

Genetic components for fodder yield and agronomic characters in maize lines

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Abstract. In maize hybrid development, it is essential to know the parent's performance per se in different environments as well as the genetic base in populations in order to facilitate selection of superior lines. The objective of this work was to estimate the genetic variance and heritability while assessing agronomic behavior in 237 maize fodder lines featuring different inbred levels and origin in two different locations. Traits such as plant height, cob height, stem diameter, and fodder yield were taken. A combined variance analysis was carried out using this information. The variable mean squares showing significant differences were used to estimate the genetic variance components. Significant differences were observed ($p \leq 0.01$) for the line variation source and location \times line interaction in all assessed characteristics. The genetic parameter estimation provided information on the existing genetic variance and heritability among the population which is important for the progress of the selection process. Lines CLWN701, CLWN345, CML476, CML216, CLWQ232, and CML 528 measured 74.8, 72.2, 67.7, 65.8, 63.8 and 62.5 t ha⁻¹, respectively showed the highest yield potential for green fodder.

Key words: heritability, additive variance, green fodder, inbred lines, coefficient of variation genetic.

INTRODUCTION

In Mexico, maize is cultivated in diverse environments ranging from sea level to upper valleys (above 2,200 m.a.s.l.) with a wide variety of thermal rainfall systems from very drastic to mild ones. From self-consumption to highly commercial production schemes (Preciado et al., 2005), maize cultivated area in Mexico, accounted for 7.3 million hectares for grains and 602617 hectares for green fodder with an average 36.12 t ha⁻¹ yield (SADER-SIAP, 2018).

Because there are no highly productive maize lines, double or three-way hybrids are used in commercial hybrid production. Besides, high costs of simple hybrid-seed have limited its commercial production (Luna et al., 2012). Parents are of underlying importance in maize hybrid formation in both behavior per se in different environments and their combining ability. Knowledge of combining ability allows for recognition and identification of parents with desirable characteristics for seed production and hybrid formation (Pérez et al., 1992). According to Marquez (1988), in order to obtain high-yielding maize lines, it is necessary to have big-size, variable, and high-yield populations. Hallauer (1970) reported that yield may be increased through selection and enhancement of existing lines.

In genetic enhancement programs, it is desirable to be genetically acquainted with base populations in order to facilitate ideal line selection. In order to select the enhancement scheme, it is necessary to first know the type of heredity or specific gene action for quantitative characters of agronomic concern (Peyman et al., 2009).

The genetic parameters estimate in maize populations provide information on the existing genetic variation among the population and supports progress on the selection process. The heritable genetic variance ratio is therefore broken down into an additive portion associated to the average output of genes effect, a dominance portion resulting from the allelic interaction of a genetic locus and epistasis (Hallauer, 1970). Current variations among the population resulting from genetic additive effects are measured by additive variance (Rovaris et al., 2011).

During genetic enhancement by selection and hybridization, the plant breeder besides knowing the agronomic aspects of the species in question, must also know the genetic characteristics of the populations to be enhanced (Moreno et al., 2002). According to Marquez (1985), the additive effects are used in the selection process both intra locus and inter loci for population improvement. In addition, it was further stated that the general procedure consists of: 1) Selection of the best individuals among the population; 2) Utilization of the selected individuals as parents for the next generation; 3) Inception of a selection cycle in the population resulting from the selected individuals mating; and 4) Realization of various additional cycles up to reduction of the additive variance.

Estimation of the genetic variability extent shown by the different quantitative characters in any vegetal species is essential to begin their genetic enhancement. Answer to the selection being performed in any individual depends primarily genetic variability, heritability and gene frequency present in the population to be enhanced.

The objective of this work was to estimate both the genetic variance and heritability as well as to evaluate the agronomic behavior in 237 fodder maize lines at two locations. This was with a view to select those lines that consistently manifest high yield potential for fodder.

MATERIALS AND METHODS

Location of the experiment

The current investigation was carried out in two locations: The Dr. Ernest W. Sprague Experimental Station from the International Maize and Wheat Improvement Center in Agua Fria, Puebla (812 m.a.s.l.), 20° 27' Lat. N, 97°38' Long. O) and Rancho Santa Margarita, Puerto Vallarta, Jalisco (731 m.a.s.l.), 20° 44' Lat. N, 105°10' Long. O). Cultural practices on typical handling were carried out for each region in such a way that cultivation was kept free of pests and diseases. Sowing and harvesting were performed manually.

