# Genetic Variability, Correlation and Path Analysis on the Storage Tuber Yield and Yield Components of Yam (*Dioscorea* spp.) from Southwest Ethiopia

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## Abstract

*The study was conducted to estimate the extent of genetic variation, association between storage tuber yield and yield related traits and to identify the most persuasive character(s) involving 36 yam genotypes for selection and conservation. Field evaluation was conducted at Jimma Agricultural Research Center in Ethiopia using a 6x6 lattice design with two replications. Variance analysis of characters revealed significant differences ($p \leq 0.01$) among the genotypes. Estimate of phenotypic and genotypic coefficients of variation showed variability among the genotypes. High genotypic (14.87, 8.36 and 5.38%) and phenotypic coefficients of variation (40.11, 24.03 and 15.17%) were observed for tuber fresh weight, petiole length and number of vine hill$^{-1}$ in the order of magnitudes. Heritability (13.70% and 12.10%) coupled with genetic advance as percent of mean (11.56% and 5.94%) were recorded for tuber fresh weight and petiole length, respectively. Correlation study between different traits showed highly significant association among characters. At genotypic level, tuber fresh weight showed significant and positive correlated with leaf length (r=97), leaf width (r=1.00), vine length (r=0.99), petiole length (r=1.00), days to maturity (r=1.00), number of internodes vine$^{1}$ (r=0.57), internodes length (r=1.00), tuber length (r=1.00), tuber diameter (r=1.00) and harvest index (r=0.73). Tuber fresh yield is a complex agronomic trait induced by many associated traits directly and indirectly and thus, selection of yams based on these traits will enhance tuber yield and need high concern towards tuber yield improvement. Analysis of path coefficients at genotypic level revealed that days to maturity (p=1.0183) had maximum positive direct effect on tuber fresh weight followed by tuber length (p=0.2126). This study revealed that selection of later maturing genotypes may improve genetic gain in storage tuber yield in yam breeding. Based on the above results, genotypes: 27/02, 56/76, 08/02, 10/002, 39/87, 45/03, 6/02, 116, and 7/83 were selected for breeding and conservation.*

**Keywords:** Association, direct selection, diversity, genotype, indirect selection

# Introduction

Yam (*Dioscorea* species) belonging to the family *Dioscoreaceae* is cultivated in Africa, Asia, parts of South America, as well as Caribbean and the South Pacific islands for its storage tubers (Asiedu and Alieu, 2010; Sesay *et al.,* 2013). The genus comprises over 600 species (Dansi*et al.*, 2013; Marcos *et al.*, 2014), and only 10 of them are cultivated for human food and have real economic significance in Africa (Lebot, 2009; Asiedu and Alieu, 2010; Norman *et al.*, 2012). Ethiopia is considered to be the center of origin and diversity of most yam species (Coursey, 1967; Terauchi *et al.,* 1992; Tamiru *et al.,* 2011). In the country a large number of yam genotypes are cultivated for food, medicine and economical uses (Hildebrand *et al.*, 2003; Girma *et al.*, 2012).

Despite its food security and economic benefits, production of yams in the Southwest region of Ethiopia is mostly on a small scale and average crop yield is too low about 4 t/ha (Okoli, 1988; Tamiru *et al.*, 2011) as compared to West African countries (15 t/ha) (Asiedu and Alieu, 2010; Dansi *et al*. 2013). Hence, there is urgent need to increase the production of yam in order to meet the growing demand and genetic resource conservation. In Southwest Ethiopia, a large number of yam genotypes are cultivated, but no serious attempt has been made before to improve them for higher productivity and acceptability (Hildebrand *et al.*, 2002). Thus, there is a need to boost productivity of the crop through breeding. Yam breeders are interested to develop cultivars with high yield and other desirable agronomic characters through selection. Selection of important traits depends on the amount of genetic variation present in the area (Mulualem and Dagne, 2013; Mazid*et al.*, 2013). Evaluation of genetic variability and association between agronomic traits in the existing genotype is the key component of any breeding program (Appalaswamy and Reddy, 2004; Arshad*et al.*, 2006). Moreover, estimates of heritability and genetic advance offers the best instrument of any crop including yam in any trait by selection of superior genotypes (Larik and Rajput, 2000; Surek and Beser, 2003; Male *et al.*, 2014).

Tuber yield and yield components are important traits in yam improvement program (Mulualem and Mohammed, 2012; Terfa, 2023). Tuber yield is directly or indirectly affected by yield components requiring selection of relevant traits positively correlated with it. Thus, knowledge on the interrelationship and degree of association between yield and yield components are useful to improve selection efficiency in yam breeding and conservation efforts. According to Kumar and Shukla (2002) information of association such as genotypic and phenotypic correlation between yield and its component traits is vital for yield improvement through selection programs. Further, Mulualem and Mohammed (2012), described the association of yield and yield related traits on yam collected from different areas of Ethiopia. As correlation alone hardly explain the relationships among the characters, therefore partitioning of total correlation into direct and indirect effects by path analysis helps make selection more effective (Faisal *et al*., 2007; Biabani and Pakniyat, 2008). Path coefficients give the relative contribution of various yield determining traits, enabling breeders to decide between direct and indirect selection procedures (Paul *et al*., 2013). The direct and indirect effects of traits on economic yield can be determined through path analysis. Path analysis has been used in a number of crops to study the relationships between yield and yield components (Christopher, 2000). In this regards, there is little information on direct and indirect effects of traits on yam through path analysis in southwest Ethiopia. Hence, this information could provide valuable insight when evaluation yam genotypes for breeding. Therefore, the objectives of this study were to determine the magnitude of variability, character association between tuber yield and related traits and to identify the most influential character(s) involving 36 yam genotypes for effective selection and conservation.

