

## Morpho-Biochemical Characterization of Chayote [*Sechium edule* (Jacq.)] Genotypes from Sikkim Himalayas

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### ABSTRACT

Twenty chayote genotypes with different accession numbers maintained at ICAR-NEH region, Gangtok were used in the study and observations were recorded for seventeen quantitative traits during the year 2018-19. All the genotypes genetically differed from each other based on their mean performance. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters. High values for PCV, GCV, heritability and genetic advance as per cent of mean

were observed for seed weight (61.2 %, 61.1 %, 99 % and 125.6 %) and non-reducing sugar (59.2 %, 58.1 %, 96 % and 117.4 %) respectively, which indicates a wide range of variation for crop improvement through selection. The correlation coefficient (genotypic and phenotypic) showed that fruit weight expressed significant positive correlation with seed length (0.93), seed breadth (0.92) and total sugar (0.65). Path coefficient analysis revealed that fruit breadth, fruit length, seed weight would be of selection criteria for further crop improvement. The genotypes were grouped into three clusters and the maximum intra-cluster distance was observed in cluster I (25.12) and maximum inter cluster distance was found between the cluster I and III (41.47). Seed weight exhibited the highest percentage contribution towards total genetic divergence.

**Keywords** Chayote, Characterization, Genetic divergence, Genotypes, Variability.

### INTRODUCTION

Chow-Chow [*Sechium edule* (Jacq.)] is an herbaceous, perennial, monoecious climber belongs to the family Cucurbitaceae. Chayote is considered as one of the important fruits in tropical and subtropical regions of the world (Morton 1981), it provides three seasonal edible products widely utilized in Sikkim and Darjeeling region of India. These products include a young twig available during the summer time known as “Munta”, the fruit available in the rainy to the winter season, is known as ‘Dana’, and root

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available between winter to spring season, is known as “Jara”. It is popularly known by different names, as Chow-Chow and Squash in North-Eastern India. It is known with different names in different dialects such as Eskush, among the Nepali-speaking people of India, is a deformation of English word ‘squash’, which is a misnomer for chayote, Iskut (in Mizoram), Piskot (Khasi) in Meghalaya, Daskus in Manipur and Lonku in Himachal Pradesh (Verma *et al.* 2017). Variation in color, size and fruit habit has been observed in these regions. So far, the crop remained neglected and underutilized, and only a few studies have been carried out regarding its crop improvement. Its characteristics like higher and potential nutritional aspects, tolerance to biotic and abiotic stresses and very low manurial requirements make it potential crop in changing climate scenario. Fruit extract has an antihypertensive property (Gordon *et al.* 2000), antibacterial properties, antifungal properties, antioxidant properties (Ordenez *et al.* 2009, Ordenez *et al.* 2003, Sibi *et al.* 2013), anti-hyperglycaemic properties (Tiwari *et al.* 2013), anticonvulsant and central nervous system depressant activity (Firdous *et al.* 2012). Biochemical and nutritional characterization of chayote (*Sechium edule* Jacq.) would render further information for its rational use and benefit to the mankind. Analysis of biochemical parameters is found to be a helpful tool for crop improvement with regards to fruit quality. An improvement in yield and quality in the crop like chayote is normally achieved by selection of superior genotypes with agronomical desirable traits or by hybridization. Therefore, the study of phenotypic variation among chayote genotypes could be utilized for genetic improvement. A wide range of genetic variability is available in chayote, providing good scope for improvement in quality and other yield attributing characters through selection. The correlation coefficient measures the mutual relationship between various characters and determines the component characters on which selection could be made for genetic improvement for yield and yield contributing traits (Rao 1952, Bamaniya *et al.* 2018). The path coefficient analysis provides an effective mean for partitioning of direct and indirect cause of association (Sharma *et al.* 2020). Hence, there is a prerequisite for preliminary investigations of different quantitative traits in the genotypes for the development of superior hybrids in chayote. A

very few researchers have worked upon chayote to estimate the amount of genetic diversity under Sikkim Himalayan region for future genetic improvement of the crop. So, this study was conducted to determine genetic divergence based upon the morphological and biochemical parameters in chayote genotypes available here.

## MATERIALS AND METHODS

Fruits from twenty chayote genotypes with different accessions numbers (ACC-02, ACC-03, ACC-05, ACC-06, ACC-13, ACC-23, ACC-25, ACC-27, ACC-28, ACC-30, ACC-31, ACC-43, ACC-44, ACC-45, ACC-46, ACC-65, ACC-70, ACC-72, ACC-80 and ACC-88) were collected from ICAR Research complex for NEH region, Tadong, Gangtok, East-Sikkim which were statistically laid out in Randomized Block Design (RBD) with three replications. Ten fruits were randomly selected from every replication for observing the data under each genotype. The morphological and biochemical study was carried out at Department of Horticulture, Sikkim University with 25°09.66’N - 27°31.733’N latitude and 88°8.54’E- 94°6.44’E longitude during *rabi* season of 2018-2019.

The data was recorded on morphological characters viz., fruit weight (g) which was measured by an electronic balance ranging from 0.00 kg-25.00 kg, fruit length, fruit breadth, peel thickness, seed length and seed breadth was measured by measuring tape and seed weight (g) was measured by a digital electronic balance ranging from 0.00 g to 250.00 g. The biochemical parameters like total soluble solids (TSS) were examined by using Hanna Digital Refractometer, Moisture % in fruit and seed, were measured using hot air oven drying method.

