Genetic Variability and Characters Association in Hot Pepper (Capsicum annuum L.) Genotypes in Central Zone of Tigray, Northern Ethiopia

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Abstract
Hot pepper production in most areas of Ethiopia especially in Tigray region is constrained by shortage of varieties, the prevalence of fungal and bacterial as well as viral diseases. Sixty-four hot pepper genotypes were evaluated to obtain the extent of genetic variability, association among characters. The experiment was laid out using 8x8 simple lattice design at Axum Agricultural Research center in 2017/2018. Data were collected for 19 agronomic characters and analysis of variance revealed significant differences ($p<0.01$) among the genotypes for all characters. Fruit yield ranged from 0.83 to 4.55 t ha^{-1} with a mean of 2.67 t ha^{-1}. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from 3.57and 3.84 for days to maturity to 42.04 and 42.88% for average single fruit weight. All the traits had moderate to very high broad sense heritability while genetic advance as percent of mean (GAM) ranged from 8.34 for days to maturity to 85.03% for average single fruit weigh. High heritability coupled with high GAM was obtained for average single fruit weight, fruit length, dry fruit yield per plant, fruit diameter and thousand seed weight reflecting the presence of additive gene action for the expression of these traits and improvement of these characters could be done through selection. Fruit yield per hectare had positive and highly significant phenotypic and genotypic correlations with dry fruit yield per plant, average single fruit weight, fruit pericarp thickness, thousand seed weight, fruit diameter and fruit length, but it had negative and highly significant genotypic and phenotypic correlations with days to maturity. Estimates of genotypic and phenotypic direct and indirect effects of various characters on fruit yield (t ha^{-1}) showed that dry fruit yield per plant, fruit pericarp thickness had the highest positive direct contribution to fruit yield indicating that selection based on these characters will improve fruit yield. In conclusion, the research results showed the presence of significant variations among genotypes for agro-morphology traits. Therefore, it is recommended further evaluation of genotypes/hybrids that exhibited highest yield, quality and disease resistance in subsequent breeding programs to improve the productivity of the crop.
Keywords: Capsicum, Direct effect, Genetic advance and Heritability
DOI: 10.7176/JBAH/9-13-02
Publication date:July 31st 2019

Introduction

The genus Capsicum belongs to the family Solanaceace and it includes 30 species, including five domesticated and commercially cultivated species (*C. annuum* L., *C. baccatum* L., *C. chinensis* Jacq., *C. frutescence* L. and *C. pubescence*) (Dagnoko *et al*., 2013). However, from the five-domesticated species of the genus *C. annuum* L. is the most widely cultivated species worldwide (Pickersgill, 1997). It is the world's most important vegetable after tomato and used as fresh, dried or processed products, as vegetables and spices or condiments (Berhanu *et al*., 2011). Nutritionally, hot pepper like any other *Capsicum* species is rich in vitamin A and C, calcium, phosphorus and potassium. It has been reported that peppers are highly appreciated for their spicy flavor and nutritional value. Currently, it is produced in many parts of the country, because food is tasteless without hot pepper for most Ethiopians. The crop is also one of the important vegetables that serve as the source of income particularly for smallholder producers in many parts of rural Ethiopia (Berhanu *et al*., 2011; Shimeles, 2018). Moreover, hot pepper contributes 40 - 60% to the household income (Shimeles, 2018).

According to CSA (2017) the national average yields of hot pepper are 6.3 t ha^{-1} for green pod and 1.8 t ha^{-1} for the dry pod, which is far below the dry pod yield (2.5-3.7 t ha^{-1}) of improved varieties harvested at research fields of Ethiopia (MoANR, 2016) and world average yield of 3 - 4 t ha^{-1} (FAO, 2015). The productivity of the crop is low due to many limiting factors such as shortage of adapted high yielding varieties, using unknown seed sources and poor-quality seeds, poor irrigation system, lack of information on soil fertility, the prevalence of fungal and bacterial as well as viral diseases, lack of awareness on existing improved technologies and poor marketing system.

In the past decades, diverse pepper genotypes (>300) were introduced from different regions of the world (Fekadu *et al*., 2008) adding to the diversity of the crop in Ethiopia**.** However, Ethiopia has less benefited from research activities although some research centers are working on hot pepper variety development which mainly focused on adaptation and release of locally adapted varieties. For efficient and effective breeding work investigation and better understanding of the variability of existing genotypes is essential. Very few studies have been conducted on hot pepper genetic variability using morphological traits (Berhanu *et al*., 2011; Shimeles et al., 2016; Abrham *et al*., 2017 and Birhanu, 2017).

