

DROUGHT TOLERANCE ASSESSMENT OF TEMPERATE MAIZE INBRED LINES BY VARIABILITY ESTIMATES OF ROOT AND SHOOT TRAITS

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INTRODUCTION

Maize is a versatile crop grown over a range of agro climatic zones. In fact the suitability of maize to diverse environments is unmatched by any other crop. Maize requires 500-800 mm of water during the life cycle of 80 to 110 days. Unfortunately, maize is prone to many kinds of biotic and abiotic stresses. One of the major concerns among abiotic stress includes drought. Drought stress or water deficit is an inevitable and recurring feature of global agriculture. As the water becomes limiting, identification of techniques for selection of drought tolerant lines becomes necessary. Much evidence suggests that variation exists in water availability in field (Kitchen *et al.*, 1999) implying need to develop reasonable drought tolerant inbred lines which ultimately pave way for hybrid development.

Effective approaches to combat current impacts of drought are of utmost importance, more so as the situation is set to become even worse as climate change progresses (Thornton *et al.*, 2009). Nevertheless, a breeding program focused on identifying traits linked to drought tolerance will help in increasing productivity under water-limiting condition. A promising strategy to encounter drought stress relies on deep roots which suck water from deep layers of soil when water becomes limiting in upper layers which eventually help in increasing yield (Parthasarathi *et al.*, 2014). Such a program requires a good definition of major drought scenarios in the target environment and needs to be conducted under repeatable experimental conditions reflecting those scenarios.

Roots are generally considered to have much role in absorption of water and nutrients with anchorage. Very few attempts have been laid in dissecting drought under phenotypic traits like root traits like root depth, root volume etc. especially in maize. Even though, numerous studies have been conducted to understand the molecular mechanism and the genes responsible for these traits (Reddy *et al.* 2013). This paper aims to highlight the need for selecting drought tolerant inbred lines using root traits as a phenotypic marker.

MATERIALS AND METHODS

The material used for the present study consisted of 28 inbred lines (Table 1) and two checks (GM-6 and CML-442) maintained at Dryland (Karewa) Agriculture Research Station, Budgam (SKUAST-K) were used for phenotyping roots and shoots during Rabi 2015-16 at Crop Physiology Field, UAS, GKVK, Bangalore. In the first of its kind maize inbred lines primarily consisting of temperate germplasm was used to screen for drought adaptive traits encompassing various root traits.

Plants were raised in specially constructed root structures that measured 150 cm

ABSTRACT

28 inbred lines and two checks (GM-6 and CML-442) maintained at Dryland (Karewa) Agriculture Research Station, Budgam (SKUAST-K) were used in the present study. Plants were raised in specially constructed root structures in a randomized block design (RBD) with three replications. Plant population was maintained with 60 x 20 cm spacing, Root structure was dismantled by removing each brick units at 40 days after sowing. Significant genetic variability in drought tolerance traits was revealed among the maize germplasm lines. Shoot length varied between 38.33cm (CML-442) to 82.0cm (KDM-442) and total biomass ranged from 3.87 (CML-442) to 20.03 (KDM-440A) g/plant. The promising lines identified like KDM-932A (82.00 cm) for root length, KDM-1095 for root volume (51.67ml), KDM-918A for root weight (5.31g/plant), can be used as trait donor lines to transfer specific traits into a recipient genotype for drought tolerance in maize. Thus, this study provides impetus on trait assisted breeding instead of empirical breeding.

KEY WORDS

Inbred lines
Drought tolerance
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tall, 300 cm wide and 1800 cm long An additional 150 cm tall wall was built in the middle of the structure all along the length to make two halves each 150 cm wide. Top soil dug out from another field was transported to fill these structures. (Sheshshayee *et al.* 2011, Rajuet *et al.* 2014). Soil was compacted to mimic the real field conditions.

Seedlings were transplanted in a randomized block design (RBD) with three replications. Plant population was maintained with 60 x 20 cm spacing, which ensured that plants experienced the inter-plant competition as in field conditions thus leading to more realistic phenotypic expression. The soils in the GKVK campus had been previously estimated to hold 23 percent water (W/W) at 100 percent field capacity. On an average, surface irrigation was provided once every 5 –7 days to bring the soil to 100 percent FC. On the 40th day after sowing (DAS), the side walls of root structures were dismantled and roots were extracted carefully with a jet of water to wash away the soil from roots. Roots were separated from the shoot and several parameters including root length, root volume were recorded before transferring the plant parts to a drying hot air oven. The samples were oven-dried at 70°C and their weights recorded after the dry weights reached constant values.

Parameters recorded

Shoot length (cm): The shoots were separated from the plants and the shoot length was recorded using a graduated scale.

Root length (cm): The roots were separated from the plants and the root length was recorded using a graduated scale.

Root volume (cm³): A known volume of water was taken in a measuring cylinder, and the separated roots were immersed into this beaker and then the volume of displaced water was taken as the root volume.

Shoot weight (g): All shoots were collected separately and oven dried at 70°C for 48 h to determine the dry weight for other biometric analysis.

