

## Genetic Variance and Correlation of Forage Yield and Quality Traits in Tropically Adapted Maize

(Varians Genetik dan Kolerasi Hasil Foraj dan Ciri Kualiti terhadap Jagung Disesuaikan Tropika)

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### ABSTRACT

*Two  $F_2$  populations segregating for biomass yield and forage quality traits were developed from two separate crosses of tropically adapted maize inbred lines. The parental,  $F_1$  and  $F_2$  generations of both crosses were evaluated to estimate broad sense heritability, genetic advance and correlations for these traits to suggest the best traits as selection criteria towards breeding forage maize with high yield and quality. In Cross 1, biomass yield trait with the highest broad-sense heritability was plant height (70.03%), whereas forage quality trait with the highest heritability estimate was crude protein content (66.60%). Heritability estimates in Cross 2 were high for all biomass yield traits and forage quality traits (>50% for all traits). Indigestible cell wall component represented by acid detergent lignin content was found to be highly heritable in both populations. High genetic advance as percent of mean were found for fresh and dry plant yield as well as for lignin content in both populations. Correlation analysis on all traits showed that all biomass yield components were significantly correlated. All traits related to cell wall content were positively correlated and acid detergent lignin was positively correlated with dry plant yield. Traits with high to moderate heritability and high predicted genetic advance, namely plant height, fresh plant yield and protein content can be used as selection criteria to improve maize biomass yield and nutritive quality for forage utilization. Selecting for higher biomass yield would also result in selecting individuals with higher lignin content as shown by the correlation analysis.*

*Keywords: Correlation; forage yield and quality traits; genetic advance; heritability; maize*

### ABSTRAK

*Dua populasi  $F_2$  yang bersegregasi bagi ciri hasil biojisim dan kualiti foraj dihasilkan daripada kacukan dua pasangan baris biak baka jagung tropika. Induk, generasi  $F_1$  dan  $F_2$  bagi kedua-dua kacukan tersebut dinilai untuk menganggar kebolehwarian luas, kemajuan genetik, dan kolerasi bagi ciri hasil biojisim dan kualiti foraj untuk mencadangkan ciri terbaik sebagai kriteria pemilihan ke arah menghasilkan baka jagung foraj berhasil tinggi dan berkualiti. Bagi Kacukan 1, ciri biojisim yang mempunyai kebolehwarian tertinggi adalah ketinggian tumbuhan (70.03%) manakala ciri kualiti foraj dengan nilai kebolehwarian tertinggi adalah kandungan protein (66.60%). Anggaran kebolehwarian bagi Kacukan 2 adalah tinggi bagi semua ciri hasil biojisim dan kualiti foraj (<50%). Komponen dinding sel yang tidak terhadam iaitu kandungan lignin asid detergen mempunyai anggaran nilai kebolehwarian yang tinggi bagi kedua-dua populasi. Anggaran kemajuan genetik sebagai peratus min untuk kedua-dua populasi dilaporkan tinggi bagi hasil tumbuhan segar dan kering, juga bagi kandungan lignin asid detergen. Analisis kolerasi bagi semua ciri menunjukkan bahawa semua ciri hasil biojisim berkolerasi secara signifikan. Semua ciri yang berkaitan dengan kandungan dinding sel berkolerasi secara positif dan kandungan lignin detergen asid juga berkolerasi secara positif dengan hasil tumbuhan kering. Ciri yang mempunyai nilai kebolehwarian sederhana kepada tinggi dan mempunyai nilai kemajuan genetik sebagai peratus min yang tinggi, seperti ketinggian tumbuhan, hasil tumbuhan segar dan kandungan protein boleh dijadikan sebagai kriteria pemilihan dalam menambah hasil biojisim dan kualiti nutrisi jagung foraj. Pemilihan bagi tanaman berbiojisim tinggi juga turut meningkatkan kandungan lignin seperti yang didapati dalam analisis korelasi.*

*Kata kunci: Hasil biojisim dan kualiti foraj; jagung; kebolehwarian; kemajuan genetik; kolerasi*