### Ascorbic acid content (mg/100g)

It was estimated through the method suggested by Rangana (1976). In this method 10 to 20 mg of sample is taken and volume was made up to 100 ml with 3 % HPO<sub>3</sub> and filtered. An aliquot (2-10 ml) of the HPO<sub>3</sub> extract of the sample is taken and titrated with the standard dye till it showed pink color which persist for at least 15 sec. The aliquot of sample was taken such that the titre did not exceed 3-5 ml. Ascorbic

acid (mg /100g) was calculated as:

$$= \frac{\text{Titre} \times \text{dye factor} \times \text{volume made up.}}{\text{Aliquot of extract taken for estimation} \times \text{wet/volume of sample for estimation}} \times 100$$

#### Titrateable acidity (%)

It was estimated by the method suggested by Rangana (1976). Approximately 10 ml of sample was diluted with 100 ml of distilled water and few drops of phenolphthalein indicator was added. Acids in the juice were titrated with 0.1 N NaOH. The per cent of citric acid was calculated as:

$$\text{Titrateable Acidity (\%)} = \frac{\text{Titre vol} \times \text{normality of NaOH} \times \text{vol made up} \times \text{eq wt of acid}}{\text{Aliquot of sample} \times \text{vol of sample} \times 1000} \times 100$$

#### Total sugar %

Total sugar was determined by the method described in AOAC (2005) using following formula:

$$\text{Total sugar \%} = \frac{\text{Factor} \times \text{dilution}}{\text{Weight of sample} \times \text{titre value}} \times 100$$

#### Reducing sugar %

Reducing sugar was determined by the method as described in AOAC (2005). Firstly 50 ml of filtered solution (A) is taken and filled it in a burette and 210 ml of mixed Fehling's solution (A and B) in two 250 ml conical flasks is pipetted and mixed with the contents in flask which was moderately boiled for 2 minutes, later 3 drops of the methylene blue solution were added after 2 minutes. Titration is completed by adding 2 to 3 drops of prepared solution at 5 to 10 seconds intervals, until the red brick color is appeared.

$$\text{Reducing sugar \%} = \frac{\text{Factor} \times \text{dilution}}{\text{Weight of sample} \times \text{titre value}} \times 100$$

#### Non-reducing sugar %

Non-reducing sugar was the value obtained after subtracting the value of reducing sugar from total sugar.

#### Phenol content

Total phenol content estimation was carried out with Folin-Ciocalteu reagent along with other reagents like 80 % Ethanol, 20 % Na<sub>2</sub>CO<sub>3</sub> and Standard (100 mg catechol in 100 ml of water). It is diluted 10 times for a working standard.

#### Crude fiber %

Crude fiber estimation was done as per AOAC (2005) by Fibra plus apparatus (Pelican Equipment) using 1.25% H<sub>2</sub>SO<sub>4</sub> and 1.25% sodium hydroxide.

#### Statistical analysis

The data were statistically analyzed to find out the significance of the difference among the chayote genotypes. The mean values of all the characters were evaluated and ANOVA was set for Randomized Block Design.

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967). Phenotypic and Genotypic coefficients of variation were estimated by the method given by Burton and De Vane (1953). Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance was calculated as per formula suggested by Lush (1949) and expressed in percentage. Genetic advance is the improvement in mean genotypic value of selected plants over the base population. Genetic advance at 5% selection intensity was worked out using the formula given by Lush (1949) and Johnson *et al.* (1955). The correlation coefficients among at phenotypic (rp) and genotypic (rg) level were estimated by formulae given by Al-Jibouri *et al.* (1958). The path coefficient analysis was performed as per the formula given by Wright (1921) and adopted by Dewey and Lu (1959). The data collected on different morphological and quality traits were subjected to D<sup>2</sup> analysis (Mahalanobis 1936) to estimate the genetic diversity among the genotypes by measuring intra-cluster and inter-cluster distance.

## RESULTS AND DISCUSSION

In the investigation, genotypes of chayote exhibited

significant differences for all the seventeen characters studied and a wide range of variability was observed for morphological as well as biochemical parameters. While studying the mean performance, there was a significant difference with all the characters under investigation (Table 1 and Fig. 1). ACC-45 showed maximum fruit weight (796.67 g) and maximum fruit length (17.04 cm). ACC-46 was promising in seed length (6.84 cm) and seed weight (13.46g). ACC-80 was highest in case of seed breadth (3.69 cm) and

fruit breadth (10.58 cm) and peel thickness was high in ACC-65 (0.32 cm). Significant differences among the mean performance indicated that there were significant variations among the collected genotypes. Variation in the seed length and fruit weight could be possibly due to genetic makeup of the cultivar, edaphic conditions and particular set of environments which results in better nutrient diversion towards fruit development with a better source to sink capacity (Shiga *et al.* 2015, Kapoor *et al.* 2014, Ragasa *et al.*

