

## Correlation and Path Coefficient Analysis for Root Yield and Related Characters of Cassava (*Manihot esculenta Crantz*) Accessions in Southwest Ethiopia

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### Abstract

An experiment was conducted to study the interrelationship of yield related characters and extent of their contribution to cassava fresh storage root yield using correlation and path coefficient analysis in the Southwest Ethiopia during the 2019–2021 cropping season. The design of the experiment was a simple lattice with two replications using sixty four cassava accessions. Genotypic correlation analysis showed that fresh storage root yield ( $t\ ha^{-1}$ ) observed significant and highly significant positive correlation with root diameter ( $r=0.65^{**}$ ), root length ( $r=0.31^*$ ), stem diameter ( $r=0.63^{**}$ ), root number per plant ( $r=0.54^{**}$ ), petiole length ( $r=0.47^{**}$ ), plant height ( $r=0.34^{**}$ ), weight fresh aboveground biomass per plot ( $r=0.56^{**}$ ) and harvest index ( $r=0.57^{**}$ ). Only magnitude difference Similarly result were found phenotypic correlation these character with fresh storage root yield ( $t\ ha^{-1}$ ). Hence, improvement in fresh storage root yield per hectare is possible by considering these characters as criteria in selection scheme. Path coefficient analysis revealed that weight fresh above ground biomass per plot (0.770) the highest and positive direct effect was exerted on fresh storage root yield per hectare, followed by harvest index per plot (0.763), root diameter (0.121) and petiole length (0.120). These character that exerted positive direct effect and strong positive correlation coefficient with fresh storage root yield were known to influences cassava fresh storage root yield in the favorable direction and needs much attention during the process of selection cases in point are weight of above ground biomass per plot, harvest index per plot, root diameter and petiole length.

**Keywords:** Cassava; Correlation; Direct Effect; Path analysis; yield Components; Root Yield

### Introduction

Cassava is a significant food security and industrial crop, contributing as food, feed and industrial biomass in Africa, Asia and South America. The study stated that crop improvement efforts have focused to the development of cassava cultivars having desirable characters such as increased root, flour, and starch yield, reduced toxicity, reduced pest/disease susceptibility and improved nutrient contents. In sub-Saharan Africa cassava is the second to maize utmost staple food being the major source of food energy contribution up to 285 calories per person per day and it could be a track to food security and resilient to climate change. Nevertheless, in the East African region, cassava yield is on average 10 t/ha (10 t/ha in Ethiopia, 9.8 t/ha in Tanzania, 10.6 t/ha in Kenya and 12 t/ha in Uganda). These yields are about half compared to yields in some South Asian countries: China (16.7 t/ha), Thailand (22.26 t/ha), Indonesia (23.36 t/ha) and India (35.6 t/ha). In Ethiopia, cassava has been found to have an excellent adaptation and growth performance in different agro ecologies with productivity variation. Since the economic importance of cassava and the low average productivity in Ethiopia, there is tremendous scope to increase the yield per unit area and there by the total production. The main goal in any crop improvement program is to enhance yield. It is well recognized that economic yield is the final product and many characters contribute to its performance [1]. Meanwhile yield is a complex character and is dependent on a number of its component characters; yield cannot be improved to a greater extent on its own. Hence, selection of plants based directly on yield would not be very reliable and the information on the nature of

association between yield and its components helps in simultaneous selection for many characters associated with yield improvements. The efficiency of breeding programme depends mainly on the direction and magnitude of association between yield and its components and also the relative importance of each factor involved in contributing to yield. Understanding the relative contribution of each character to yield may be accomplished using correlation studies. The estimates of correlation co-efficient analysis are more useful in the estimation of inter-relationship among the yield contributing component but simple correlation does not provide adequate information about the contribution of each factor towards yield. So, it becomes

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becomes necessary to study path coefficient analysis, which takes in to account the casual relationship in addition to degree of relationship. Furthermore, stated that path coefficient analysis is a standard partial regression coefficient that measures the direct influence of one variable up on others, and permits the separation of the correlation coefficient into components of direct and indirect effects. Therefore, a clear picture of contribution of each component in final expression of complex character is essential.