### INTRODUCTION

Maize (*Zea mays* L.) is a favorable source of animal feed or fodder due to having qualities such as high protein content, good palatability and good digestibility (Ballard et al. 2001;

O'Mara et al. 1998). In the temperate region especially in the Europe, maize is widely used as conserved high quality forage and processed feed due to having seasonal climate change (Deinum 1988). Despite the extensive development in breeding for temperate forage maize, development and

improvement of varieties with high biomass yield and quality (nutritive and digestibility) traits in the tropics still falls behind due to lack of interest and need. An initiative to produce high yielding and high quality forage maize was conducted in Universiti Putra Malaysia to promote the potential utilisation and production of maize as forage crop. Thus, the identification of traits as the selection criteria to be applied in breeding programmes towards developing new forage maize varieties with high biomass yield and forage quality on tropically adapted populations is imperative.

The progress and success in genetic improvement of a crop is dependent on the genetic variability and the effectiveness of selection procedure in any breeding program. The study of variation is done to partition components that are attributable to genetic, environment, and the interaction between these two. These variance components can be estimated using the values of variances retrieved from each generation involved (Kearsey & Pooni 2004). Broad sense heritability is the estimation of the relative magnitude of genetic variation to the overall phenotypic variation ( $V_G/V_p$ ). Estimate of heritability can influence breeder to effectively determine the selection procedures for trait improvements and to predict gain from selection (Bekele & Rao 2014; Kapoor 2017; Maruthi & Rani 2015). Forage traits are mostly quantitative traits which are not only polygenic but possibly have complex gene architecture (Ali et al. 2006; Kumar et al. 2014). Identifying traits with considerably medium to high heritability values could increase the effectiveness of selection. Genetic advance is a function of heritability that gives an indication of the effectiveness of selection in any breeding programme, which is a great interest to plant breeders. Relative genetic advance value gives the magnitude of genetic improvement that can be achieved for a particular trait (Bekele & Rao 2014; Kapoor 2017; Kumar et al. 2014). High genetic advance with high heritability estimates suggest the most promising condition for selection. Traits with high heritability may not necessarily give high genetic advance, as another important function of genetic advance is available variability on the traits in question and the population involved. For instance, traits such as days to silking and tasseling in maize are often reported to have high heritability, but with low genetic variability (Asghar & Mehdi 1999; Kashiani et al. 2010). Therefore, not much genetic improvement could be made for these traits. Consequently, traits with moderate to high heritability and high genetic advance would be suitable to be utilised as selection criteria in breeding programs.

Correlation analysis establishes relationship among agronomic traits in genetically diverse population for crop improvement (Silva et al. 2016). Phenotypic correlation includes both genetic and environmental effects on the

traits while genetic correlation analysis gives the heritable association between two variables (Kashiani & Saleh 2010). Many studies showed strong correlation among related traits. Positive correlations were reported for yield and yield related components namely ear yield, grain yield, biomass yield, plant height, number of leaves per plant, stem girth and leaf to stem ratio (Bekele & Rao 2014; Kapoor 2017; Saleh et al. 2002; Umakanth et al. 2000). The same correlation patterns were also found among the cell wall components, namely the neutral and acid detergent fibre contents (Cardinal et al. 2003).

Biomass yield and quality traits in forage maize are mostly quantitative in nature, having complex genetic control with generally moderate heritability (Ali et al. 2006; Deinum 1988; Kapoor 2017). Preliminary understanding of heritability, predicted genetic advance and correlations among biomass yield and forage quality traits is essential in order to plan and set a proper selection criterion for the improvements of the desired characters. Keeping in view the potential of maize as forage crop, this study was undertaken to estimate heritability and genetic advance of maize biomass yield and forage quality traits and suggest practical selection strategies based on the correlation study for forage maize breeding program under tropical conditions.