Genetic material

In this study, 237 maize lines of different origins and inbreeding levels were evaluated. These lines came from tropical and subtropical genetic enhancement programs and the germplasm bank from the International Maize and Wheat Improvement Center.

Experiment initiation and agronomic management

Sowing at the Agua Fria and Puerto Vallarta location took place on December 19 and 21, 2018 respectively. Planting density was 83,000 plants per hectare. Experimental unit was made up of two 5-meter-long furrows with 0.80 distance in between furrows and 0.15 meter space in between plants. Irrigation water supply was achieved by means of a trickle irrigation ribbon with 15 cm separation. Approximately 20% urea was applied at sowing, two additional applications (40%) were carried out at bloom period and grain filling stage. Weeds were controlled through the application of Callisto® at 300 cm³ ha⁻¹ dose. Insect pests were controlled with Denim® 19 CE and Lorsban™ 4 EC applications at 100 mL ha⁻¹ and 1.0 L ha⁻¹ dose accordingly.

Evaluated variables

Cob Height (CH) in five randomly selected plants was taken from the soil surface to the point where the first ear was inserted.

Plant height (PH) was measured when the plants reached harvest maturity. It was recorded in five plants taken at random from the plot, measuring from the point of the union of the root and stem to the base of the male inflorescence.

Stem diameter (ST) in five central plants was measured with a vernier with results reported in centimeters.

Forage yield (FY) was taken when the plants reached physiological maturity and the weight of five plants per experimental unit was recorded, and extrapolated to green forage yield per hectare.

Statistical analysis

A double-repetition, random combined-analysis following a full-block design was carried out. Two hundred and thirty-seven (237) lines were sowed and split into 26, 9-line groups by repetition in two locations. The significant agronomic characteristics ($p \leq 0.01$) were used to estimate variance components.

The model used for phenotype dissection in different environments was $y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + (\gamma_k)_j + \alpha\beta_{ij} + (\delta_l)_j + (\alpha\delta_{il})_j + \varepsilon_{ijkl}$, where y_{ijkl} – line phenotypic value;

μ – target feature mean; α_i – effect of the i -th location; β_j – effect of the j -th group; γ_k – effect of the k -th repetition; δ_l – effect of the l -th line; $(\gamma_k)_j$ – k -th repetition nested in the j -th group; $\alpha\beta_{ij}$ – interaction of the i -th location and the j -th group; $(\alpha\delta_{il})_j$ – interaction of the i -th location and the l -th line nested in the j -th group; ε_{ijkl} – experimental error. The combined-variance analysis was carried out using the R 3.6.0 statistical program (R Core Team, 2013).

Genetic variability estimates

Data were recorded for each genotype. The variance components estimate was calculated taking the mean squares from the line variation sources as well as from the lines \times location obtained from the mixed variance analysis. Variance components were used to make estimates of genetic variance.

The genotypic variance is the part of that total variation explained by the genotypes effect evaluated in different environments. As for lines S_1 , it provides a direct estimate of the additive genetic variance (σ^2_A). This occurs under the assumption that dominant effects and epistasis are minimized during inbred. Likewise, the reference population from which study lines were developed is supposed to be in Hardy-Weinberg equilibrium.

Genetic variance (σ^2_g), phenotypic variance (σ^2_f), variance interaction (σ^2_{ga}) and broad sense heritability (H^2) was determined by the method of the mean squares of the variance components (Barriga et al., 1983). Phenotypic (CV_F), genotypic (CV_G) and environmental (CV_A) variation coefficients were calculated, considering the methodology proposed by Pistorale et al. (2008).

Best linear unbiased predictor (BLUP)

In order to eliminate the environmental effect, a mixed linear model was adjusted to calculate the best linear unbiased predictor (BLUP) value for each line. The model used for phenotype dissection in different environments was: $y_{ijk} = \mu + g_i + e_j + \varepsilon_{ijk}$. In this equation, y_i represents the " i " line phenotype, μ represents the great mean value for the environment target feature, g_j represents the genetic effect, e_j represents the environmental effect and ε_{ijk} represents the random error. All effects were considered as random except for the mean (Li et al., 2016). The BLUP value estimate was therefore denoted as the sum of the great mean and the genetic effect of each line. Such values were obtained using the lme4 statistical package (Linear Mixed-Effects Model version 1.1-21) from the R 3.6.0 statistical program (Bates et al., 2015).