In southwest Ethiopia, cassava is a crop grown as a food security and income source. Since the economic importance of cassava and despite a few research efforts, the national average yield of cassava in Ethiopia (10 t ha<sup>-1</sup>) is still very low with compared to the genetic potential of the crop (80 t ha<sup>-1</sup>) and twice below productivity per unit area of some South Asian countries for example India (35.6 t ha<sup>-1</sup>). So as to achieve the target of increased production by increasing the yield potential of the cassava, understanding on direction and magnitude of association between yield and yield related character is essential for a cassava breeder. Hence, continuous improvement efforts of this crop are needed using suitable selection criteria in national or regional cassava improvement program. This warrants that there has research gap of study on interrelationships among various characters and amount of their contribution to root yield. Therefore, the major contributors of the characters for such important features of the crop need to be studied and exploited to design appropriate selection criteria in cassava breeding program. The object of this study was conducted to estimate the interrelationship of yield related characters and extent of their contribution to cassava fresh storage root yield using correlation and path coefficient analysis. Specific objectives: to determine the magnitude of correlation among characters and to determine the direct and indirect contribution of characters to cassava fresh storage root yield [2].

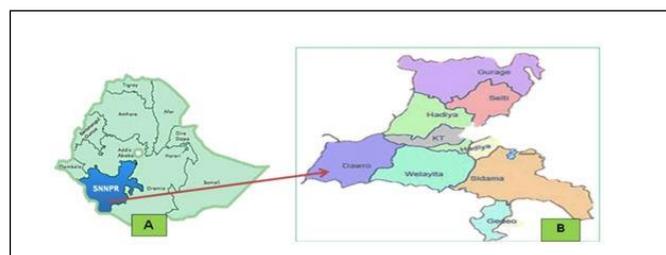
## Materials and Methods

### Description of the study area

The experiment was conducted at Tarcha research site in Dawuro zone of Southern Nation And Nationality People Regional State

(SNNPRS) of Ethiopia during in 2019-2021 cropping season. Tarcha research site is located at latitude 07°09'32"N and longitude 037°10'16"E (Figure 1) with an altitude 1250 meters above sea level (M.A.S.L). The area receives mean annual rainfall of 1392 mm with mean maximum and minimum temperatures of 30°C and 17.0°C, respectively.

The soil of the study site is Nitosol (weathered brown) with pH of 5.6 (EMA) [3].



**Figure 1:** (A) Map and position of the study region in Ethiopia. (B) Zones map of the study area in region.

### Experimental materials

The study used 64 cassava accessions among which 15 accessions were provided by International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. The remaining 49 accessions were obtained from two national research centers namely Jimma Agricultural Research Center and Hawassa [4] Agricultural Research Center (Table 1).

Genotype	Code	Source	Genotype	Code	Source
J-local	G1	JARC	46330/12	G33	HARC
50583014	G2	HARC	1051741	G34	HARC
F-100	G3	HARC	AWC-4	G35	HARC
5028/73	G4	HARC	1071393	G36	ITTA
26/84	G5	HARC	1061630	G37	ITTA
5338-19	G6	HARC	191/0427	G38	HARC
1070952	G7	IITA	WALAMO	G39	HARC
45/72 white	G8	HARC	101	G40	HARC
156	G9	HARC	5532-4	G41	HARC
AWC-5	G10	HARC	1070337	G42	ITTA
MM96/3280	G11	HARC	Wajo bohe	G43	HARC

1011224	G12	ITTA	Korre(original)	G44	HARC
5048-33	G13	HARC	Gamo dhaske	G45	HARC
NALINDAM 96-41	G14	HARC	Korre- dhaske-8	G46	HARC
1050125	G15	ITTA	Bajk-8	G47	HARC
Klgoma Red	G16	HARC	1038	G48	HARC
1062630	G17	ITTA	M-94/0114	G49	HARC
1070593	G18	ITTA	1630	G50	HARC
AWC-3	G19	HARC	869	G51	HARC
45/72 Red	G20	HARC	1554	G52	HARC
MM 96/9361	G21	HARC	196/624	G53	HARC
10540	G22	ITTA	M-94/0125	G54	HARC
1980510	G23	ITTA	Umbure	G55	HARC
1011206	G24	ITTA	1708	G56	HARC
104	G25	HARC	Bajk-1	G57	HARC
200	G26	HARC	Korre-dhaske-7	G58	HARC
1061365	G27	ITTA	AAGT 192	G59	JARC
7070824	G28	HARC	Melko 108	G60	JARC
1070539	G29	ITTA	AAGT 191	G61	JARC
MM 96/9308	G30	HARC	Hawassa -04	G62	JARC
1010085	G31	ITTA	Kello	G63	HARC
1050127	G32	ITTA	Qulle	G64	HARC

