Variability and Association of Quantitative Traits in *Plectranthus edulis* (Vatke) Agnew

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Abstract: Thirty six accessions of *Plectranthus edulis* were evaluated to estimate the nature and magnitude of variability and associations among tuber yield and related characteristics. Analysis of variance for each characters indicated highly significant ($p<0.01$) variation among the accessions for all characters except tuber length. Relatively high phenotypic (43.17, 37.85, and 24.25 %) and genotypic coefficients of variation (42.42, 36.47 and 18.40%) were observed for tuber weight per hill, number of tuber per hill and stem number per hill in the order of magnitudes. High heritability (96.50 and 92.84%) coupled with high genetic advance as percent of mean (86.85 and 72.38%) were recorded for tuber weight per hill and number of tubers per hill respectively. Analysis of phenotypic correlation indicated that tuber yield per hill was significantly and positively associated with number of branches ($r =0.366$), tuber diameter ($r = 0.435$), and number of tuber per hill ($r =0.567$). Path coefficient analysis at genotypic level also revealed that number of tubers per hill ($p=0.982$) exerted a high magnitude of positive direct effect on tuber weight per hill. Nevertheless, the need for confirmation of genotypic-environment interaction and widening of the genetic base for *P. edulis* improvements are suggested.

Keywords: Correlation Analysis; Genetic Variability; Path Analysis; *Plectranthus edulis*

1. Introduction

Plectranthus edulis is an indigenous annual tuber crop grown widely in the central, southern, western, northwestern and southwestern parts of Ethiopia (Uphof, 1968; Westphal, 1975; Zeven and Zhukovsky, 1975; PGRC/E, 1986; Edward, 1991; Edossa, 1996; Abdissa, 2000; GRIN, 2005). It is a dicotyledonous plant and belongs to the family Lamiaceae/Labiatae; subfamily Nepetoideae and tribe Ocimeae (GRIN, 2005).

In the various growing areas of Ethiopia, different vernacular names are used for *Plectranthus edulis*. Among these are '*Dinicha Oromo*' in Oromia, meaning "potato of the Oromo people" (Abdissa, 2000), '*Wolaita Dinich*' (potato of the Wolayita people) around Wolaita (Endale, 1997), '*Agew Dinch'* (potato of the Agew people) in the northwest and '*Gurage Dinich'* (potato of the Gurage people) around Gurage zone (Westphal, 1975). For generations, farmers in different parts of the country have been cultivating *Plectranthus edulis,* primarily for its edible tuber. The leaves are also eaten as a green vegetable in some regions (Abebe, 1988). Moreover, the edible tubers are good for people with asthma (IAR, 1980) and, because of its abundant nectar, the plant is a good source of honey (Reinhard and Admasu, 1994).

Despite its importance for food security as well as its medicinal value, only limited research has been conducted on the crop (Abebe, 1988). On the other hand, changes in agricultural practices and environmental degradation are causing genetic loss in the local gene pool of this crop (Amsalu and Tesfaye, 2004). In response to these problems and the expressed need for making useful germplasm readily available for crop improvement programs, some collection and conservation work has been started. However, the collected accessions have not been properly characterized and evaluated, their attributes remaining unknown to breeders. Admasu (2002) indicated that lack of knowledge about the genetic diversity of the enset crop complicated the conservation, improvement and utilization by farmers, conservationists and breeders. He also noted that knowledge about clonal diversity allows the selection of clones prioritized for conservation, by removing duplication and optimizing genetic diversity and hence optimizing cost benefit ratio in maintaining the crop germplasm.

Therefore, the value of the conserved germplasm depends greatly upon the information available on each accession. Furthermore, the effectiveness of selection also depends upon the amount of variability existing in the material, the extent to which the character is heritable and the association/correlation between traits. This study, therefore, was undertaken to characterize the accessions in the collection and identify the nature and magnitude of variability of traits and their association with each other, with the ultimate goal of providing a basis for conservation and utilization in a breeding program.

2. Material and Methods

The study was carried out at Jimma Agricultural Research Centre. The site is located at $7^0$46' N and 36^0 E with an altitude of 1753 meters above sea level. The soil type of the experimental area is Eutric Nitosol (reddish brown) with a pH of around 5.2. The area receives mean annual rainfall of 1536 mm with a mean annual maximum and minimum temperatures of 25.9 ^oC and 11.2 ^oC, respectively (IAR, 1997).