# Materials and Methods

## Description of the study area

The study was conducted at Jimma Agricultural Research Center (JARC). The center is located at latitude 7$^{o}$ 40.00' N and longitude 36$^{o}$ 47’.00’ E with an altitude of 1753 meters above sea level (m.a.s.l.). The area receives mean annual rainfall of 124.6 mm with mean maximum and minimum temperatures of 26.2 $^{0}$C and 12.0 $^{0}$C, respectively. The soil of the study site is Eutric Nitosol (reddish brown) with $p^{H}$ of 5.3. These environmental conditions are conducive for yam cultivation.

## Experimental materials, design and management

A total of 36 yam genotypes were collected from Jimma, Sheka and Bench-maji zones of Southwest Ethiopia (Table 1). The experiment was laid out in a 6 x 6 simple lattice design with two replications. Plants were field established using a 7m long rows using inter and intra row spacing of 1.5m and 1m, respectively. Tubers of the same size which started sprouting were used as planting material. All other agronomical practices were followed according to the recommendations and farmers practices in southwest Ethiopia. Each yam plant was tended using dried coffee stick of 3.5 - 4.5 meters long to provide support and induce good canopy and vine development. Five middle plants within a row were sampled and tagged for data collection and final harvest.

**Table 1. List of 36 yam accessions and** their areas of collection

| No. | Name of landraces | Zone | District | Latitude | Longitude | Altitude |
|---|---|---|---|---|---|---|
| 1 | 59/02 | Jimma | Mana | 07$^0$40’37N | 036$^0$49’10E | 1718 |
| 2 | 68/01 | Jimma | Dedo | 07$^0$30’63N | 036$^0$53’45E | 1784 |
| 3 | 6/02 | Bench maji | Sheko | 06$^0$59’66N | 035$^0$34’11E | 1728 |
| 4 | 75/02 | Jimma | Kersa | 07$^0$40’43N | 036$^0$48’76E | 1734 |
| 5 | 3/87 | Jimma | Manna | 07$^0$40’58N | 036$^0$48’75E | 1731 |
| 6 | 56/76 | Jimma | Manna | 07$^0$41’89N | 036$^0$48’06E | 1837 |
| 7 | 54/02 | Bench maji | Sheko | 07$^0$02’03N | 035$^0$32’77E | 1892 |
| 8 | 46/83 | Jimma | Dedo | 07$^0$31’28N | 036$^0$53’59E | 1771 |
| 9 | 08/02 | Jimma | Kersa | 07$^0$40’46N | 036$^0$48’79E | 1740 |
| 10 | 116 | Jimma | Dedo | 07$^0$31’28N | 036$^0$53’63E | 1683 |
| 11 | 01/75 | Sheka | Yeki | 07$^0$11’30N | 035$^0$26’22E | 1171 |
| 12 | 06/83 | Jimma | Dedo | 07$^0$31’32N | 036$^0$53’64E | 1692 |
| 13 | 17/02 | Sheka | Yeki | 07$^0$11’27N | 035$^0$26’26E | 1176 |
| 14 | 07/03 | Jimma | Dedo | 07$^0$31’50N | 036$^0$53’60E | 1733 |
| 15 | 45/03 | Jimma | Mana | 07$^0$41’86N | 036$^0$48’08E | 1810 |
| 16 | 27/02 | Jimma | Sekachekorsa | 07$^0$35’06N | 036$^0$41’91E | 1877 |
| 17 | 37/87 | Jimma | Mana | 07$^0$41’87N | 036$^0$48’13E | 1940 |
| 18 | 10/002 | Bench maji | Sheko | 07$^0$02’91N | 035$^0$29’76E | 1668 |
| 19 | 76/02 | Jimma | Kersa | 07$^0$40’64N | 036$^0$48’84E | 1728 |
| 20 | 06/2000 | Jimma | Sekachekorsa | 07$^0$35’43N | 036$^0$41’86E | 1850 |
| 21 | 7/83 | Jimma | Sekachekorsa | 07$^0$35’06N | 036$^0$41’91E | 1898 |
| 22 | 58/02 | Sheka | Yeki | 07$^0$11’22N | 035$^0$26’25E | 1192 |
| 23 | 39/87 | Jimma | Sekachekorsa | 07$^0$35’42N | 036$^0$42’94E | 1885 |
| 24 | 32/83 | Jimma | Shebesombo | 07$^0$26’74N | 036$^0$24’01E | 1372 |
| 25 | 24/02 | Jimma | Shebesombo | 07$^0$26’75N | 036$^0$24’07E | 1379 |
| 26 | 2/87 | Jimma | Shebesombo | 07$^0$26’76N | 036$^0$24’12E | 1365 |
| 27 | 60/87 | Sheka | Yeki | 07$^0$11’72N | 035$^0$26’48E | 1199 |
| 28 | 15/2000 | Bench maji | Sheko | 07$^0$04’13N | 035$^0$37’74E | 1320 |
| 29 | 34/87 | Jimma | Dedo | 07$^0$31’37N | 036$^0$53’44E | 1911 |
| 30 | 21/02 | Jimma | Sekachekorsa | 07$^0$36’48N | 036$^0$45’09E | 1785 |
| 31 | 57/76 | Bench maji | Sheko | 07$^0$02’88N | 035$^0$29’74E | 1654 |
| 32 | 0001/07 | Jimma | Shebesombo | 07$^0$26’74N | 036$^0$24’12E | 1367 |
| 33 | 0004/07 | Jimma | Kersa | 07$^0$40’55N | 036$^0$48’75E | 1741 |
| 34 | 7/84 | Bench maji | Sheko | 07$^0$02’88N | 035$^0$29’74E | 1661 |
| 35 | 7/85 | Sheka | Yeki | 07$^0$14’30N | 035$^0$26’17E | 1173 |
| 36 | 06/2001 | Bench maji | Sheko | 06$^0$59’69N | 035$^0$34’09E | 1387 |

## Data collection and analysis

A total of 19 quantitative data was collected according to the descriptor of yam *(Dioscor*ea spp.) developed by Bioversity International (IPGRI, 1997). Data were collected from individual plant and the whole plot basis from the middle of five plants and the average value was used for analysis.