#### MATERIALS AND METHODS

The four parental maize inbred lines used in this study to develop the two segregating population were obtained from International Center for Maize and Wheat Improvement. The first cross (Cross 1) was made between CML 152 (high yield and protein content) and CML 383 (low yield and protein content), while the second cross (Cross 2) involved CML 491 (high yield but low protein content) and CML 331 (low yield but high protein content) as parents. The  $F_1$  plants of both crosses were self-pollinated to produce the  $F_2$  seeds. Sufficient seeds of all generations ( $P_1$ ,  $P_2$ ,  $F_1$  and  $F_2$ ) were produced from both crosses under field conditions with controlled pollinations. The evaluation was conducted at Experimental Field 2, Faculty of Agriculture, Universiti Putra Malaysia (UPM), Serdang, Selangor, Malaysia (Latitude = 3.0077, Longitude = 101.7026). The parental lines,  $F_1$  and  $F_2$  populations were arranged in randomised complete block design with three replications. Each plot consisted of 4 m rows of both parents, the  $F_1$  (one row, respectively) and  $F_2$  populations (four rows), with planting spacing of 0.75 m between rows and 0.20 m between plants in a row. All experimental plots were subjected to uniform and good agronomic practices to ensure cultivation of good crop growth.

Six plants were randomly sampled from each replicate for the four parental lines and both  $F_1$ s, and the average value were taken for all measurements. For

the segregating F<sub>2</sub> population, data were collected from healthy (not heavily infested by pests and free from diseases) and surviving F<sub>2</sub> individuals of Cross 1 (166 individuals) and Cross 2 (162 individuals). Traits related to biomass yield were plant height, number of leaves per plant, fresh plant yield and dry plant yield, while traits for quality were crude protein content, neutral detergent fibre content, acid detergent fibre content and acid detergent lignin content. Data of plant height (cm), days to tasseling and days to silking were recorded at pre-harvest. At three weeks after tasseling, whole plants were cut 20 cm above soil. Number of leaves per plant were counted and recorded. Whole plant was weighed and recorded as fresh plant yield (g). Samples were oven dried in 60 °C for at least 72 h (>85% dry matter content) and their dry plant yield were determined in gram. Dried samples were ground and screened through a 1.0 mm steel mesh to prepare for forage quality traits determination. Ground samples were collected in labelled pill bottles for crude protein content (% CP), neutral detergent fibre content (% NDF), acid detergent fibre content (% ADF) and acid detergent lignin content (% ADL) measurements using Near Infrared Reflectance Spectroscopy (NIRS) (Foss Analytical, Denmark, M6500).

Mean, standard deviation and variance of the parental, F<sub>1</sub> and F<sub>2</sub> generations for both crosses were obtained from basic statistics option using the Minitab® Statistical Software (LEAD Technologies, Inc.). Significant means were compared using least significant difference at  $p \leq 0.05$ . Phenotypic ( $\delta_p^2$ ) (1) and genotypic ( $\delta_g^2$ ) (2) variances were according to Kearsley and Pooni (2004).

$$\delta_p^2 = VF_2 \quad (1)$$

$$\delta_g^2 = VF_2 - [(VP_1 + VP_2 + VF_1)/3] \quad (2)$$

where  $VF_2$ ,  $VP_1$ ,  $VP_2$ , and  $VF_1$  are variances of F<sub>2</sub>, P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub> population, respectively. The mean values were used for genetic analyses to determine phenotypic coefficient of variation (PCV) (3) and genotypic coefficient of variation (GCV) (4):

$$PCV (\%) = \frac{\sqrt{\delta_p^2}}{\bar{x}} \times 100 \quad (3)$$

$$GCV (\%) = \frac{\sqrt{\delta_g^2}}{\bar{x}} \times 100 \quad (4)$$

where  $\delta_g^2$  is the genotypic variance;  $\delta_p^2$  is the phenotypic variance; and  $\bar{x}$  is the sample mean. Broad-sense heritability ( $h_B^2$ ) estimate of each trait was calculated using (5).

$$h_B^2 = (\delta_g^2) / (\delta_p^2) \quad (5)$$

Level of heritability estimates were assigned according to Stansfield's classification (Stansfield 1986) where values of more than 50% is considered high, 20-50% as moderate and below 20% as low.