A total of 36 *Plectranthus edulis* accessions collected from six different regions of the country by Jimma Agricultural Research Centre and Institute of Biodiversity Conservation were grown in single row plots during the 2005 main cropping season (April-October) in 6 x 6 simple lattice design. Each row was 3.5 m long with a space of 1 m between rows. Plants were spaced 50 cm apart within the row. Tubers which had just started sprouting were used as planting material. Planting was done at the beginning of the rainy season (April) in well-drained, loose soil on flat ground. Three kg/plot of

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ISSN 1992-0407

farmyard manure (8.571 t/ha) was applied along the rows. One month later, when the crop was well established, earthing up with loose soil was undertaken. Hand weeding was conducted as required to keep plots weed-free.

A total of 16 quantitative traits were recorded on plant basis on five selected plants. The average of five plants was used for statistical analysis. Days to flower initiation and days to 50 percent flowering were recorded on plot basis. The collected traits included : Plant height (cm): the height measured from the mounding to the tip of the plant at crop maturity (the longest height); Stem girth (cm): the diameter (girth) of the main stem measured at the fourth internode from the mound at 50 % flowering; Number of tubers per hill: the actual count of the number of tubers at harvest; Tuber length (cm): the average length of five tubers per hill measured at harvest; Tuber diameter (cm): the average diameter of five tubers measured per hill at harvest using vernier calliper; Number of nodes: the number of nodes on the main stem counted at 50% flowering; Internodes length (cm): the length of nodes on the main stem measured at 50% flowering; Tuber weight per hill (kg): the total weight of tubers per hill (tuber yield per hill or plant);Tuber dry matter content (%): estimated by drying 500 g tuber in a forced air circulation oven at 70^{0}C for about 72 hours and expressed in percentage of the total tuber weight and Number of stems per hill: the number of stems at crop maturity per hill.

Days to initiation of flowering: number of days from planting until the appearance of the first open flower in any of the sampled plants; Days to flowering: number of days from planting to the stage when 50% of the sampled plants have begun to flower; Number of primary branches: number of primary branches on the main stem counted at crop maturity; Leaf length (cm): length of the leaf on the main stem originating at the fourth node below the main stem inflorescence; Leaf width (cm): width of the leaf on the main stem originating at the fourth node below the main stem inflorescence and Flower length (cm): length of flowers measured at 50% flowering.

Since the relative efficiency of simple lattice design over randomized complete block design was low, mean values of the characters were subjected to RCBD ANOVA to derive variance components as setout below.

Phenotypic σ^2_p and genotypic σ^2_g variances and coefficient of variations PCV and GCV were calculated according to the method suggested by Burton and Devane (1953) considering genotypes as random effects using SAS Statistical Package (SAS, 2001).

Genotypic variance component

$$(\sigma^2 g) = \frac{MS_g - MS_e}{r}$$

Where MS_g is genotypic mean square, MS_e is Error mean square and r is replication

Environmental variance component (on genotype mean basis) $(\sigma^2 e) = \frac{MS_e}{r}$

Phenotypic variance component

$$(\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

The phenotypic and genotypic coefficients of variation were calculated according to the method suggested by Burton and Devane (1953) as:

Genotypic Coefficient of Variation

$$(GCV) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} * 100$$

Phenotypic Coefficient of Variation

$$(PCV) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} * 100$$

Where $\bar{X}$ is the grand mean value of the trait

Broad sense heritability (h^2) in percents was estimated for each character using variance components as described by Allard (1960).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} * 100$$

The expected gain or genetic advance (GA) with one cycle of selection, assuming the selection intensity (k) of 5%, was predicted as suggested by Poehlman and Sleeper (1995).

$$GA = h^2 \kappa \sigma p$$

Expected genetic advance (GA) in percent of the mean

$$= \frac{GA}{\bar{X}} * 100$$

Covariance analysis was carried out in the same way as that of analysis of variance, and the mean cross products were equated with the expected mean square product to calculate the covariance component used to compute the correlation coefficients.

Genotypic covariance of traits x and y

$$(\sigma gxy) = \frac{MSCP_{gxy} - MSCP_{exy}}{r}$$

Where, MSCPgxy is the genotypic mean cross product of traits x and y

MSCPexy is the error mean cross product of traits x and y

Phenotypic covariance

$$(\sigma_{pxy}) = \sigma_{gxy} + \frac{\sigma_{exy}}{r}$$

Genotypic and phenotypic correlation coefficients for tuber yield and its components were estimated by calculating the variance and covariance at phenotypic and genotypic levels by using the formula suggested by Singh and Chaudhury (1985).

Phenotypic correlation, the observable correlation between two variables, which includes both genotypic and environmental components between two variables,

was estimated using the formula suggested by Miller *et al.* (1958) as: $r_{pxy} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px})(\sigma^2_{py})}}$

Genotypic correlation between traits x and y was computed as: $r_{gxy} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2 gx)(\sigma^2 gy)}}$

Where, σ^2_{gx} and σ2px are genotypic and phenotypic variance components of trait x.

