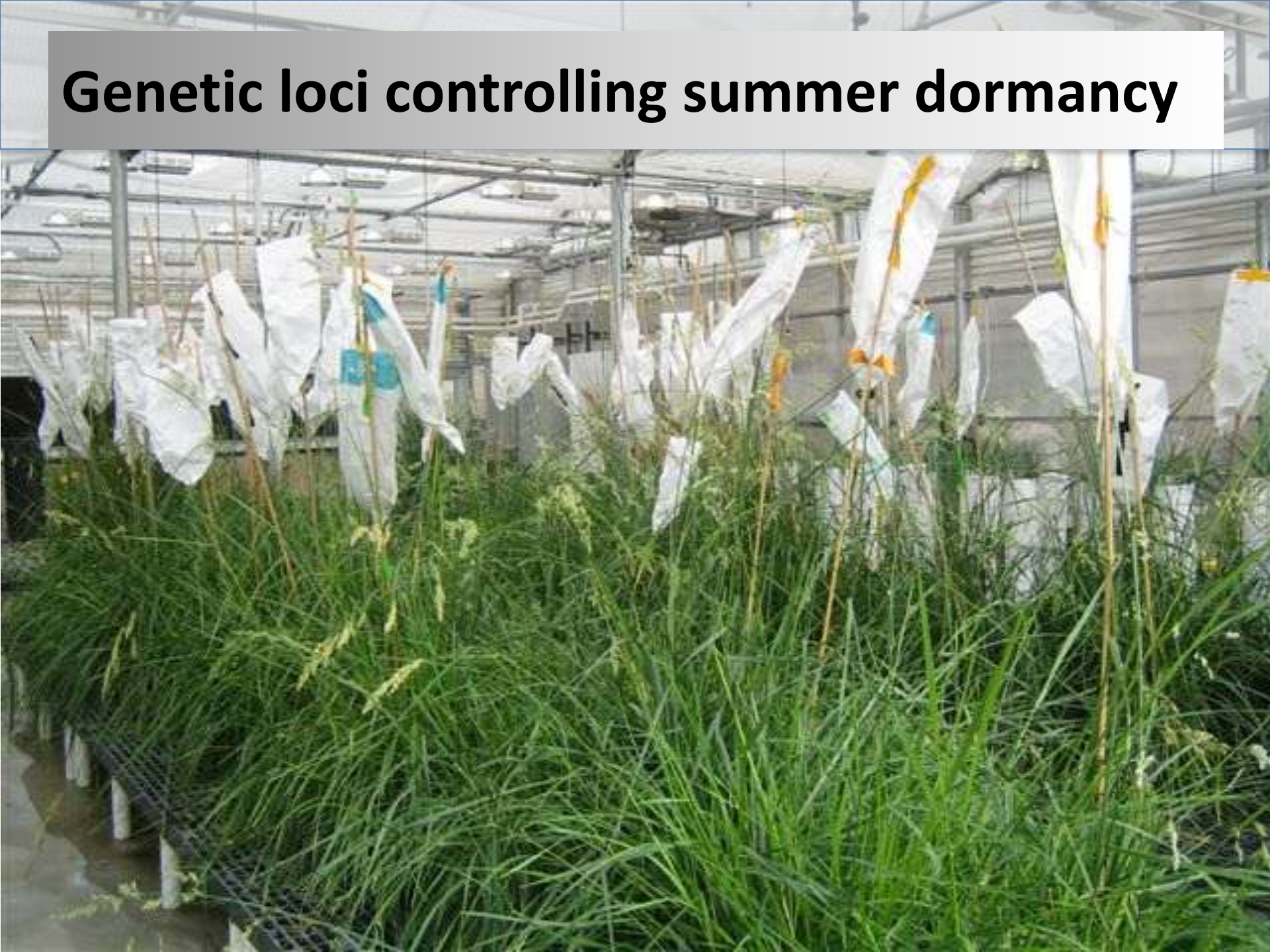
Noble Foundation Forage Analysis core facility included the NFTCHL045 primer assay in their services

Chloroplast genome based phylogeny



- Very similar relationships among the Fescue grasses were obtained from the SSR-STS marker analysis