RESULTS AND DISCUSSION

Variance analysis

The mixed variance analysis results from the 237 maize inbred lines evaluated at Agua Fria and Puerto Vallarta, Mexico are shown in Table 1. Highly significant differences ($p \leq 0.01$) are observed in lines and interactions line \times location in fodder yield variables (FYG), plant height (PH), cob height (CH) and stem diameter (ST). Upon detection of such differences, these were used to estimate variance components. The mean for the evaluated agronomic variables is also shown. As for fodder yield, the mean value was 37.77 t ha^{-1} . Variation coefficient ranged from 3.4 (plant height) to 16.06 (stem diameter).

Table 1. Mean squares for the mixed variance analysis for yield and agronomic characters in 237 maize lines evaluated at Agua Fria and Puerto Vallarta, Mexico

SV	DF	Fodder yield (t ha ⁻¹)	Plant height (cm)	Cob height (cm)	Stem diameter (mm)
Loc	1	17,001.28**	22,363.88 **	42,153.78**	324.10**
Groups	25	1,083.00*	6,908.48*	3,093.72*	244.70*
Repetitions (Groups)	26	0.9914 ns	21.25 ns	21.773 ns	13.75 ns
Loc*Groups	25	170.81**	388.19**	249.33**	16.88 *
Lines (Groups)	208	500.85**	1245.59**	721.91**	40.14**
Loc*Lines(Groups)	208	107.69**	226.66**	116.87**	13.91**
Error	454	11.81	41.03	8.53	11.58
R ²		0.95	0.95	0.96	0.79
CV(%)		9.1	3.8	3.4	16.06
Mean		37.77	168.97	86.21	21.18

*, ** significant at 5% and 1% level, respectively; ns = Non-significant; SV = Variation source; DF = Degree of freedom; Loc = Locations; CV = Variation coefficient.

The frequency distribution of agronomic characters (Fig. 1) shows the way in which variable data were distributed in both environments. As for fodder yield, distribution frequency ranged from 10 to 80 t ha⁻¹, thus showing the differences of the genotypes under study in which the highest frequency fell to within 30 to 40 t ha⁻¹.

According to the mixed variance analysis results, highly significant values for lines variation sources and lines × location were present across both locations. Thus, showing that at least one out of the 237 lines was different compared to the rest, highlighting the differences in the lines' genetic origin besides the effect caused by climate conditions during cultivation development. Garcia & Villa (1995) pointed out that growth and development directly depend on the plant's genetic structure, soil and climate conditions in which evaluation had been conducted. The statistical differences observed from one line to another, are the result of the genetic variability relevant to the germplasm used in the process.

The significant line interaction per location is noteworthy as it shows that production was not kept relatively equal in the two evaluation environments by the parents. Due to random environmental fluctuations, maize germplasm agronomic evaluation needs to be carried out in different environments allowing for a more accurate estimate of the genetic components value thus, detaching the environmental genetic effect (Gutiérrez-Del Rio et al., 2004).

As for the plant and cob height variables, mean values noted were 168.97 and 86.21 centimeters, respectively. In general, lines evaluated in this study are considered as low height due to the inbreeding depression occurring when lines are self-fertilized successively with the purpose to achieve homogeneity and consistency. The inbreeding depression depends directly on the level of dominance, so that no changes in the mean are expected under inbreeding when genes controlling the trait follow a strictly additive model (Falconer, 1984).