Effectiveness of selection depends on the amount of variability, heritability and genetic advance, interrelations among themselves and genetic divergence present in the genetic material for yield and yield related characters. Hence, developing of varieties with the desired traits has a significant contribution to increase the yield of hot pepper in the region. Therefore, the first step in the development of varieties is assessing the genetic variability of available genotypes for the characters of interest. Similarly, information on the extent and nature of interrelationship among plant characters' help formulating efficient index selection and the relative contribution of various components traits to yield (Singh, 1993). Besides, knowledge of the naturally occurring diversity in a population helps identify diverse groups of genotypes that can be useful for the breeding program. Greater the variability in a population, there are the greater chance for effective selection for desirable types (Vavilov, 1951). Therefore, assessment of variability, association and heritability of traits in hot pepper genotypes in case of Central zone of Tigray agro-ecology is essential for planning an appropriate breeding strategy for genetic improvement of the crop. Hence, the present study was undertaken with the objectives to estimate phenotypic and genotypic variations, heritability and expected genetic advance of agronomically important traits in the hot pepper genotypes and to assess the extent of associations among yield and yield related traits and to identify the most yield predicting traits.

2. MATERIALS AND METHODS

Experimental Site: The study was conducted at Axum Agricultural Research Center (AxARC) experimental field, Mereb Leke District, in the central zone of Tigray, northern Ethiopia during 2017/2018 irrigation season. The site is located at about 1041 kms away from Addis Ababa and 67kms to the north of Aksum town, at 14^o 25'26" and 14^{o}18'48" N latitude, and 38^o 42'15" and 38^{o}48'30" E longitude with an altitude of 1390 m.a.s.l. The site is found in semi-arid tropical belt of Ethiopia with "kola" agro climatic zone and the rainy season is mono - modal concentrated in one season from late July to early September and receives from 400 - 600 mm of rain fall per annum. The mean minimum and maximum temperatures ranged from 13.33 ^{0}C to 33.71 ^{0}C, respectively. The soil texture of the specific site of the study area is sandy clay loam textural class with bulk density of 1.72 gm cm^{-3}, very low in organic carbon (0.73%) with an alkaline pH of (8.2).

Experimental Materials: Sixty-three local hot pepper Ethiopian landraces along with one released variety Mareko fana as a check were used in this study. The landraces were collected from different agro-ecologies of varying altitude, rainfall, temperature, and soil type by the Ethiopian Biodiversity Institute (EBI), Shire Maitsebri Agricultural Research Center (SMARC) and Melkassa Agricultural Research Center (MARC). The accession numbers and source of the genotypes are shown in Table 1.

Experimental Design: The experiment was laid out in 8x8 simple lattice design with two replications. The experimental materials were planted at Axum Agricultural Research Center main research site during 2017/2018 cropping season under irrigation condition. Seeds of each hot pepper genotypes were sown in seed bed of 0.6 m2 (3 rows, 0.2 m spacing between rows, 1m row length) during October 2017 to raise seedlings. Seedlings were transplanted to main field 48 days after seed sowing i.e. when the seedlings attained 15 cm height. Each genotype was planted in the main field in a plot size of 8.4m2 (2.8 m x 3 m). Each plot consisted of four rows of 3m length with inter and intra-row spacing of 0.7m and 0.3m, respectively, containing a total of 40 plants. Each incomplete block and replication was spaced 1 and 1.5 meters, respectively. The middle two rows were used for data collection leaving the two rows as borders. Fertilizer, Di-ammonium phosphate (DAP) as a source of Phosphorus was applied at the rate of 200 kg ha-1 during planting and nitrogen fertilizer was applied in the form of Urea at the rate of 150 kg ha-1 in splits, half during transplanting and the rest as side dressing at 45 days after transplanting. For this experiment was irrigated, furrow irrigation method, scheduled at 7days interval (AxARC, 2016) was used. Weeding, hoeing and other field management and crop protection activities were done as required.

Table 1. Hot pepper accessions, their local name, area of collection, origin and sources