All quantitative data were subjected to analysis of variance (ANOVA) using the lattice procedure as suggested by Gomez and Gomez (1984) using SAS version 9.0 (SAS, 2000) and Genres (2008) statistical software packages.Treatment means were separated using the Least Significant Difference (LSD) procedure at the 5% and 1% level of significance. The analysis of variance (ANOVA) was made using model for simple lattice design as follow:

$Yijklm = \mu + ti + \beta j + \chi k + yl + \pi m + \Sigma ijklm$

Where, $Y_{ijklm}$ = response of Y trait from the $i^{th}$ genotypes, $j^{th}$ replication, μ= Overall mean effects, ti= Effects of $i^{th}$ level of treatments, β= Effects of $j^{th}$ level of replication, $\chi_k$= Effects of $K^{th}$ level of blocks within replications (adjusted for treatments),$y_l$ = Effects of $l^{th}$ level of intra block error, $\pi_m$= Effects of the $m^{th}$ randomized complete block error andΣijklm= is a random error component.

Analysis of covariance was done for each pair of characters to obtain the sum of cross products to be used in covariance calculation.

$\sigma^2_{g\,xy} = MSCP_{axy} - MSCP_{exy})/r$

Where: $\sigma^2_{gxy}$= genotypic covariance between character x and y; $\sigma^2_{exy}$= environmental covariance between character x and y, $MSCP_{rxy}$= Mean sum of cross product of replication for variable x and y, $MSCP_{axy}$= Mean sum of cross product of accessions for variable x and y,$MSCP_{exy\,=}$ Mean sum of cross product of error for variable x and y.

Variability was estimated by simple measures, viz., range, standard error, phenotypic and genotypic variances and coefficient of variations. Based on the expected mean squares, phenotypic variations and coefficient of variations were calculated according to the method suggested by Burton (1953) and Burton and de Vane (1953).

$\sigma^2_p = \sigma^2_g + \sigma^2_e$

Where, $\sigma^2_p$ = phenotypic variance
$\sigma^2_g$ = genotypic variance
$\sigma^2_e$ = environmental variance

Phenotypic Coefficient of Variation (PCV) = $(\sqrt{\sigma^2_p}$ / grand mean) x 100

Genotypic Coefficient of Variation (GCV) = $(\sqrt{\sigma^2_g}$ / grand mean) x 100

Heritability in broad sense ($H^2_B$) = $(\sigma^2 g/\sigma^2 p)$ x 100 (Allard, 1960). The expected genetic advance (GA) for each trait was computed using the formula adopted by Johnson *et al.* (1955) as: GA = (k) $(\sqrt{\sigma^2 p})$ $(h^2)$, and GA as % of the mean (GAM) = (GA/ $\bar{X}$ ) x 100; where, k= selection differential at 5% selection intensity (k= 2.06), $\sigma^2_p$ = phenotypic variance,$h^2$ = heritability in broad sense and $\bar{X}$ is grand mean of the population in which selections was employed.

The Genotypic ($r_g$) and phenotypic ($r_p$) correlation coefficients for tuber yield and its components were estimated by calculating the variance and covariance at phenotypic and genotypic levels using the formula suggested by Singh and Chaudhury (1985) by using Genres statistical software (Genres, 2008).

$r_p = \sigma^2 pxy / \sigma px.\sigma py$

$r_g = \sigma^2 gxy / \sigma gx.\sigma gy$

Where, $r_{p=}$ Phenotypic correlation coefficient, $r_{g\,=}$ Genotypic correlation coefficient, $\sigma^2_{pxy=}$Phenotypic covariance between traits x and y and$\sigma^2_{gxy}$= Genotypic covariance between traits x and y.

The values of phenotypic correlation coefficient were tested for significance using tabulated value at a-2 degree of freedom, where a= number of accessions and the values of genotypiccorrelation coefficients were tested for significance employing 't' statistics as follows:

$t= r_g /\sqrt{} (1-r^2gxy)^2/2H_xH_y$

Where, $H_x$ and $H_y$ are the heritability value for character x and y, respectively. The calculated t–value was compared with 't' tabulated value for a-2 degrees of freedom at 5% and 1% levels of significance.

Path coefficient analysis was carried out to partition the total genotypic correlation coefficients into direct and indirect effects. Total tuber fresh yield was considered as dependent variable, while the rest of the variables were considered as independent variables. The independent characters that showed relatively high correlation with total tuber fresh yield at genotypic level were used for path analysis. It was computed according to the method suggested by Dewey and Lu (1959).

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

Where, $r_{ij}$= mutual association between the independent character (i) and dependent characters (j) as measured by correlation coefficients, $p_{ij}$ = components of direct effects of the independent characters (i) on the dependent characters (j), $\sum r_{ik} p_{kj}$ = summation of components of indirect effect of a given independent character (i) on the dependent characters (j) via all other independent characters (k). The residual effect (h) was estimated using the formula shown below (Dewey and Lu, 1959).

$h = \sqrt{} 1-R^2$ Where, $R^2 = \sum r_{ij} p_{ij}$

# Results and Discussion

The analysis of variance of quantitative characters revealed highly significant difference ($p\leq0.01$) among the genotypes for 13 of the 19 characters. Significant differences among accessions in most traits indicated the existence of inherent genetic variability among accessions. The observed variability among accessions was made due to: leaf length, leaf width, petiole length, vine length, internodes length, number of internodes vine$^{-1}$, number of vine hill$^{-1}$, days to maturity, tuber length, tuber diameter, tuber fresh weight, tuber dry weight and harvest index (Table 2).

## Variability of quantitative traits

The analysis of variance of quantitative characters revealed significant difference at ($p\leq0.01$) among the genotypes for 13 of the 19 characters suggested high degree of genetic variability in the materials evaluated and the existence of considerable genetic diversity among accessions for selection (Table 2). The characters that manifested significant difference genotypes for leaf length, leaf width, petiole length, vine length, internodes length, number of internodes vine$^{-1}$, number of vine hill$^{-1}$, days to maturity, tuber length, tuber diameter, tuber fresh weight, tuber dry weight and harvest index.

