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Estimates of Variability, Heritability and Genetic Advance for Fodder Traits in Two Maize Populations

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Abstract: Broad sense heritability estimates, genetic advance and Relative Expected Genetic Advance (REGA) were computed for different fodder yield related traits in two maize populations during Kharif 2002 and 2003. Two maize populations, DRS; developed through recurrent selection and DMS developed through mass selection, were grown in modified RCBD with two replications. Mean squares from the analysis of variance among S_1 families for both maize populations indicated highly significant ($p \leq 0.01$) differences for all the studied traits. Estimates of genetic variances were significant for all traits except stem girth in both populations. Genetic variances in comparison to respective environmental variances were greater for majority of the traits in both populations. Heritability estimates were high and significant for all the traits in both populations. Comparison of two populations revealed that heritability estimates were higher for internode length and fresh fodder yield in the DRS population and for plant height, stem girth, flag leaf area and dry matter content in the DMS population. Genetic advance was higher for internode length, flag leaf area, fresh fodder yield in the DRS population and for plant height, stem girth and dry matter content in DMS population. REGA% was higher for internode length and fresh fodder yield in DRS population while DMS population attained higher values for plant height, stem girth, flag leaf area and dry matter content. The higher heritability estimates, genetic advance and REGA for fresh fodder yield in DRS population indicates that recurrent selection method was comparatively more effective in improving maize population for fodder yield parameters.

Key words: Variability, heritability, genetic advance, relative expected genetic advance, maize, fodder

INTRODUCTION

Maize (*Zea mays* L.) is an important Kharif fodder crop of NWFP and Northern Areas of Pakistan. It provides the cheapest and most valuable fodder for animals. Maize green fodder contains 1.56% protein, 0.30% fats and 5.20% fiber (Nazir *et al.*, 2003). The production of maize fodder crop ha^{-1} is low in Pakistan as compared to many other countries of the world. This is because very little attention has been paid in the past to the improvement of maize as fodder crop. In order to provide an adequate and regular supply of nutritious fodder especially during summer season, exhaustive efforts are needed to develop maize varieties both for grain and fodder purposes and suitable for wide range of environmental conditions.

For conducting any breeding program successfully, some basic information such as the magnitude and pattern of genetic variation, its components and heritability are helpful for the breeders to select a suitable breeding procedure. Estimates of genetic parameters obtained from

well designed experiments provide the breeder with the information necessary to determine the best breeding procedures for a particular species. The progress in any breeding program depends primarily upon genetic diversity and the effectiveness of selection procedure involved (Asghar and Mehdi, 1999).

The basic idea in the study of variation is its partitioning into components attributable to different causes. The relative magnitude of these components determines the genetic properties of the breeding populations, in particular the degree of resemblance between relatives. The measurements and evaluation of variability in breeding populations is desirable to draw meaningful conclusion from given observations. Genetic variability could be explored by detecting environmental variations (Asghar and Khan, 2005).

The ratio of genotypic and phenotypic variance (V_G/V_P) expresses the extent to which individual's phenotypes are determined by their genotypes. Reliable estimates of the additive component of variation estimate the heritability or the breeding value of a certain character.

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However, many genes or quantitative traits display a different expression in different genetic backgrounds (Kearsey and Pooni, 1966). In addition to genetic variance, environmental variance cannot be ignored because it includes by definition all non genetic variance and much of this is beyond experimental control. Hence selection in the S_1 families is more effective for characters, having high heritability. Heritability estimates help to predict the progress from selection for any breeding system. Since expected genetic advance is function of heritability, therefore, such guided selection produces genetic advance. These changes are of great interest to plant breeder, since it changes the population mean.

Keeping in view the importance of maize as a fodder crop, the present study was conducted to compute genetic parameters including genetic variances, estimates of heritability and genetic advance in two maize populations for different fodder characteristics.

MATERIALS AND METHODS

Two maize populations viz, DRS; developed through recurrent selection while DMS; developed by successive use of mass selection from the same broad base populations, were compared for various fodder yield related traits.