Expected genetic advance percentage of mean (GA) after one generation of selection was calculated at 5% selection intensity ( $k=2.06$ ) on the segregating population (F<sub>2</sub> population) using (6):

$$GA (\%) = \frac{k \cdot \delta_p \cdot h_B^2}{\bar{x}} \quad (6)$$

where  $k$  is the constant for selection differential at 5%;  $\delta_p$  is the phenotypic standard deviation of F<sub>2</sub> population; and  $h_B^2$  is the broad-sense heritability.

Simple phenotypic correlation estimates among the traits measured were determined from the data collected from the segregating F<sub>2</sub> populations using Pearson's correlation formula (Gomez & Gomez 1984). Genetic correlation coefficient estimates among the traits measured were determined from the variance components based on the formula (Falconer & Mckay 1996) as follows (7):

$$r_G = \frac{\frac{\delta_{G(XY)}}{r}}{\sqrt{\frac{\delta_{G(X)}^2}{r} \cdot \frac{\delta_{G(Y)}^2}{r}}} \quad (7)$$

where  $r_G$  is the genotypic correlation between the traits X and Y;  $\delta_{G(XY)}$  is the genetic covariance between the traits X and Y;  $\delta_{G(X)}^2$  is the genotypic variance of the trait X;  $\delta_{G(Y)}^2$  is the genotypic variance of the trait Y; and  $r$  is the number of replication.

## RESULTS AND DISCUSSION

### VARIANCE COMPONENTS AND HERITABILITY ESTIMATES FOR BIOMASS YIELD AND FORAGE QUALITY IN MAIZE

Genetic and phenotypic variances as well as broad-sense heritability estimates for biomass yield and quality traits in the two populations were presented in Table 1. In both crosses, broad-sense heritability estimates for days to tasseling and silking were high (more than 70%) which is expected for flowering traits. Broad-sense heritability for plant height, fresh and dry plant yield were high in both populations. However, heritability values for number of leaves per plant were different in these two populations, which was moderate in Cross 1 and high in Cross 2. All forage quality traits were found to have medium to high heritability values in both crosses.

TABLE 1. Variance components and broad-sense heritability estimates of forage yield and quality traits of two F<sub>2</sub> maize populations

Trait	Cross 1 (CML 152 × CML 383)			Cross 2 (CML 491 × CML 331)		
	$\sigma_g^2$	$\sigma_p^2$	$h_B^2$	$\sigma_g^2$	$\sigma_p^2$	$h_B^2$
Days to tasseling	5.24	7.47	70.07	6.41	7.90	81.10
Days to silking	11.05	14.59	75.74	12.95	14.92	86.85
Fresh plant yield	16900.84	37906.3	44.59	36006.55	51717.40	69.62
Dry plant yield	1526.89	3170.74	48.16	1978.47	3875.43	51.05
Plant height	267.71	382.25	70.03	330.17	392.24	84.17
Number of leaves per plant	0.52	2.02	25.66	1.94	2.85	68.01
Crude protein content	1.71	2.56	66.60	2.06	2.36	87.32
Neutral detergent fibre	4.15	9.31	44.58	5.95	11.78	50.54
Acid detergent fibre	11.73	32.11	36.53	19.19	24.29	79.02
Acid detergent lignin	3.27	4.08	80.06	2.33	2.76	84.68

$\sigma_g^2$  = Genotypic variance,  $\sigma_p^2$  = Phenotypic variance,  $h_B^2$  = Broad-sense heritability

In general, high phenotypic variances were found for biomass yield and their components in both populations. It was also observed that almost equivalent portion of genetic and environmental variances contributed to the overall phenotypic variance. This was in accordance with the nature of these traits being quantitative traits, thus, having a wide range of variation and subjected to environmental influence. Similar results were also reported by Ali et al. (2006) for fresh fodder yield, dry matter content, and plant height in two S<sub>1</sub> maize populations and Anshuman et al. (2013) for biological yield and plant height in 20 maize genotypes. Estimates of phenotypic variances for forage quality traits were low to moderate in both populations. However, the genetic variance estimates were higher than the environmental variance. Consequently, heritability estimates for all quality traits in both populations were moderate to high. Similar findings were reported by Cardinal et al. (2003), where heritability for leaf sheath and stalk fibre and lignin content in RIL populations were estimated to be from 51-78%. Heritability values for protein content were 66.6 and 87.3% in Cross 1 and 2, respectively. Bekele and Rao (2014) reported a higher heritability estimate for protein content (96.1%) but the findings were observed on Quality Protein Maize (QPM) hybrids and lines, therefore were expected to have high heritability estimates for this trait.