ITTA=International Institute for Tropical Agriculture, JARC=Jimma Agriculture Research Center, HARC=Hawassa Agriculture Research Center [5].

**Table 1:** List of cassava accessions with their code and source of collection.

### Experimental design and management

The field experiment was laid out in 8 × 8 simple lattice designs with two replications (Figure 2) Mature cassava cuttings measuring 25-30 cm [6] long were planted (7 m<sup>2</sup>) in a single row plot of 7 m long using inter row spacing of 1 m and intra-rows spacing of 1 m on the top of ridge at an angle of 45° to the ground surface. All agronomic practices were done according to the recommendations and farmers' practices of the areas. Five middle plants within a row were sampled and tagged for data collection and final harvest [7].



**Figure 2:** Cassava at seedling stage in field.

### Data collection

Quantitative data measures and counting were taken on 3 plants for each accession per repetition. Five middle plants within a row were sampled and tagged for data collection and final harvest. All quantitative characters were measured as per described [8] in Table 2.

Evaluation Period	Traits measured	Code	Scoring
6MAP	length of leaf lobe(cm)	Ll	measured three leaves from the middle of the plant, measure from the intersection of all lobes to the end of the middle lobe
	width of leaf lobe(cm)	Wl	measured three leaves from the middle of the plant, measure from the widest part of the middle lobe
	Ratio: length lobe/width lobe	R	ratio between length and width was performed with Excel
	Petiole length (cm)	Pl	measured two leaves/plant from the middle third
18MAP	Plant height (cm)	Ph	measured vertical height from the ground to the top of the canopy, record measurements from three plants
(Harvest)	Canopy diameter (cm)	Cd	measured the top of the canopy diameter, record measurements from three plants
	Diameter of stem at 50 cm from ground (cm)	Sd	measured the main stem diameter using caliper at height of 50 cm, record measurements from three plants
	Level of branching	Lb	Counted level of branch from the ground to the top canopy from three plant
	Height of first branch (cm)	Hfb	measured vertical height from ground to first primary branch from three plant
	Number of storage roots per plant	Nsr	recorded from each of three plants
	Weight of fresh roots yield (t/ha)	Wfr	Was weighed the root fresh weight/plot then converted to tonnes per hectare (t/ha)
	Weight of fresh aboveground biomass per plot (kg)	Wfab	measured the weight of aboveground biomass
	Harvest index (%)	HI	Measured the weight of 5 plant

**Table 2:** Quantitative data used and technique of measurement 64 cassava accessions.

### Data analysis

All data generated were subjected to analysis of variance (ANOVA) using R-software (version 4.0.3). Phenotypic and genotypic correlation coefficients and co-variance analysis was estimated using the formula [9] suggested by Singh and Chaudhury and Miller. Direct and indirect contributions of various characters to root yield was calculated through path coefficient analysis according to the team of expert [10].

### Variance and co-variance analysis

Phenotypic and genotypic variances and co-variances was calculated according to the method suggested by

### Genotypic variance component

- Genotypic variance ( $\sigma^2_g$ )=(MSg -MSe)/r
- Where MSg is genotypic mean square, MSe is error mean square and r is replication

- Genotypic coefficient of variation (GCV)

$$= \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

- Where is the grand mean value of the trait
- Environmental variance component (On genotypic mean basis)  
 $\sigma^2_e = MSe/r$

### Phenotypic variance component

- Phenotypic variance ( $\sigma^2_p$ )= $\sigma^2_g + \sigma^2_e$
- Phenotypic coefficient of variation (PCV)

$$= \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

## Covariance

Covariance was calculated using the following formula as:

- Genotypic covariance (CovA) =  $r_A \sigma_X \sigma_Y$
- Where  $r_A$  = correlation of breeding values arises from two sources,  $\sigma_X$  = standard deviation of trait x,  $\sigma_Y$  = standard deviation of trait y,
- Environmental covariance (CovE) =  $r_E \sigma_X \sigma_Y$

Where  $r_E$  = correlation of environmental deviations,  $\sigma_X$  = environmental standard deviation of trait x,  $\sigma_Y$  = environmental standard deviation of trait y

- Phenotypic covariance (CovP) = Genotypic covariance (CovA) + Environmental covariance (CovE)

## Correlation analysis

Correlation coefficient (r): was calculated using the standard procedure suggested by [11]

Phenotypic correlation coefficient between traits x and y is given by:

$$r_{p_{xy}} = \frac{\text{Cov } p_{xy}}{\sqrt{\sigma^2_{p_x} \sigma^2_{p_y}}}$$

Where,

$r_{p_{xy}}$  = Phenotypic correlation coefficient between traits x and y, Cov  $p_{xy}$  = Phenotypic covariance between traits x and y,  $\sigma^2_{p_x}$  = Phenotypic variance of trait x,  $\sigma^2_{p_y}$  = Phenotypic variance of trait y

Genotypic correlation coefficient between traits x and y:

$$r_{g_{xy}} = \frac{\text{Cov } g_{xy}}{\sqrt{\sigma^2_{g_x} \sigma^2_{g_y}}}$$

Where,

$r_{g_{xy}}$  = genotypic correlation coefficient between traits x and y, Cov  $g_{xy}$  = genotypic covariance between trait x and y,  $\sigma^2_{g_x}$  = genotypic variance of trait x,  $\sigma^2_{g_y}$  = genotypic variance of trait y [12].

Genotypic and phenotypic correlation coefficients were tested for their significance using the formula, using the t- table at (g-2) degrees of at 5% and 1% level of significance.

$$t = \frac{r_{g_{xy}}}{SE_{g_{xy}}} \text{ And } t = \frac{r_{p_{xy}}}{SE_{p_{xy}}}, \text{ respectively}$$

$$SE = \sqrt{\frac{(1-r_{g_{xy}})^2}{2h^2_x h^2_y}} \text{ And } SE = \sqrt{\frac{(1-r_{p_{xy}})^2}{2h^2_x h^2_y}}$$

Respectively

Where  $h^2_x$  and  $h^2_y$  are heritability values for trait x and y, respectively.

SE = standard error for genotypic and phenotypic correlation.  
G = number of genotypes.

## Path coefficient analysis

Fresh root yield was considered as the dependent variable while the rest of characters were taken as [13] the independent variables. The direct and indirect effect of the independent characters on fresh root yield/plot was estimated with the formula given by [6]

$$R_{ij} = P_{ij} + \sum r_{ik} p_{jk}$$

Where:  $R_{ij}$  = mutual association between the independent character (i) and dependent characters (j) as measured by correlation coefficients,  $P_{ij}$  = component of direct effect of independent variable (i) on the dependent variable (j) as measured by the phenotypic and genotypic path coefficient, and  $\sum r_{ik} p_{jk}$  = summation of components of indirect effect of a given independent variable (i) on a given dependent variable (j) via all other k independent variables. Residual effect (R): The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. It is estimated with the help of direct effects and simple correlation coefficient. The residual effect (R) was estimated as [14]:

$$R = \sqrt{1 - \sum P_{iy} r_{iy}}$$

Where,  $P_{iy}$  = direct effect of the independent variable i on the dependent variable y;  $r_{iy}$  = the correlation coefficient of the independent variable i with the dependent variable y [15].