The coefficients of correlation at phenotypic level were tested for their significances using the t – test as

$$t = \frac{r_{pxy}\sqrt{g-2}}{\sqrt{1-r^2_{pxy}}}$$

The calculated 't' value was compared with the tabulated 't' at g-2 degree of freedom, where g is the number of genotypes.

The correlation coefficients at genotypic level were tested with the following formula suggested by Robertson (1959).

$$t = \frac{r_{gxy}}{SEr_{gxy}}$$

Where r_{gxy} is the genotypic correlation coefficient, SEr_{gxy} is the standard error of genotypic correlation coefficient and

$$SEr_{gxy} = \sqrt{\frac{(1-r^2 gxy)^2}{2h^2 xh^2 y}}$$

Where, h^2_x and h^2_y are broad sense heritability for characters x and y respectively. The calculated t value for each genotypic correlation coefficient was tested against tabulated 't' at (g-2) degrees of freedom.

In path coefficient analysis which indicates causal relationship, tuber weight per hill was considered as the dependent variable while the rest of the variables were used as independent variables.

Path coefficient analysis was calculated using the formula suggested by Dewey and Lu (1959) to assess direct and indirect effects of different variables on tuber yield as:

$$r_{ij} = p_{ij} + \sum r_{ik}p_{kj}$$

Where r_{ij} is mutual association between the independent traits (i) (tuber weight/hill) and any independent variable j as measured by the correlation coefficient, p_{ij} is component of direct effect of the independent trait (j) on the dependent variable (i); and $\sum r_{ik}p_{kj}$ is summation of components of indirect effect of a given independent trait (j) via all other independent traits (k). The residual effect (U), or the unexplained variation of the dependent variable that is not accounted for by path coefficients, was calculated as: $U = \sqrt{1-R^2}$, where $R^2 = \sum r_{ik}p_{kj}$

3. Result and Discussion

3.1. Analysis of Variance

The analysis of variance for each character revealed highly significant ($P < 0.01$) difference among the accessions for all the characters examined except tuber length (Table 1), which was omitted from further analysis, indicating the presence of considerable amount of variability for the characters. Amsalu (2003) and Baye *et al.* (2005) also reported similar results for the majority of the characters in potato and cassava, respectively.

The wide range, not only for tuber yield (0.37 to 3.15 kg/hill), but for almost all the other quantitative traits studied is an indication that Ethiopian farmers have maintained the genetic variability of this crop. The yield of this crop is comparable to that of other root and tuber crops. For example, Baye *et al.* (2005) reported a yield range of 536.9 to 1008.9 gram/plant for potato. The breeder has the raw material in which selection in any direction (early or late, tall or dwarf, high yielding or low yielding, etc) can be successful (Table 1)

The average dry matter content of *P. edulis* is 20.75%, which is similar to that of Irish potato (20%), but less than that of sweet potato (30%), cassava (40%), taro (30%) and yam (27%) (Admasu, 2002).

Table 1. Mean performance values for 16 characters of 36 *P. edulis* germplasm accessions evaluated at Jimma in 2005.

