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Genetic variability of maize stover quality and the potential for genetic improvement of fodder value

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ABSTRACT

Maize stover left after grain harvest constitutes an important source for livestock feed in most parts of East Africa, particularly during the dry season. In spite of its wide use and greater importance, breeding programs have given little attention to the improvement of stover quality and quantity. The objectives of this study were to assess the genetic variability of experimental and released (checks) maize varieties for stover feed quantity and quality, and their relationship with grain yield. Results from different trials conducted across locations using randomized complete block design (RCBD) in different sites in Ethiopia and Tanzania from 2004 to 2006 showed higher genotypic variation for grain and stover yields and stover feed quality traits. This confirmed the existence of exploitable genetic variation not only for grain yield but also for stover fodder quality and quantity. Positive relationship was also observed between grain and stover yields but the relation between stover fodder quality traits and grain yield, in most cases, was weak. Generally, the study pinpointed the possibility for simultaneous improvement of grain yield and stover traits to address the high demand existing for dual purpose food-feed type of maize genotypes in maize-livestock mixed farming system of East Africa.

1. Introduction

In East Africa, maize is planted on more than 15 million hectares (ha) where it is the staple food of millions of poor families, and its importance is growing with time (Byerlee and Eicher, 1997; CIMMYT, 1999; Thorne et al., 2002). The dominant farming mode in the region is a small scale crop-livestock mixed system, which involves the simultaneous production of food crops and livestock on the same unit. The by-product from one enterprise usually supplements the production of the other (Adugna et al., 1998; Kang'ara et al., 2003). Despite diversified uses and the large number of livestock in this particular production system, livestock production faces several constraints, with provision of quantity and quality of feed being the major ones. In major maize producing areas, the maize stover left after grain harvest constitutes the main diet for livestock particularly in the dry season (Diriba et al., 2002). However, maize breeding programs in the region are mainly designed to improve the grain yield and quality for direct human consumption with little attention to the improvement of stover quality for feed. With the current population increase and subsequent shrinkage of agricultural land, farmers can hardly allocate separate land for food grain production and grazing. In much of the region, communal grazing lands have already being converted to crop production. Such scenarios will further exacerbate the shortage of feed. On the other hand, a crop residue, maize stover, which is poor in nutritional quality, is abundant after grain harvest. In the future, stover yield and quality traits should be considered in the development and release of maize varieties in order to sustain the maize-livestock mixed farming system in which the two entities of the system are mutually benefited.

Genetic variation for most traits in maize is incredibly high and amenable to enhancements (Vasal, 2000). Information on the nature and magnitude of genetic variability present in a crop species is important for developing effective crop improvement program and for the improvement of any trait of interest (Dabholkar, 1999). For stover yield and quality, some preliminary studies involving released varieties have indicated the existence of exploitable genetic variability among genotypes (Adugna et al., 1998, 1999; Diriba et al., 2002). However, since the studies were conducted in a single location and/or season, it should be supported by studies conducted across different locations in the region to

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Table 1
Combined mean, probability and range for maize grain and stover yields in trials conducted at different sites and years.

Trial code	No. of entries	No. of reps	Testing sites	Year	Grain yield (t/ha)			Stover yield (t/ha)		
					Mean	Probability	Range	Mean	Probability	Range
AMB04H13-1	24	2	Ambo, Holeta and Kulumsa	2004/05	6.4	<0.0001	3.7–8.9	5.3	<0.0001	3.3–6.7
AMB04H14-1	21	2	Ambo, Holeta and Kulumsa	2004/05	5.6	<0.0001	3.5–7.2	4.5	<0.0001	1.7–6.8
AMB04TW112	24	2	Holeta and Kulumsa	2004/05	5.5	0.001	4.4–7.2	5.0	<0.0001	3.4–6.2
AMB04TW812	24	2	Holeta and Kulumsa	2004/05	6.2	<0.0001	4.5–7.5	4.4	<0.0001	3.0–6.4
HRVT043-1	28	2	Ambo, Holeta and Kulumsa	2004/05	6.3	<0.0001	4.0–8.2	5.3	0.0070	4.1–6.1
HRVTO41-1	33	2	Ambo, Holeta and Kulumsa	2004/05	5.4	0.002	4.0–6.5	4.6	<0.0001	3.4–5.6
HRVT044-2	36	2	Ambo, Holeta and Kulumsa	2004/05	6.2	<0.0001	4.9–8.1	5.9	<0.0001	3.4–7.2
Ambo5DTC2	26	2	Ambo and Holeta	2005/06	5.7	<0.0001	4.7–7.3	5.5	<0.0001	4.4–8.5
Ambo5H91	26	2	Ambo and Holeta	2005/06	5.9	0.017	4.9–7.2	5.9	<0.0001	4.7–7.4
AmboNVT1	15	3	Ambo and Holeta	2005/06	7.5	0.003	6.6–8.9	7.4	<0.0001	6.2–9.3
Ambo5H101	30	2	Ambo	2005/06	6.0	0.001	4.6–8.6	6.1	<0.0001	4.4–9.8
Ambo5H53	36	2	Ambo	2005/06	7.2	0.61	5.1–10.2	8.4	0.1000	5.5–15.5
Ambo6NVT1	12	3	Ambo, Arusha, Bako and Holeta	2006/07	7.4	<0.0001	6.6–8.6	9.7	<0.0001	8.4–11.1

$P < 0.01$ indicates highly significant genotype mean square. $P < 0.05$ indicates significant genotype mean square.

draw concrete conclusion on the genetic variability and relationship among food and feed traits. Therefore, the objectives of this study were (1) to determine genetic variability existing in maize germplasm for both food and feed traits and (2) to determine the relationship between food and feed traits in maize for simultaneous improvement.