## Results and Discussion

### Correlation root yield with other character

The Genotypic (rg) and [16] Phenotypic (rp) correlation coefficients for fifteen characters in 64 cassava accessions were presented in (Table 3). The genotypic correlation coefficient for fresh storage root yield per hectare showed significant and highly significant positive correlation with root diameter (rg=0.65), root length (rg=0.31), stem diameter (rg=0.63), root number per plant (rg=0.54), petiole length (rg=0.47), plant height (rg=0.34), weight fresh aboveground biomass

per plot ( $rg=0.56$ ) and harvest index ( $rg=0.57$ ) (Table 3). On the other hand, fresh storage root yield had significant negative correlation with ratio leaf lobe length to leaf lobe width ( $rg=-0.31$ ) and also it had non-significant correlation with leaf lobe [17] length and width, height of first branch and canopy diameter (Table 3). In the same way at phenotypic level, fresh storage root yield per hectare showed significant and highly significant positive correlation with root diameter ( $rp=0.37$ ), root length ( $rp=0.24$ ), stem diameter ( $rp=0.30$ ), root number per plant ( $rp=0.39$ ), petiole length ( $rp=0.32$ ), weight fresh aboveground biomass per plot ( $rp=0.49$ ) and harvest index ( $rp=0.59$ ) (Table 3). Likewise genotypic level, fresh storage root yield per hectare at phenotypic level had significant negative correlation with ratio leaf lobe length to leaf lobe width ( $rg=-0.18$ ) but it had non-significant correlation with the rest of the characters (Table 3) [18].

Correlations among characters play a vital role in plant breeding by refining selection efficiency. Stronger and positive correlations are observed between fresh storage root yield per hectare with root diameter, root length, stem diameter, root number per plant, petiole length, plant height, weight fresh aboveground biomass per plot and harvest index characters indicating that any increase in such characters will do the boosting in root yield (Table 3). This genotypic and phenotypic correlation results is agreed with research findings of earlier workers with respect to positive correlation of root yield with stem diameter and number of commercial roots per plant, root length, root diameter. However, fresh storage root yield per hectare has negative correlation with ratio leaf lobe length to leaf lobe width, suggesting that when selection for high root fresh yield one should go for accessions with low leaf length to width ratio (Table 3) [19].

In generally, the attributes of genotypic and phenotypic correlation coefficients value either positive or negative are exhibited roughly similar in respect of the majority of the characters studied (Table 3). In [20] those characters in which fresh storage root yield show positive and significant correlation, there are component interactions in which a gene get ready an increase in one character will influence another character as long as other conditions are kept constant. Hence, improvement in fresh storage root yield per hectare is possible by considering above characters as criteria in selection design (Table 3). Furthermore, the significantly higher magnitudes of positive genotypic correlation than the corresponding phenotypic correlation in respect to some of the characters (Table 3) suggest that these characters are strong [21] association with root yield and genetically controlled. Larger genotypic correlation coefficients indicate greater contribution of genetic factors and reduced effects of the environment. These results agree with the study by expert team, they found cassava root yield genotypic correlation magnitude higher than phenotypic correlation with respect to the characters studied. In contrary, noted that in sweet potato accessions, the genotypic correlation coefficients are lower than the phenotypic correlation coefficients among different sweet potato traits, indicating the significant effects of the environment [22]. The magnitude may be varied among crop types.

### Correlation among other character

Many Several remarkable genotypic and phenotypic associations were revealed among themselves (Table 3). The Genotypic ( $rg$ ) association results showed that stem diameter had highly significant positive association with leaf lobe width ( $rg=0.34$ ), petiole length ( $rg=0.40$ ), plant height ( $rg=0.80$ ), root number per plant ( $rg=0.48$ ), root diameter ( $rg=0.28$ ), root length ( $rg=0.41$ ) and [23] weight fresh above ground biomass per plot ( $rg=0.65$ ) and it had non-significant association with the rest of the characters (Table 3). Likewise, root diameter had positive and significant correlation with petiole length ( $rg=0.37$ ), height first branch ( $rg=0.34$ ), weight fresh above ground biomass per plot ( $rg=0.25$ ), harvest index per plot ( $rg=0.42$ ) and it revealed non-significant association with the rest of the characters except stem diameter (Table 3). Further, stronger and positive associations were observed between root number per plant with root length ( $rg=0.33$ ) and weight fresh aboveground biomass per plot ( $rg=0.66$ ) suggesting that as cassava root length and aboveground biomass per plot increases correspondingly it will increase in root number per plant. Most of the characters have negative genotypic associations with number of root per plant (Table 3).