Kahrman and Egesel (2017) reported high heritability estimate for protein content (>60%) when as well in their analysis using F<sub>1</sub> and F<sub>2</sub> generations in maize. Estimation of heritability values using population variances of highly segregating population (F<sub>2</sub> population) could lead to low to moderate heritability due to heterozygous allele segregation during meiosis from the F<sub>1</sub> to the F<sub>2</sub> generation (Klein 1974).

#### EXPECTED GAIN FROM SELECTION FOR BIOMASS AND QUALITY TRAITS IN FORAGE MAIZE

The phenotypic and genotypic coefficients of variation (PCV and GCV) for the F<sub>2</sub> populations are presented in Table 2. In both populations, high PCV and GCV were recorded for all biomass yield traits. Low values of GCV and PCV were found for days to tasseling and silking, number of leaves per plant, neutral detergent fibre content and acid detergent fibre content in both populations. Wide difference (more than 10%) between GCV and PCV for fresh and dry plant yield in both populations indicated the influence of environment on genotype.

The results on genetic advance (at 5% selection intensity,  $k = 2.06$ ), as percentage of mean for biomass yield and forage quality traits for both populations were given in Table 2. High to moderate genetic advance were found for all biomass yield components and

acid detergent lignin content in both populations, with expected gain from selection of more than 20% from their respective means. Low gain from selection (as percentage

of mean) were found for days to tasseling, days to silking and neutral detergent fibre content.

TABLE 2. Genotypic and phenotypic coefficient variation and estimated genetic gain at 5% selection intensity of forage yield and quality traits for both the  $F_2$  populations

Trait	Cross 1			Cross 2		
	(CML 152 × CML 383)			(CML 491 × CML 331)		
	GCV (%)	PCV (%)	GA as % mean	GCV (%)	PCV (%)	GA as % mean
Days to tasseling	3.70	4.42	6.22	4.25	4.72	7.89
Days to silking	5.22	6.00	9.06	5.80	6.22	11.13
Fresh plant yield	36.56	54.75	51.58	46.97	56.29	80.73
Dry plant yield	31.35	45.17	49.46	31.92	44.68	46.98
Plant height	14.68	17.54	23.15	14.60	15.92	27.61
Number of leaves per plant	7.64	15.08	7.96	14.19	17.20	24.11
Protein content	12.62	15.47	25.20	16.48	17.63	31.72
Neutral detergent fibre	2.99	4.48	1.94	3.55	5.00	5.20
Acid detergent fibre	10.37	17.16	13.60	12.34	13.88	22.60
Acid detergent lignin	22.57	25.22	50.77	24.02	26.10	45.54

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance

The variance components used to estimate broad sense heritability for all traits were obtained using the values of generation variances in both populations. Therefore, the genetic variances of biomass yield and quality traits in this study were the combination of dominance, additive and epistatic gene effects. Both heritability and genetic advance estimates could give a suggestion on the genetic control of traits (Anshuman et al. 2013; Bekele & Rao 2014; Kumar et al. 2014). For instance, traits like days to tasseling and silking have high heritability and low GCV and PCV, suggesting that the observed variation in these traits were attributed to a small number of genes with dominance effects (Saleh et al. 2002). This was in accordance with the findings of Kashiani et al. (2010) and Saleh et al. (2002) in their studies of heritability for yield traits in sweet corn and Ravindra and Karan (2018) for grain corn.