ACC	PH	SG	NN	NS	NB	FL	LW	DFI	DF	IL	LL	TL	TD	TW	NT	TDM
028/02	112.33	2.06	20.83	2.28	17.58	14.13	5.13	137.0	151.0	4.81	15.68	16.44	1.98	2.02	141.60	23.36
076/03	115.42	1.65	18.55	1.90	15.93	21.50	4.67	143.0	147.0	5.46	14.91	16.90	1.97	1.50	134.70	21.48
106/03	117.00	1.63	20.30	1.50	17.03	20.88	5.00	143.0	151.0	5.34	17.16	15.34	2.09	1.76	141.05	21.62
073/02	130.85	1.91	23.00	2.80	13.10	15.77	4.54	140.0	154.5	5.29	14.07	16.06	1.86	1.69	113.60	21.36
066/02	101.85	1.58	21.90	1.80	18.80	14.98	4.16	158.0	168.0	4.51	13.07	16.86	1.64	0.84	97.90	23.57
102/03	117.25	1.44	19.40	2.20	18.30	18.53	4.44	132.0	140.0	5.26	14.82	16.02	2.05	2.69	196.80	20.96
107/03	117.00	1.67	24.00	2.50	14.70	16.58	3.72	135.0	163.0	4.44	11.65	14.58	1.55	1.52	181.50	22.45
082/02	107.25	1.92	20.80	1.80	13.90	20.28	3.84	97.0	143.0	4.34	12.83	17.00	1.74	1.43	136.08	20.81
010/02	106.50	2.02	17.10	1.90	17.50	17.17	4.66	143.0	154.5	5.45	14.81	18.76	2.25	2.07	138.90	20.74
018/02	100.10	1.63	15.40	1.90	22.20	18.15	4.66	110.0	124.0	5.08	12.05	19.28	2.01	1.48	141.10	19.81
049/02	103.75	1.57	16.70	1.88	18.60	17.50	3.50	109.0	154.0	4.66	13.09	16.72	1.67	1.69	184.45	21.97
067/02	102.25	1.50	19.60	2.30	15.30	16.40	4.08	159.5	171.0	4.66	13.20	20.60	1.72	2.20	219.33	21.80
022/02	90.50	1.89	21.10	1.40	20.70	16.77	4.31	151.0	164.5	4.12	13.16	19.20	2.15	2.46	126.00	18.14
099/03	113.50	1.58	22.60	2.20	18.50	16.80	3.00	162.0	166.0	4.95	12.29	16.56	1.88	1.20	98.00	22.51
052/02	110.75	1.84	20.80	2.60	19.70	18.73	4.86	149.0	163.0	5.03	14.28	18.90	2.22	1.87	82.90	18.47
235969	121.50	1.69	19.10	2.30	19.80	23.88	4.49	143.0	143.0	5.96	13.93	19.94	1.99	2.37	121.80	18.86
044/03	146.75	1.66	27.00	4.10	12.40	12.82	3.58	159.5	168.0	5.10	11.75	15.64	1.56	1.53	167.20	22.50
003/02	113.85	1.75	22.30	3.00	17.60	16.60	4.43	148.5	158.0	4.68	13.28	22.02	1.95	3.15	118.00	17.83
063/02	97.00	1.48	20.03	2.40	14.18	15.23	4.06	151.0	164.5	4.28	13.17	19.38	1.52	1.67	190.50	23.33
079/02	90.38	1.49	17.78	2.10	15.20	18.83	4.08	114.5	143.0	4.52	12.67	17.46	1.74	1.34	85.10	19.70
064/02	104.25	1.83	20.93	2.60	16.80	19.57	4.72	84.5	154.5	4.53	13.78	19.70	2.06	2.28	122.10	19.10
011/02	91.75	1.73	18.35	1.93	15.60	17.23	4.05	135.0	158.0	3.89	12.71	17.68	2.44	1.46	75.40	16.93
235976	108.50	1.25	17.33	2.10	16.00	25.50	4.73	110.0	124.0	4.97	15.34	19.14	2.01	0.57	49.50	20.76
046/02	92.25	1.44	21.00	1.70	15.00	15.10	4.05	158.5	169.5	4.02	12.62	14.46	1.71	0.81	125.20	23.17
014/03	109.25	1.56	25.80	2.70	12.50	14.48	3.48	153.5	164.5	4.40	11.28	13.24	1.59	0.97	93.00	21.22
242494	89.00	1.01	15.10	1.80	15.30	20.42	4.42	144.5	147.0	4.25	14.20	15.08	1.81	0.74	64.10	20.53
071/02	104.25	1.86	19.43	3.10	15.80	18.12	4.58	144.5	144.5	4.93	13.65	16.92	1.83	1.39	119.30	21.30
004/02	93.25	1.42	18.50	2.33	14.58	15.17	4.22	158.0	171.5	4.51	14.86	15.86	1.51	0.59	84.68	20.86
242493	89.69	1.36	15.63	1.73	17.68	18.83	4.86	109.0	139.0	4.38	14.42	16.36	1.66	0.37	37.77	20.23
Lu-bo	87.50	1.70	20.40	2.50	15.80	16.92	4.30	151.0	158.0	3.92	12.76	18.18	2.09	1.42	83.00	20.61
113/03	96.35	1.65	20.33	3.10	16.30	17.45	4.42	148.5	154.5	4.22	12.88	17.02	2.02	1.60	70.60	19.17
045/02	89.75	1.78	19.20	1.90	15.90	18.12	4.23	143.0	151.0	4.17	13.20	15.60	1.85	1.17	113.80	22.06
041/02	107.00	1.71	18.55	1.80	14.30	24.47	4.80	124.0	143.0	5.68	15.66	18.94	1.96	1.58	74.80	18.31
235975	93.75	1.39	20.38	2.92	15.13	15.92	3.61	147.0	151.0	4.30	11.77	15.12	1.43	1.18	141.96	21.71
235978	102.25	1.43	20.00	1.80	15.80	22.10	4.63	129.0	143.0	4.75	15.39	14.28	1.85	0.48	42.10	19.91
242491	91.25	1.58	18.90	2.50	13.20	13.15	3.50	147.0	150.5	4.47	11.53	13.13	1.72	0.72	92.43	19.84
LSD(5%)	24.36	0.38	3.27	1.02	4.08	4.36	0.73	16.58	17.49	0.96	1.67	NS	0.35	0.35	33.94	2.09
CV (%)	11.48	11.35	8.07	22.33	12.34	11.99	8.43	5.91	5.62	10.07	6.07	15.10	9.13	11.35	14.32	4.96