Genetic loci controlling summer dormancy



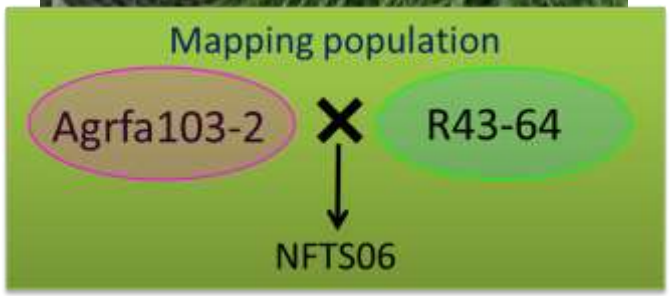
Development of a mapping population

Parental selection

Flecha MaxQ

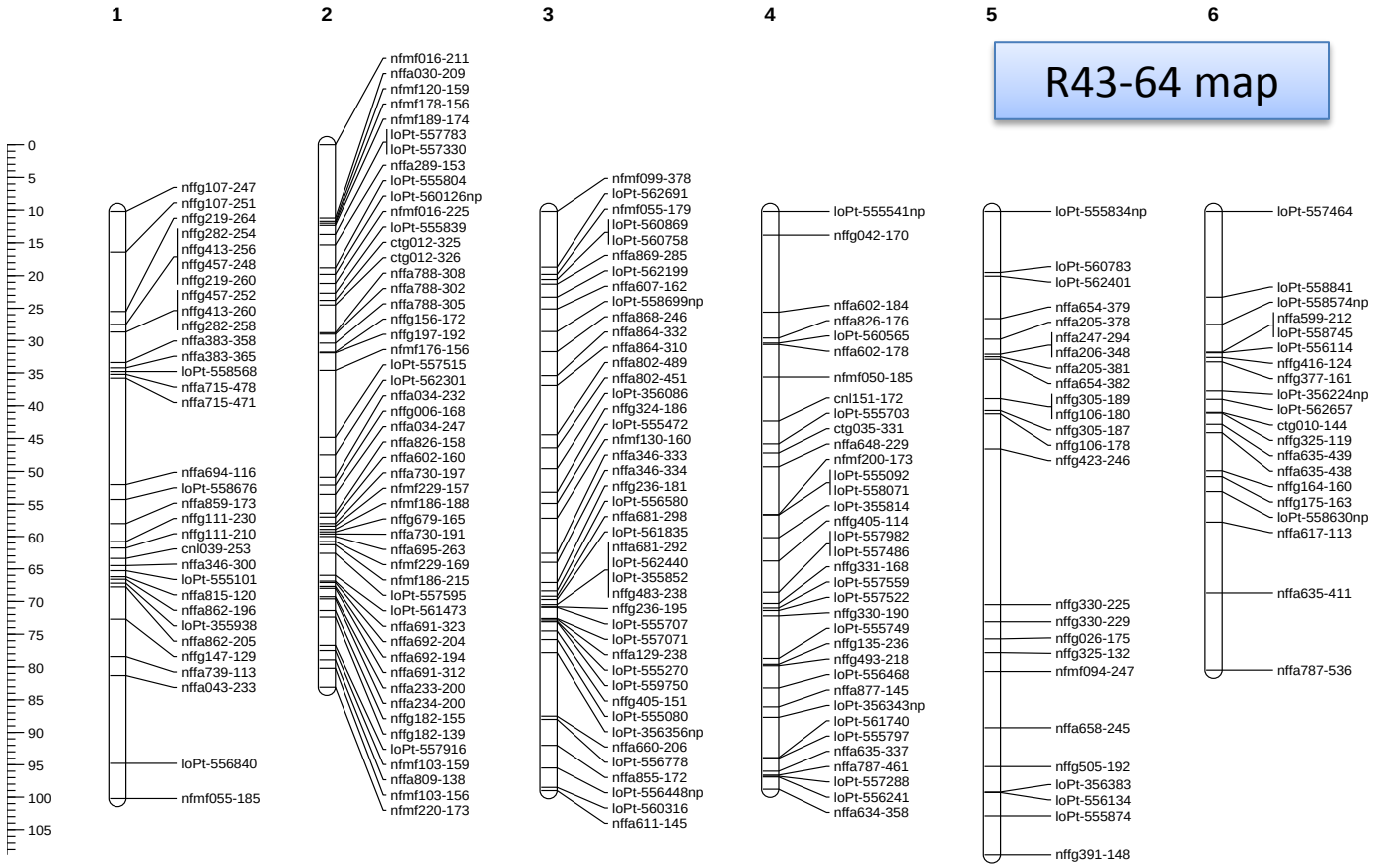
- Dormant plants selected from Flecha field
- Re-grown in greenhouse
- Selected most dormant plant