Generally, traits related to biomass yield such as fresh and dry plant yield were found to have high PCV and GCV, with substantial genetic advance values in

both populations. These traits were also found to have moderate heritability. It is possible to suggest that these traits are governed by multiple genes with additive effects (Ali et al. 2007; Maruthi & Rani 2015). Hence, selection based on biomass yield traits can be done to accumulate favorable additive alleles. In addition to that, substantial improvements on biomass yield traits in both populations based on the high estimates of genetic advance if selections were to be made from these two segregating populations. Protein and acid detergent fibre contents were found to have moderate to high heritability with moderate genetic advance, which could suggest similar genetic control as biomass yield traits.

#### CORRELATION BETWEEN BIOMASS YIELD AND FORAGE QUALITY TRAITS

The results on phenotypic and genetic correlations among characters measured in the segregating  $F_2$  populations derived from Cross 1 and 2 were presented in Tables 3 and 4, respectively.



TABLE 3. Phenotypic (below diagonal) and genetic (above diagonal) correlation coefficients for forage yield and quality traits measured among F<sub>2</sub> individuals derived from Cross 1 (CML152 × CML383)

Trait	FPY	DPY	PH	NLP	DTT	DTS	CP	NDF	ADF	ADL
FPY		0.84**	0.60**	0.86**	-0.40*	-0.48**	0.13 <sup>ns</sup>	-0.19 <sup>ns</sup>	0.14 <sup>ns</sup>	0.11 <sup>ns</sup>
DPY	0.87**		0.55**	0.83**	-0.37*	-0.50**	0.11 <sup>ns</sup>	-0.20 <sup>ns</sup>	0.17 <sup>ns</sup>	0.20 <sup>ns</sup>
PH	0.75**	0.66**		1.00**	-0.36*	-0.37*	0.04 <sup>ns</sup>	-0.18 <sup>ns</sup>	0.21*	0.22*
NLP	0.65**	0.61**	0.78**		-0.54**	-0.64**	0.05 <sup>ns</sup>	-0.09 <sup>ns</sup>	0.11 <sup>ns</sup>	0.16 <sup>ns</sup>
DTT	-0.50**	-0.44*	-0.36*	-0.33*		0.80**	-0.11 <sup>ns</sup>	0.22*	0.14 <sup>ns</sup>	-0.05 <sup>ns</sup>
DTS	-0.63**	-0.63**	-0.39*	-0.38*	0.85**		-0.01 <sup>ns</sup>	0.31*	0.10 <sup>ns</sup>	-0.03 <sup>ns</sup>
CP	0.16 <sup>ns</sup>	0.12 <sup>ns</sup>	0.04 <sup>ns</sup>	0.08 <sup>ns</sup>	-0.10 <sup>ns</sup>	-0.08 <sup>ns</sup>		-0.13 <sup>ns</sup>	0.02 <sup>ns</sup>	0.21*
NDF	-0.19 <sup>ns</sup>	-0.19 <sup>ns</sup>	-0.15 <sup>ns</sup>	-0.11 <sup>ns</sup>	0.17 <sup>ns</sup>	0.24*	-0.11 <sup>ns</sup>		0.00 <sup>ns</sup>	-0.11 <sup>ns</sup>
ADF	0.13 <sup>ns</sup>	0.15 <sup>ns</sup>	0.15 <sup>ns</sup>	0.13 <sup>ns</sup>	0.10 <sup>ns</sup>	0.07 <sup>ns</sup>	0.01 <sup>ns</sup>	0.00 <sup>ns</sup>		0.24*
ADL	0.15 <sup>ns</sup>	0.26*	0.24*	0.29*	-0.05 <sup>ns</sup>	-0.03 <sup>ns</sup>	0.23*	-0.15 <sup>ns</sup>	0.35*	

N = 166, \*\* and \* = significant at  $p \leq 0.01$  and  $p \leq 0.05$ , respectively, <sup>ns</sup> = not significant

FPY = fresh plant yield, DPY = dry plant yield, PH = plant height, NLP = number of leaves per plant, DTT = days to tasseling, DTS = days to silking, CP = crude protein, NDF = neutral detergent fibre, ADF = acid detergent fibre and ADL = acid detergent lignin