Acc= accession number; PH= Plant height(cm); SG=Stem girth (cm); NN=Number of nodes(n); NS=Number of stem per hill(n); NB=number of branches(n); FL= Flower length(cm); LW=Leaf width(cm); DFI=Days to flower initiation; DF=Days to 50% flowering; IL=Internodes length(cm); LL=Leaf length(cm); TL=Tuber length(cm); TD=Tuber diameter(cm)); TW=Tuber weight per hill(kg); NT=Number of tubers per hill and TDM=Tuber dry matter (%)

3.2. Range and Mean Performance

The mean values of the accessions for the various characters showed differences among the accessions (Table 2). A wide range of variation in the characters studied was observed. The highest value (25.50 cm and 2.06 cm) was almost twice of the minimum value (12.82 cm and 1.01 cm) for flower length and stem girth, three fold for number of stems per hill (4.1 and 1.4), sixfold for number of tubers per hill (219.33 and 37.77) and eight fold for tuber weight per hill (3.15 and 0.37 kg) respectively.

3.3. Phenotypic and Genotypic Variation

Phenotypic coefficients of variation (PCV) ranged from 7.76 for days to 50 percent flowering to 43.17 percent for tuber weight per hill, whereas genotypic coefficients of variation (GCV) ranged from 6.67 for days to 50 percent flowering to 42.42 percent for tuber weight per hill (Table 2). This indicates that tuber weight per hill, on average, had the largest PCV and GCV; and days to 50 percent flowering had the lowest PCV and GCV. Number of tubers per hill had also PCV and GCV values of 37.85% and 36.47%, respectively, suggesting the existence of high genetic variability among the accessions for effective selection. These high PCV and GCV values for tuber weight per hill and number of tubers per hill could be evidence for the existence of a wide range of variation for such characters. This view is in agreement with the observation of Baye *et al.* (2005) on potato with respect to number of tubers per hill, and Ruth and Ramaswamy (2002) who also found high PCV and GCV for yield per plant in cassava. On the other hand, genetic variability for days to 50 percent flowering, tuber dry matter content, internode length, leaf length, plant height and leaf width were lower (Table 2), suggesting a need to search for diverse accessions in order to ensure effective selection.

Moreover, a narrow range of difference between PCV and GCV was recorded for days to flower initiation, tuber weight per hill, tuber dry matter content and leaf length (Table 2) indicating less environmental influence on the phenotypic expression of these characters and that they are mostly governed by genetic factors .Hence, selection based on phenotypic values may be effective for these traits. This is in agreement with Baye *et al.* (2005) who found narrow range between PCV and GCV for tuber dry matter content and days to maturity in potato. On the contrary, a wide difference between PCV and GCV were observed for number of stems per hill, number of branches, and plant height and internodes length (Table 2) indicating the high influence of the environment on these characters. Thus, selection on a phenotypic basis may not be effective for the genetic improvement of such traits.

3.4. Estimates of Heritability and Expected Genetic Advance

Heritability estimates ranged from 56.73 for internode length to 96.5 % for tuber weight per hill (Table 2). Maximum heritability was obtained for tuber weight per hill, followed by number of tubers per hill, days to flower initiation, leaf length, tuber dry matter content and number of nodes. Although yield is a complex characters, liable to have more environmental influence, heritability of tuber weight per hill was the maximum in this study. For example, Baye *et al.* (2005) found heritability of only 18.22% for tuber yield per plant in potato, which is very low compared to the heritability obtained in this study even although the crop is different**.** Therefore, further investigation should be undertaken in order to verify such a useful result. On the other hand, internode lengths, number of stems per hill, plant height, number of branches and stem girth have relatively low heritability estimates (Table 2). The expected genetic advance values expressed as a percentage of the accession mean also indicated which the progress that could be expected from selection of the top 5% of the accessions ranged from 11.80% for days to 50% flowering to 86.86% for tuber weight per hill (Table 2). High genetic advance as a percentage of the mean was recorded for tuber weight per hill and number of tubers per hill.

High heritability coupled with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals. In this investigation, high heritability along with high genetic advance as a percentage of mean was obtained for tuber weight per hill and number of tubers per hill. High GCV along with high heritability and high genetic advance will provide better information than single parameters alone (Saha *et al.,* 1990). Hence, in this study, tuber weight per hill, number of tubers per hill, and days to flower initiation exhibited high genotypic coefficients of variation, high heritability together with high genetic advance as percentages of means. This indicates that these characters would be very useful as a base for selection in *P. edulis* improvement programs.

