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Genetic variability and heritability of vegetative, fruit and seed yield traits in fluted pumpkin (*Telfairia occidentalis* Hook F)

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Telfairia occidentalis (fluted pumpkin) is a leafy vegetable crop popularly cultivated in the South-eastern part of Nigeria for its economic value and important role in nutrition and poverty alleviation. Nine genotypes of fluted pumpkin collected from different localities in Ogun, Lagos and Oyo States Nigeria were grown in the teaching and research farm of the School of Agriculture, Babcock University during the rainy season of 2011, in order to determine genetic variability and heritability of 15 characters comprising of seven vegetative, five fruit and three seed yield traits in fluted pumpkin. The experiment was laid out in a randomized complete block design with three replications. The results reveal huge genetic diversity among the genotypes studied. Number of branches per plant, vine length and number of fruits per plant were the most genetically divergent traits measured. Vine length (21.72, 97.38 and 44.16), number of branches per plant (23.86, 96.59, 48.31), seed weight per plant (18.43, 79.31 and 33.81) and leaf width (11.36, 80.73 and 21.03) showed high genotypic coefficient of variability (GCV), heritability and genetic advance (GA). These characters are most likely under additive gene control and can be effective in the prediction of vegetative, fruit and seed yield in *Telfairia*. Correlation analysis revealed that selection directed towards leaf length, leaf width, petiole length, vine length, vine width, number of fruit per plant, fruit length and fruit width will be efficient in improving vegetative and seed yield in *T. occidentalis*.

Key words: Fluted pumpkin, cucurbitaceae, divergent, vegetative, genetic advance.

INTRODUCTION

Telfairia occidentalis also known as fluted pumpkin is a leafy vegetable crop commonly cultivated in the South-eastern part of Nigeria (Odiaka et al., 2008); however, it

is gradually gaining prominence in the western part of the country (Schippers, 2002). It belongs to the family Cucurbitaceae having over 90 genera (Akoroda, 1990). It

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has a creeping growth habit that spreads across the ground to produce an efficient cover to the ground against erosion (Horsfall and Spiff, 2005) and produces large fruits with many large seeds. The seed is a rich source of oil and protein in the proportion of 30.1 and 47%, respectively (Akoroda, 1990; Ehiagbonare, 2008); while the leaf is a veritable source of protein, iron, saponin, tannins, phytic acid, vitamins and minerals (Akwaowo et al., 2000; Akanbi et al., 2007; Ehiagbonare, 2008). The leaf extract is commonly used in the treatment of anaemia, high blood pressure, convulsion and diabetes (Ehiagbonare, 2008; Fayeun et al., 2012); whereas the seed oil extract can be used in the production of margarine and pomade (Asiegbu, 1987). Beyond its nutritional and medicinal values, farmers prefer to grow fluted pumpkin because it generate appreciable cash to small family holdings thus alleviating poverty (Akoroda, 1990; Fayeun et al., 2012). It also portrays an ethnobotanical importance in the folklore of the Igbo's in the South-eastern part of Nigeria (Oyekunle and Oyelere, 2005)

The success of any crop breeding programme largely depends on the availability of huge genetic variability, genetic advance and character association, direct and indirect effects on yield and its attributes (Nwangburuka et al., 2012). Genetic diversity is important for selection of parents to recover transgressive segregants (Kiran Patro and Ravisankar, 2004). Genetic variability and heritability studies have been conducted on various vegetable crops in their breeding programme. For instance, *Solanum anguivi* (Denton and Nwangburuka, 2011), okra (Nwangburuka et al., 2012), *Corchorus olitorius* (Nwangburuka and Denton, 2012), kenaf (Mostofa et al., 2002), roselle (Ibrahim and Hussein, 2006), tomato (Foolad et al., 2006), cowpea (Aremu et al., 2007) or eggplant (Islam and Uddin, 2009). However, there is sparse information on the heritability studies in fluted pumpkin (Aremu and Adewale, 2012). The few information on heritability in fluted pumpkin has focused more on the vegetative yield characters (Oyekunle and Oyelere, 2005; Fayeun et al., 2012, Aremu and Adewale, 2012). Meanwhile, abundance and availability of improved seeds is a major factor in the continuous cultivation of fluted pumpkin for economic purpose and nutrition. Hence, there is need to evaluate the diversity in fluted pumpkin in both vegetative, seed and fruit characters and the heritability of these characters as a tool in the improvement of the overall yield of this crop.