**Table 1.** Mean performances of seventeen characters of chayote genotypes.

ACC. NO.	FW	FL	FB	PT	SW	SL	SB	SM	FM	PC	TA	TSS	AA	RS	TS	NRS	CF
ACC- 2	342.67	11.67	8.52	0.30	2.40	4.07	2.46	74.63	92.49	131.60	0.34	3.30	19.79	6.74	7.33	0.59	15.93
ACC- 3	418.33	10.67	9.40	0.28	4.24	4.66	2.97	83.44	92.72	156.23	0.34	3.93	22.17	6.97	7.57	0.60	16.10
ACC- 5	360.00	13.07	8.52	0.27	3.73	4.42	2.96	79.13	93.96	137.97	0.29	2.90	22.00	6.13	8.53	2.40	25.38
ACC- 6	533.33	15.80	8.82	0.28	2.37	3.66	2.19	73.39	93.15	104.20	0.42	3.37	25.81	6.40	8.47	2.07	33.00
ACC- 13	440.00	11.88	9.22	0.28	4.92	4.90	2.94	81.72	95.55	109.83	0.45	3.47	20.59	7.23	8.70	1.47	15.43
ACC- 23	266.67	9.42	7.72	0.29	9.36	6.04	3.33	77.78	85.10	152.40	0.63	3.40	28.50	6.70	7.73	1.03	36.60
ACC- 25	536.67	12.83	10.12	0.29	7.79	5.72	3.26	78.90	92.51	142.83	0.61	3.47	20.59	6.63	8.23	1.60	46.83
ACC- 27	396.67	12.26	8.60	0.31	2.64	2.68	2.17	75.72	93.67	128.63	0.46	2.93	22.96	6.13	7.57	1.43	17.67
ACC- 28	520.00	12.49	9.50	0.30	10.68	6.04	3.28	78.91	88.83	162.30	0.75	3.53	27.71	4.77	7.10	2.33	13.56
ACC- 30	243.33	10.26	7.25	0.28	2.05	3.90	1.75	72.85	95.94	133.80	0.49	3.67	20.59	5.30	6.10	0.80	27.60
ACC- 31	480.00	14.33	8.61	0.28	9.21	5.40	3.07	78.59	91.75	128.70	0.58	3.43	27.71	7.67	8.10	0.43	16.16
ACC- 43	353.33	11.34	8.30	0.29	3.26	3.56	2.40	77.02	92.64	139.33	0.57	3.53	19.00	6.50	7.53	1.03	45.22
ACC- 44	418.33	12.39	8.96	0.31	2.86	3.18	2.32	75.51	96.55	119.60	0.55	3.10	21.38	4.23	6.57	2.33	26.42
ACC- 45	796.67	17.04	10.54	0.30	8.58	5.30	3.03	80.59	93.59	174.93	0.48	3.23	30.96	6.37	6.73	0.37	17.60
ACC- 46	448.33	12.69	8.85	0.27	13.46	6.84	3.62	74.44	93.08	128.53	0.49	3.27	26.13	6.13	6.47	0.33	16.08
ACC- 65	408.33	12.62	8.29	0.32	6.84	5.06	3.06	80.62	91.38	166.10	0.48	3.80	20.59	5.30	6.37	1.07	17.37
ACC- 70	271.67	11.75	8.09	0.19	2.62	3.11	2.23	77.60	96.30	169.00	0.46	3.37	27.71	6.23	6.83	0.60	14.20
ACC- 72	391.67	14.97	8.06	0.29	3.17	3.48	2.36	76.69	93.87	166.83	0.55	3.60	21.38	5.40	6.33	0.93	22.77
ACC- 80	560.00	11.50	10.58	0.28	12.81	6.37	3.69	75.68	92.69	137.33	0.65	3.00	28.59	5.97	6.47	0.50	17.92
ACC- 88	403.33	13.10	8.10	0.31	9.29	5.61	3.35	78.00	89.38	129.50	0.66	3.40	26.67	6.47	8.33	1.87	15.76
GM	429.47	12.60	8.80	0.29	6.12	4.70	2.82	77.56	92.76	140.98	0.51	3.39	24.04	6.16	7.35	1.19	22.88
SE (m)	11.30	0.35	0.22	0.01	0.22	0.14	0.10	0.85	0.50	2.64	0.02	0.10	1.08	0.16	0.17	0.13	1.53
CD 5 %	32.34	1.00	0.63	0.02	0.62	0.41	0.30	2.43	1.44	7.55	0.05	0.28	3.10	0.45	0.49	0.38	4.38
Lowest range	243.33	9.42	7.25	0.19	2.05	3.11	1.75	72.85	85.1	104.2	0.29	2.9	19	4.23	6.1	0.33	13.56
Highest range	796.67	17.04	10.58	0.32	13.46	6.84	3.69	83.44	96.55	174.93	0.75	3.93	30.96	7.67	8.7	2.4	46.83

FW = Fruit weight (g), FL = Fruit length (cm), FB = Fruit breadth (cm), PT = Peel thickness (mm), SW = Seed weight (g), SL = Seed length (cm), SB = Seed breadth (cm), SM = Seed moisture (%), FM = Fruit moisture (%), PC = Phenol content (mg/100g), TA = Titrable acidity (%), TSS = TSS (%), RS = Reducing sugar (%), AA = Ascorbic acid (mg/100g), TS = Total sugar (%), NRS = Non-reducing sugar (%), CF = Crude fibre (%).