3.5. Correlation Analysis

The value of phenotypic correlation coefficients indicated that tuber yield per hill was significantly and positively correlated with plant height, stem girth, number of branches, tuber diameter and number of tubers per hill (Table 3). This is in agreement with Murat and Vahdettin (2005) who also reported positive correlations of tuber yield per plant with plant height, tuber number per hill and tuber diameter in potato. On the other hand, tuber weight was negatively correlated with flower length and tuber dry matter content although the correlation was non-significant. In addition to tuber yield per hill, tuber dry matter content showed a non-significant and negative correlation with stem girth, number of branches, leaf width, internode length, leaf length and tuber weight per hill. It was significantly and positively correlated with number of tubers per hill. Number of tubers per hill, the major yield component in root and tuber crops (IITA, 1990), exhibited no significant correlation with most of the traits investigated except plant height, tuber dry matter content and tuber weight per hill. Diameter of the tuber was significantly and positively correlated with stem girth, number of branches, leaf length and width, flower length and tuber weight per hill. The trait was significantly

and negatively correlated with tuber dry matter content. Based on the correlations between characters at phenotypic level, accessions with tall plant height, wide in stem girth, a higher number of branches and tubers and large tuber diameter should be given due consideration in efforts towards tuber yield improvement. Such a view is also in agreement with the works of Amsalu (2003) on cassava for most of the characters.

Unlike the phenotypic correlation coefficients, the value of genotypic correlation coefficient for the majority of the characters showed a non-significant ($P > 0.05$) correlation (Table 3). For example, no character that showed significant association with tuber weight per hill although some of them have a higher degree of correlation with it. This may suggest that the phenotypic association of such characters with tuber weight per hill is not genotypic inheritance but more likely environmental influence. Tuber diameter was significantly and negatively correlated with tuber dry matter content, concurring with the result found at phenotypic level. In addition to this, genotypic correlation between the two characters is higher than its phenotypic correlation coefficient, indicating that the association between them is genetically inherited but not environmentally influenced. Therefore, during selection attention must be paid to the size of tubers because the bigger tubers have a low dry matter content. Plant height was significantly and positively correlated with number of stems per hill. This genotypic correlation coefficient is also higher than its phenotypic correlation coefficient (Table 3). The result demonstrated that, as stem numbers per hill increased, plant height also increased, which could be due to competition for light.

In general, the nature of phenotypic and genotypic correlation coefficients observed were more or less similar among most of the characters studied. It is of interest to note that the significant positive correlation coefficients estimated at genotypic level were also found to be significant and positive at phenotypic level. Moreover, the significantly higher magnitudes of positive genotypic correlation compared to the corresponding phenotypic correlation for some of the characters suggest that they were genetically controlled. Furthermore, although there was no statistically significant difference between the correlations of plant height, stem girth, number of branches, internode length, tuber diameter and number of tubers per hill with tuber weights per hill at genotypic level, their magnitude was moderately higher. This indicates that it may be possible to exploit these characters in an attempt to improve the tuber yield in *Plectranthus edulis*.

Table 2. Estimates of means, ranges, components of variance, PCV, GCV, heritability and genetic advance for 15 traits in *Plectranthus edulis*.

Trait	Mean	Range	σ^2_p	σ^2_g	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
PH	104.61 ± 1.87	87.50 – 146.75	169.692	97.701	12.45	9.45	57.58	15.45	14.77
SG	1.63 ± 0.03	1.01 – 2.06	0.048	0.030	13.38	10.69	63.77	0.29	17.58
NN	19.95 ± 0.33	15.10 – 27.00	6.775	5.481	13.05	11.74	80.90	4.34	21.75
NS	2.26 ± 0.08	1.40 – 4.10	0.300	0.173	24.25	18.40	57.59	0.65	28.76
NB	16.30 ± 0.32	12.40 – 22.20	5.229	3.207	14.03	11.00	61.33	2.89	17.73
FL	17.89 ± 0.40	12.82 – 25.50	9.091	6.789	16.85	14.56	74.67	4.64	25.92
LW	4.27 ± 0.07	3.00 – 5.13	0.247	0.182	11.62	10.00	73.66	0.75	17.63
DFI	138.11 ± 2.34	97.00 – 162.00	367.487	334.131	13.88	13.24	90.92	35.91	26.00
DF	153.18 ± 1.56	124.00 – 171.50	141.474	104.376	7.76	6.67	73.78	18.08	11.80
IL	4.70 ± 0.07	3.89 – 5.96	0.259	0.147	10.81	8.14	56.73	0.59	12.63
LL	13.55 ± 0.17	11.28 – 17.16	1.876	1.537	10.11	9.15	81.95	2.31	17.06
TD	1.86 ± 0.03	1.43 – 2.44	0.055	0.040	12.55	10.76	73.49	0.35	19.01
TW	1.49 ± 0.08	0.37 – 3.15	0.416	0.402	43.17	42.42	96.50	1.28	86.86
NT	116.84 ± 5.36	37.77 – 219.33	1955.229	1815.299	37.85	36.47	92.84	84.53	72.38
TDM	20.75 ± 0.21	16.93 – 23.57	2.787	2.257	8.05	7.24	81.00	2.79	13.42