NO.	Accession Name	Local Name	Site of Collection	Sources	NO.	Accession Name	Local Name	Site of collection	Sources
1	Acc-1	Berebere Hormat	Raya Kobo	Amhara	33	Acc-229701	Hulet Ejenese	Misrak Gojam	Amhara
2	Acc-2	Berbere Aberegelle	Tanqua Abergelle	Tigray	34	Acc-237528	Enticho	Ahferom	Tigray
3	Acc-3	Berebere Birisheleko	Bure	Amhara	35	Acc-9102	Achefer	Mirab Gojam	Amhara
4	Acc-4	Felege Da'ero	Mekelle	Tigray	36	Acc-9094	Gooda	Mirab Gojam	Amhara
5	Acc-5	Berebere Agew	Ofla(Zata)	Tigray	37	Acc-9098	Achefer	Mirab Gojam	Amhara
6	Acc-6	Berebere Dibdibo	Ahferom	Tigray	38	Acc-9104	Merwi	Mirab Gojam	Amhara
7	Acc-7	Shamba berbereAdi	Welkait	Tigray	39	Acc-9099	Amestya	Mirab Gojam	Amhara
8	Acc-8	Berebere korir	Kilte Awulalo	Tigray	40	Acc-9082	Meacha	Mirab Gojam	Amhara
9	Acc-9	Berebere Tsalaiet	Kola Temben	Tigray	41	Acc-9101	Achefer	Mirab Gojam	Amhara
10	Acc-10	Berebere Agbe	Abergelle	Tigray	42	Acc-9086	Kudmie	Mirab Gojam	Amhara
11	Acc-11	Laelay Dayu	Alamata	Tigray	43	Acc-229696	Dibata	Metekel	B/Gumz
12	Acc-12	Berebere Hewane	Walkait	Tigray	44	Acc-9106	Bure Wemberma	Mirab Gojam	Amhara
13	Acc-13	Abat Berebere	Walkait	Tigray	45	Acc-9007	Galioch Buare town	Mirab Gojam	Amhara
14	Acc-14	Bora(Gemelo)	Embalaje	Tigray	46	Acc-9107	Guzamn	Misrak Gojam	Amhara
15	Acc-15	Abat Berebere	Welkait	Tigray	47	Acc-28334	Abdigudina	Illubabor	Oromiya
16	Acc-16	Berbere Rama	Mereb Leke	Tigray	48	Acc-48	Berbere Alaba	Alaba	SNNPRS
17	Acc-28336	Durame	Illubabor	Oromiya	49	Acc-49	Tedele	Guragae	SNNPRS
18	Acc-230800	Bedeno	Misrak Harerge	Oromiya	50	Acc-229694	Mentawuha	Metekel	B/Gumz
19	Acc-28337	Elammo	Illubabor	Oromiya	51	Acc-51	Abeshigie	Guragie	SNNPRS
20	Acc-229699	Adet	Misrak Gojam	Amhara	52	Acc-52	Wegedadi	Mirab Gojam	Amhara
21	Acc-212912	Kedida Gameala	Kembata Alaba	SNNPRS	53	Acc-9093	Solmeda	Mirab Gojam	Amhara
22	Acc-9097	Achefer/Durbate	Mirab Gojam	Amhara	54	Acc-229692	Dinkara	Agew Awi	Amhara
23	Acc-9084	Merawi	Mirab Gojam	Amhara	55	Acc-55	Debremarkos	Misrak Gojam	Amhara
24	Acc-229697	Wonbera	Metekel	B/Gumz	56	Acc-56	Finote Selam	Mirab Gojam	Amhara
25	Acc-212913	Humbo	Semen Omo	SNNPRS	57	Acc-57	Guragie Berebere	Butajira	SNNPRS
26	Acc-229700	Bibugn (Astero M.)	Misrak Gojam	Amhara	58	Acc-58	Berebere Merb	Mereb Leke	Tigray
27	Acc-9085	Merawi	Mirab Gojam	Amhara	59	Acc-59	Adiha Local	Abi Adi	Tigray
28	Acc-230798	Dogo Midi Jara	Misrake Harerge	Oromiya	60	Acc-23880	Meskele Kirstos	Semien Gonder	Amhara
29	Acc-230799	Girawa	Misrake Harerge	Oromiya	61	Acc-61	Myweni	Mereb Leke	Tigray
30	Acc-236436	Bako Tibe	Mirab Shewa	Oromiya	62	Acc-62	Berebere Hesea	Mereb Leke	Tigray
31	Acc-229698	Dibate	Metekel	B/Gumz	63	Acc-63	Yeyeju Bereberie	Woldia	Amhara
32	Acc-229698	Dibate	Metekel	B/Gumz	64	Acc-64	Mareko fana (St. check)	Melkassa	Oromiya

Data collected: Seventeen quantitative characters on recorded on five randomly selected plants from the two middle rows of each plot by adopting descriptors list for hot pepper (IPGRI, 1995).

Data Analysis: Data for quantitative characters were subjected to analysis of variances (ANOVA) for simple lattice design using proc lattice and Proc lattice procedures of SAS Version 9.2(SAS Institute Inc., 2010) to test the presence of significant differences among genotypes. Mean separations were estimated using Duncan Multiple Range Test (DMRT) at 5% probability levels.

Variability among accessions was estimated using genotypic variances and coefficients of variations as suggested by Burton and De vane (1953) as: Genotypic Variance ($\sigma^2 g$) = $\frac{\text{MSg}-\text{MSe}}{\text{r}}$

Phenotypic variance ($\sigma^2 p$) = [$\sigma^2 g$ + ($\sigma^2 e/r$)], Phenotypic coefficient of variation (PCV) =$\frac{\sqrt{\sigma 2p}}{\bar{x}} * 100$, Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma 2g}}{\bar{x}} * 100$, Where, r = number of replication; MSg = mean square due to genotypes and Mse = mean square of error, $\sigma^2 p$ = phenotypic variance, $\sigma^2 g$ = genotypic variance and $\bar{x}$ = grand mean of the character under consideration. Both phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) was categorized depending up on cut points suggested by Deshmukh *et al*. (1986) as low (<10%), moderate (10-20%) and high (>20%).