**Table 2:** Analysis of variance for 19 quantitative characters of yam

| Trait | Replication (DF=1) | Mean square of Genotypes (DF=35) | | Mean square of Blocks within Reps (Adj.) (DF=10) | Mean square of error | | LSD | Efficiency relative to RCBD (%) | CV (%) |
|---|---|---|---|---|---|---|---|---|---|
| | | Unadjusted | A | | Intrablock(25) | RCBD (35) | 0.01 | | |
| LL | 1.11 | 3.75 | 3.15** | 1.49 | 0.34 | 0.67 | 1.81 | 159.24 | 5.59 |
| LW | 0.10 | 0.49 | 0.46** | 0.25 | 0.07 | 0.12 | 0.85 | 138.69 | 6.53 |
| PL | 1.04 | 8.59 | 7.56** | 4.36 | 3.23 | 3.55 | 4.89 | 102.43 | 17.5 |
| LLO | 0.45 | 0.65 | 0.44ns | 0.80 | 0.62 | 0.67 | ns | 101.64 | 39.8 |
| DBL | 0.17 | 0.35 | 0.35ns | 0.34 | 0.56 | 0.45 | ns | 86.40 | 23.6 |
| VL | 950.4 | 339.38 | 192.7** | 418.2 | 34.29 | 143.9 | 18.3 | 332.63 | 2.29 |
| IL | 0.03 | 0.51 | 0.32** | 0.43 | 0.13 | 0.22 | 1.13 | 134.88 | 3.84 |
| TiL | 0.08 | 0.22 | 0.22ns | 0.21 | 0.47 | 0.40 | ns | 84.20 | 27.3 |
| NIPV | 0.04 | 13.05 | 10.76** | 3.27 | 2.22 | 2.52 | 4.05 | 104.02 | 5.73 |
| NVPH | 0.43 | 0.59 | 0.57** | 0.32 | 0.21 | 0.24 | 1.26 | 104.14 | 10.9 |
| DM | 325.2 | 230.25 | 175.9** | 83.5 | 64.13 | 69.67 | 21.8 | 101.88 | 5.78 |
| NTPH | 0.17 | 0.11 | 0.10ms | 0.15 | 0.12 | 0.13 | ns | 100.93 | 8.12 |
| TL | 0.63 | 8.27 | 5.22** | 6.97 | 2.22 | 3.58 | 4.54 | 134.85 | 3.84 |
| TuDi | 0.01 | 7.00 | 5.59** | 1.57 | 1.96 | 1.85 | 3.82 | 94.36 | 9.40 |
| VFW | 76.50 | 10.11 | 13.21ns | 20.15 | 17.43 | 18.20 | ns | 100.58 | 33.7 |
| VDW | 0.73 | 1.02 | 0.95ns | 0.95 | 1.08 | 1.05 | ns | 96.44 | 33.5 |
| TFW | 13.66 | 333.03 | 219.1** | 16.42 | 9.53 | 11.50 | 9.10 | 107.74 | 10.3 |
| TDW | 0.004 | 5.58 | 5.01** | 1.09 | 1.04 | 1.06 | 2.78 | 100.06 | 4.93 |
| HI | 325.3 | 230.25 | 175.9** | 83.52 | 64.13 | 69.67 | 21.8 | 101.88 | 11.7 |

** = Highly significant at 0.01 level of probability. ns= non-significant

LL= Leaf length (cm), LW= Leaf width (cm), PL=Petiole length (cm), LLO= Length of leaf lobe (cm), DBL= Distance between lobs (cm), VL= Vine length (cm), IL= Internodes length (cm), TiL= Tip length (cm),NIPV= Number of internodes vine$^{-1}$,NVPH= Number of vine hill$^{-1}$, DM= Days to maturity, NTPH= Number of tubers hill$^{-1}$,TL= Tuber length (cm), TuDi= Tuber diameter (cm), VFW= Vine fresh weight (t/ha), VDW= Vine dry weight (t/ha), TFW= Tuber fresh weight (t/ha),TDW= Tuber dry weight (t/ha) and HI= Harvest index (%). RCBD= Randomized complete block design, LSD= Least significant difference, CV=Coefficient of variation

In contrary, non-significant difference was observed among the genotypes for length of leaf lobe, distance between lobs, tip length, number of tubers hill$^{-1}$, vine fresh weight and vine dry weight revealed that the contribution of these characters for the variability was low and therefore, it was discarded from further analysis. In line with this, Baye *et al*. (2005), Kifle (2006), Mulualem and Dage, (2013) also reported similar results for the majority of the characters in potato, taro and aerial yam, respectively.

## Estimates of variability

### Phenotype and genotype variation

The value of phenotype and genotype variation cannot be used for comparing the magnitude of variance for different characters since the mean and units of measurement of the character may be different. Hence, the coefficient of variation expressed at phenotype and genotype levels have been used to compare the observed variability among the characters. In the present study, the genotype coefficients of variation (GCV) ranged from 1.034% for tuber length to 14.87% for tuber fresh weight, whereas phenotype coefficients of variation (PCV) ranged from 6.107% for vine length to 40.11% for tuber fresh weight (Table 3).

Table 3: Estimates of components of variance, PCV, GCV, heritability and genetic advance for 13 quantitative characters of 36 *Dioscorea* spp. grown at Jimma.