2. Material and methods

For this study, 13 trials consisting of 335 experimental highland maize hybrids, including standard checks, from the East and Central Africa Highland Regional Maize Improvement Program coordinated by CIMMYT and the Ethiopian Institute of Agricultural Research (EIAR) were used. The crosses were generated using S_3–S_5 inbred lines. All inbred lines were derived from mid-altitude and highland transitional maize lines obtained from CIMMYT-Zimbabwe and Mexico (Twumasi-Afriyie et al., 2002). Genotypes in HRVT041-1 were top crosses formed between inbred lines and three known highland population testers; Kitale Syn II, Ecuador 573 and Kuleni (Pool 9A) (Twumasi-Afriyie et al., 2002). In AMB05DTC2, double top crosses formed between single crosses and four synthetic varieties as male parent were evaluated. Genotypes in AMB04TW112, AMB04TW812, AMB0NVT1 and AMB06NVT1 were three way crosses. Crosses in all the remaining trials were single crosses which were randomly formed using inbred lines from different heterotic groups. Heterotic classification was the basis for forming the random crosses evaluated under the different trial sets. In all the trials a unique set of materials were evaluated except that inbred lines used as male/female parent in one trial could be used as parent in another trial but with different cross combination. Selected genotypes from across location evaluation are promoted to advanced trail evaluation stage, i.e., national variety trail (NVT) to see their performance in more location and over years.

The trials were planted during the main rainy season from 2004 to 2006 at 1–3 sites in Ethiopia and Tanzania (Arusha) (Table 1). All trials were replicated 2–3 times. For all trails, one row plot was used except for AMB0NVT1 and AMB06NVT1 which were planted on two row plots. The row length was 5.1 m with 0.25 m and 0.75 m intra and inter row spacing, respectively. The randomized complete block design (RCBD) was used for laying out the trials in the field and for data analysis. All Trials were hand planted and received optimal level of crop management practices recommended for each location. Trials at Ambo, Holeta and Kulumsa were supplied with 69 kg P_2O_5 ha^{-1} and 92 kg N ha^{-1} while at Bako 100 kg ha^{-1} of both nutrients were applied. At Arusha, the rate of fertilizer used was 80 kg N ha^{-1} and 60 kg P_2O_5 ha^{-1} at all sites, the whole dose of recommended phosphorous was applied during planting as basal application while urea was applied as split application. At Ambo nitrogen was split three times; 1/3rd at planting, 1/3rd at knee high stage and the remaining 1/3rd at flowering. In all other locations, it was split twice, half at planning and the other half at knee high stage.

Data were collected on grain yield, stover yield, crude protein (CP), true in vitro organic matter digestibility (TIVOMD) and acid detergent fiber (ADF). Adjusted grain yield was calculated from the total field weight of all ears in a plot adjusting to 12.5% moisture (measured by Dickey-John multi grain moisture tester) level and 80% shelling percentage. The adjusted yield was latter divided to plot area and multiplied by 10 to estimate grain yield per ha in tons. Stover yield, which includes leaves, stems and husk, was determined from fresh weights adjusted to a dry matter basis based upon oven dried sample weights. The samples were oven dried for 24 h at 100 °C. For laboratory analysis of stover fodder quality parameters, five plants were randomly samples from each plot of all trials after grain harvest, chopped manually and sun-dried in muslin bags. After sun-drying the samples were ground to pass through 1 mm particle mesh and shipped to the ILRI laboratory in Patancheru, India. These stover samples were analyzed by Near Infrared Spectroscopy (NIRS) as described by Ramana Reddy et al. (2013). Validation procedures were blind-predictions of laboratory measurements by the NIRS equations developed in the calibration procedures. Relationships between blind-predicted and measured variables were described by R^2 and standard error of prediction (SEP). Laboratory traits analyzed were nitrogen (N) by Technicon Auto Analyzer, neutral (NDF) and acid detergent fiber (ADF) according to Van Soest et al. (1991). In vitro organic matter digestibility (IVOMD) content was analyzed according to Menke and Steingass (1988) in the modification of Blümmel and Ørskov (1993).

Analysis of variance (ANOVA) was done using General Linear Model (GLM) procedure in SAS 9.2. The general model used for data analysis was

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{jk} + e_{ijk},$$

where μ is mean, G_i is the effect of ith genotype, E_j is the effect of jth environment, GE_{ij} is the interaction of ith genotype with jth environment, B_{jk} is the effect of kth replication in the jth environment and e_{ijk} is the random error.

GraphPad Prism (1994) was used for graphs and simple correlation analysis.