PH= Plant height (cm); SG=Stem girth(cm); NN=Number of nodes(n); NS=Number of stems per hill(n); NB=number of branches(n); FL= Flower length(cm); LW=Leaf width(cm); DFI=Days to flower initiation; DF=Days to 50% flowering; IL=Internodes length(cm); LL=Leaf length(cm); TD=Tuber diameter(cm); TW=Tuber weight per hill(kg); NT=Number of tubers per hill and TDM=Tuber dry matter content(%); GA=genetic advance in absolute units; GAM= genetic advance as percent of mean

Table 3. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient among 15 traits of *Plectranthus edulis*.

	PH	SG	NN	NS	NB	FL	LW	DFI	DF	IL	LL	TD	TW	NT	TDM
PH	1	0.305	0.564**	0.460**	-0.094	0.024	0.015	0.077	0.046	0.686**	0.138	0.005	0.375*	0.362*	0.192
SG	0.243	1	0.322	0.140	0.158	-0.175	0.199	-0.047	0.142	0.209	0.030	0.431**	0.542**	0.221	-0.138
NN	0.650	0.300	1	0.567**	-0.362*	-0.467**	-0.393*	0.416*	0.593**	-0.046	-0.363*	-0.249	0.192	0.235	0.268
NS	0.852*	0.231	0.734	1	-0.382*	-0.415*	-0.252	0.272	0.248	0.046	-0.400*	-0.261	0.180	0.157	0.057
NB	-0.437	-0.040	-0.528	-0.527	1	0.227	0.341*	-0.143	-0.237	0.218	0.192	0.481**	0.366*	0.039	-0.238
FL	0.228	-0.215	-0.528	-0.531	0.271	1	0.494**	-0.503**	-0.665**	0.445**	0.573**	0.380*	-0.012	-0.333*	-0.393*
LW	-0.256	0.243	-0.534	-0.360	0.323	0.680	1	-0.279	-0.445**	-0.365*	0.787**	0.529**	0.199	-0.240	-0.287
DFI	0.030	-0.037	0.503	0.356	-0.179	-0.525	-0.381	1	0.671**	-0.068	-0.177	-0.150	0.004	0.112	0.280
DF	0.042	0.278	0.729	0.343	-0.122	-0.738	-0.527	0.761*	1	-0.342*	-0.319	-0. 251	0.113	0.268	0.275
IL	0.615	0.215	-0.163	0.233	0.179	0.882*	0.299	-0.118	-0.598	1	0.499**	0.230	0.322	0.160	-0.047
LL	-0.077	-0.028	-0.496	-0.589	0.129	0.800*	0.775*	-0.257	-0.402	0.483	1	0.398**	0.091	-0.179	-0.083
TD	-0.113	0.514	-0.382	-0.574	0.700	0.570	0.668	-0.169	-0.278	0.234	0.498	1	0.435**	-0.212	-0.596**
TW	0.454	0.678	0.218	0.211	0.467	-0.017	0.203	0.001	0.137	0.402	0.075	0.484	1	0.567**	-0.280
NT	0.484	0.290	0.302	0.181	0.087	-0.395	-0.314	0.099	0.315	0.214	-0.245	-0.247	0.571	1	0.446**
TDM	0.343	-0.244	0.323	0.019	-0.315	-0.440	-0.351	0.300	0.366	-0.083	-0.117	-0.802*	-0.291	0.500	1

**, ** Significant at 0.05 and 0.01 levels of significance, respectively.*

PH= Plant height(cm); SG=Stem girth(cm); NN=Number of nodes(n); NS=Number of stem per hill(n); NB=number of branches(n); FL= Flower length(cm); LW=Leaf width(cm); DFI=Days to flower initiation; DF=Days to 50% flowering; IL=Internodes length(cm); LL=Leaf length(cm); TD=Tuber diameter(cm); TW=Tuber weight per hill(kg); NT=Number of tubers per hill (n) and TDM=Tuber dry matter (%)

3.6. Path Coefficient Analysis

Path coefficient analysis at the genotypic level revealed that 4 of the 15 quantitative traits (number of nodes on the main axis, leaf length, number of tubers per hill and tuber dry matter content in %) affected tuber weight per hill to the greatest extent (Table 4). The residual from these four traits was only 0.07; path analysis explained 93% of the genotypic correlation of these traits with tuber weight. All four traits had positive direct effects on tuber weight except tuber dry matter content which had a relatively large negative direct effect on the main trait. Number of tubers per hill and tuber dry matter content had the largest direct effects (in absolute value) and, are, therefore the most important determinants of tuber weight per hill. Ntawuruhunga *et al.* (2001) reported that the direct effect of storage root weight on cassava yield was also high and positive (p= 0.45) while its indirect effect through storage root number was negative.