| Traits | Range | | Mean | $\sigma^2_g$ | $\sigma^2_p$ | GCV | PCV | $H^2$ (%) | Genetic advance | GAM (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| | Min | Max | | | | | | | | |
| LL | 7.34 | 14.32 | 10.55 | 0.150 | 2.233 | 3.661 | 14.143 | 6.70 | 0.206 | 1.953 |
| LW | 2.72 | 5.60 | 4.27 | 0.047 | 0.308 | 5.076 | 12.944 | 15.40 | 0.176 | 4.121 |
| VL | 224 | 303.00 | 254.61 | 19.16 | 241.759 | 1.719 | 6.107 | 7.90 | 2.530 | 0.994 |
| PL | 4.83 | 14.47 | 10.25 | 0.735 | 6.074 | 8.362 | 24.038 | 12.10 | 0.614 | 5.993 |
| DM | 98.98 | 161.2 | 138.44 | 3.143 | 149.957 | 1.280 | 8.845 | 2.10 | 0.529 | 0.382 |
| NIPV | 20.75 | 33.60 | 25.97 | 0.902 | 7.811 | 3.655 | 10.757 | 11.50 | 0.662 | 2.558 |
| NVPH | 3.20 | 6.20 | 4.27 | 0.053 | 0.419 | 5.377 | 15.175 | 12.60 | 0.168 | 3.935 |
| IL | 8.54 | 11.35 | 9.70 | 0.012 | 0.368 | 1.144 | 6.254 | 3.30 | 0.041 | 0.422 |
| TL | 34.16 | 45.39 | 38.82 | 0.161 | 5.930 | 1.034 | 6.273 | 2.70 | 0.135 | 0.348 |
| TuDi | 10.88 | 20.0 | 14.91 | 0.118 | 4.431 | 2.301 | 14.120 | 2.60 | 0.113 | 0.757 |
| TFW | 6.80 | 65.60 | 29.90 | 20.608 | 149.996 | 14.869 | 40.114 | 13.70 | 3.456 | 11.558 |
| TDW | 16.04 | 24.60 | 20.70 | 0.796 | 3.321 | 4.300 | 8.782 | 24.00 | 0.900 | 4.348 |
| HI | 28.98 | 91.21 | 68.40 | 3.143 | 149.961 | 2.590 | 17.892 | 2.10 | 0.529 | 0.773 |

LL=Leaf length (cm); LW= Leaf width (cm); PL= Petiole length (cm); VL= Vine length (cm); IL= Internodes length (cm); NIPV= Number of internodes vine$^{-1}$; NVPH= Number of vine hill$^{-1}$; DM= Days to maturity, TL=Tuber length (cm); TDi= Tuber diameter (cm); TFW=Tuber fresh weight (t/ha); TDW=Tuber dry weight (t/ha) and HI= HarvestIndex (%). Min= Minimum, Max= Maximum, $\sigma^2_g$= Genetic variance, $\sigma^2_p$= Phenotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, $H^2$= Broad sense heritability, GAM= genetic advance as percent of mean.

This revealed that tuber length and vine length had the least GCV and PCV and tuber fresh weight had the highest GCV and PCV value. The least value of PCV and GCV on tuber length and vine length indicated the limited scope for improvement of these traits through selection of yams. The result obtained from this study is supported by the report of Sendek (2004) who reported that that bulb length and plant height showed the lowest PCV and GCV in shallot. High GCV values on tuber fresh weight indicated the existence of genetic variation for such character. Therefore, selection based on tuber fresh yield is effective. This view is also in agreement with the observation of Baye *et al*. (2005) and Terfa, (2023) who reported selection based on tubers yield and number of corm per hill are effective on potato and aerial yam improvement.

Genetic variability of internodes length, leaf width, number of vine hill$^{-1}$, tuber diameter, leaf length, tuber length and tuber dry weight were relatively lower (Table 3) suggesting that there is a need to search for diverse accessions in order to ensure effective selection and hybridization. In this study, wide variations between GCV and PCV were observed in most of the characters, for example, harvest index, petiole length, tuber diameter, number of vine hill$^{-1}$ and tuber fresh weight, indicated presence of high pressure of the environment on these characters and less effect of genetic factors. Thus, selection on phenotype basis may not be effective for the genetic improvement of the crop. On contrary, the narrow gap between PCV and GCV for tuber dry weight, tuber length, internodes length and number of internodes vine$^{-1}$, suggesting the influence of environment in phenotypic performance is minimal.

## Estimates of heritability and expected genetic advance

The heritability estimates provides information on the magnitude of the inheritance of quantitative traits, but it has no indication of the amount of genetic progress that would result from the selecting of best individuals (Bekele, 2006; Hefney, 2013). In the present study, the heritability estimates ranged from 2.1% for harvest index and days to maturity to 24.0% for tuber dry weight (Table 3). Maximum heritability was obtained from tuber dry weight followed by leaf width. On the other hand, harvest index, days to maturity, tuber diameter, tuber length and internodes length have relatively low heritability estimates (Table 3). Moderate heritability estimates were observed for tuber fresh weight, number of vine hill$^{-1}$ and petiole length. Heritability indicates the ease with which a trait can be improved through selection and could vary with materials studied and the environment. It also indicated the relative importance of genetic makeup in the expression of the characters. The higher value of heritability suggests that selection will be more effective and improvement can be expected for that trait in future breeding programs for similar condition. In most cases, high heritability alone does not guarantee a large enough to make sufficient improvement through selection in advance generations unless accompanied by a substantial amount of genetic advance (Sendek, 2004; Hefny, 2013). It has been emphasized that without genetic advance, the heritability values would not be practical importance in selection based on phenotypic appearance. In this study, the values of genetic advance for different characters of *Dioscorea* spp. accessions were different. These values are also expressed as percentage of the accession mean for each character, so that comparisons could be made among various characters, which had different units of measurement. The result revealed that the progress that could be expected from selection of accessions ranged from 0.35% for tuber length to 11.56% for tuber fresh weight (Table 3).

Genetic advance along with high heritability is a key instrument for selection of the best individuals. In this study, high heritability along with high genetic advance as percent of the mean was obtained for tuber dry weight, tuber fresh weight, leaf width and petiole length. Besides, high GCV along with high heritability and high genetic advance will provide better information than single parameters alone (Sahel *et al.*, 2004; Garedew, 2006). Hence, tuber fresh weight, petiole length, leaf width and number of vineshill$^{-1}$ exhibited high genotype coefficients of variation, high heritability together with high genetic advance as percent of means. Therefore, selection based on these characters would be very useful for genetic improvement of yam.