Broad sense heritability (h^2) of the all traits were calculated according to the formula as described by Allard (1960) as follow:

$$h^2_{bs} = [(\sigma^2 G) / (\sigma^2 P)] \times 100,$$

Where: h^2_{bs}= heritability in broad sense; $\sigma^2 G$ = Genotypic variance; $\sigma^2 P$ = Phenotypic variance. According to Singh (2001) that heritability values ≥80% were very high, values from 60-79% were moderately high, values from 40-59% were medium and values less than 40% were low.

Genetic Advance (GA) for selection intensity (K) at 5%was computed according to Allard (1960) as given here:

$$GA = K * \sigma p * H^2$$

Where, GA = expected genetic advance, K = the standardized selection differential at 5% selection intensity (K = 2.063), σp = is phenotypic standard deviation on mean basis and H^2 = heritability in the broad sense. The genetic advance as percentage of population means (GAM) was also estimated with the methods described by Johnson *et al*. (1955). Genetic advance as % of mean (GAM) was computed as: GAM = $\frac{GA}{\bar{x}} * 100$

Where, GA = Genetic advance under selection and $\bar{x}$ = mean of the population. According to Johson *et al.* (1955) genetic advance as percent of mean was classified as low (<10%), moderate (10-20%) and high (>20%).

Characters associations at genotypic and phenotypic levels were calculated from the genotypic and phenotypic and environmental covariance according to Singh and Chaundhary (1985). In Path analysis, Total yield per hectare was taken as the resultant (dependent) variable while the rest of the characters were considered as casual (independent) variables. The direct and indirect effects of the independent characters on fruit yield per hectare were estimated by the simultaneous solution of the formula suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

The results of analysis of variance (ANOVA) of 19 quantitative characters for the 64 hot pepper genotypes are presented in Table 2. There were highly significant differences (P<0.01) among the tested genotypes for all characters studied indicating presence of adequate variability among genotypes. This significant genetic variation among genotypes suggested that the genotypes were genetically diverse and it could be a good opportunity for breeders to select genotypes for trait of interest for variety development. This finding was in agreement with the findings of Berhanu *et al*. (2011), Nsabiyera *et al*. (2013), Birhanu (2017) and Shimeles (2018).

Mean Performance of Genotypes: Genotypes had 57.5 to 76.5 days to flowering, 67.5 to 84.5 days to fruiting and 113.5 to133 days to maturity with a mean of 62.27, 75.78 and 122.6 days, respectively. The result showed a wide range of variations for days to flowering, fruiting and maturity. Similarly, Shimeles (2018) and Berhanu *et al.* (2011) reported the existence of wide genetic variation for those phenological characters on for 49 and 20 hot pepper genotypes respectively. Acc-1 (113.5 days), Acc-49 (114.5 days) and Acc-57 (114 days) had significantly shorter days to maturity while Acc-5 (133 days), Acc-9 (130.5days) and Acc-59 (130.5days) had significantly delayed maturity. About 54.68% of the genotypes exhibited shorter number of days to maturity than the genotypes mean (122.6). Moreover, 25 genotypes were significantly earlier in maturity than the check variety (Mareko fana) that had the earliest days to maturity (Appendix Table 1). Most of the genotypes have also yield advantage over the early maturing check variety. Hence, there is an opportunity to select early maturing and high yielder genotypes better than the check variety (Mareko fana).

The magnitude of genetic variability for plant height ranged from 37.1 (Acc-9097) to 66.5 cm (Acc-3) with average value of 53.29 cm. Genotypes codded as Acc-63, Acc-9007, Acc-8, Acc-212912, Acc-1, Acc-9, Acc-59, Acc-5 and Acc-9102 had tall plant stature (59.4 - 65 cm), so can be used as parents in developing varieties with maximum plant height, as it may contribute to fruit yield.

The minimum and maximum canopy diameter was exhibited by genotypes Acc-229697 and Acc-59, respectively. Genotypes Acc-59, Acc-15 and Acc-9101 have also yield advantage and can be used as parents in developing varieties with high canopy diameter over the check variety. However, Shimeles (2018) reported a wide range of 40.9 - 76.6 cm for canopy diameter. This wide range of variability may attribute to differences in the materials used in the experiment and /or may be due to the differences of the testing environments.

The fruit pericarp thickness of genotypes also ranged from 1.7 to 2.7 mm with an overall mean of 2.1 mm. The genotypes Acc-212912, Acc-212913, Acc-230798, Acc-236436, Acc-229698, Acc-16, Acc-11, Acc-48, and Acc-51 had thicker pericarp than the check variety. The highest fruit pericarp thickness was Acc-212912 (2.7 mm) which indicated that Acc-212912 should be given consideration for selection designed for the improvement of this trait. This is in agreement with the finding of Nsabiyera *et al.* (2013) and Shimeles (2018) who reported a wide range of variation for fruit pedicel length, fruit length and fruit diameter. Average single fruit weight varied from 1.55 to 7.1 gm with a mean of 3.6 gm. Acc-49, Acc-212912, Acc-61, Acc-1, Acc-11, Acc-212913 and Acc-229694 depicted highest fruit weight per plant comparing to the check variety in that order.