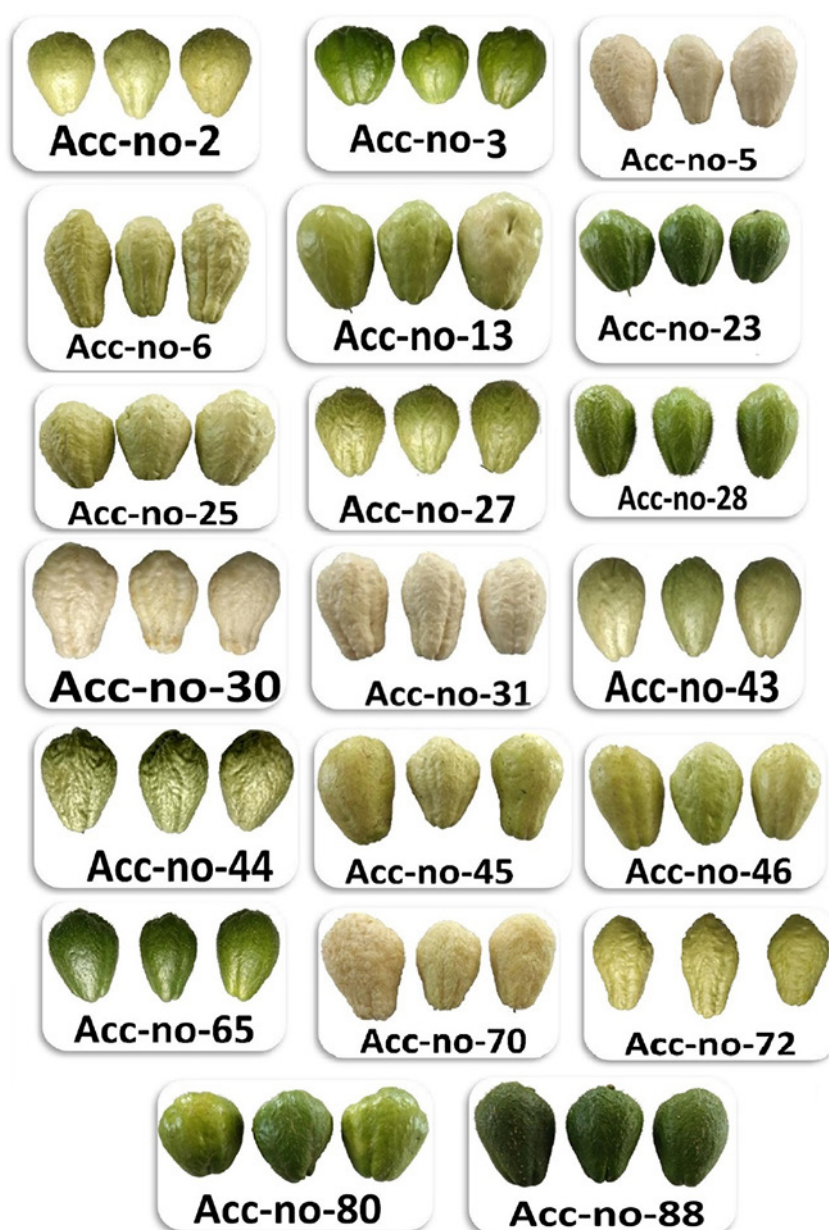


Fig. 1. Genetic variability among the various chayote genotypes.

2014, Kumar *et al.* 2018). Similarly, the length of chayote fruit varies from 10 to 20 cm, similar results were obtained in the findings of Kapoor *et al.* (2014), with fruit length range of 4.8 to 11.8 cm. Whereas in quality attributing traits, ACC-45 was found to be significantly superior in ascorbic acid (30.96 mg/100 g) and phenol content (174.93 mg/100g),

value regarding fruit moisture was high in ACC-44 (96.55 %), similarly seed moisture (83.44 %) and TSS (3.93 %) were recorded high in ACC-3, titrable acidity was high in ACC-28 (0.75 %). Reducing sugar (7.67 %), non-reducing sugar (2.4 %) and total sugar (8.7 %) were high in ACC-31, ACC-5 and ACC-13 respectively, whereas crude fiber was high in ACC-25



(46.83 %). Variations in quality attributing traits were due to genetic makeup of the corresponding genotype, which also results in better nutrient diversion towards fruit development with a better source to sink capacity which ultimately results in significant enzymatic activity and corresponding pathways for biosynthesis (Mishra and Das 2015, Jat *et al.* 2014). The data on genotypic and phenotypic coefficients of variation of different characters as presented in Table 2 revealed that the highest phenotypic and genotypic coefficient of variation was recorded in case of seed weight (61.18 % and 61.08 %) followed by non-reducing sugar (59.15 % and 58.07 %), while fruit moisture (2.9 % and 2.85 %) recorded lowest value among genotypic and phenotypic coefficient of variation, respectively. It has also been shown that phenotypic and genotypic coefficient of variation values were expressed high in crude fiber (44.48 % and 43.98 %), fruit weight (28.93 % and 28.81 %), seed length

(25.69 % and 25.51 %) and titrable acidity (22.78 % and 22.49 %), respectively. It is apparent from the data that value for PCV was marginally higher than GCV for all the traits indicating lesser degree of environmental influences upon them (Gaikwad *et al.* 2011, Kumar *et al.* 2008). Similarly, it has been observed that highest phenotypic and genotypic coefficient of variation was obtained for the yield attributing traits like seed weight (Rakhi and Rajamony 2005). The higher degree of the coefficients of variation clearly revealed that these traits were produced additively amongst the genotypes. This could be of a criterion for selection of superior genotypes for crop improvement. The results revealed that the heritability in broad sense was ranged from 87- 99 % (Table 2). High heritability percentage was recorded in fruit weight and seed weight (99 %) followed by seed length and phenol content (98 %), it was apparent from the table that TSS (87%) was found to be lowest amongst all. Her-

**Table 2.** Mean, range, co-efficient of variation, heritability, genetic advance and genetic advance as % of mean.

Characters	General mean	Range	Co-efficient of variation (%)		Heritability % (broad sense)	Genetic advancement at 5 %	Gen adv as of % mean at 5 %
			GCV	PCV			
FW	429.47	243.33-796.67	28.81	28.93	99	253.81	59.11
FL	12.60	9.42-17.04	14.24	14.51	96	3.63	28.8
FB	8.80	7.25-10.58	9.72	10.03	93	1.7	19.39
PT	0.29	0.19-0.32	8.7	9	93	0.04	17.33
SW	6.12	2.05-13.46	61.08	61.18	99	7.68	125.62
SL	4.70	3.11-6.84	25.51	25.69	98	2.45	25.2
SB	2.82	1.75-3.69	18.9	19.26	96	1.07	38.21
SM	77.56	72.85-83.44	3.42	3.59	90	5.21	6.72
FM	92.76	85.1-96.55	2.85	2.9	96	5.35	5.77
PC	140.98	104.2-174.93	14.05	14.17	98	40.46	28.7
TA	0.51	0.29-0.75	22.49	22.78	97	45.76	58.46
TSS	3.39	2.9-3.93	7.4	7.93	87	0.48	14.24
AA	24.04	19-30.96	14.63	15.31	91	6.92	28.8
RS	6.16	4.23-7.67	13.17	13.41	96	1.64	26.65
TS	7.35	6.1-8.7	11.22	11.46	95	1.66	22.64
NRS	1.19	0.33-2.4	58.07	59.15	96	1.39	117.44
CF	22.88	13.56-46.83	43.98	44.48	97	20.49	89.57