High heritability with low genetic advance was recorded for tuber dry weight and leaf width indicating less influence of environment but prevalence of non-additive gene action for which simple selection will be less effective. Thus, heterosis breeding would be recommended for these traits improvement. In line with this, Desalegn (2005) who reported characters such as bean width, bean thickness and fruit width of coffee showed higher heritability and lower genetic advance. In quantitative traits, the poor estimates of heritability and genetic advance indicate that inheritance of these traits is being influenced by inter allelic interaction rather than intra allelic interaction (Birenda *et al*., 2014).

## Association between characters

### Genotype correlation coefficients

Tuber yield is the result of the expression and association of several plant growth components (Arshad *et al*., 2006; Keya *et al*., 2015). Although, correlation coefficient is useful in quantifying the size and direction of trait association can be misleading if the high correlation between two traits is a consequence of the indirect effect of the traits (Dewey and Lu, 1959). Hence, association analysis was undertaken to determine the direction of selection and number of characters to be considered in improving tuber yield.In the present study, more traits were found having high correlation coefficients at genotypic level than at phenotypic level, indicating the inherent association between the traits studied. In agreement with the current study, higher genotype correlation coefficients than their respective phenotype correlation coefficients were reported similarly by Sarkar *et al*. (2007), Anbanandan *et al.* (2009), Sabesan *et al*. (2009), Jayasudha and Sharma (2010) and Keya *et al.* (2015) on different crops.

Tuber fresh weight (t/ha) had strong positive correlation with leaf length (r =0.97**), leaf width (r =1.00**), vine length (r =0.99**), petiole length (r =1.00**), days to maturity (r =1.00**), number of internodes vine$^{-1}$ (r =0.57**), internodes length (r =1.00**), tuber length (r =1.00**), tuber diameter (r =1.00**) and harvest index (r =0.73**) at genotypic level (Table 4). On the contrary, number of vine hill$^{-1}$ exhibited significant and negative correlation with tuber fresh weight. This result is in agreement with Terfa, (2023) who reported positive association in plant height and days to flowering, days to maturity, with tuber yield in yam. Garedew, (2006) who also reported positive association in plant height, stem girth, number of nodes, number of stem hill$^{-1}$, number of branches, number of tubers hill$^{-1}$ and tuber dry weight in Ethiopian potato. Similarly, Dagne (2007) reported positive and significant association of petiole length, leaf length, leaf width and tuber length with tuber fresh yield in taro from south Ethiopia. Thus, selection of yams having these characters will enhance tuber yield improvement.

Table 4: Genotypic (above diagonal) and phenotypic correlation coefficient among 36 yam (*Dioscorea* spp) accessions grown at Jimma.

| **Traits** | **LL** | **LW** | **VL** | **PL** | **DM** | **NIPV** | **NVPH** | **IL** | **TL** | **TUDi** | **TFW** | **TDW** | **HI** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LL | **1.00** | -1.00** | 0.53** | -1.00** | 1.00 ** | 1.00** | 0.47** | -1.00 ** | -1.00 ** | -1.00** | 0.97** | -0.49** | 1.00** |
| LW | 0.77* | **1.00** | -0.47** | -0.74** | 1.00** | 1.00** | 0.57** | -1.00** | -1.00** | -1.00** | 1.00** | -0.39* | 1.00** |
| VL | 0.25 | 0.11 | **1.00** | 1,00** | 1.00** | 0.57** | 0.80** | 0.39* | 0.38* | -0.63** | 0.99** | 0.11 | 1.00** |
| PL | 0.32* | 0.29 | -0.13 | **1.00** | 1.00** | 0.99** | 0.82** | 1.00** | 1.00** | 1.00** | 1.00** | -1.00** | 1.00** |
| DM | -0.01 | 0.13 | 0.33* | 0.09 | **1.00** | 0.47** | -1.00** | 1.00** | 1.00** | 1.00** | 1.00** | 1.00** | 0.99** |
| NIPV | -0.27 | -0.31 | 0.53** | -0.42** | 0.16 | **1.00** | -0.60** | 0.21 | 0.21 | 1.00** | 0.57** | 0.12 | 0.47** |
| NVPH | -0.30 | -0.19 | 0.30 | -0.36* | 0.08 | 0.48** | **1.00** | 1.00** | 1.00** | -0.58** | -0.42** | 0.07 | -1.00** |
| IL | 0.51** | 0.37 * | 0.71** | 0.11 | 0.19 | 0.08 | -0.04 | **1.00** | 1.00** | -1.00** | 1.00** | 0.08 | 1.00** |
| TL | 0.51** | 0.37* | 0.71** | 0.11 | 0.19 | 0.09 | -0.04 | 1.00 ** | **1.00** | -1.00** | 1.00** | 0.08 | 1.00** |
| TuDi | 0.33* | 0.45** | 0.06 | 0.28 | 0.26 | -0.17 | -0.11 | 0.23 | 0.22 | **-1.00** | 1.00** | -1.00** | 1.00** |
| TFW | 0.16 | 0.24 | 0.32* | 0.09 | 0.74** | 0.13 | 0.14 | 0.29 | 0.29 | 0.40* | **1.00** | 0.46** | 1.00** |
| TDW | -0.06 | -0.26 | 0.11 | -0.34* | -0.18 | 0.24 | 0.08 | -0.03 | -0.03 | -0.47** | -0.30 | **1.00** | 1.00** |
| HI | -0.01 | 0.13 | 0.33* | 0.09 | 1.00** | 0.16 | 0.08 | 0.19 | 0.19 | 0.26 | 0.73** | -0.18 | **1.00** |

* Significant 0.05 probability level; **= highly significant at 0.01 probability level.

LL=Leaf length (cm); LW= Leaf width (cm); VL= Vine length (cm); PL= Petiole length (cm); DM= Days to maturity, NIPV= Number of internodes vine$^{-1}$,NVPH= Number of vine per hill; IL= Internodes length (cm); TL=Tuber length (cm); TDi= Tuber diameter (cm); TFW=Tuber fresh weight (t/ha); TDW=Tuber dry weight (t/ha) and HI= Harvestindex (%).