- R43-64, parent of another population selected as the summer active parent



Construction of parental linkage maps

- Mapping population was genotyped with SSR, STS, and DArT markers
- Parental maps were constructed following CP model of JoinMap 4.0



- R43-64 map: length 1509 cM, total loci 541, density 2.79 cM/marker
- 103-2 map: length 1044 cM, total loci 141, density 7.41 cM/marker

Field evaluation of NFTS06 population

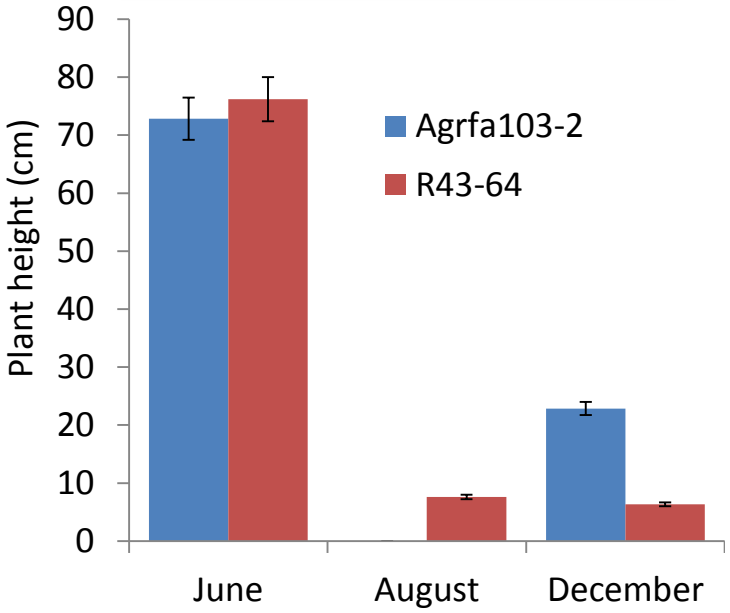
208 genotypes and parental ramets evaluated in replicated trials at two locations

Segregation for senescence can be observed in extreme weather conditions

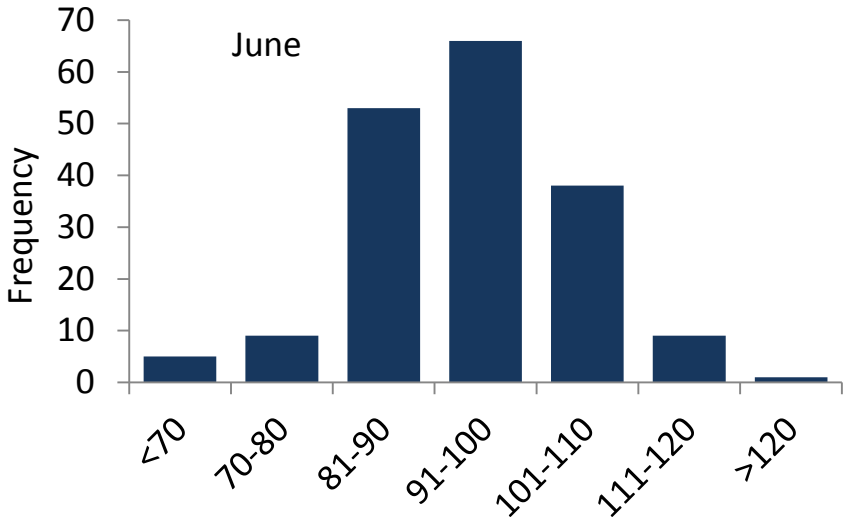
Phenotyping summer dormant mapping population