The genotypes exhibited significant variability in fruit number per plant which ranged from 14.75 to 55.5 with a mean of 31. The lowest number of fruits per plant depicted by genotypes Acc-57, Acc-56, Acc-229698 and Acc-49 whereas the highest number of fruits per plant was recorded for Acc-5, Acc-2, Acc-59, Acc-229700, Acc-212913, Acc-8 and Acc-229697. On the other hand, number of seeds per fruit ranged between 93 and 231 with a mean value of 139.1. The lowest number of seeds per fruit was counted for Acc-229697 and Acc-14, whereas the highest seeds per fruit were recorded for Acc-212912, Acc-3, Acc-48 and Acc-4 respectively. Accordingly, in the current study 42 genotypes scored greater than 65% number of fruits per plant and 33 genotypes scored greater than 51% number of seeds per fruit as compared with the best performing check variety (Mareko fana) (Table 5). Similar results for number fruits per plant were reported by kadwey et al. (2015), Birhanu (2017), Kumari (2017) and Shimeles (2018).

A wide range of variation was observed for 1000 seed weight among genotypes which ranged from 4 to 7.2g with a mean of 5.6g. Genotypes Acc-212913, Acc-58, Acc-229694, Acc-212912 and Acc-11 had high seed weight of 7.2, 6.9, 6.9, 6.8 and 6.6 g while Acc-9085, Acc-9101, Acc-9099 and Acc-9086 had low 1000 seed weight of 4g each as compared to the check variety.

Average dry fruit yield per plant ranged from 53.96 to 172.5g with an overall mean of 107.34g. The highest yield per plant was recorded from Acc-212913 (172.5g) and Acc-4 (168g) while Acc-13 (54.5 g), Acc-237528 (56 g) and Acc-9102 (64 g) produced lowest yield per plant as compared to the check variety. Similar results for dry fruit yield per plant were reported by kadwey *et al*. (2015), Rosmaina *et al*. (2016) and Shimeles (2018).

Table 2. Mean squares of variance for 19 characters of 64 hot pepper genotypes evaluated at Mereb Leke in, 2017/2018

Characters	Mean squares							
				Error				
	Replication(1)	Treatments Adji (63)	Blocks with in replication (Adj)(14)	Intra Block(49)	RCBD(63)	R^2 (%)	RE to RCBD (%)	CV (%)
DFL	8.508	27.51**	13.936	6.528	8.175	86.95	111.99	3.8
DFR	0.008	30.17**	8.820	6.347	6.897	87.19	102.29	3.3
DM	3.445	44.26**	6.222	5.856	5.937	91.20	100.08	2.0
PH	526.500	62.76**	15.390	17.487	17.021	84.70	97.33	7.8
CD	7.703	14.69**	3.318	3.550	3.499	86.89	98.55	5.0
NPB	0.797	13.45**	1.100	1.117	1.113	94.65	99.66	15.0
SD	1.144	3.37**	1.241	0.963	1.025	84.00	101.37	7.7
FPL	0.054	0.79**	0.119	0.074	0.084	94.29	104.71	7.8
FL	0.002	22.28**	0.426	0.407	0.411	98.66	100.04	7.8
FD	1.533	49.14**	2.355	1.638	1.797	97.70	102.77	7.1
FPT	0.918	0.13**	0.026	0.029	0.028	87.87	97.27	8.3
FW	0.463	4.82**	0.144	0.187	0.177	97.30	94.96	11.9
NFP	2.820	294.20**	8.135	4.555	5.351	98.93	107.00	6.9
NSF	17.331	1453.86**	80.555	18.524	32.309	99.14	148.93	3.1
TSW	0.538	1.50**	0.213	0.189	0.194	91.78	100.32	7.8
DFYP	12.500	1741.51**	37.670	20.676	24.452	99.21	107.49	4.2
MFY	1.304	0.81**	0.069	0.131	0.117	90.52	89.57	14.6
UNMFY	0.008	0.01**	0.001	0.001	0.001	92.09	91.35	19.7
TFY	1.533	0.82**	0.065	0.135	0.120	90.46	88.52	13.8

*and** = significant at 5% and 1% probability level, respectively. Number in parenthesis represented degree of freedom adj = adjusted treatment mean squares, RCBD = Randomized completed block design, RE to RCBD = Relative efficiency to randomized completed block design CV = coefficient of variation, R^2 (%) = coefficient of determination, DFL = days to 50% flowering, DFR = days to 50% fruiting, DM = days to maturity, PH = Plant height (cm), CD = canopy diameter (cm), number of primary branches per plant, SD = stem diameter (mm), FPL = fruit pedicel length (cm), FL = fruit length (cm), FD = fruit diameter (mm), FPT = fruit pericarp thickness (mm), FW = average single fruit weight (g), NFP = number of fruits per plant, NSF = number of seeds per fruit, TSW = thousand seed weight(g), DFYP = dry fruit yield per plant (g), MFY = marketable fruit yield (t ha^{-1}), UNMFY = Unmarketable fruit yield (t ha^{-1}) and TFY = total fruit yield (t ha^{-1}).