Selecting accessions with many nodes on the main axis, with longer leaves and producing many tubers per hill is believed to result in identifying genotypes with high tuber yield. Since the indirect effect of both number of nodes and leaf length on tuber weight via number of tubers per hill is negative, precautions should be taken when selecting genotypes with many nodes and longer leaves. This finding was in line with the result of Pandey *et al.* (2005). They reported that number of tubers per plant showed a positive direct effect on tuber yield in potato and suggested that these traits be given due consideration during selection. Simultaneous selection should be made to assure that these genotypes have many tubers per hill. Accessions with high dry matter content should not be selected. Such genotypes give minimum tuber weight per hill. Both the genotypic correlation of tuber dry matter with tuber weight and its direct effect on tuber weight were negative. If accessions are sorted according to their tuber dry matter content, the bottom fourth of the accessions by this trait (accessions with the lowest tuber dry matter content) have an average tuber yield of 2.01 kg/hill, while the top fourth by tuber dry matter content have a mean tuber weight of only 1.38 kg/hill. Murat and Vahdettin (2005) also found that tuber yield per hill, dry matter content and number of tubers per hill had the greatest direct effect on tuber yield per unit area in their order of magnitude in potato. Baye *et al.* (2005) also reported that average tuber weight had the maximum positive direct effect (p = 3.546) followed by tuber number per plant (p = 3.114), leaf area (p = 2.261), days to maturity (p = 1.006), tuber dry matter content (p = 0.742) and plant height (p = 0.703) on tuber yield per plant on potato.

Table 4. Genotypic direct (bold and underlined) and indirect effects of four quantitative traits on tuber weight per hill of *Plectranthus edulis*.

	Number of Nodes	Leaf Length	No of Tubers Per hill	Tuber Dry Matter content	r_g
Number of nodes	**0.4064**	-0.2061	0.2965	-0.2794	0.2174
Leaf Length	-0.2014	**0.4159**	-0.2406	0.1009	0.0748
Number of tuber per hill	0.1227	-0.1019	**0.9822**	-0.4322	0.5709
Tuber dry matter content	0.1313	-0.0485	0.4910	**-0.8646**	-0.2907

h=0.07

4. Conclusions

This study clearly illustrated the existence of a wide range of variation among the germplasm accessions collected from different regions of Ethiopia. This indicates the presence of a considerable amount of variability for the different characters. However, this investigation was carried out at a single location and in a single season. It is possible that the trends could vary across location and the need for ascertaining genotypic-environment interaction through appropriate studies should be highlighted. The requirement for broadening the genetic base is also emphasized from the point of view of diversifying the prevailing gene pool. *P. edulis* collection representing diverse eco-geographical areas of the country should be organized for diversity analysis to derive further guidelines for conservation activities than reported here. Furthermore, the conventional approaches of characterization as adopted in this study have certain limitations in identifying duplicates, whereas the use of advanced biochemical (isozyme polymorphism) and molecular (RFLP, RAPD etc) approaches could precisely contribute to germplasm characterization, management and utilization and are needed for efficient characterization of *P. edulis* which would, in turn, be invaluable for the conservation and improvement of the crop.

5. Acknowledgement

We deeply appreciate the assistance and cooperation extended to us by the staff of the Horticulture section at Jimma Agricultural Research Center: Mr. Dawit Ashenaf, Mr. Belay Y/birhan, Mr. Abate Guangul, Mr. Haile Abshiro, Mrs. Tirfalem H/wold, Mr. Jebel Abalulessa, Mr. Teferi Siraj and Miss. Biritu Girma for their unreserved cooperation by way of material support and facilities, creating a very good working atmosphere, and their feeling of a sense of belongingness to the field trial. Special thanks are extended to Mr. Abate Guangul and Haile Abshiro who were involved with us in all challenges of land preparation, planting, and trial management and data collections. We would also like to extend and express our sense of deep appreciation to the staff of the

Horticulture unit at the Institute of Biodiversity Conservation (IBC): Mr. Zenebe Woldu (head of the division) and Mr. Yeshitila Mekbeb for the assistance rendered to us in supplying the planting materials for research work.

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