Determination of heritability estimates, using different methods (Obilana and Fakorede, 1981; Wray and Visscher, 2008) will provide information on the proportion of phenotypic variance that is due to genetic factors for different traits but heritability estimate alone is not a sufficient measure of the level of possible genetic progress that might arise not even when the most outstanding individuals are selected in a breeding programme. The value of heritability estimates is enhanced

when used together with the selection differential or genetic advance (Ibrahim and Hussein, 2006). Information on the amount and direction of association between yield and yield related characteristics is important for rapid progress in selection and genetic improvement of a crop (Asish et al., 2008). This will indicate the interrelationship between two or more plant characters and yield, providing suitable means for indirect selection for yield.

This study is aimed at evaluating the genetic variability in fluted pumpkin and further determining the traits associated with the seed, fruit and vegetative yield in fluted pumpkin. The heritability of those traits will be evaluated for indirect selection to improve fluted pumpkin fruit, seed and leaf yield.

MATERIALS AND METHODS

The nine accessions of fluted pumpkin used for this study were collections from different localities in Ogun, Lagos and Oyo State, where fluted pumpkin is intensively cultivated and deposited in the germplasm of the Department of Agriculture Babcock University, Ogun State, Nigeria.

This study was conducted in the Teaching and Research Farm of the Department of Agriculture Babcock University, Ilishan-Remo, Ogun State, Nigeria located on 6° 5'N, 6° 43'E during the rainy season of May 2011 to December 2011. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each replication consists of nine plots of double rows of *Telfairia* genotypes identified as follows: BUTEL001, BUTEL002, BUTEL003, BUTEL004, BUTEL005, BUTEL006, BUTEL007, BUTEL009 and BUTEL010. Each row was 9 m long with intra-row spacing of 1 m and inter row spacing of 1 m whereas the distance between each plot was 2 m following the procedure provided in the Department of Agriculture Babcock University. The seeds lot were confirmed viable after germination test before planting. There were a total of nine plants per row, given a total of 18 plants per plot of genotype. The seeds were sown directly into the already prepared soil after allowing it under the sun for about 6 h as a pre-germination condition to enhance early germination.

Data collection

Data were collected on the following vegetative and seed yield characters as shown in Table 1.

Data analysis

The plot means for each character was subjected to analysis of variance using SAS (1999) employing the method prescribed by Steel and Torrie (1980). The yield and its component were used to determine the genotypic and phenotypic variances according to Prasad et al. (1981).

$$\text{Genotypic variance } (\delta^2_g) = (\text{MSG} - \text{MSE})/r$$

$$\text{Phenotypic variance } (\delta^2_{ph}) = \text{MSG}/r$$

$$\text{Error variance } (\delta^2_e) = \text{MSE}/r$$

Where, MSG = Genotype mean squares; MSE = error mean squares; R = number of replications

Table 1. Quantitative characters of *Telfeiria occidentalis* and the method of measurement.

Quantitative characters	Method/Unit of Measurement
Leaf length at 9 weeks	Measured from five middle row plants (cm)
Leaf width at 9 weeks	Same as in above using a ruler (cm)
Vine length at 9 weeks	Same as in above using a tape (cm)
Vine width	Same as in above using a vernier caliper (cm)
Number of branches at 9 weeks	Same as in above
Petiole Length at 9 weeks	Same as in above using a ruler (cm)
Number of leaflet at 9 weeks	Determined from 5 random leaves on the vine
Number of fruit per plant at harvest	Average Count of all fruits per plot/rep
Fruit weight per plant at harvest	Average weight of 10 fruits/plot (kg)
Fruit length at harvest	Same as in above using a ruler (cm)
Fruit width at harvest	Same as in above using a tape (cm)
Number of seeds per fruit at harvest	Mean from 5seeds/ 10 random fruit per row (g)
Seed length at harvest	Mean from 20 bulked seeds per row(cm)
Seed width at harvest	Same as in above using a ruler (cm)
Total seed weight per fruit harvest	Mean of seeds from 5 random fruits /row (g)

The variance components was used to compute the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) as follows according to the methods of Burton (1952), Johnson et al. (1955) and Kumar et al. (1985).

Genotypic coefficient of variability = $100 \times [(\delta g)/x]$

Phenotypic coefficient of variability = $100 \times [(\delta ph)/x]$

Where, δg and δph are the genotypic and phenotypic standard deviations, respectively and X is the grand mean for the character under consideration.