Marketable fruit yield per hectare ranged from 0.7- 4.34 t with an overall mean of 2.48 t ha^{-1}. The highest marketable fruit yield per hectare was recorded for Acc-4, Acc-212913, Acc-212912, Acc-1, Acc-49, and Acc-50 while Acc-9102, Acc-52, Acc-9099, Acc-9098, Acc-230798 and Acc-230799 gave the lowest yield as compared to the check variety (Appendix Table 2). Hence, there is an opportunity to select high yielder genotypes better than the check variety to develop high yielding varieties. Total fruit yield per hectare ranged from 0.83 to 4.55 t ha^{-1} which showed wide variation with a mean value of 2.67 t ha-1. The maximum yield was obtained from Acc-4 (4.55 t ha-) followed by Acc-212912 (4.49 t ha^{-1}), Acc-212913 (4.32 t ha^{-1}) and Acc-3 (4.27 t ha^{-1}) (Appendix Table 2). Nearly, 43.75 % of the tested genotypes had fruit yields above the grand mean of genotypes. As compared with the best performing check variety (Mareko fana), 54.6% of the genotypes had yield advantages. Most of these high yielding genotypes were also earlier in maturity than the check variety (Appendix Table 2). This wide range of variability of genotypes for most traits in the study indicated the high possibility for genetic improvement of traits under consideration.

Phenotypic and Genotypic Variations: Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances and phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) along with the mean and the range of various characters investigated in the present study depicted in Table 3. For all characters studied, the magnitude of environmental variance was lower than the corresponding genotypic variance. This indicates that the genotypic component of variation was the major contributor to the total variation in the studied characters. Genetic variance ranged from 0.05 for fruit pericarp thickness to 860.42 for dry fruit yield per plant while phenotypic variance values ranged from 0.07 to 870.76 for fruit pericarp thickness. The GCV ranged from 3.57% for days to maturity to 42.04% for average fruit weight. Similarly, PCV ranges from 3.84% for days to maturity to 42.88% for average fruit weight per plant. In general, the phenotypic coefficient of variation (PCV) was relatively higher than the corresponding genotypic coefficient of variation (GCV). The difference between PCV and GCV was narrow indicating little influence of environment on the expression of these characters and considerable amount of variation was observed for all the characters. The GCV and PCV values are normally categorized as low (<10%), moderate (10-20%) and high (>20%) as indicated by Deshmukh *et al*. (1986). High values of PCV and GCV indicated the existence of substantial variability for such characters and selection may be effective based on these characters.

Average fruit weight had the highest GCV and PCV (42.04 and 42.88) followed by fruit length (40.33 and 40.7), number of fruits per plant (38.86 and 39.16), number of primary branches per plant (35.17 and 36.73), dry fruit yield per plant (27.33 and 38.88), fruit diameter (24.57 and 27.49), total fruit yield (21.99 and 24.05), number of fruits per plant (38.86 and 39.16). Medium GCV and high PCV were observed for fruit pericarp thickness (10.94 and 12.41), fruit pedicel length (17.23 and 18.1), number of seeds per fruit (19.26 and 19.38) and thousand seed weight (14.54 and 15.56). GCV and PCV were low for days to 50% flowering (7.32 and 7.80), days to 50% fruiting (6.87 and 7.26) and days to maturity (5.24 and 5.43), plant height (8.93 and 10.51) and canopy diameter (6.31 and 7.25). Similarly, Pujar *et al*. (2017) reported a relatively low GCV and PCV for days to flowering in 63 chilli genotypes. The high PCV and GCV are evident for the high variability that in turn offers good scope for selection. Similar finding was reported by Berhanu *et al*. (2011) indicating that days to flowering and days to maturity had low GCV and PCV values, while fruit weight, number fruits per plant, number of primary branches per plant had high GCV and PCV. Datta and Das (2013) reported high GCV and PCV with high heritability and GAM for fruit number per plant and fruit yield per plant. Razzaq *et al*. (2016) reported high values of GCV and PCV for weight of red fruit (110.02% and 112.02%) and number of fruits per plant (85.02% and 86.05%). Shimeles et al. (2016) also reported high estimates of GCV and PCV for fruit weight, number of branches per plant and number of fruits per plant. In addition, similar findings were also reported by (Sharma et al., 2010; Janaki *et al*., 2015; Rosmaina *et al*., 2016; Sahu *et al*., 2016).