One hundred and twenty five S_1 families from each population were evaluated during Kharif crop season of 2002 and 2003. Families from each population were assigned to five blocks, each containing 25 S_1 progenies in a modified randomized complete block design (replicates in block design) with two replications. Each family was planted in single row plots of 2.5 m length with row to row and plant to plant distances of 0.30 and 0.12 m, respectively. Normal cultural practices were applied to the crop throughout the experimental period. Ten randomly selected plants plot^{-1} were tagged from each plot of every replication for recording the observations. Data were recorded on important fodder yield related parameters viz., plant height, internode length, stem girth, flag leaf area and dry matter content whereas, fresh fodder yield was measured on whole plot basis. Plant height was measured as the distance from the ground to the base of the tassel main axis. Internode length was measured 30 cm above the soil surface. Stem girth was measured using vernier caliper. Flag leaf area was measured by calculating the entire length of the flag leaf and width at the maximum width point and was adjusted by a factor according to Montgomery (1962). For dry matter content a sample of 1,000 g of green fodder from each treatment was taken and sun dried for approximately 15 days to ensure constant moisture

content and then re-weighed using electronic balance. Fresh fodder yield was measured by weighing the fresh green plants on the plot basis and then converted to ha^{-1} yield.

Genetic and environmental variances were computed from the expected mean squares in each year as well as across two years for both populations to estimate broad sense heritabilities on entry mean basis (Fehr, 1987). The Standard Error (SE) for the genetic variance and heritability were computed following Lothrop *et al.* (1985). Heritability estimates were grouped as high (>50%), moderate (20-50%) and low (<20%) as proposed by Stansfield (1986). Response to selection or expected genetic advance after one generation of selection was calculated at 10% selection intensity using the following formula:

$$GA = i\,\sigma\hat{}p\,h^2$$

Where,
GA = The expected genetic advance
i = selection intensity
$\sigma\hat{}p$ = the phenotypic standard deviation
h^2 = broad sense heritability

Relative Expected Genetic Advance (REGA) was calculated with the following formula:

$$REGA = \frac{GA}{\overline{x}} \times 100$$

Where,
GA = Expected genetic advance and
$\overline{x}$ = Grand mean for a given trait

RESULTS AND DISCUSSION

Genetic and environmental variances: Genetic and environmental variances for various characters under study from S_1 families of DRS and DMS populations during 2002, 2003 and across two years are presented in Table 1 and 2. The estimates of genetic variances were significant for all traits except stem girth in both populations. During crop season 2002, genotypic and environmental variances were 206.18 and 27.95 for plant height, 1.77 and 0.29 for internode length, 0.01 and 0.01 for stem girth, 260.39 and 155.63, for flag leaf area, 1111.81 and 168.51 for dry matter content and 300062.40 and 88840.80 for fresh fodder yield respectively, in DRS (Table 1) whereas variances were 349.02 and 24.85 for plant height, 1.62 and 0.57 for internode length, 0.02 and 0.01 for stem girth, 142.40 and 63.76 for flag leaf area, 1382.80 and 186.93

Table 1: Estimates of genetic and environmental variances for fodder traits, among DRS and DMS populations during 2002 and 2003

	DRS			DMS		
Plant trait	σ^2_g	±SE	σ^2_e	σ^2_g	±SE	σ^2_e
Year 2002						
Plant height	206.18	1.39	27.95	349.02	1.75	24.85
Internode length	1.77	0.13	0.29	1.62	0.13	0.57
Stem girth	0.01	0.01	0.01	0.02	0.01	0.01
Flag leaf area	260.39	1.85	155.63	142.40	1.30	63.76
Dry matter content	1111.81	3.24	168.51	1382.80	3.59	186.93
Fresh fodder yield	300062.40	56.46	88840.80	503452.80	69.56	86889.60
Year 2003						
Plant height	196.99	1.54	91.47	221.09	1.41	21.67
Internode length	0.99	0.11	0.49	0.44	0.10	0.89
Stem girth	0.01	0.01	0.00	0.01	0.01	0.00
Flag leaf area	273.51	1.94	185.58	136.33	1.36	91.43
Dry matter content	431.29	2.41	277.24	307.47	1.85	109.89
Fresh fodder yield	1031552.00	97.48	127667.20	591129.60	74.38	68241.60

Table 2: Estimates of genetic, genetic × year and environmental variances for fodder traits of DRS and DMS populations across the two years