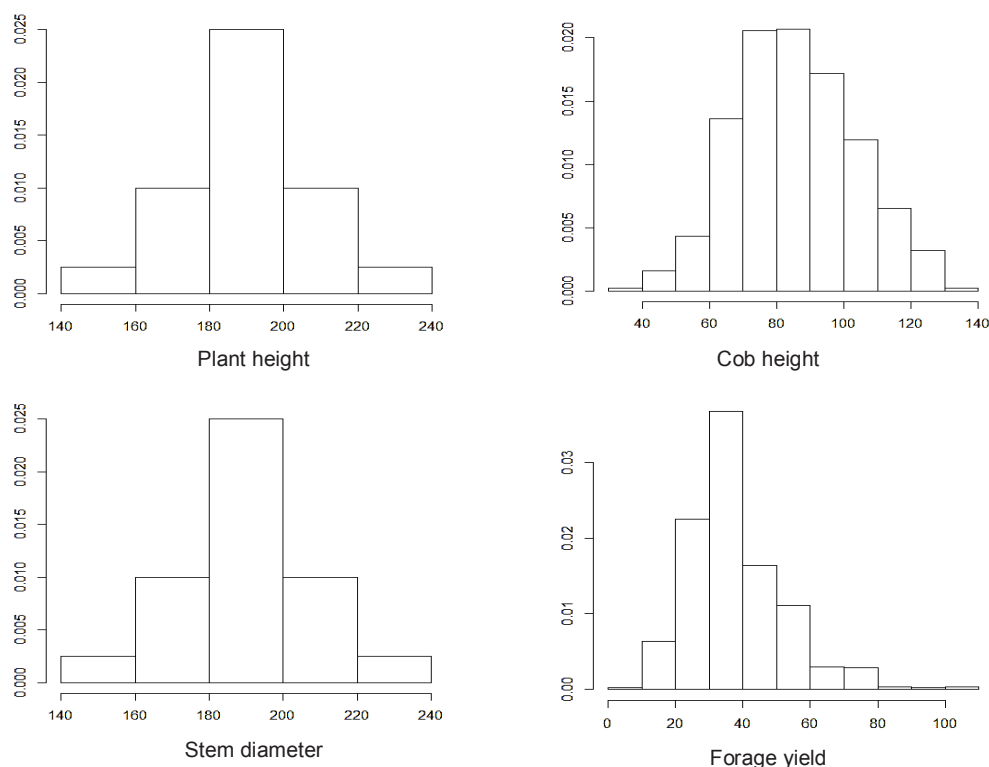


Figure 1. Frequency distribution for agronomic characters; Plant height (cm), cob height (cm), stem diameter (cm) and fodder yield (t ha^{-1}) from 237 maize lines evaluated at Agua Fria and Puerto Vallarta, Mexico.

Similar results for the variables plant height and cob height were reported by Alfaro & Segovia (2009), when maize cultivars were characterized in the Southern part of Venezuela. Bejarano et al. (2000) reported significant differences regarding the environmental effects for PH and CH evaluated in simple breeds of maize coming from lines featuring different inbred levels. Silva et al. (2009) also noted significant differences in maize lines for these characteristics in each evaluated environment. In a study to estimate the genetic variability degree in maize genotypes, Sabiell et al. (2014) found highly significant differences among plant height (PH) genotypes in two locations. A similar conclusion was reported by Salami et al. (2007) and Hajibabae et al. (2012).

As for fodder yield, the significant differences observed among the lines suggests the presence of a vast genetic diversity in the evaluated genotypes despite the yield mean in both evaluated environments (37.84 t ha^{-1}). Values of 74.8, 72.2, 67.7, 65.8, 63.8 and 62.5 t ha^{-1} for CLWN701, CLWN345, CML476, CML216, CLWQ232, CML528 lines, respectively correspond to the highest yield potential and up to 21.46, 21.31, 21.30, 21.26, 20.92, 17.42 t ha^{-1} for CSL1619, CML527, CML327, CML506, CLYN531, CML529 lines were observed as the lines with the lowest yield, respectively.

Yield values in higher potential lines exceeded the 36.12 t ha^{-1} national average (SADER-SIAP, 2018) and are similar to those recorded by Peña-Ramos et al. (2008) and Castillo et al. (2009), with yields ranging between 70 and 95 t ha^{-1} . With the purpose to

identify outstanding fodder cultivars for upper valleys, Franco-Martinez et al. (2015) assessed 29 maize cultivars with 86.96 and 88.28 t ha⁻¹ average fodder yields for SBA-470 and AS-722 cultivars. Sánchez-Hernandez et al. (2011) reported 44.2 and 32.5 t ha⁻¹ average fodder yields in maize genotypes evaluated in Oaxaca, Mexico. On the other hand, Nunez et al. (2001) evaluated fodder production in early and intermediate tropical and mild weather maize under irrigated conditions, cultivated in the Northern part of Mexico. The green fodder yield found ranged from 52.8 to 75.6 t ha⁻¹.