FW = Fruit weight (g), FL = Fruit length (cm), FB = Fruit breadth (cm), PT = Peel thickness (mm), SW = Seed weight (g), SL = Seed length (cm), SB = Seed breadth (cm), SM = Seed moisture (%), FM = Fruit moisture (%), PC = Phenol content (mg/100g), TA = Titrable acidity (%), TSS = TSS (%), RS = Reducing sugar (%), AA = Ascorbic acid (mg/100g), TS = Total sugar (%), NRS = Non-reducing sugar (%), CF = Crude fibre (%).

**Table 3.** Estimation of phenotypic and genotypic correlation co-efficient between different characters in chayote.

		FL	FB	PT	SW	SL	SB	SM	FM	PC	TA	TSS	AA	RS	TS	NRS	CF	FW
FL	P	-	<b>0.345</b>	0.116	0.051	-0.039	-0.002	0.032	0.176	0.052	-0.054	-0.176	0.304	0.015	0.086	0.085	-0.123	0.713
	G		<b>0.358</b>	0.119	0.053	-0.039	-0.009	0.032	0.179	0.058	-0.059	-0.171	0.330	0.012	0.087	0.089	-0.135	0.713
FB	P		-	<b>0.100</b>	0.444	0.410	0.505	0.342	0.064	0.075	0.128	-0.238	0.305	0.085	0.053	-0.037	-0.091	0.856
	G			<b>0.103</b>	0.457	0.422	0.519	0.351	0.065	0.079	0.133	-0.240	0.333	0.086	0.039	-0.055	-0.105	0.856
PT	P			-	<b>0.118</b>	0.122	0.134	-0.006	-0.351	-0.157	0.214	0.015	-0.229	-0.264	-0.012	0.296	0.073	0.248
	G				<b>0.121</b>	0.136	0.142	0.02	-0.371	-0.162	0.222	0.021	-0.246	-0.287	-0.027	0.305	0.073	0.248
SW	P				-	<b>0.934</b>	0.907	0.156	-0.546	0.147	0.591	-0.088	0.623	0.090	-0.090	-0.214	-0.199	0.446
	G					<b>0.943</b>	0.928	0.162	-0.553	0.146	0.600	-0.097	0.651	0.092	-0.092	-0.218	-0.201	0.446
SL	P					-	<b>0.923</b>	0.254	-0.582	0.110	0.446	0.070	0.476	0.199	0.041	-0.185	-0.116	0.379
	G						<b>0.936</b>	0.256	-0.603	0.115	0.457	0.074	0.506	0.203	0.040	-0.190	-0.122	0.379
SB	P						-	<b>0.422</b>	-0.571	0.148	0.388	-0.063	0.455	0.232	0.147	-0.097	-0.168	0.411
	G							<b>0.439</b>	-0.601	0.153	0.392	-0.065	0.477	0.236	0.151	-0.098	-0.177	0.411
SM	P							-	<b>-0.177</b>	0.432	-0.078	0.366	0.036	0.319	0.306	-0.008	-0.206	0.263
	G								<b>-0.190</b>	0.454	-0.087	0.435	0.044	0.343	0.316	-0.025	-0.219	0.263
FM	P								-	<b>-0.216</b>	-0.496	-0.169	-0.377	-0.184	-0.226	-0.054	-0.122	-0.002
	G									<b>-0.215</b>	-0.506	-0.194	-0.387	-0.204	-0.242	-0.049	-0.129	-0.002
PC	P									-	<b>0.148</b>	0.334	0.251	-0.204	-0.476	-0.331	-0.146	0.097
	G										<b>0.153</b>	0.352	0.261	-0.209	-0.494	-0.344	-0.146	0.097
TA	P										-	<b>0.075</b>	0.384	-0.255	-0.160	0.108	0.153	0.172
	G											<b>0.070</b>	0.406	-0.251	-0.153	0.113	0.156	0.172
TSS	P											-	<b>-0.27</b>	0.07	-0.13	-0.24	0.05	-0.18
	G												<b>-0.317</b>	0.100	-0.097	-0.233	0.047	-0.177
AA	P												-	<b>0.120</b>	-0.051	-0.203	-0.333	0.448
	G													<b>0.140</b>	-0.041	-0.213	-0.353	0.448
RS	P													-	<b>0.65</b>	-0.40	0.03	0.06
	G														<b>0.644</b>	-0.406	0.034	0.064
TS	P														-	<b>0.440</b>	0.230	0.036
	G															<b>0.438</b>	0.237	0.036
NRS	P															-	<b>0.236</b>	-0.032
	G																<b>0.243</b>	-0.032
CF	P																-	<b>-0.119</b>
	G																	<b>-0.119</b>

FW = Fruit weight (g), FL = Fruit length (cm), FB = Fruit breadth (cm), PT = Peel thickness (mm), SW = Seed weight (g), SL = Seed length (cm), SB = Seed breadth (cm), SM = Seed moisture (%), FM = Fruit moisture (%), PC = Phenol content (mg/100g), TA = Titrable acidity (%), TSS = TSS (%), RS = Reducing sugar (%), AA = Ascorbic acid (mg/100g), TS = Total Sugar (%), NRS = Non-reducing sugar (%), CF = Crude Fibre (%).

itability in broad sense in similar range also reported by other workers (Kumar *et al.* 2008, Tamang *et al.* 2018). Thus, the above-mentioned findings reveal that heritability in the most of the traits is due to additive

**Table 4.** Direct and indirect effect of various traits in relation to fruit weight of chayote at phenotypic and genotypic level.