	DRS				DMS			
Plant trait	Gen Var	±SE	Gen × Yr_Var	Envir_Var	Gen Var	±SE	Gen × Yr_Var	Envir_Var
Plant height	92.45	1.77	133.06	128.40	106.33	1.85	182.10	46.20
Internode length	1.64	0.13	1.08	1.03	1.16	0.13	0.97	1.55
Stem girth	0.01	0.01	0.015	0.01	0.02	0.01	0.01	0.01
Flag leaf area	261.69	1.88	281.04	337.03	170.00	1.43	103.43	159.57
Dry matter content	877.72	3.04	639.735	500.28	1076.37	3.17	633.42	301.62
Fresh fodder yield	1062219.00	97.80	295887.28	209457.70	751694.23	83.25	330383.02	167599.54

for dry matter content and 503452.80 and 86889.60 for fodder yield respectively, in DMS population. During crop season 2003, the genetic and environmental variances were: 196.99 and 91.47 for plant height, 0.99 and 0.49 for internode length, 0.01 and 0.00 for stem girth, 273.51 and 185.58 for flag leaf area, 431.29 and 277.24 for dry matter content and 1031552.00 and 127667.20 for fodder yield, respectively, in the DRS population while values were 221.09 and 21.67 for plant height 0.44 and 0.89 for internode length, 0.01 and 0.00 for stem girth, 136.33 and 91.43 for flag leaf area, 307.47 and 109.89 for dry matter content and 591129.60 and 68241.60 for fodder yield, for genotypic and environmental variances, respectively in DMS population. Genetic and environmental variances across the two years in DRS population were 92.45 and 128.40 for plant height, 1.64 and 1.03 for internode length, 0.01 and 0.01 for stem girth, 261.69 and 337.03 for flag leaf area, 877.72 and 500.28 for dry matter content and 1062219.00 and 209457.7 for fresh fodder yield, respectively (Table 2). Similarly, the genotypic and environmental variances for the DMS population were 106.33 and 46.20 for plant height, 1.16 and 1.55 for internode length, 0.02 and 0.01 for stem girth, 170.00 and 159.57 for flag leaf area, 1076.37 and 30162 for dry matter content and 751694.23 and 167599.54 for fodder yield, respectively (Table 2).

In the present studies, the estimates of genetic variances were significant for all traits except stem girth in both populations as their absolute magnitude exceeded twice their respective standard errors. In addition, the estimates of genotypic variance were larger than respective environmental variances. The presence of sufficient genetic variation in these populations for the studied traits could be helpful for further improvement of maize populations. Similarly significant estimates of genetic variance were reported by El-Hosary and Abd-El-Sattar (1997) for plant height, ear height and kernel row cob[−1] in maize populations. Our results are in conformity with the findings of Asghar and Mehdi (1999), Walters *et al.* (1991) and Zieger (1987), who reported significant genetic variances for different quality traits in maize. Similarly Malvar *et al.* (1996) also found larger estimates of genetic variance in maize for lodging, ear and kernel traits suggesting good potential for improvement through intra population selection. Similarly, Ahmad and Mehdi (2001) reported significant genetic variation in a popcorn population.

Estimates of heritability: Heritability estimates in DRS population (Table 3) were high (>50%) during 2002for all fodder related traits. On the basis of magnitude of estimates, traits could be ranked as plant height (0.88), dry matter content (0.87), internode length (0.86) and fresh fodder yield (0.77), flag leaf area (0.63) and stem girth (0.53). Similarly, heritability estimates were higher in DMS population for plant height (0.93), dry matter content (0.88) fresh fodder yield (0.85), stem girth (0.81), internode length (0.74) and flag leaf area (0.69). Estimates

Table 3: Broad sense heritability (h²), genetic advance (GA) and relative expected genetic advance (REGA) of fodder traits, in DRS and DMS population during 2002 and 2003

