Evaluation of tall fescue genotypes for drought stress

Francis Kirigwi, Konstantin Chekhovskiy, Jennifer Black, Andrew Hopkins and Malay C. Saha
The Samuel Roberts Noble Foundation, Forage Improvement Division, 2510 Sam Noble Parkway, Ardmore, Oklahoma 73401 USA

THE SAMUEL ROBERTS NOBLE FOUNDATION

ABSTRACT

Tall fescue (*Festuca arundinacea* Schreb.) is a cool-season perennial forage grass. Persistence, yield and quality are severely affected by drought stress during the hot, dry summers in the southern Great Plains. The objective of this study was to evaluate and identify genotypes with contrasting drought tolerance for genomic studies and develop mapping populations. Initially, 1000 genotypes of a tall fescue population were evaluated for relative water content (RWC), osmotic potential (OP) and chlorophyll content. The genotypes differed for RWC (33.7-97.3%, mean 79.7%) and had an almost fivefold difference for OP (-0.5 to -2.4 MPa, mean -1.2 MPa). Fifty genotypes with contrasting levels of performance for RWC, OP and chlorophyll content were identified. Selected genotypes were re-evaluated in the greenhouse and in field experiments. No significant correlation was found between RWC and OP in the greenhouse experiment, but a significant negative correlation (r=-0.36 *P*= 0.0154) was found under field conditions. Genotypes with consistently high (TD400, TD348) and low (TD279, TD947) drought tolerance based on RWC and OP under both field and greenhouse conditions were identified and used for the construction of mapping populations. Here we present preliminary phenotyping data of the mapping population (TD400 × TD279) planted in the field and greenhouse.

INTRODUCTION

Tall fescue is an important cool-season perennial hay and pasture grass grown on over 14 million hectares in the United States. Tall fescue is adapted to the transitional zone, the zone of successful cultivation of cool- and warm-season grasses. Summers in the Midwest are characterized by increasing temperatures and diminishing water resources in the root zone, and severe drought conditions prevail at least part of every year.

Heat and drought during summer lead to poor persistence of tall fescue in field plantings. Cultivars do not generally persist for more than two to four years in the southcentral U.S. due to drought stress. Persistence may be attributable to one or more physiological traits, including drought tolerance. The development and release of drought-tolerant cultivars would benefit livestock farmers in these regions.

The Forage Improvement Division of the Noble Foundation has initiated projects to address the constraints of tall fescue production in the southcentral U.S. The specific objectives of the projects are:

- To identify contrasting tall fescue genotypes to drought stress;
- To develop mapping populations and carry out multi-location testing and genotyping; and
- Quantitative trait loci (QTL) analysis and identification of markers for marker-assisted selection (MAS).

Here we present some preliminary data from this project.

MATERIALS AND METHODS

Plant material

Tall fescue genotypes used in this experiment descend from a population collected from pastures in southern Oklahoma originally planted in the 1970s with seed of an unknown source, possibly KY31.

Initially, 1000 genotypes were evaluated for drought tolerance in two replicates in 4.5-inch pots. The plants were randomly placed on greenhouse benches and watered to field capacity. Stress was imposed after one month and was achieved by withholding water until the values of relative water content in the leaves reached around 60%. Generally this occurred after seven days. The plants were then re-watered and the stress treatment repeated. RWC, OP and chlorophyll content were determined.

Twenty-five genotypes from each end of performance for RWC, OP and chlorophyll content were identified and used to conduct a replicated trial in the greenhouse (as above) and in the field (Iowa Park, Texas).

Ten genotypes were eventually selected for a root study.

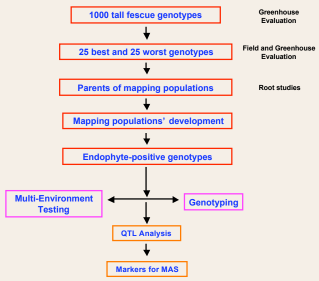

Fig. 1. Tall fescue drought-tolerance mapping project outline

Measurements

RWC was determined using leaf samples cut from the three leaves collected per genotype and fresh weight (FW) determined. Samples were then immersed in distilled water for four hours under darkness and turgid weight (TW) determined. The samples were dried and dry weight (DW) determined. RWC was calculated as: (FW-DW)/(TW-DW).

Samples for determination of OP were hydrated using distilled water under dark for four hours and then frozen at -80°F overnight. Samples were then thawed, and the cell sap was obtained using a syringe. The OP of the cell sap from each sample was determined using Westcor's vapor pressure osmometer (Westcor, Logan, Utah). The Osmolality units (mmol kg⁻¹) were converted to MPa using the Van't Hoff relation.