The Broad-sense heritability and expected genetic advance, assuming a selection intensity of 5% were estimated according to the formula of Allard (1960) and Miller et al. (1958) as follows:

Heritability (Broad-sense) = $(\delta^2g) / [\delta^2g + \delta^2e]$

Where, δ^2g is the estimate of genotypic variance and δ^2e is the estimate of environmental variance.

Genetic advance = heritability $\times k \times \delta ph$

Where, K (selection differential expressed in phenotypic standard deviations) = 2.06

Estimates of genotypic and phenotypic correlation coefficients among the characters were obtained using the formula of Miller et al. (1958):

$$r_{x,y} = \frac{CoV_{(x,y)}}{\sqrt{(\delta^2x)(\delta^2y)}}$$

Where, $r_{x,y}$ is either genotypic or phenotypic correlation between variables x and y ; $CoV_{(x,y)}$ is the genotypic or phenotypic covariance between two variables; δ^2x is the genotypic or phenotypic variance of the variable x , δ^2y is the genotypic or phenotypic variance of the variable y .

In order to determine the interrelationships amongst the character traits (yield characters) correlations were calculated. Experimental correlation coefficients were determined according to Falconer (1981).

RESULTS AND DISCUSSION

The result of analysis of variance indicated significant differences ($p > 0.01$ and 0.05) in genotypes in all the characters studied except in number of fruits per plant at harvest, fruit weight per plant at harvest, fruit length at harvest, fruit width at harvest, seed length at harvest and seed width at harvest (Table 2). This suggests significant diversity among the genotypes studied. This finding is at variance with earlier observation by Ajayi et al. (2006), who reported a narrow genetic diversity in *T. occidentalis*. However, our finding agrees with the reports of Aremu and Adewale (2012) and Fayeun et al. (2012) who observed significant genetic variability in *Telfairia* genotypes in vegetative characters such as number of branches per plant, vine length and vine width, number of foliage and foliage width.

This observation further suggests that there is relatively low variability in fruit and seed traits compared to the vegetative traits in *T. occidentalis*. Table 3 shows the means, genotypic and phenotypic variances, genotypic coefficient of variability (PCV and GCV), estimates of broad-sense heritability and genetic advance in all the characters studied in the nine *Telfairia* genotypes. Generally, the genotypic variance is higher than the environmental variance, except in number of fruits per plant and fruit yield per plant. This may suggest that the genotype component contributed more to the expression of the vegetative and few of the seed and fruit characters compared to the contribution of the environment. This information will enhance selection towards vegetative yield as well as seed yield in *Telfairia*.

This observation is contrary to the report of Fayeun et al. (2012), who observed higher environmental variance in number of branches over genotypic variance. Meanwhile, procurement of sufficient seeds has been

Table 2. Mean Squares of leafy vegetable and seed yield related characters of Nine *Telfairia* accessions.

Source of Variation	df	Leaf length at 9 weeks	Leaf width at 9 weeks	Vine length at 9 weeks	Vine width at 9 weeks	Number of branches at 9 weeks	Petiole length at 9 weeks	Number of leaflets at 9 weeks	Number of fruits per plant at maturity	Fruit weight per plant at maturity	Fruit length at maturity	Fruit width at maturity	Number of seeds per fruit at maturity	Seed length at maturity	Seed width at maturity	Total seed weight per fruit at maturity
Block	2	27.97**	6.46**	144.05	0.007	0.02	0.21	0.02	61.18*	5.50*	8.44	14.78	278.86	0.12	0.003	0.06*
Genotype	8	6.02*	5.35**	3526.15**	0.01*	2.11**	3.63**	0.15**	26.62	1.76	62.82	20.75	291.13*	0.06	0.04	0.06**
Error	16	2.19	1.03	92.37	0.002	0.07	0.10	0.01	14.92	1.25	17.53	8.69	120.84	0.07	0.04	0.01
CV %		9.99	9.61	6.17	9.23	7.76	2.48	3.26	39.44	32.01	12.27	10.62	26.21	7.47	5.50	10.24

*Significant at 5% ($p > 0.05$) level of probability; **significant at 1% ($p > 0.01$) level of probability.

Table 3. Estimates of Phenotypic and Genotypic variance, Phenotypic and Genotypic coefficient of variability, Broad sense Heritability and Genetic Advance in 15 characters of *T. occidentalis*.