		FL	FB	PT	SW	SL	SB	SM	FM	PC	TA	TSS	AA	RS	TS	NRS	CF
FL	P	<b>0.427</b>	0.147	0.050	0.022	-0.017	-0.001	0.014	0.075	0.022	-0.023	-0.075	0.130	0.007	0.037	0.036	-0.053
	G	<b>0.383</b>	0.137	0.046	0.020	-0.015	-0.004	0.012	0.068	0.022	-0.022	-0.066	0.126	0.005	0.033	0.034	-0.052
FB	P	0.222	<b>0.643</b>	0.064	0.285	0.263	0.325	0.220	0.041	0.048	0.082	-0.153	0.196	0.055	0.034	-0.024	-0.059
	G	0.216	<b>0.604</b>	0.062	0.277	0.255	0.314	0.212	0.039	0.048	0.080	-0.145	0.201	0.052	0.023	-0.033	-0.063
PT	P	0.020	0.017	<b>0.172</b>	0.020	0.021	0.023	-0.001	-0.060	-0.027	0.037	0.003	-0.039	-0.045	-0.002	0.051	0.012
	G	0.031	0.027	<b>0.259</b>	0.031	0.035	0.037	0.005	-0.096	-0.042	0.058	0.006	-0.064	-0.074	-0.007	0.079	0.019
SW	P	0.021	0.185	0.049	<b>0.417</b>	0.389	0.378	0.065	-0.227	0.061	0.246	-0.037	0.260	0.038	-0.038	-0.089	-0.083
	G	0.005	0.042	0.011	<b>0.091</b>	0.086	0.085	0.015	-0.051	0.013	0.055	-0.009	0.060	0.008	-0.008	-0.020	-0.018
SL	P	-0.006	0.068	0.020	0.154	<b>0.165</b>	0.152	0.042	-0.096	0.018	0.073	0.012	0.078	0.033	0.007	-0.031	-0.019
	G	-0.006	0.066	0.021	0.147	<b>0.156</b>	0.146	0.040	-0.094	0.018	0.071	0.012	0.079	0.032	0.006	-0.030	-0.019
SB	P	0.001	-0.287	-0.076	-0.515	-0.524	<b>-0.567</b>	-0.239	0.324	-0.084	-0.220	0.036	-0.258	-0.132	-0.083	0.055	0.095
	G	0.003	-0.140	-0.038	-0.250	-0.253	<b>-0.270</b>	-0.118	0.162	-0.041	-0.106	0.018	-0.129	-0.064	-0.041	0.026	0.048
SM	P	0.007	0.069	-0.001	0.032	0.051	0.086	<b>0.203</b>	-0.036	0.088	-0.016	0.074	0.007	0.065	0.062	-0.002	-0.042
	G	0.006	0.069	0.004	0.032	0.051	0.087	<b>0.198</b>	-0.038	0.090	-0.017	0.086	0.009	0.068	0.062	-0.005	-0.043
FM	P	-0.004	-0.001	0.007	0.011	0.012	0.011	0.004	<b>-0.020</b>	0.004	0.010	0.003	0.008	0.004	0.005	0.001	0.002
	G	0.017	0.006	-0.036	-0.054	-0.059	-0.059	-0.019	<b>0.097</b>	-0.021	-0.049	-0.019	-0.038	-0.020	-0.024	-0.005	-0.013
PC	P	-0.004	-0.006	0.012	-0.011	-0.008	-0.011	-0.032	0.016	<b>-0.074</b>	-0.011	-0.025	-0.019	0.015	0.035	0.024	0.011
	G	-0.008	-0.011	0.022	-0.020	-0.016	-0.021	-0.062	0.030	<b>-0.137</b>	-0.021	-0.048	-0.036	0.029	0.068	0.047	0.020
TA	P	0.004	-0.010	-0.017	-0.046	-0.035	-0.030	0.006	0.039	-0.012	<b>-0.078</b>	-0.006	-0.030	0.020	0.013	-0.008	-0.012
	G	0.004	-0.008	-0.013	-0.036	-0.028	-0.024	0.005	0.031	-0.009	<b>-0.060</b>	-0.004	-0.025	0.015	0.009	-0.007	-0.009
TSS	P	-0.003	-0.004	0.000	-0.001	0.001	-0.001	0.006	-0.003	0.005	0.001	<b>0.016</b>	-0.004	0.001	-0.002	-0.004	0.001
	G	-0.013	-0.019	0.002	-0.008	0.006	-0.005	0.034	-0.015	0.028	0.006	<b>0.079</b>	-0.025	0.008	-0.008	-0.018	0.004
AA	P	0.043	0.043	-0.033	0.089	0.068	0.065	0.005	-0.054	0.036	0.055	-0.038	<b>0.142</b>	0.017	-0.007	-0.029	-0.047
	G	0.118	0.119	-0.088	0.233	0.181	0.170	0.016	-0.138	0.094	0.145	-0.113	<b>0.358</b>	0.050	-0.015	-0.076	-0.126
RS	P	0.002	0.014	-0.043	0.015	0.032	0.038	0.052	-0.030	-0.033	-0.041	0.012	0.020	<b>0.162</b>	0.104	-0.065	0.005
	G	0.000	0.000	-0.001	0.000	0.001	0.001	0.001	-0.001	-0.001	-0.001	0.000	0.001	<b>0.004</b>	0.003	-0.002	0.000
TS	P	-0.017	-0.011	0.003	0.018	-0.008	-0.029	-0.061	0.045	0.095	0.032	0.026	0.010	-0.129	<b>-0.199</b>	-0.088	-0.046
	G	-0.009	-0.004	0.003	0.009	-0.004	-0.015	-0.032	0.024	0.050	0.015	0.010	0.004	-0.065	<b>-0.101</b>	-0.044	-0.024
NRS	P	0.010	-0.004	0.035	-0.025	-0.022	-0.012	-0.001	-0.006	-0.039	0.013	-0.028	-0.024	-0.048	0.052	<b>0.119</b>	0.028
	G	-0.002	0.002	-0.008	0.006	0.005	0.003	0.001	0.001	0.009	-0.003	0.006	0.006	0.011	-0.012	<b>-0.028</b>	-0.007
CF	P	-0.011	-0.008	0.006	-0.017	-0.010	-0.014	-0.018	-0.011	-0.013	0.013	0.004	-0.029	0.003	0.020	0.020	<b>0.086</b>
	G	-0.022	-0.017	0.012	-0.033	-0.020	-0.029	-0.035	-0.021	-0.024	0.025	0.008	-0.057	0.006	0.038	0.039	<b>0.162</b>
FW	P	0.713	0.856	0.248	0.446	0.379	0.411	0.263	-0.002	0.097	0.172	-0.177	0.448	0.064	0.036	-0.032	-0.119
	G	0.722	0.874	0.257	0.447	0.383	0.417	0.272	-0.001	0.096	0.175	-0.181	0.471	0.064	0.028	-0.041	-0.123