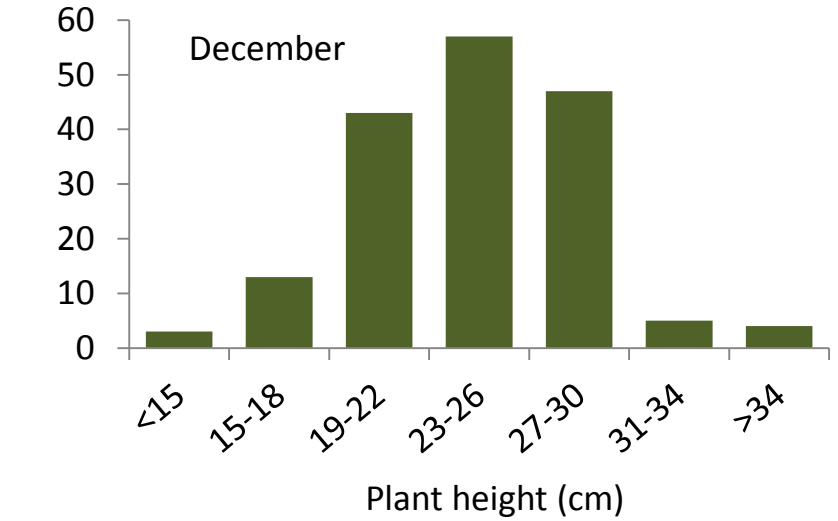
Plant height distribution at Research Park , Ardmore, Okla.

Parental distribution



- Both the parents grew equally in June
- Summer dormant parent didn't grow in August but actively grew in December