At [24] Phenotypic ( $rp$ ) level, stem diameter had significant and highly significant positive association with petiole length ( $rp=0.28$ ), plant height ( $rp=0.22$ ), root number per plant ( $rp=0.26$ ), root diameter ( $rp=0.18$ ), weight fresh above ground biomass per plot ( $rp=0.38$ ) and it had non-significant association with the rest of the characters (Table 3). Root diameter had strong positive association with petiole length ( $rg=0.28$ ), weight fresh above ground biomass per plot ( $rg=0.25$ ), harvest index per plot ( $rg=0.20$ ) whereas rest of the characters showed non-significant association except stem diameter. Similarly, root number per plant had highly significant and positive association with root length ( $rp=0.23$ ) and weight fresh above ground biomass per plot ( $rp=0.47$ ). Among the characters, petiole length, plant height, root number per plant, root diameter and weight fresh above ground biomass per plot are strong positively associated with stem diameter at both genotypic and phenotypic levels (Table 3) [25].

In the present study, many genotypic and phenotypic associations are observed among themselves (Table 3). The character has more and strong positive correlation with respect to the character studied, suggest that any increase in such characters will do the boost more than one character among themselves. Also the observed associations among the agronomic characters indicate that improvement of one character would also result in simultaneous improvement to the other character. The results are in [26] accordance with who reported genotypic and phenotypic associations are observed among themselves for sweet potato. As compared to genotypic correlation, the value of phenotype correlation coefficients between most of the characters is lower than among themselves [27].

Traits	LLL	WLL	R	PL	PH	CD
LLL		0.64**	0.32*	0.49**	0.55**	-0.09NS
WLL	0.49**		-0.49**	0.74**	0.47**	-0.27*
R	0.42**	-0.55 **		-0.32*	-0.01NS	0.22NS
PL	0.41**	0.60**	-0.23**		0.54**	-0.16NS

PH	0.33**	0.22*	0.05NS	0.28 **		-0.13NS
CD	0.03NS	-0.09 NS	0.13NS	-0.07NS	0.18*	
SD	0.11NS	0.11NS	-0.06NS	0.28 **	0.22*	0.02NS
LB	-0.17NS	-0.24 **	0.06NS	-0.12NS	-0.11NS	0.08NS
HFB	0.09NS	0.05 NS	0.03NS	0.11NS	0.15NS	-0.02NS
RN	-0.06NS	0.03 NS	-0.14NS	0.09NS	0.09NS	0.03NS
RD	0.14 NS	0.01NS	0.12NS	0.28 **	0.12 NS	-0.05NS
RL	-0.08NS	-0.14 NS	0.01NS	-0.07NS	0.06NS	0.02NS
WFAB	-0.21 *	-0.06 NS	-0.15NS	0.22*	0.26 **	0.14NS
HI	0.12NS	0.14NS	-0.06NS	0.08NS	-0.10NS	0.02NS
FSRY	-0.04NS	0.10NS	-0.18 *	0.32 **	0.14NS	0.13NS

Traits	SD	LB	HFB	RN	RD	RL	WFAB	HI	FSRY
LLL	0.19NS	-0.23NS	0.14NS	-0.06NS	0.22NS	-0.1NS	-0.2NS	0.14NS	-0.04NS
WLL	0.35**	-0.28*	0.11NS	0.12 NS	0.19NS	-0.16NS	-0.03NS	0.27*	-0.21NS
R	-0.24NS	0.04NS	0.01NS	-0.28*	-0.02NS	-0.04NS	-0.21NS	-0.17NS	-0.31*
PL	0.40**	-0.13NS	0.14NS	0.10NS	0.37 **	-0.11NS	0.26*	0.21NS	0.47**
PH	0.80**	-0.34**	0.27*	0.12NS	0.24NS	0.18NS	0.51**	-0.10NS	0.34**
CD	0.18NS	0.09NS	-0.05NS	0.09NS	-0.15NS	-0.07NS	0.21NS	0.04NS	0.21NS
SD		-0.08NS	0.04NS	0.48**	0.29*	0.41**	0.65**	0.06NS	0.63**
LB	-0.05NS		-0.19NS	-0.07NS	-0.16NS	0.09NS	0.04NS	0.01NS	0.01NS
HFB	0.03NS	-0.17NS		0.03NS	0.34**	-0.11NS	0.07NS	0.06NS	0.16NS
RN	0.26**	-0.02NS	-0.04NS		0.16NS	0.33**	0.66**	0.03NS	0.54**
RD	0.18*	-0.15NS	0.17NS	0.10NS		-0.06NS	0.25*	0.42**	0.65**
RL	0.07NS	0.04NS	-0.06NS	0.23**	0.14NS		0.47**	-0.07NS	0.31*
WFAB	0.37**	0.03NS	0.05NS	0.47**	0.18*	0.29**		-0.35**	0.56**
HI	-0.02NS	0.02NS	0.05NS	0.02NS	0.20*	0.01NS	-0.39 **		0.57**
FSRY	0.30**	0.03 NS	0.11NS	0.39**	0.37**	0.24**	0.49**	0.59**	