Table 2. BLUP values applicable to the agronomic characteristics from the 237 maize lines fraction evaluated at Agua Fria and Puerto Vallarta, Mexico

Variables Lines	Fodder yield (t ha ⁻¹)		Plant height (cm)		Cob height (cm)		Stem diameter (mm)	
CLWN345	71.0	a	209.8	bcd	110.2	b	25.6	cd
CLWN701	68.5	b	239.5	a	127.7	a	28.3	a
CLRCW96	62.1	c	190.0	degf	91.5	cdef	25.3	cd
CML563	56.5	d	198.0	bcde	97.0	c	25.5	cd
CLWN509	55.3	e	196.5	cdef	91.7	cdef	20.9	ghi
CLWN379	55.2	e	203.3	bcde	106.0	b	24.4	de
CLQRCWQ8	54.2	f	220.1	ab	104.5	b	26.3	bc
CSL1676	52.9	g	156.4	ijk	70.0	jk	22.1	fgh
CLWN630	52.3	g	221.5	ab	109.2	b	27.5	ab
CLWN775	52.1	g	219.0	abc	111.5	b	22.8	ef
CLWN750	38.59	h	191.5	defg	82.5	gh	26.6	cd
CLRCW97	38.25	hi	165.5	hij	70.0	j	22.7	efg
CLRCW100	38.06	hi	157.9	ijk	83.8	fgh	20.8	hi
CLYQ266	37.81	hi	198.8	bcde	92.0	cde	17.9	klm
CLWN603	37.75	i	204.8	bcde	94.0	cd	22.0	fgh
CLYN619	37.65	i	183.3	efgh	87.0	defgh	12.6	n
CLYN460	37.50	ij	172.0	ghi	70.0	jk	20.5	hij
CLWN496	37.50	ij	172.6	ghi	72.0	j	20.5	hij
CML444	36.81	lk	155.4	ijk	88.2	defg	18.8	jkl
CLYN548	36.62	k	199.0	bcde	85.5	efgh	11.3	n
CSL1673	23.28	l	175.1	fghi	73.0	ij	17.1	lm
CSL1656	23.28	l	165.8	hij	82.6	gh	19.8	ijk
CSL1643	22.96	l	138.1	lm	70.0	jk	20.3	hij
CSL1671	22.65	lm	147.4	jkl	62.2	k	19.2	ijk
CLYN631	22.62	lm	174.3	fghi	94.5	cd	18.2	klm
CSL1669	22.03	mn	153.9	ijk	65.0	jk	17.03	m
CML537	21.40	n	144.5	jkl	80.0	hi	19.7	ijk
CSL1612	20.06	o	129.8	lm	49.0	l	12.8	n
Mean	37.77		168.9		86.2		21.1	

Different superscripts denote statistical significance at $p \leq 0.05$ by Tukey's post-hoc test.

Best linear unbiased predictor (BLUP) values for yield and concerned agronomic characteristics were obtained. The upper fraction values for the 237 lines evaluated in two environments are shown in Table 2. As for fodder yield, the general mean was 37.84 t ha⁻¹ while an important group of lines showed values higher than the mean. This is probably as a result of the vast genetic diversity present in the assessed line population.

Variance components estimate

All evaluated agronomic variables showed significant differences ($p \leq 0.05$), therefore the variance components were estimated. Under the assumption that dominant effects and epistasis are minimized during the inbred process and taking into consideration that the lines under study showed a high inbred level (S_{10}), the genetic variance provides a direct estimate of the additive genetic variance. The genetic parameter estimates for the population under study are shown in Table 3. It was observed that phenotypic variance estimate, in all evaluated characters; showed a greater scale with regard to the additive variance estimate. Characters heritability showed values ranging from 34% (stem diameter) up to 65% (plant height).