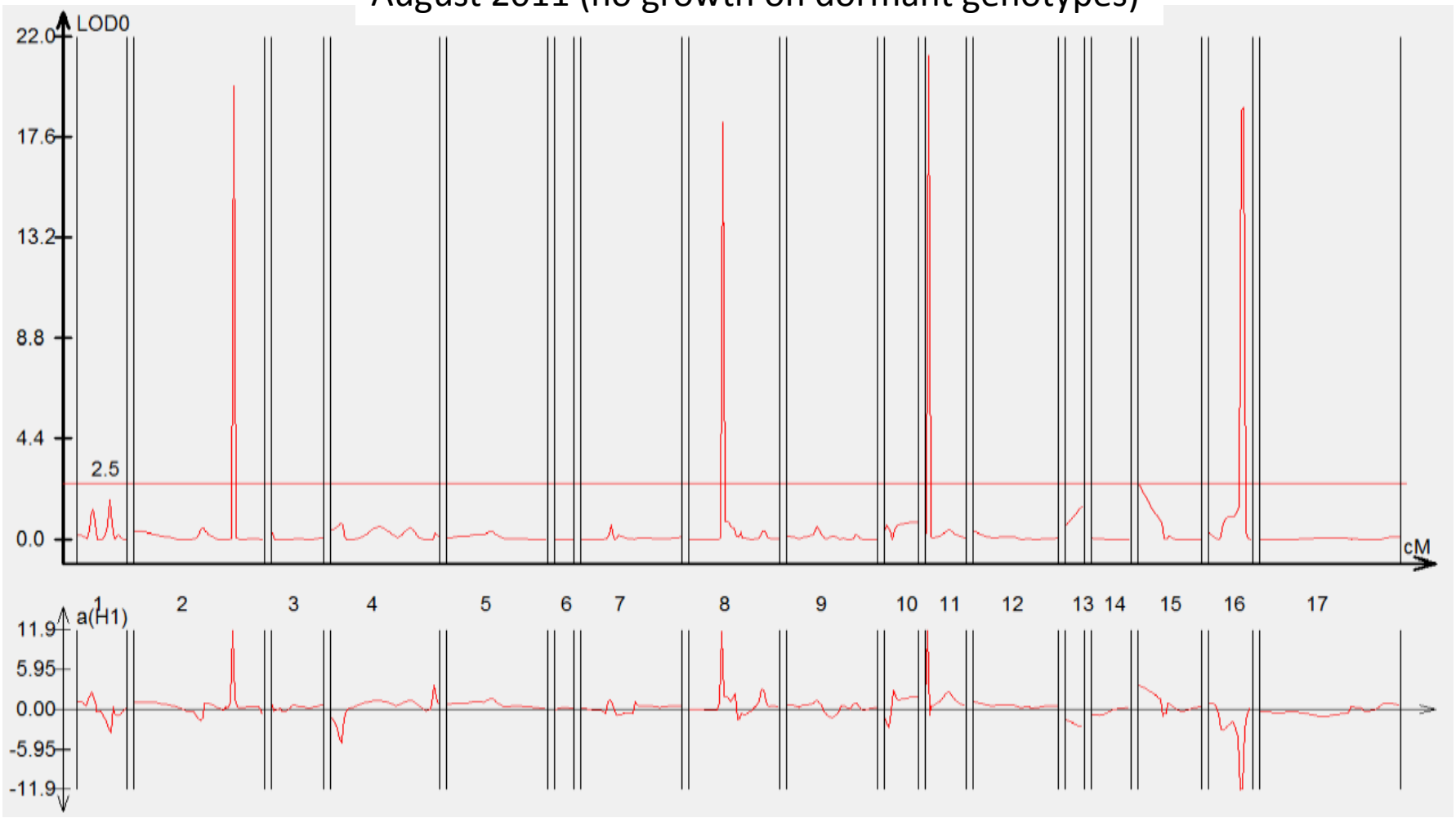




Population distribution

QTL for plant height on Agrfa103-2 map

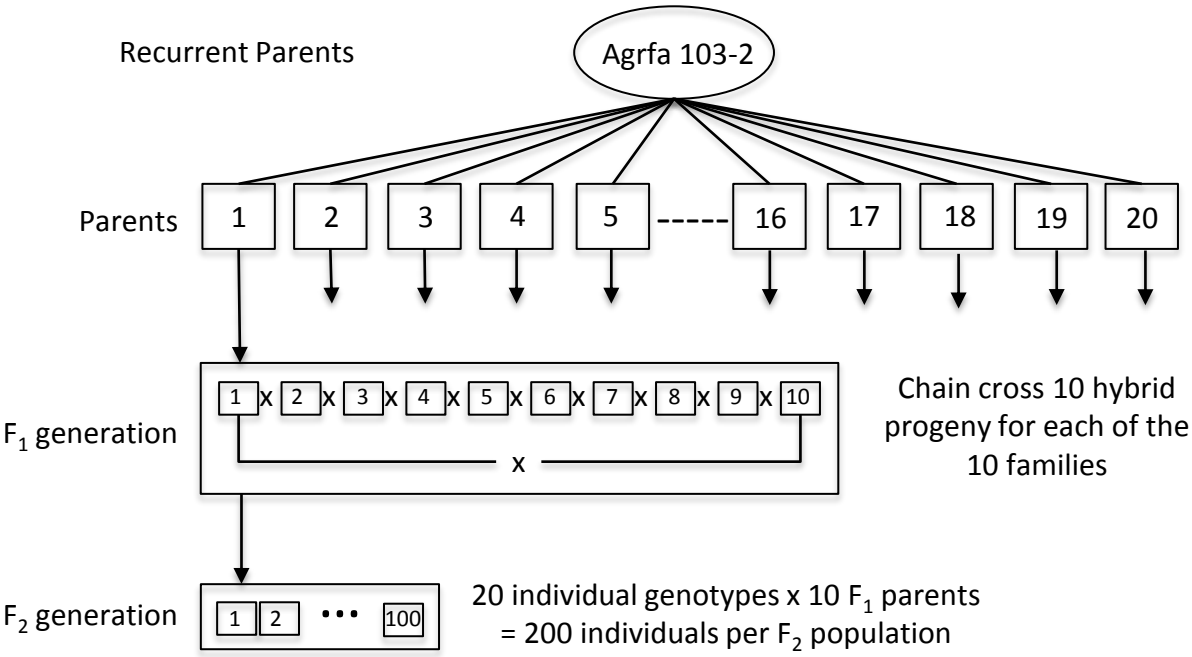
August 2011 (no growth on dormant genotypes)



Linkage groups

Development of a nested association population

Crossing program to develop a NAM population of 4,000 genotypes



Summer-dormant breeding population evaluations

- Summer-dormant breeding populations have been developed at the Foundation
- Populations evaluated at multiple locations in TX and OK
    - NFTF1800 had the best stand at Burneyville, OK
    - NFTF1700 ranked top at Vernon, TX
    - Across locations, NFTF1700 ranked #1
    - Plant stand of Flecha was statistically identical

Summary

- Summer-dormant tall fescue has great potential in the southern Great Plains
- Long day is critical for inducing summer dormancy
- Morphotype specific molecular markers have developed
- Identification of QTLs associated with summer dormancy is in progress
- Summer dormant breeding populations developed at the Foundation showed their promise in the region

Acknowledgements

Collaborators within Foundation

Forage improvement Division
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- Yuhong Tang

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University of Missouri

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Thank you