Residual effect (rg) = 0.0224, Residual effect (rp) = 0.0712.

FW = Fruit weight (g), FL = Fruit length (cm), FB = Fruit breadth (cm), PT = Peel thickness (mm), SW = Seed weight (g)  
 SL = Seed Length (cm) SB = Seed Breadth (cm), SM = Seed moisture (%), FM = Fruit moisture (%), PC = Phenol content  
 (mg/100g), TA = Titrable acidity (%). TSS = TSS (%), RS = Reducing sugar (%) AA = Ascorbic acid (mg/100g), TS = Total  
 sugar (%), NRS = Non-reducing sugar (%), CF = Crude fibre (%).



gene action and simple recurrent selection might be effective for these traits. The traits with high heritability with high genetic advance would respond better towards selection rather than those traits with high heritability but with low genetic advance (Ragasa *et al.* 2014). Genetic advance as a percentage of mean at 5 % ranged from 5.77 to 125.62 % for different characters (Table 2). The highest genetic advance as a percentage of mean was recorded in seed weight 125.62 % followed by 117.44 % in non-reducing sugar and lowest was recorded in fruit moisture with the value 5.77 %. The above findings demonstrated that these characters were distributed additively and selection against these traits might be effective for the improvement (Jat *et al.* 2014).

It was evident from the Table 3 that fruit weight was positively and significantly correlated with fruit breadth ( $r_g=0.856$  and  $r_p=0.856$ ) and fruit length ( $r_g=0.713$  and  $r_p=0.713$ ) at both genotypic and phenotypic level respectively. Fruit weight also recorded the positive correlation with ascorbic acid ( $r_g=0.448$  and  $r_p=0.448$ ) and seed weight ( $r_g=0.446$  and  $r_p=0.446$ ) at both genotypic and phenotypic level respectively. It was revealed from the investigation that correlation coefficient (genotypic) was similar in nature and higher in their magnitude than the correlation coefficient (phenotypic) revealed that there were inherited relationship among all traits under investigation and environment has not played any significant role in reducing their actual association. However, the highest magnitude of association was ascertained in fruit yield contributing traits like fruit breadth and fruit length (Singh *et al.* 2006, Samadia 2007). Path coefficient analysis was carried out by taking fruit weight as dependent variable (Table 4).

**Table 5.** Clustering patterns of twenty genotypes of chayote on the basis of genetic divergence.

Clusters	No. of genotypes	Name of genotypes
1	17	ACC- 2, ACC- 3, ACC- 5, ACC- 6, ACC- 13, ACC- 23, ACC- 25, ACC- 27, ACC- 28, ACC- 30, ACC- 31, ACC- 43, ACC- 44
2	2	ACC- 46, ACC- 80
3	1	ACC- 45

**Table 6.** Average cluster distance of twenty genotypes of chayote.

	Cluster – 1	Cluster – 2	Cluster – 3
Cluster – 1	25.48	35.66	41.47
Cluster – 2		15.09	39.88
Cluster – 3			0

Path coefficient analysis of the different characters showed that fruit breadth (0.643 and 0.604) imparted highest direct and positive effect on fruit weight at both genotypic and phenotypic level respectively via indirect effect of fruit length and seed weight. It was closely followed by fruit length (0.427 and 0.383) which also showed positive direct effect on fruit weight via indirect effect of fruit breadth and peel thickness at both phenotypic and genotypic level respectively. Seed breadth showed negative direct effect on fruit weight at genotypic level (Manivannan *et al.* 2005, Mishra and Das 2015, Mashilo *et al.* 2016).