**Table 3:** Genotypic (above diagonal) and Phenotypic (below-diagonal) correlations of 15 cassava traits grown at Tarcha, 2019-2021.

### Path-coefficient analysis

Based on genotypic path coefficient analysis result revealed that weight fresh above ground biomass per plot (0.770) the highest and positive direct effect was applied on fresh storage root yield per hectare, followed by harvest index per plot (0.763), root diameter (0.121) and petiole length (0.120) (Table 4). On the other hand, canopy diameter, root length and height of first branch were employed weak positive direct effects 0.079, 0.034 and 0.014, respectively on fresh storage root yield per plot, whereas plant height (-0.006), stem diameter(-0.029), level of branch per plant (-0.029), root number (-0.035), leaf lobe length to width ratio(-0.042) and width of leaf lobe

(-0.058) had negative direct influence (Table 4). The residual factor (0.037) showed that about 96.3% of the variability in fresh storage root yield per hectare was contributed by the fourteen characters studied in path analysis. This means, those characters considered in this study are sufficient to adequately explain the variation in fresh storage root yield in cassava (Table 4) [28].

As correlation coefficients analysis does not permit the separating of both phenotypic and genotypic correlation coefficients in to direct and indirect effect, they are further analyzed by path coefficient analysis. Therefore [29], Path coefficient analysis is a tool to separation the showed association into direct and indirect effects of yield components on fresh storage root yield per hectare offers clearer

picture of character association for expressing efficient component approach (Table 4). A very high positive direct contribution to fresh storage root yield per hectare is employed by weight fresh above ground biomass per plot. Harvest index per plot, root diameter, petiole length, canopy diameter and root length are also major positive direct contribution to the fresh storage root yield per hectare (Table 4). Also all these characters were correlated strongly and positively with fresh storage root yield per hectare (Table 4), suggest that indirect selection of these characters would be worthwhile to improve cassava fresh storage root yield. In other words, positive direct effects of these characters on fresh storage root yield per hectare indicate that, with other variables kept constant, improvement of these characters will increase fresh storage root yield per hectare (Table 4). Similar results are reported by for root diameter, number of branch per plant and for root diameter, number root per plant, weight fresh above ground biomass per plot and for stem diameter, root diameter and negative direct effect petiole length on fresh storage root yield. All those authors are found root diameter the most important components contributing to fresh storage root yield. On other study [10,29,30] are also reported that above ground fresh weight per plot and harvest

index per plot have direct positive effects on tuber yield of sweet potato which is supported by present findings.

The negative direct effect of these six characters on fresh storage root weight might be explained by the fact that selection based on these six characters might reduce fresh storage root weight (Table 4). But from these root number, stem diameter and plant height characters are also exhibited strong and positive genotypic correlations with fresh storage root yield (Table 4). This finding is in agreement with who are stated that plant height and root number per plant are negative direct effect on fresh storage root yield of cassava but opposite results are reported by for canopy diameter, stem diameter and level of branch per plant. Similarly, for leaf length and leaf width are negative and positive direct effect respectively on tuber yield of yam. Within the scope of the path analysis is carried out in the present study, it is, hence, suggested that the weight of above ground biomass per plot, harvest index per plot, root diameter and petiole length are the main components of yield should be given high attentions in the selection process [30].