TABLE 4. Phenotypic (below diagonal) and genetic (above diagonal) correlation coefficients for forage yield and quality traits measured among F<sub>2</sub> individuals derived from Cross 2 (CML491 × CML331)

Trait	FPY	DPY	PH	NLP	DTT	DTS	CP	NDF	ADF	ADL
FPY		1.00**	0.70**	0.71**	-0.30*	-0.38*	0.17 <sup>ns</sup>	-0.23*	0.10 <sup>ns</sup>	0.05 <sup>ns</sup>
DPY	0.96**		0.56**	0.03 <sup>ns</sup>	-0.31*	-0.37*	0.14 <sup>ns</sup>	-0.20 <sup>ns</sup>	0.09 <sup>ns</sup>	0.02 <sup>ns</sup>
PH	0.77**	0.72**		0.60**	-0.29*	-0.31*	0.03 <sup>ns</sup>	-0.14 <sup>ns</sup>	0.15 <sup>ns</sup>	0.24*
NLP	0.70**	0.63**	0.80**		-0.03 <sup>ns</sup>	-0.12 <sup>ns</sup>	0.15 <sup>ns</sup>	-0.31*	0.00 <sup>ns</sup>	0.12 <sup>ns</sup>
DTT	-0.32*	-0.39*	-0.15 <sup>ns</sup>	-0.02 <sup>ns</sup>		0.86**	-0.14 <sup>ns</sup>	-0.01 <sup>ns</sup>	-0.11 <sup>ns</sup>	0.06 <sup>ns</sup>
DTS	-0.43*	-0.48**	-0.24*	-0.11 <sup>ns</sup>	0.89**		-0.10 <sup>ns</sup>	-0.01 <sup>ns</sup>	-0.15 <sup>ns</sup>	0.05 <sup>ns</sup>
CP	0.19 <sup>ns</sup>	0.19 <sup>ns</sup>	0.03 <sup>ns</sup>	0.17 <sup>ns</sup>	-0.14 <sup>ns</sup>	-0.22*		-0.28*	-0.14 <sup>ns</sup>	0.34*
NDF	-0.20 <sup>ns</sup>	-0.20 <sup>ns</sup>	-0.12 <sup>ns</sup>	-0.27*	-0.01 <sup>ns</sup>	-0.01 <sup>ns</sup>	-0.22*		0.18 <sup>ns</sup>	-0.16 <sup>ns</sup>
ADF	0.11 <sup>ns</sup>	0.11 <sup>ns</sup>	0.12 <sup>ns</sup>	0.01 <sup>ns</sup>	-0.11 <sup>ns</sup>	-0.15 <sup>ns</sup>	-0.13 <sup>ns</sup>	0.23*		0.00 <sup>ns</sup>
ADL	0.06 <sup>ns</sup>	0.03 <sup>ns</sup>	0.08 <sup>ns</sup>	0.14 <sup>ns</sup>	0.06 <sup>ns</sup>	0.05 <sup>ns</sup>	0.33*	-0.21*	0.00 <sup>ns</sup>	

N = 162, \*\* and \* = significant at  $p \leq 0.01$  and  $p \leq 0.05$ , respectively, <sup>ns</sup> = not significant

FPY = fresh plant yield, DPY = dry plant yield, PH = plant height, NLP = number of leaves per plant, DTT = days to tasseling, DTS = days to silking, CP = crude protein, NDF = neutral detergent fibre, ADF = acid detergent fibre and ADL = acid detergent lignin