Based on  $D^2$  values, the twenty genotypes were grouped into three highly divergent clusters, where cluster I comprising of 17 genotypes namely ACC- 2, ACC- 3, ACC- 5, ACC- 6, ACC- 13, ACC- 23, ACC- 25, ACC- 27, ACC- 28, ACC- 30, ACC- 31, ACC- 43 and ACC- 44, cluster II comprising of two genotypes namely ACC- 46 and ACC- 80 and cluster III was with only one genotype namely ACC- 45 (Table 5). The intra-cluster distance was maximum in cluster I ( $D_2 = 25.48$ ) revealed maximum genetic diversity within the cluster followed by cluster II ( $D_2 = 15.09$ ), whereas cluster III recorded intra-cluster distance of  $D_2 = 0$  (Table 6). The inter-cluster  $D_2$  values of the three clusters presented in the Table 6 revealed that maximum inter-cluster distance ( $D_2 = 41.47$ ) was recorded between cluster I and III followed by cluster II and III ( $D_2 = 39.88$ ) and the lowest was found in between cluster I and II ( $D_2 = 35.66$ ). Inter-cluster distance was greater than that of intra-cluster distances which revealed considerable amount of genetic diversity among the genotypes under study of all three clusters (Shiga *et al.* 2015; Debnath *et al.* 2020). The cluster means for different characters have been shown in the table 7. It was quite obvious from the table that Cluster I has produced highest mean values for crude fiber (23.88 %), TSS (3.42 %), total sugar (7.49 %), non-reducing sugar (1.33 %), whereas cluster II has

**Table 7.** Cluster wise mean values of nineteen characters in chayote.

	FW	FL	FB	PT	SW	SL	SB	SM	FM
Cluster - 1	399.08	12.4	8.59	0.29	5.14	4.44	2.71	77.68	92.69
Cluster - 2	504.17	12.1	9.72	0.28	13.14	6.61	3.65	75.06	92.88
Cluster - 3	796.67	17.04	10.54	0.3	8.58	5.3	3.03	80.59	93.59

**Table 7.** Continued.

	PC	TA	TSS	AA	RS	TS	NRS	CF
Cluster - 1	139.93	0.51	3.42	23.24	6.17	7.49	1.33	23.88
Cluster - 2	132.93	0.57	3.13	27.36	6.05	6.47	0.42	17
Cluster - 3	174.93	0.48	3.23	30.96	6.37	6.73	0.37	17.6

FW = Fruit weight (g), FL = Fruit length (cm), FB = Fruit breadth (cm), PT = Peel thickness (mm), SW = Seed weight (g), SL = Seed length (cm), SB = Seed breadth (cm), SM = Seed moisture (%), FM = Fruit moisture (%), PC = Phenol content (mg/100g), TA = Titrable acidity (%), TSS = TSS (%), RS = Reducing sugar (%), AA = Ascorbic acid (mg/100g), TS = Total sugar (%), NRS = Non-reducing sugar (%), CF = Crude fibre (%).

**Table 8.** Contribution of various characters towards total genetic divergence.

Source	Contribution %	Times ranked 1 <sup>st</sup>
Fruit weight (g)	7.89%	15
Fruit length (g)	0.00%	0
Fruit breadth (cm)	0.00%	0
Peel thickness (mm)	1.05%	2
Seed weight (g)	34.21%	65
Seed length (cm)	5.79%	11
Seed breadth (cm)	0.00%	0
Seed moisture %	0.53%	1
Fruit moisture %	0.53%	1
Phenol content (mg/100g)	10.53%	20
Titrable acidity %	4.74%	9
TSS %	0.53%	1
Ascorbic cid (mg/100g)	0.00%	0
Reducing ugar %	5.79%	11
Total ugar %	18.95%	36
Non reducing sugar %	0.00%	0
Crude fiber %	9.47%	18

shown highest mean values for seed weight (13.14 g), seed length (6.61 cm), seed breadth (3.65 cm), titrable acidity (0.57 %) and cluster III has produced high mean values for fruit weight (796.67 g), fruit length (17.04 cm), fruit breadth (10.54 cm), peel thickness (0.3 mm), seed moisture (80.59 %), fruit moisture (93.59 %), phenol content (174.93 mg/100g), ascorbic acid (30.96 mg/100g) and reducing sugar (6.37 %). Cluster mean values were differed in different morphological and biochemical traits (Mahapatra 2017). Seed weight (34.21 %) contributed maximum towards the total genetic divergence followed by total sugar (18.95 %) and phenol content (10.53 %). It was also quite evident from the table that ascorbic acid, fruit length, fruit breadth, seed breadth and non-reducing sugar have no contribution towards total genetic divergence as presented in Table 8. The results have shown no association between geographical distance and genetic divergence of the genotypes under investigation (Ahmed *et al.* 2016, Hasan *et al.* 2015).

## CONCLUSION

Chayote is a potential vegetable crop for the Sikkim Himalayan region for both nutrition and economic point of view, since the crop is underutilized and literally ignored by the scientists and other horticultural practitioners, genetically improved varieties are not developed so far for the region. However, the utilization of the genetic resource makes the task very easy for the scientific community. Our study was an attempt to draw the valid conclusion regarding the genetic variation of the crop which may be further utilized in future breeding program. On the basis of result and discussion made so far, it may be concluded that the collected and maintained material of chayote has a wide range of genetic variability for all the traits which can be utilized for further crop improvement program for yield and quality breeding. Being a complex trait, yield is governed by polygenes, so selection towards simple contributing traits paves the path very easy towards genetic improvement of such an important vegetable which possesses several health benefits. As the traits studied in present investigation produced fair degree of genetic variability parameters, and most of the contributing traits expressed additively, simple recurrent selection may be used for further improvement. Highly divergent clusters

can be utilized as pre-breeding materials towards hybrid breeding.

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