Tuber dry weight was negative and significantly correlated with leaf length (r =-0.49**), leaf width (r = -0.39**), petiole length (r = -1.00**) and tuber diameter (r =-1.00**); positively with days to maturity (r=1.00**) and tuber fresh weight (r =0.46). The positive association of internodes length with tuber length will make easy simultaneous improvement through selection for two traits. However, simultaneous improvement of tuber length and internodes length in yam is very difficult due to the negative association of tuber length and internodes length with tuber diameter; thus, an independent selection should be done for improvement of such traits.Petiole length was negatively and significantly associated with leaf length (r = -1.00**), leaf width (r = -0.74**), number of internodes vine$^{-1}$ (r =-0.42**), number of vine hill$^{-1}$ (r= -0.36*) and tuber dry weight (r =-0.34*) and non-significantly with days to maturity, internodes length, tuber length, tuber diameter tuber fresh weight and harvest index. Whereas, longer and wider leaves may leads to decrease tuber length due to negative associations with these traits at genotypic level.Tuber length and diameter was positive and significant association with tuber fresh yield and with days to maturity at genotypic level. The result showed that late maturity would increase tuber yield significantly. Besides similar trends was evident for harvest index. Based on the associations between characters, accessions with longer vine, late maturity and higher harvest index will maximize fresh tuber yield and may need high concern towards tuber yield improvement. Harvest index showed significant positive association with almost all characters except number of vine hill$^{-1}$. Higher harvest index produced lower vine hill$^{-1}$. Tuber length showed perfect negative association with leaf length and leaf width and positive significant with days to maturity (r =1.00**), petiole length (r =1.00**), number of vine hill$^{-1}$ (r =1.00**) and internodes length (r =1.00**). Increase in leaf length and leaf width may lead to reduce tuber length; tuber diameter and tuber dry weight due to negative and significant correlation of the traits. Moreover, vine number hill$^{-1}$ showed significant and positive genotypic associations with leaf length, leaf width, vine length and petiole length. Ghafoor *et al*. (2003) showed that more number of vine produced longer and wider leaves which had a chance to fix more carbon dioxide and to produce higher tuber yield through photosynthesis.

## Phenotype correlation coefficients

The value of phenotype correlation coefficients between most of the characters was non- significant (Table 4). Except vine length, days to maturity and tuber diameter, there was no character showing significant association with tuber fresh weight.

This may suggest that the association of genotypic in most characters with tuber fresh weight is stronger than the environmental correlation which is similarly justified by (Arshad *et al*., 2003). Besides, tuber dry weight also showed non-significant and positive correlation with vine length, number of internodes vine$^{-1}$ and number of vine hill$^{-1}$.

There was significant negative association between petiole length and tuber diameter with tuber dry weight at phenotype level revealed that longer petiole and wider tuber reduced tuber dry weight, it might be due to yam tuber might have high moisture content. The result is in agreement with that of Dagne (2007) who also reported that petiole length and tuber diameter reduced tuber dry weight in taro. In this study, the nature of phenotype and genotype correlation coefficients either positive or negative was observed to be more or less similar in respect of the majority of the characters studied. It is of interest to note that the significant positive correlation coefficients estimated at genotypic level was also found significant and positive at phenotypic level. Moreover, the significantly higher magnitudes of positive genotypic correlation than the corresponding phenotypic correlation in respect to some of the characters suggested that these characters were genetically controlled. Under complex situation the estimates of correlation alone does not provide the true contribution of the characters towards the yield, these genotypic correlation was partitioned into direct and indirect effects through path coefficient analysis. Besides, tuber yield is a complex character associated with a number of component characters that may be interrelated. Rakesh *et al*. (2013), who indicated that, interdependence of contributing factors often affects their direct relationship with yield, making correlation coefficients unreliable as selection indices. Thus, assessments of direct and indirect effects of different characters on yield are essential (Weber and Moorthy, 1952).

## Path coefficient

Partitioning of the total correlation into direct and indirect effects provides information on contributions of traits and forms the basis for selection to improve yield (Shipley, 1997; Rakesh *et al*., 2013; Birenda *et al*., 2014). In this study, path coefficient analysis was used (Dewey and Lu, 1959) by assign tuber fresh weight as the response character as summarized in Table 5. The results showed that days to maturity had maximum positive direct effect on tuber fresh weight (p=1.0183) followed by tuber length (p=0.2130) suggesting simultaneous selection of the two traits may improve genetic gain of tuber yield in yam breeding. This finding is in agreement with Mulualem and Mohammed (2012) who reported that days to maturity and tuber length is an important character in making selection in aerial yam. Further, Tsegaye *et al.* (2006) reported storage tuber length and dry matter contents are the best character to select Ethiopian sweet potato accessions. Hence, selection on the bases of later days to maturity and increased tuber length may maximize storage tuber yield in yam. The negative direct effect of internodes length on tuber fresh weight may be explained by the fact that selection based on internode length might reduce tuber yield. Similar finding was reported by Monkola (2013) who indicated, the direct effect of internodes length on tuber fresh weight of cassava was small and negative. Whereas these are in contradiction to the result of Mulualem and Dagne (2013) and Dominic *et al.* (2014) who reported that number of verticals contributed more for tuber yield on taro and cassava, in that order. However, tuber length, number of vine hill$^{-1}$, number of internodes vine $^{-1}$ and tuber dry weight had positive direct effects (Table 5). Vine length also had positive indirect effect on tuber fresh weight through most of the traits except, leaf width and number of internodes vine$^{-1}$ where the direct effect of vine length is negative (Table 5). Vine yield components seem to have less competitive effect with tuber fresh weight at path coefficient analysis level and have not been selected against. Leaf width had negative indirect effect through days to maturity, number of internodes vine$^{-1}$, number of vine hill$^{-1}$ and tuber dry weight. It is interesting to note that days to maturity had positive direct effect on tuber fresh weight and positive indirect effect through all characters except number of vine hill$^{-1}$. This finding is similar with the result of Mulualem and Dagne (2013) who reported days to maturity being the novel character and had higher direct effect on fresh root yield on cassava. The low negative association of tuber dry weight with tuber fresh weight (t/ha), which is not as such important on the basis of correlation estimates, revealed positive direct and indirect supplier to tuber fresh weight *via* path analysis. Thus selecting accessions based on this character would contribute for rapid in yam tuber yield enhancement program.