Character	Phen var	Gen var	Env var	PCV	GCV	Heritability	Gen adv%
leafL9wk	2.01	1.28	0.73	9.57	7.63	63.62	12.54
leafW9wk	1.78	1.44	0.34	12.64	11.36	80.73	21.03
Petlgt9wk	1.21	1.18	0.03	8.53	8.41	97.16	17.08
Vinelgt9wk	1175.39	1144.60	30.79	22.02	21.72	97.38	44.16
Vinewidth9wk	0.00	0.00	0.00	11.23	10.16	81.82	18.93
Nobranches9wk	0.70	0.68	0.02	24.28	23.86	96.59	48.31
Noleaflet	0.05	0.04	0.00	6.52	6.24	91.72	12.32
Nofruit	8.87	3.90	4.98	30.41	20.15	43.93	27.52
Fruityield	0.59	0.17	0.42	21.93	11.82	29.03	13.12
Noseed	97.04	56.76	40.28	23.49	17.96	58.49	28.30
Fruitlgt	20.81	14.96	5.84	13.37	11.34	71.92	19.81
Fruitwdt	6.92	4.02	2.90	9.47	7.22	58.10	11.33
Seedlgt	0.02	0.00	0.02	4.33	1.68	15.15	1.35
Seedwdt	0.01	0.00	0.01	3.46	1.38	15.91	1.13
Wgtseed	0.02	0.02	0.00	20.69	18.43	79.31	33.81

LeafL9wk = Leaf length at 9 weeks; leafW9wk = leaf width at 9 weeks; Petlgt9wk = petiole length at 9 weeks; Vinelgt 9wk = vine length at 9 weeks; Vinewidth9wk = vine width at 9 weeks; Nobranches9wk = number of branches at 9 weeks; Noleaflet = number of leaflets; Nofruit = number of fruits per plant; Fruityield = fruit yield per plant; Noseed = number of seeds per fruit; Fruitlgt = fruit length; Fruitwdt = fruit width; Seedlgt = seed length; Seedwdt = seed width; Wgtseed = weight of seed per plant; Phen var = phenotypic variance; Gen var = genotypic variance; Env var = environmental variance; PCV = phenotypic coefficient of variability; GCV = genotypic coefficient of variability; Gen adv% = genetic advance.

observed as a major challenge confronting *Telfairia* farmers (Oyekunle and Oyelere, 2005)

and can be significantly addresses via selections towards vegetative and seed yield. The higher

environmental variance observed in number of fruits per plant and fruit yield per plant may be due

to environmental interference encountered during the commonly practiced exercise of removing more of the male plants in order to allow for more of female plants to favour fruit production in *T. occidentalis*.

This practice can lead to abortion of young developing fruits. Hence, selection on the basis of number of fruits and fruit yield per plant for yield improvement is environment specific. There was higher genotypic variance over environmental variance in number of branches per plant, indicating a significant contribution of the genotypic component in the branching of the accessions. This further suggests adequate genetic gain when selection favours number of branches per plant. This observation is contrary to the report of Fayeun et al. (2012) who observed higher environmental variance against genotypic variance in branching per plant. Similarly, phenotypic variance was slightly higher than the genotypic variance in all the characters studied as expected, since the phenotype variance is the sum of both the genotypic and environmental variance. This report agrees with the observation of Fayeun et al. (2012), who observed higher phenotypic variance in all the character studied above the genotypic variance. High genotypic variance facilitates selection for improvement and widens the probability for heritability of traits from parents to offsprings (Ayanley et al., 2012).

The values of phenotypic coefficient of variability (PCV) and the genotypic coefficient of variability (GCV) are useful in comparing the relative amount of phenotypic and genotypic variation among different characters. The PCV values were slightly higher than the GCV values in all the characters studied, confirming slight environmental influence on the expression of all the characters studied. This corresponds to the report of Fayeun et al. (2012), who observed higher PCV in all the vegetative characters studied in *T. occidentalis*, except in vine width and leaf length.

Similarly, Nwangburuka and Denton (2012), also observed higher PCV above GCV in all the vegetative characters studied in *Corchorus olitorius*. Number of branches per plant, Vine length and Number of fruits per plant were the most genetically variable traits compared to the others with values (23.86, 21.72 and 20.15%) respectively and therefore may be considered in the distinguishing the genotypes. This also agrees with the report of Aremu and Adewale (2012) as well as Fayeun et al. (2012), who observed high GCV in number of branches per plant and vine length in *Telfairia*. Similarly, the relatively high PCV and GCV values recorded in the above mentioned three traits suggests huge prospects for selection based on these traits in the improvement of the crop (Denton and Nwangburuka, 2011; Ayanley et al., 2012).