Root weight (g): Roots were washed from the structure, then oven-dried at 80°C for 48 h and dry weights were recorded.

Total biomass (g): The biomass accumulated during the experimental period was computed by summing up leaf, stem and root dry weights.

Root: Shoot ratio: It was computed by dividing the root biomass by the shoot biomass

RESULTS AND DISCUSSION

Ability to extract water from deeper soil profiles is an extremely important determinant of crop growth under water-limited conditions. The presence of genetic variability among the accessions under study holds the key for maize crop improvement under stress conditions. The maize germplasm accessions were screened for various root and shoot traits in specially built root structures.

Significant genetic variability (Plate 1) was observed for various root and shoot traits like shoot length, shoot weight, root length, root volume, root weight, ratio of root to shoot and total biomass. Shoot length varied from 38.33cm (CML-442) to 82.0cm (KDM-442) with a mean of 64.09 cm. Root length varied from 23.0cm (KDM-895A) to 61.67cm (KDM-932A)

with a mean of 36.93 cm. Root length showed a continuous variability and a positively skewed mesokurtic distribution towards the lower values. Root volume varied between a minimum of 11.67mL (CML-442 and KDM-913A) to a maximum of 51.67mL (KDM-1095) with a mean of 30.56mL. Continuous variability was observed for root volume among maize germplasm accessions. Root weight, one of the important root traits that determine root system architecture varied from 1.17 (KDM-332A) to 5.31gplant⁻¹(KDM-918A) with a mean of 2.42g plant⁻¹. Root weight showed positively skewed mesokurtic distribution towards lower values. Shoot weight varied from 4.17 (KDM-332A) to 15.57gplant⁻¹(KDM-440A) with a mean of 10.25 gplant⁻¹.

Total biomass ranged from 3.87 (CML-442) to 20.03 (KDM-440A) g/plant with a mean of 12.33 gplant⁻¹, Root: Shoot ratio ranged from 0.12(KDM-892A) to 0.65 (KDM-930A) with a mean of 0.24 (Table 1.)

One of the limiting factors for crop production is drought. During drought conditions plants manifest some of unique traits classified under adaptive traits like deep roots or more root biomass etc. for maximum utilization of receding water. This complexity of drought can be reduced by employing analytical breeding approaches to specifically target traits having major roles in drought tolerance like roots traits (Gowda *et al.*, 2011; Jung and McCouch. 2013; Uga *et al.*, 2013) or water use efficiency (Sheshshayee *et al.*, 2013) which have a direct effect on yield (Suma *et al.*, 2014). These adaptive traits can maintain higher leaf water potential and relative water content under water limited condition and hence can tolerate

Table 1: List of Inbreds and Checks used in the study

S.No	Accessions
1.	KDM 927A
2.	KDM 930A
3.	KDM 332A
4.	KDM 921A
5.	KDM 408
6.	KDM 1156
7.	KDM 941A
8.	KDM 932A
9.	NGB17094-1
10.	KDM 892A
11.	KDM 362A
12.	NGB 17099-1
13.	KDM 895A
14.	KDM 1095
15.	KDM 343A
16.	KDM 329
17.	KDM 945
18.	KDM 963A
19.	KDM 925B
20.	KDM 440A
21.	KDM 926B
22.	NGB 17097-1
23.	KDM 954
24.	KDM 913A
25.	KDM 443
26.	KDM 918A
27.	KDM 944A
28.	NGB13905
29.	GM-6 (C)
30.	CML-442 (C)

stress better.

On the other hand “Constitutive traits” are inherent traits expressed all the times irrespective of the stress occurrence. Constitutive traits such as root traits (not deep roots), water use efficiency, water conservation, cellular level tolerance, flowering time and stay green traits can be routinely screened without a drought challenge. These traits have implications for drought protection and survival (Kamoshita et al., 2008). These constitutive traits besides improving drought tolerance, significantly contribute to growth rates under any given condition. Therefore exploiting such traits has great relevance in improving productivity under water-limited conditions (Sheshshayee et al., 2011). To increase growth rates under drought conditions, abilities to mine water associated with roots and WUE becomes crucial.

Taking into account the potential of improving drought tolerance in crops using root traits special root structure was constructed. Unlike, other approaches our approach mimics the real field condition and provides a vivid picture of the other half of plant. In spite of significant development of root phenomics (Gowda et al. 2011; Courtois et al. 2013), our approach seems more amenable, cheap and depicts the real field conditions which does not need sophisticated techniques. This alone could be major improvisation than any other techniques reported so far. Hence, this approach will help in capturing variability, which is a key step in breeding process.

However, all these traits are quantitatively inherited polygenic traits and their introgression can be effectively achieved only through a focused molecular breeding approach. Conventionally DNA-based molecular markers flanking QTL are discovered using a bi-parental mapping population segregating for a specific trait. Since diverse trait are needed for improving drought tolerance, the bi-parental linkage mapping strategy becomes very cumbersome and laborious. Thus, attempts to increase root traits and WUE has great relevance.

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