Plant trait	DRS			DMS		
	h²	GA	REGA (%)	h²	GA	REGA (%)
Year 2002						
Plant height	0.88*	23.65	22.46	0.93*	31.68	25.02
Internode length	0.86*	2.16	18.25	0.74*	1.92	14.69
Stem girth	0.53*	0.11	9.63	0.81*	0.21	18.24
Flag leaf area	0.63*	22.40	48.72	0.69*	17.41	42.81
Dry matter content	0.87*	109.06	32.36	0.88*	61.25	30.17
Fresh fodder yield	0.77*	844.44	44.78	0.85*	1149.96	52.93
Year 2003						
Plant height	0.68*	20.36	14.15	0.91*	24.90	17.48
Internode length	0.67*	1.43	11.89	0.33*	0.67	5.50
Stem girth	0.85*	0.19	17.81	0.70*	0.14	12.57
Flag leaf area	0.60*	22.40	38.46	0.60*	15.85	33.68
Dry matter content	0.61*	56.88	15.31	0.74*	26.41	13.92
Fresh fodder yield	0.89*	1681.46	68.63	0.90*	1277.60	59.15
Means over two years (2002-2003)						
Plant height	0.48ns	11.74	9.42	0.51ns	12.91	9.60
Internode length	0.67*	1.84	15.45	0.57*	1.42	11.27
Stem girth	0.55*	0.15	13.34	0.78*	0.21	18.78
Flag leaf area	0.54*	20.82	39.95	0.65*	18.45	42.06
Dry matter	0.66*	84.72	23.91	0.73*	98.60	25.10
Fresh fodder yield	0.84*	1659.09	76.53	0.78*	1347.28	62.19

* = Significant at p = 0.05 probability levels, ns = non significant

of heritability in DRS population during crop season 2003, were high for plant height (0.68), internode length (0.67), stem girth (0.85), flag leaf area (0.60), dry matter content (0.61) and fodder yield (0.89), respectively. In DMS population, heritability estimates for plant height, internode length, stem girth, flag leaf area, dry matter content and fodder yield were 0.91, 0.33, 0.70, 0.60, 0.74 and 0.90, respectively. The pooled broad sense heritability estimates across the two years in the DRS population were 0.48 for plant height, 0.67 for internode length, 0.55 for stem girth, 0.54 for flag leaf area, 0.66 for dry matter and 0.84 for fresh fodder yield (Table 3). In DMS, population the values were 0.51 for plant height, 0.57 for internode length, 0.78 for stem girth, 0.65 for flag leaf area, 0.73 for dry matter content and 0.78 for fresh fodder yield.

These values indicated that broad sense heritability estimates were high for all traits in both populations. Higher heritability estimates suggested the feasibility of early selection for these traits. These heritability estimates could be considerably useful for the expected genetic advance manipulations in S₁ family selection program. Based on the significant broad sense heritability estimates, the selection among S₁ families for the traits under study may result in substantial improvement in these populations through both methods. Higher estimates of broad sense heritability were reported by Aziz *et al.* (1992) for agronomic traits in maize, whereas, moderate estimates were found by Mehdi and Ahsan (2000a, b) for fresh shoot weight, dry root weight, fresh shoot length and fresh root length. Asghar and Khan (2005) observed significant estimates of broad sense

heritability for the seedling parameters. Ahmad and Mehdi (2001) recorded maximum estimates of broad sense heritability for 100 kernel weight, plant height and number of kernel 100⁻¹ g whereas lower estimates were recorded fro number of kernel row cob⁻¹. Similarly, Saleh *et al.* (2002) found plant height, days to tasseling and ear length most heritable in populations of sweet corn.

Since majority of the traits studied in the present experiment possessed high heritability, it is, therefore, expected that improvement in fodder is possible by using these traits as selection criteria. This information would be greatly helpful to breeders in making appropriate selection for the desired genetic improvement in maize populations.

Genetic advance at 10% selection intensity: The estimates of Genetic Advance (GA) in DRS population during 2002 were 23.65 cm for plant height, 0.11 cm for internode length, 2.16 cm for stem girth, 22.40 cm² for flag leaf area, 109.06 g kg⁻¹ dry matter content and 844.44 kg ha⁻¹ for fresh fodder yield. In case of DMS population, the values of GA were 31.68 cm for plant height, 1.92 cm for internode length, 0.21 cm for stem girth, 17.4 cm² for flag leaf area, 61.25 g kg⁻¹ for dry matter content and 1149.96 kg ha⁻¹ for fresh fodder yield (Table 3). The estimates of genetic advance for S₁ families in DRS population during crop season 2003 were 20.36 cm for plant height, 1.43 cm for internode length, 0.19 cm for stem girth, 56.88 g kg⁻¹ for dry matter content, 22.40 cm² for flag leaf area and 1681.46 kg ha⁻¹ for fresh fodder yield. Whereas the GA for the above mentioned fodder parameters in DMS population were 24.90 cm for plant