Estimates of broad-sense heritability varied from 15.91 in seed width to 97.38 in vine length. Estimates of broad-sense heritability has been categorized (Dabholkar 1992) as low (5-10%), medium (11-30%) and high (>30%). All

the traits expressed heritability between medium and high, with the following characters exhibiting extremes of high heritability petiole length (97.16), vine length (97.38), number of branches per plant (96.59), number of leaflet (91.72), vine width (81.82) and leaf width (80.73). This agrees with the reports of Aremu and Adewale (2012), who observed high broad-sense heritability in foliage numbers, vine and branching traits in *Telfairia*. These high estimates of heritability observed in the traits mentioned above suggests that inheritance of these traits are under additive control, hence selection on the basis of these character will result in crop improvement and therefore reliable (Ullah et al., 2011). However, predictions of an individual's response to selection is more reliable when the estimate of broad-sense heritability is combined with GCV and genetic advance (GA) (Ibrahim and Hussein, 2006), instead of relying on GA values alone. Thus characters such as vine length and number branches per plant with high combination GCV, heritability and GA are most likely under additive gene control and will be effective in the prediction of yield (Bello et al., 2006). This agrees with the recent observation by Mohammed et al., (2012) on their report on wheat. Meanwhile high heritability and GA is an estimate of how much selection to improve a character in plants can be based on phenotypic observation (Johnson et al., 1955; Idahosa et al., 2010).

Estimates of genotypic and genotypic correlation of characters was also determined and expressed in Table 4. The result shows that there was strong significant positive phenotype and genotypic correlation between seed weight per pod and vine width (0.62, 0.81), number of fruits per plant (0.59, 0.86), fruit yield (0.77, 1.28), fruit length (0.73, 0.75) and fruit width (0.69, 0.70). This suggests that selections directed to any of the traits mentioned above may likely favour seed weight in *T. occidentalis*.

Similar reports have been presented by Nwangburuka et al. (2012) in okra. However, significant positive genotype correlation was observed between seed weight per pod and seed length (0.69), number of leaflet (0.40) and leaf width (0.40). This suggests that selection made on the basis of the genotypic expression of these characters will result in seed weight increase in *T. occidentalis*. Similarly, there was strong negative significant phenotypic and genotypic association between seed width and leaf length (-0.43, -1.70), vine width (-0.52, -1.47) and number of seeds per pod (-0.56, -1.03). This strongly suggests that a selection that is based on leaf length and vine width will not favour seed width. Seed width is one of the seed characters in *T. occidentalis* that determine seedling vigour and early crop performance. Meanwhile strong genotypic association exists between seed width and petiole length (0.71), vine length (0.40), number of branches per plant (0.79), number of leaflet (1.13), fruit width (0.75), but very strong negative genotypic association with seed length (-2.41).

Table 4. Contd

Seedwdt	
P	-0.14
G	-0.19

LeafL9wk = Leaf length at 9 weeks; leafW9wk = leaf width at 9 weeks; Petlgt9wk = petiole length at 9 weeks; Vinelgt 9wk = vine length at 9 weeks; Vinewidth9wk = vine width at 9 weeks; Nobranches9wk = number of branches at 9 weeks; Noleaflet = number of leaflets; Nofruit = number of fruits per plant; Fruityield = fruit yield per plant; Noseed = number of seeds per fruit; Fruitlgt = fruit length; Fruitwdt = fruit width; Seedlgt = seed length; Seedwdt = seed width; Wgtseed = weight of seed per plant; P = phenotypic correlation; G = genotypic correlation.

This suggests that selection base on seed length may yield seeds with small width, whereas those based on petiole length, number of branches number of leaflet, may affect seed width positively. Result further shows that there was significant phenotypic and genotypic correlation between seed length and number of leaflets (90.46, 1.19). Whereas seed length had negative genotypic correlation with number of branches (-0.97), number of fruits per plant (-0.91), fruit length (-0.470) and fruit width (-1.02), there was a positive significant genotypic association between seed length and petiole length (0.71), vine width (0.97) and number of seeds per pod (0.63). This suggests that selection based on number of branches, number of fruits per plant, fruit length and fruit width may depress seed length expression, while selection based on petiole length, vine length will favour seed length. Seed size is a function of seed length and seed width. However, large seed sizes have a reproductive advantage over small seed sizes under adverse shaded conditions and hence promotes seedling vigour. It is very important for the establishment of seedlings (Kenji and Kihachiro, 1999). The result for fruit width indicated strong positive phenotypic and genotypic correlation between leaf width (0.72, 1.19), vine length (0.51, 0.66), vine width (0.41, 0.63), number of fruits per plant (0.54, 0.97), fruit yield per plant (90.69, 1.52) and fruit length (0.95, 1.03). This result suggests that fruit width increase is dependent on the vegetative