Phenotypic correlation coefficients in both populations showed positive and significant associations (at  $p < 0.01$ ) between fresh plant yield and dry plant yield, with  $r$  values ranging from 0.64 to 0.97 for Cross 1 and 0.78 to 0.98 for Cross 2. Fresh and dry plant yields were also observed to be positively and significantly correlated (at  $p < 0.01$ ) with plant height ( $r$  values ranging from 0.57 to 0.79) and number of leaves per plant ( $r$  values ranging from 0.52 to 0.76) in both populations. Significant positive correlation coefficients were also found between grain yield and yield components (Ravindra & Karan 2018). Biomass yield and yield components were inversely correlated with days to tasseling ( $r = -0.33$  to  $-0.50$  for Cross 1,  $r = -0.23$  to  $-0.43$  for Cross 2) and days to silking ( $r = -0.38$  to  $-0.63$  for Cross 1,  $r = -0.24$  to  $-0.53$  for Cross 2) in both populations, which implied that earlier maturing individuals had lower biomass yield. Similar results were reported by Kashiani et al. (2014) and Saleh et al. (2002). The results on the genetic correlations amongst biomass yield its components were consistent with those of the phenotypic correlations such that the correlation coefficients were high and significant (at  $p < 0.01$ ), suggesting that all biomass yield traits (fresh and dry plant yield) and their components were genetically correlated.

Correlation analyses were also performed to understand the underlying relationships among biomass yield traits and forage nutritive and digestibility components. The results were different in both populations. In the  $F_2$  population derived from Cross 1, it was observed that acid detergent lignin content had positive correlations (at  $p < 0.05$ ) with dry plant yield ( $r$  values ranging from 0.20 to 0.36), number of leaves per plant ( $r = 0.29$ ) and plant height ( $r = 0.24$ ), suggesting that taller and leafy plants with high dry plant yield had high lignin content. Acid detergent lignin content was also found to have positive correlation with acid detergent fibre content ( $r = 0.35$ ). When analysing the correlations amongst forage quality traits, the phenotypic and genetic correlation coefficients for protein content and acid detergent fibre content were found to be negative and significant (at  $p < 0.05$ ). In the  $F_2$  population derived from Cross 2, protein content was found to be negatively correlated (at  $p < 0.05$ ) with days to silking ( $r = 0.22$ ), indicating that plants that reached silking stage early were also those having high protein content. However, these traits were not significantly correlated genetically. This was expected as the genes controlling protein content and flowering should be different. Neutral detergent fibre content had negative phenotypic and genetic correlations (at  $p < 0.05$ ) number of leaves per plant ( $r = -0.27$ ). Analysis of correlation in this population also showed that protein content had negative correlations (significant at  $p < 0.05$ ) with neutral detergent fibre content ( $r = 0.22$ ) and acid detergent lignin content ( $r = 0.33$ ).

Selection strategies can be made by referring to correlation analysis among the traits. Fresh plant yield was positively correlated to all fresh and dry plant yield components, as well as plant height. On the other hand, biomass yield was negatively correlated to days to flowering. These findings were also in accordance with Kashiani et al. (2010), indicating that higher maize biomass yield was associated with early maturity. Significant correlation values between biomass yield traits could suggest that these traits were controlled by genes with pleiotropic effect or controlled by multiple genes that are tightly linked (Chen & Lübberstedt 2010). The genetic coefficient estimates showed stronger relationship for these traits compared to phenotypic correlation, thus supporting that these traits were genetically correlated. In both populations, fresh plant yield was found to be phenotypically and genetically correlated with dry plant yield, plant height and number of leaves per plant. For selection purposes, it is recommended to emphasize on these traits to improve for biomass yield improvement. The findings in correlation analysis also reported positive, although low correlation between dry plant yield traits and cell wall components that affect digestibility of the forage. This indicated that selection for traits related to high biomass yield would also increase fibre and lignin content in plants. This was in accordance with Chen and Lübberstedt (2010) who reported that the decrease in digestibility (high lignin content) was correlated to the increase in biomass yield. Nevertheless, since the heritability estimate of ADL were considerably high, selection against individuals with high fibre content can be made earlier in forage maize breeding program.

## CONCLUSION

Traits with moderate to high heritability and substantial genetic advance such as plant height and fresh plant yield can be used as selection criteria in forage maize breeding program to allow significant genetic improvement in biomass yield. On the same note, crude protein content can also be used as selection criterion to improve forage maize nutritive quality. Significant correlations were found among biomass yield traits as well as with lignin content. Therefore, selecting higher biomass yield would increase plant lignin content, hence decreasing the digestibility. It is suggested that marker assisted selection approach would be appropriate in order to select high yielding individuals with acceptable lignin content in developing forage maize varieties.

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