height, 0.67 cm for internode length, 0.14 cm for stem girth, 15.85 cm² for flag leaf area, 26.41 g for dry matter content and 1277.60 kg ha⁻¹ for fresh fodder yield in 2003 (Table 3). The pooled Genetic Advance (GA) across the two years in DRS population regarding fodder characteristics were 11.74 cm for plant height, 1.84 cm for internode length, 0.15 cm for stem girth, 20.82 cm² for flag leaf area, 84.72 g kg⁻¹ for dry matter content and 1659.09 kg ha⁻¹ for fresh fodder yield (Table 3). GA in DMS population was 12.91 cm for plant height, 1.42 cm for internode length, 0.21 cm for stem girth, 18.15 cm² for flag leaf area, 98.60 g kg⁻¹ for dry matter content and 1347.28 kg ha⁻¹ for fresh fodder yield (Table 3).

Higher GA values observed for fodder yield in DRS population showed the effectiveness of recurrent selection over mass selection for selecting superior genotypes for fresh fodder yield. Present findings are supported by earlier reports of Casanas *et al.* (1998) who reported 5% increased for stalk diameter with an average of 4% generation⁻¹ after applying 5% selection intensity. They further reported overall increases in ear yield (16%), stover yield (31%) and total dry matter yield (24%). Similarly Mehdi and Ahsan (2000b) found greater genetic advance for different seedling traits. El-Hosary and Abd-El-Sattar (1997) reported genetic advances selection⁻¹ cycle of 2.57, 3.01, 7.53, 6.26, 12.04 and 8.79% for mass selection, ear-to-row selection, half-sib family selection, full-sib family selection, progeny test and S₁ family selection, respectively. Similarly, Kumar and Mishra (1995) found high estimates of heritability and genetic advance for grain yield and ear length. Mahdy *et al.* (1987) concluded that S₁ family selection and recurrent reciprocal selection significantly increased grain yield plant⁻¹ and ear length in maize.

Relative Expected Genetic Advance (REGA%): The estimates of Relative Expected Genetic Advance (REGA) of S₁ families in DRS population during 2002 were 22.46% for plant height, 18.25% for internode length, 9.63% for stem girth, 48.72% for fresh flag leaf area, 32.36% for dry matter content and 44.78% for fresh fodder yield (Table 3). In DMS population, these values were 25.02% for plant height, 14.69% for internode length, 18.24% for stem girth, 42.81% for flag leaf area, 30.17% for dry matter content and 52.93% for fresh fodder yield. REGA values of S₁ families in DRS population during 2003 were 14.1% for plant height, 11.89% for internode length, 17.81% for stem girth, 38.46% for flag leaf area, 15.31% for dry matter content and 68.63% for fresh fodder yield (Table 3). For DMS population, REGA values were 17.48% for plant height, 5.50% for internode length, 12.57% for stem girth, 33.68%

for flag leaf area, 13.92% for dry matter content and 59.15% for fresh fodder yield. Pooled relative expected genetic advance (REGA) across two years in DRS population was 9.42% for plant height, 15.45% for internode length, 13.34% for stem girth, 39.95% for flag leaf area, 23.91% for dry matter content and 76.53% for fresh fodder yield. REGA values in DMS population were 9.60% for plant height, 18.78% for stem girth, 11.27% for internode length, 42.06% for flag leaf area, 25.10% for dry matter content and 62.19% for fresh fodder yield when averaged over the two years (Table 3).

REGA values showed that DRS population surpassed DMS for internode length and fresh fodder yield, while DMS surpassed DRS population for rest of the traits. The superiority of DRS over DMS population especially for fresh fodder yield suggested the advantage of recurrent selection over mass selection whereas for other traits mass selection was found effective over recurrent selection. Our results are supported by the earlier findings of Vasal *et al.* (1995) who found a significant positive linear response for days to silk, grain moisture at harvest, plant height and ear length. Ahmad and Mehdi (2001) found quite high estimates of relative expected genetic advance for plant height and number of kernel 10⁻¹ g at 15% selection intensity. However, Backtash (1986) reported an increase of 24.5% in yield for mass selection and 17.5% increase for recurrent selection.

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