Leaf width had comparatively high positive direct effect (0.114) on tuber fresh weight. Besides, it had positive and highly significant ($p \leq 0.01$) association with tuber fresh weight (t/ha). This is in agreement with Norman *et al.* (2011) and Himanshu *et al.*, (2016), who reported that taro accessions with wider leaves had high fresh tuber yield. It had high negative indirect effects *via* days to maturity, number of vine hill$^{-1}$, tuber dry weight and negligible indirect negative effect through number of internodes vine$^{-1}$. Therefore, it is important to consider accession with wider leaves in improving tuber yield in yam, as it was strong and positively associated with tuber fresh weight (t/ha) and its direct and indirect positive effect through yield contributing traits to tuber fresh yield (t/ha).

Table 5. Genotypic direct (bold and underlined) and indirect effects of some characters on tuber fresh weight of *Dioscorea* spp.

| Traits | LL | LW | VL | PL | DM | NIPV | NVPH | IL | TL | TDW | HI | rg |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LL | -**0.016** | 0. 156 | 0.001 | 0.146 | 0.819 | -0.003 | 0.031 | 0.287 | -0.399 | 0.083 | 0.009 | 0.97 |
| LW | -0.022 | **0.114** | -0.011 | 0.024 | 1.799 | -0.014 | 0.004 | -0.678 | 0.039 | 0.062 | -0.317 | 1.00 |
| **VL** | 0.008 | 0.053 | **-0.023** | -0.083 | 1.344 | 0.126 | 0.005 | -0.193 | 0.039 | 0.054 | -0.340 | 0.99 |
| PL | -0.122 | 0.187 | 0.060 | **-0.034** | 1.161 | -0.022 | 0.005 | -0.466 | 0.454 | -0.236 | 0.013 | 1.00 |
| DM | 0.054 | -0.202 | 0.120 | -0.066 | **1.018** | -0.014 | -0.001 | -1.038 | 1.020 | 0.127 | -0.019 | 1.00 |
| NIPV | 0.140 | -0.010 | -0.001 | -0.032 | 0.469 | **0.022** | -0.039 | -0.049 | 0.164 | 0.003 | -0.095 | 0.57 |
| NVPH | 0.260 | -0.064 | 0.187 | -0.027 | -0.958 | 0.219 | **0.065** | -0.556 | 0.509 | -0.002 | -0.054 | -0.42 |
| IL | -0.195 | 0.305 | 0.001 | -0.172 | 1.369 | -0.154 | 0.014 | **-0.238** | 0.236 | -0.117 | -0.064 | 1.00 |
| TL | -0.023 | 0.141 | 0.108 | -0.070 | 0.926 | -0.046 | 0.016 | -0.239 | **0.213** | 0.116 | -0.071 | 1.00 |
| TDW | 0.146 | -0.129 | 0.002 | -0.093 | 0.224 | -0.143 | -0.077 | -0.484 | 0.242 | **0.053** | -0.037 | -0.30 |
| HI | -0.189 | 0.086 | 0.042 | -0.087 | 1.496 | -0.218 | 0.004 | -0.284 | 0.060 | -0.063 | **-0.080** | 0.73 |

Residual effect= 0.233

LL=Leaf length (cm); LW= Leaf width (cm); VL= Vine length (cm); PL= Petiole length (cm); DM= Days to maturity, NIPV= Number of internodes vine$^{-1}$; NVPH= Number of vine hill$^{-1}$; IL= Internodes length (cm);TL=Tuber length (cm); TDW=Tuber dry weight (t/ha) and HI= HarvestIndex (%).

The direct effect of tuber length on tuber fresh weight was positive and high (0.213). Positive direct effect of tuber length on tuber fresh weight was also reported by Shipley, (1997) and Ntawuruhunga *et al.* (2001) in cassava. Besides, the indirect effect of tuber length on tuber fresh weight through petiole length, days to maturity, number of vine hill$^{-1}$, tuber dry weight, internodes length and and number of internodes vine$^{-1}$ was high and positive. In contrast, the indirect influence through leaf length was higher and negative. Therefore, selection based on tuber length is important to maximize tuber yield. Internodes length had a perfect positive association with tuber fresh weight. This positive association did not contribute to fresh tuber yield directly but, indirectly through vine length, days to maturity, number of vine hill$^{-1}$, tuber dry weight and tuber length. Besides, leaf length and vine length had contributed indirectly to fresh tuber yield. The value of harvest index had small and negative direct (-0.080) effect on tuber fresh yield. Therefore, efforts required in breeding cultivars with a higher length of storage tuber can be achieved through selection of genotypes.

Genotypes which produced the highest tuber fresh weight were 10/002, 56/76, 17/02, 39/87, 27/02, 116, 7/83, 08/02, 59/02, 45/03 and 6/02. The residual effect (h=0.233) is relatively moderate indicated that the trait considered in this study are not enough to adequately explain the variation in freshroot yield. About 76.70% of the total variability in fresh tuber yield t/ha was contributed by 12 independent traits that were assessed in this study. Therefore, it suggests that more traits should be considered to explain the existed variation in fresh root yield of yams. In this regard, Terfa, (2023) and Mulualem and Mohammed, (2012) who reported similar results on the residual effect on aerial yam collected from Southwest Ethiopia.

# Conclusion and Recommendation

In this study, more traits were found to have high correlation coefficients at genotypic level than at phenotype level. This may suggest that the inherent association of genotype in most characters with tuber fresh weight is stronger than the environmental factor.Tuber fresh weight, petiole length, leaf width and number of vines hill$^{-1}$ exhibited high genotype coefficients of variation, high heritability together with high genetic advance as percent of means. Thus, selection of yam genotypes based on these characters will enhance genetic improvement in Southwest Ethiopia.

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