Traits	LLL	WLL	R	PL	PH	CD
LLL	0	-0.038	0.013	0.059	-0.003	-0.007
WLL	0	-0.058	0.021	0.088	-0.003	-0.021
R	0	0.029	-0.042	-0.038	0	0.017
PL	0	-0.043	0.013	0.12	-0.003	-0.013
PH	0	-0.028	0.001	0.064	-0.006	-0.01
CD	0	0.016	-0.009	-0.02	0.001	0.079
SD	0	-0.02	0.01	0.048	-0.005	0.014
LB	0	0.016	-0.002	-0.015	0.002	0.007
HFB	0	-0.006	-0.001	0.017	-0.002	-0.004
RN	0	-0.007	0.012	0.012	-0.001	0.007
RD	0	-0.011	0.001	0.044	-0.001	-0.011
RL	0	0.009	0.001	-0.013	-0.001	-0.006
WFAB	0	0.002	0.009	0.031	-0.003	0.016
HI	0	-0.016	0.007	0.025	0.001	0.003

Traits	SD	LB	HFB	RN	RD	RL	WFAB	HI	rg
LLL	-0.005	0.007	0.002	0.002	0.027	-0.004	-0.158	0.106	-0.04NS
WLL	-0.01	0.008	0.002	0.004	0.023	-0.005	-0.026	0.207	-0.21NS
R	0.007	-0.001	0	0.01	-0.003	-0.001	-0.159	-0.13	-0.31*
PL	-0.011	0.004	0.002	0.004	0.044	-0.004	0.2	0.157	0.47**
PH	-0.023	0.01	0.004	-0.004	0.029	0.006	0.394	-0.073	0.34**
CD	-0.005	-0.003	-0.001	-0.003	-0.018	-0.002	0.16	0.032	0.21NS
SD	-0.029	0.002	0.001	-0.017	0.036	0.014	0.502	0.042	0.63**

<b>LB</b>	0.002	-0.029	-0.003	0.002	-0.02	0.003	0.027	0.01	0.01NS
<b>HFB</b>	-0.001	0.006	0.014	-0.001	0.041	-0.004	0.054	0.046	0.16NS
<b>RN</b>	-0.014	0.002	0	-0.035	0.019	0.011	0.511	0.026	0.54**
<b>RD</b>	-0.008	0.005	0.005	-0.006	0.121	-0.002	0.193	0.318	0.65**
<b>RL</b>	-0.012	-0.003	-0.002	-0.012	-0.007	0.034	0.363	-0.052	0.31*
<b>WFAB</b>	-0.019	-0.001	0.001	-0.023	0.03	0.016	0.77	-0.269	0.56**
<b>HI</b>	-0.002	0	0.001	-0.001	0.051	-0.002	-0.272	0.763	0.57**

**Key:** LLL=Leaf Lobe Length(cm), WLL=Width of Leaf Lobe(cm), R=Ratio Leaf lobe length to width leaf lobe, PL=Petiole Length (cm), PH=Plant Height (cm), CD=Canopy Diameter (cm), SD=Stem Diameter (cm), LB=Level of Branch per plant, HFB=Height of First Branch (cm), RN=Root Number per plant, RD=Root Diameter (cm), RL=Root Length (cm), WFAB=Weight of Fresh Above Ground Biomass (kg/plot), HI=Harvest Index(%) and FSRY=Fresh Storage Root Yield (t/ha) [31].

**Table 4:** Genotypic direct effects (bold and underlined diagonals) and indirect effects (off-diagonals) of 14 variables on fresh storage root yield of cassava at Tarcha.

Residual effect=0.037

## Conclusion

Various characters in determinants of fresh storage root yield and yield components are influenced greatly by the genotype and environment. Hence, as new cultivars are being made by crossing or selection, the breeders investigate the associations between root yield and its components. Therefore, association assessments are useful in defining the components of complex characters such as fresh storage root yield. To increase the fresh storage root yield of cassava, one has to examine of direct and indirect effects of yield components which give the basis for its effective cassava root yield improvement and thus the difficult of fresh storage root yield increase can be more successfully undertaken due to performance of yield components and selection for closely associated characters.

Based on this findings, it may be conclude character that employed positive direct effect and strong positive association value with fresh storage root yield is identified to influence cassava fresh storage root yield in the positive direction and requires much consideration during the process of selection situations in point are weight of above ground biomass per plot, harvest index per plot, root diameter and petiole length.

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