Estimates of Heritability (h^2) in broad Sense: In this study all the traits had moderate high to very high broad sense heritability percentage in the range of 71.42 to 98.81% (Table 3) indicating that the traits studied were more influenced by genetic factors (Rosmaina *et al*., 2016). According to Singh (2001) heritability values greater than 80% considered as a very high, values from 60-79% as moderately high, values from 40-59% as medium and values less than 40% as low. Accordingly, the estimates of heritability of all traits in the current study were moderate to very high. The characters having very high heritability indicated relatively small contribution of the environmental factors to the phenotype and selection for such characters could be fairly easy due to high additive effect.

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotype. Hence, knowledge on heritability coupled with genetic advance is more useful. Genetic advance as percent of the mean (GAM) in this study ranged from 6.87% to 85.03% for days to maturity and average single fruit weight respectively (Table 6). According to Jonhson *et al*. (1955) the value of GAM is categorized as low (< 10%), moderate (10-20%) and high (> 20%). The highest GAM was recorded for average single fruit weight (85.03%), followed by fruit length (82.43%), number of fruits per plant (79.54%) and number of primary branches per plant (69.47%) indicating that these characters are governed by additive genes and selection will be rewarding for improvement of hot pepper for these traits. The least GAM was recorded for days to maturity (6.87%), days to 50% fruiting (8.36%) and days to 50% flowering (8.68%). In the current result, moderately high heritability coupled with moderate GAM was observed for plant height (15.64%), canopy diameter (11.34%), stem diameter (15.06%) and fruit pericarp thickness (19.9%). These results agreed with the findings of earlier researchers (Janaki *et al*., 2015; Rosmaina *et al*., 2016; Birhanu, 2017; Kumari, 2017) who found high genetic advance as percent of mean for number of fruits per plant, average fruit weight, and number of primary branches per plant. Shimeles et al. (2016) also obtained high genetic advance as percent of mean for number of branches per plant. Similar findings were reported by earlier workers for some characters with moderate to high GCV, PCV, heritability and GAM estimates, for fruit yield per plant, fruit diameter, fruit length, average fruit weight, number of seeds per fruit and number of fruits per plant (Sharma *et al*., 2010; Sahu *et al*., 2016; Razzaq *et al*., 2016; Pujar *et al*., 2017).

Generally, characters such as dry fruits yield per plant, number of fruits per plant, number of seeds per fruit, average single fruit weight, fruit diameter, fruit length and thousand seed weight with high GCV, heritability and GAM should be considered as reliable selection criteria for crop improvement in terms of yield and yield-attributing characters in hot pepper.

Association of Characters: Estimates of genotypic and phenotypic correlation coefficients between each pairs of characters are presented in Table 4. The result showed that, in most cases, the genotypic correlation coefficients were higher than the phenotypic correlation coefficient which indicates that the inherent association among various characters independent of environmental influence. Total fruit yield per hectare showed positive and highly significant ($P<0.01$) genotypic and phenotypic correlations with dry fruit yield per plant (rg = 0.75 and rp = 0.70), average single fruits weight (rg = 0.52 and rp = 0.49), thousand seed weight (rg = 0.47 and rp = 0.41), fruit pericarp thickness (rg = 0.44 and rp = 0.42), number of seeds per fruit (rg = 0.42 and rp = 0.39) and fruit diameter (rg = 0.37 and rp = 0.33). Total fruit yield also exhibited positive and significant ($P<0.05$) genotypic and phenotypic correlations with canopy diameter, stem diameter and fruit length (Table 4). The results imply that improvement of the characters could improve the capacity of the plants to synthesize and translocate photosynthesis to the organ of economic value.

This suggested that, improvement of those characters would result in a substantial increment on fruit yield that could be used in selection of genotypes for high fruit yield. Similarly, Abrham *et al*. (2017) and Shimeles (2018) reported higher genotypic correlation coefficients than the phenotypic ones, implying the inherent associations between various characters in Ethiopian Capsicums.

Dry fruit yield per plant had a highly significant association at both genotypic and phenotypic level with average single fruit weight (0.5, 0.56), number of seeds per fruit (0.46, 0.45) and thousand seed weight (0.43, 0.40). These results agreed with the findings of earlier researchers (Kadwey *et al*., 2015; Chakrabarty and Aminul , 2017; Kumari *et.al*, 2017) indicating genotypic and phenotypic correlations between plant height, number of primary branches per plant, fruit length, fruit diameter, fruit pericarp thickness, fruit yield per plant, average fruit weight, number of fruit per plant, number of seeds per fruit and thousand seed weight.