characters such as vine length and width, which serves as connecting tissues between the leaves and the fruits. However, fruit width is positively associated in genotypic term with petiole length (0.40) and negatively associated to fruit length (-0.47). This may imply that selections directed towards petiole length will favour fruit width while selection based on fruit length will not be meaningful. The correlation between fruit length and the other characters follow the same trend like that of fruit width and the other characters except that fruit length had a positive genotypic association with leaf length (0.47) and petiole length (0.39). Though selection based on petiole length may not favour fruit width, however it favours fruit length in *T. occidentalis*. The number of seeds per pod is a strong determinant of seed yield in *Telfairia* and has a strong positive phenotypic and genotypic correlation with vine width (0.61, 0.98), while it showed a negative correlation with leaf width. This could be because the leaf width contributes to accumulation of photosynthetic assimilate which will boost seed size rather than the seed number. Similarly there was a strong positive genotypic correlation between number of seeds and the number fruit per plant. The result of the correlation analysis further reveals a positive phenotypic and genotypic correlation between fruit yield and leaf length (0.40, 0.70), vine length (0.56, 1.15), number of leaflet (0.43, 0.71) and number of fruits (0.65, 1.33). This suggests that selection on the

basis of the above mentioned characters will promote fruit yields. However, number of fruit per plant is positively associated at phenotypic and genotypic levels with vine width (0.48, 0.79), whereas, it only had a positive genotypic association with leaf width (0.66), vine length (0.52) and number of leaflets (0.43). This result portrays the strong relationship between vegetative traits and reproductive trait such as fruit and seed characters. Meanwhile, number of leaflet, a component of the vegetative yield in *Telfairia* had a strong significant phenotypic and genotypic correlation with other vegetative characters such as leaf length (0.41, 0.56), leaf width (0.51, 0.56), petiole length (0.51, 0.52) and vine length (0.67, 0.70). This also suggests that genetic improvement of *Telfairia* in vegetative yield will be effective when such characters highlighted above are considered. Number of branches per plant is negatively associated with vine width on the phenotypic and genotypic level (-0.65, -0.71) whereas it is positively associated with leaf width on phenotypic and genotypic levels (0.46, 0.53), respectively. This suggests that vine thickness in *Telfairia* may hinder the branching characteristic in *Telfairia*. Meanwhile branching characteristic in *Telfairia* is a vegetative yield component. However, a positive phenotypic and genotypic correlation exists between number of branches and leaf width, suggesting that selection directed toward leaf width will favour number of branches. This agrees with the report

of Fayeun et al. (2012), who reported positive correlation between number of branches per plant and leaf width. Vine length showed significant positive phenotypic and genotypic correlation with leaf length (0.77, 1.05), leaf width (0.58, 0.62) and petiole length (0.66, 0.67), while petiole length had a strong positive phenotypic and genotypic correlation with leaf length (0.47 and 0.67) and leaf width (0.45 and 0.49). This results suggest that vegetative yield in *Telfairia* is promoted by traits such as leaf length, width, petiole length and vine width. This agrees with the report of Fayeun et al. (2012). The higher genotypic correlation coefficient over phenotypic correlation coefficient observed in almost all the characters suggests very strong inherent association between various characters at genetic level. This is similar to the report of Ibrahim and Hussein (2006) on roselle (*Hibiscus sabdariffa*).

In conclusion, this study reveals that there is significantly large diversity in *T. occidentalis* genotypes studied which is sufficient enough for its genetic improvement. This diversity is contributed mostly by the vegetative traits. Vegetative traits such as number of branches per plant, vine length and number of fruits per plant can be used in distinguishing *T. occidentalis*, being the most genetically divergent traits in the genotypes. Characters such as vine length and number branches per plant, seed weight and leaf width with high GCV, heritability and GA were most likely under additive gene control and could be effective in the prediction of vegetative, fruit and seed yield in *Telfairia*. Hence, selection directed towards leaf length, leaf width, petiole length, vine length, will be efficient in improving vegetative yield in *T. occidentalis*, whereas selection on the basis of vine width, number of fruit per plant, fruit length, fruit width and leaf width will favour improvement in seed yield.

Conflict of Interest

The author(s) have not declared any conflict of interests.

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