RESULTS

Evaluation of 1000 genotypes

Chlorophyll content: Range- 62.8 – 25.8 Mean- 41.0

RWC : Range- 33.7 – 97.3 Mean- 79.7

OP : Range- -2.4 - -0.5 Mean- -1.2

•Selected 25 best and 25 worst genotypes

Evaluation of 50 genotypes under field and greenhouse conditions

Table 1. Phenotypic correlations between traits tested under greenhouse conditions and RWC and OP data from the field

Trait	RWC (Field)	OP (Field)
Relative water content (GH)	0.16	-0.28
Osmotic potential (GH)	-0.20	0.33*
CMS	-0.10	-0.19
Shoot dry weight (control)	-0.17	-0.12
Shoot dry weight (drought)	-0.14	-0.14
Relative water content (field)	1.0	-0.36**
Osmotic potential (field)		1.0

** Significant at P<0.01

- RWC and OP under field conditions were negatively correlated.
- The most contrasting genotypes were selected as parents of the mapping populations.

Parents of the mapping populations

- Genotypes identified as drought tolerant had higher RWC and low OP.
- TD348 and TD400 were selected for drought tolerance.
- TD947 and TD279 were selected for drought susceptibility.
- Mapping populations constructed were NFTD06 (TD400 × TD279) and NFTD07 (TD348 × TD947).

Mapping population construction

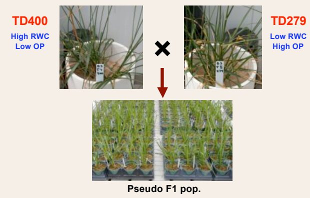

Fig. 2. Construction of the NFTD06 mapping population

Were root characteristics related to drought tolerance?

Fig. 3a. Root study with selected genotypes

Table 2. Analysis of variance for root characters and shoot weight for 10 genotypes grown in the greenhouse under water stress

Genotype	Root length (cm)	Root (R) wt. (g)	Shoot (S) wt. (g)	R/S ratio
TD039	71.2ab	5.7ab	15.7bcd	0.36ab
TD348	69.7ab	7.3a	16.0bcd	0.46a
TD794	70.7ab	6.0ab	16.7bcd	0.36ab
TD257	71.5ab	5.4b	19.0a	0.29b
TD400	72.5ab	4.7bc	14.8d	0.32b
TD592	71.5ab	3.4c	11.6e	0.29b
TD366	71.1ab	5.3b	15.7cd	0.34b
TD947	76.0a	6.3ab	18.0ab	0.35b
TD616	73.8ab	5.8ab	17.0abc	0.34b
TD279	68.1b	4.8bc	15.1cd	0.32b

Figs. 3b and 3C. Root study with selected genotypes

- Genotypes identified as drought tolerant had higher root/shoot ratios and retained a dense healthy mass of small roots.

Evaluation of the mapping population

Greenhouse

- NFTD06 was planted in three replicates in 4.5 inch diameter pots.
- Shoots were harvested after two months' growth to estimate biomass production. A second harvest was done after a month of re-growth.

Field

- Population NFTD06 was planted in a well-watered block and a drought-stressed block at Research Park in Ardmore, Oklahoma, and at Logan, Utah.
- Shoot growth from the well-watered block was harvested to estimate biomass production.
- Population NFTD07 will be planted at two sites in the fall of 2007.

Fig. 4. Planting of NFTD06 mapping population in, Ardmore, OK.

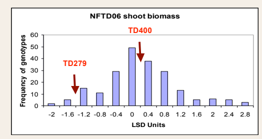

Fig. 5. Greenhouse biomass data for two harvests for NFTD06

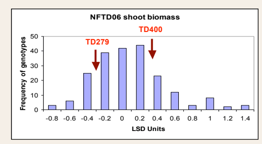

Fig. 6. Field shoot biomass data for one harvest for NFTD06

The susceptible parent, TD279, consistently produced less shoot biomass compared to the tolerant parent even without drought stress.

DISCUSSION

- Field data indicated that drought-tolerant genotypes with high RWC had low OP (Table 1).
- The presence of a healthy mass of fine roots was more important than length of roots.
- Genotypes identified as drought tolerant had higher root/ shoot ratios.
- Shoot biomass data indicates transgressive segregation both under greenhouse and field conditions (Figs. 5 and 6).
- There were sufficient amounts of moisture during the summer of 2007 at the experimental site in Ardmore, and no RWC or OP data were collected. These traits will be evaluated after one year of growth during the summer of 2008 for NFTD06 in Ardmore, Okla., and for RWC and shoot biomass at Logan, Utah.

FUTURE WORK

- Planting of NFTD07 in several environments. This mapping population is undergoing clonal multiplication.
- Biomass, RWC and OP data will be collected from both mapping populations.
- Genotyping both populations and initiating QTL analysis

REFERENCE

Barrs HD, Weatherly PE (1962). A re-examination of the relative turgidity technique for estimating water deficit in leaves. Aust J Biol Sci 15:413-428.

ACKNOWLEDGMENT

We would like to thank Mike Trammell and Kenny Word for help with field work, and Judy Grider and Greg Spencer for help with greenhouse work.