Table 3. Variance components estimate and genetic, phenotypic and environmental coefficient of variation (%) for different agronomic characters in 237 maize lines evaluated at Agua Fria and Puerto Vallarta, Mexico'

Variance components	Fodder yield	Plant height	Cob height	Stem diameter	Plant average weight
σ^2_g	98.29	254.73	151.26	6.55	26,606.01
σ^2_f	158.04	388.57	268.13	19.29	4,2075.77
σ^2_{ga}	47.94	92.81	108.34	1.16	12,447.23
σ^2_e	11.81	41.03	8.53	11.58	3,022.53
H^2	0.62	0.65	0.56	0.34	0.63
CV_G	26.25	9.44	14.26	12.08	27.01
CV_F	33.28	11.66	18.99	20.74	33.88
CV_A	18.34	5.7	12.07	5.08	18.43
CV_G/CV_A	1.4	1.6	1.1	2.3	1.3

σ^2_g = Genetic variance; σ^2_f = Phenotypic variance; σ^2_{ga} = Genotype interaction variance \times location; σ^2_e = Error variance; H^2 = Heritability in broad sense; CV_G (%) = Coefficient of variation genetic; CV_F (%) = Coefficient of variation phenotypic; CV_A (%) = Coefficient of variation environmental.

Variance components allowed for different genetic parameters estimate. Genotypic variance (σ^2_g) provided for 98.29 additive variance (σ^2_A) direct estimate in fodder yield variance. This represents sufficient line genetic variance that, when combined with each other, showed good yields in the single crossbreeding that may take place (Maphumulo et al., 2015). The magnitude of genetic variance will lead to a rapid genetic advance during selection processes (Bertoia & Aulicino, 2014).

Both phenotypic and additive variance components turned out to be according to expectations because phenotypic variance besides the genetic effect, composed of those environmental deflections as well as of genotype \times environment interaction component. Therefore, it is expected that phenotypic variance magnitudes in genetic studies exceed those of additive variance. A similar behavior of the aforementioned parameters was found in a tropical maize segregating population evaluated in Morelos, Mexico (Rebolloza-Hernandez et al., 2016).

On the other hand, additive genetic variance in intra-population genetic enhancement programs, significantly contributes to the selective response among the population. For this reason, heritability estimates are essential to predict the response of a population during the selection process. In consequence, the existence of high genetic-additive variations justifies continuance of a population enhancement program (Rovaris et al., 2011).

Heritability values observed in agronomic variables represent a good indicator to perform genetic enhancement selection. Heritability of the characters showed values ranging from 34% (stem diameter) to 65% (plant height). Heritability expresses total variance ratio attributable to the mean effects from the genes and this, in turn, determines the resemblance level among relatives (Falconer, 1984). The study of those genetic mechanisms governing the various significant characters in fodder maize indicated that fodder yield character was highly heritable (62%) thus making recurring selection effective.

The relationship between the coefficient of genetic and environmental variation (CV_G/CV_A) was high for the characteristics evaluated (Table 3). According to Vencovsky (1987), there is a very favorable situation for the selection gain when the CV_G/CV_A tends or is higher than one, since in these cases, the genetic variation is greater than the environmental variation, which indicates that the selection for these characters has the best conditions in terms of immediate genetic gain. Together, the CV_G and heritability are indicative of the potential to make any selection in genotypes analyzed.

CONCLUSIONS

The genetic parameters estimate provided information on the genetic variance and heritability existing among the population, which are essential for the progress of the selection process. In this study, the fodder yield character was highly heritable thus rendering recurring selection as effective. Lines CLWN701, CLWN345, CML476, CML216, CLWQ232, CML528 with 74.8, 72.2, 67.7, 65.8, 63.8 and 62.5 t ha⁻¹, respectively showed the highest green fodder yield. These lines may be potentially used in genetic enhancement programs for this characteristic in maize.

ACKNOWLEDGEMENTS. We would like to thank Consejo Nacional de Ciencia y Tecnología (Science and Technology National Board –CONACYT) for the graduate studies' scholarship granted to the lead author.

FUNDING. This research was funded by Universidad Autónoma Agraria Antonio Narro (UAAAN), project 2498. The MasAgro program: Sustainable modernization of traditional agriculture through the resources managed by the CIMMyT and the Secretary of Agriculture and Rural Development (SADER).

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