Table 3. Estimates of Range, Mean, Genotypic, Environmental and Phenotypic variances and Coefficient of variations, Heritability in broad sense, Genetic advance and Genetic advance as percentage of mean for 17 characters of 64 hot Pepper genotypes at Mereb Leke in, 2017/2018

Characters	Ranges	Mean ± SEM	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
DFL	57.5-75.9	67.27±1.81	10.49	6.528	13.76	4.82	5.51	76.27	5.84	8.68
DFR	67.5-84.5	75.68±1.78	11.91	6.348	15.09	4.56	5.13	78.96	6.33	8.36
DM	113.5-133	122.6±1.71	19.2	5.856	22.13	3.57	3.84	86.77	8.42	6.87
PH	37.1-66.5	53.29±2.96	22.64	17.488	31.38	8.93	10.51	72.14	8.34	15.64
CD	32.4-43.4	37.38±1.33	5.57	3.55	7.34	6.31	7.25	75.83	4.24	11.34
NPB	3.4-11.8	7.06±0.75	6.16	1.116	6.72	35.17	36.73	91.69	4.9	69.47
SD	9.85-16.05	12.7±0.69	1.2	0.962	1.68	8.64	10.22	71.42	1.91	15.06
FPL	2.29-4.65	3.47±0.19	0.36	0.074	0.39	17.23	18.1	90.64	1.17	33.85
FL	4-16.75	8.2±0.45	10.93	0.408	11.14	40.33	40.7	98.17	6.76	82.43
FD	11.21-31	18.03±0.90	23.75	1.638	24.57	27.03	27.49	96.67	9.89	54.83
FPT	1.7-2.7	2.06±0.12	0.05	0.03	0.07	10.94	12.41	77.72	0.41	19.9
DFYP	53.96-173.6	107.34±3.22	860.42	20.676	870.76	27.33	27.49	98.81	60.15	56.04
FW	1.55-7.1	3.62±0.31	2.32	0.186	2.41	42.04	42.88	96.13	3.08	85.03
NFP	14.3-55.7	30.97±1.51	144.82	4.556	147.1	38.86	39.16	98.45	24.63	79.54
NSF	90.66-233.6	139.11±3.04	717.67	18.524	726.93	19.26	19.38	98.73	54.91	39.47
TSW	4-7.2	5.56±0.31	0.65	0.188	0.75	14.54	15.56	87.39	1.56	28.05
TFY	0.83-4.55	2.67±0.26	0.34	0.136	0.41	21.99	24.05	83.61	1.11	41.48

DFL = days to 50% flowering, DFR = days to 50% fruiting, DM = days to maturity, PH = plant height (cm), CD = canopy diameter (cm), NPB = number of primary branches per plant, SD = stem diameter (mm), FPL= fruit pedicel length (mm), FL = fruit length (cm), FD = fruit diameter (mm), FPT = fruit pericarp thickness (mm), DFYP = dry red fruit yield per plant (g), FW = average fruit weight (g), NFP = number of fruits per plant, NSF = number of seeds per fruit, TSW = thousand seed weight (g) and TFY = total fruit yield (t ha^{-1}), SEM = standard error of the mean, σ^2g = genotypic variance, σ^2e = error variance, σ^2p = phenotypic variance, PCV = phenotypic coefficient of variance, GCV = genotypic coefficient of variance, H^2 = broad sense heritability, GA = genetic advance, GAM = genetic advance as percent of mean.

Genotypic path coefficient analysis: In this study, the result of genotypic path coefficient analysis showed that dry red fruit yield per plant (0.46) had the highest positive direct effect on total fruit yield per hectare followed by fruit pericarp thickness (0.37), number of primary branches per plant (0.31), canopy diameter (0.2), thousand seed weight (0.18), average single fruit weight (0.16), fruit pedicel length and stem diameter (0.11), while negative direct effect was observed for days to maturity (-0.21), fruit length (-0.2), fruit diameter (-0.15) and days to 50% flowering (- 0.08) while, days to 50% fruiting, plant height and number of seeds per fruit had very little positive direct effect on fruit yield per hectare though it exhibited significant and positive association with fruit yield (Table 5).This indicating the true relationship between these characters as a good contributor to fruit yield.

Similarly, Shimeles (2018) reported that direct influence of pericarp thickness on fruit yield was very high and positive and its indirect influence through fruit diameter was also positive. However, pericarp thickness showed high negative indirect effect on number of fruits per plant.

Generally, based on the genotypic path analysis agronomic characters which showed positive direct effects on fruit yield per hectare were: dry fruit yield per plant, fruit pericarp thickness, average single fruit weight, number of primary branches per plant, canopy diameter and number of seeds per fruit. This result agrees with that of Kumari (2017).

ISSN 2224-3208 (Paper) ISSN 2225-093X (Online) DOI: 10.7176/JBAH
Vol.9, No.13, 2019

Table 4. Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient for 17 characters in 64 Hot pepper genotypes

Traits	DFL	DFR	DM	PH	CD	NPB	SD	FPL	FL	FD	FPT	DFYP	FW	NFP	NSF	TSW	TFY
DFL	1.00	0.79**	0.58**	0.48**	0.26*	0.40*	0.49**	-0.25*	-0.30*	-0.26*	-0.31*	-0.12ns	-0.29*	0.31*	-0.11ns	-0.22ns	-0.08ns
DFR	0.72**	1.00	0.72**	0.41**	0.22ns	0.54**	0.47**	-0.34*	-0.45**	-0.44**	-0.44**	-0.18ns	-0.46**	0.43**	-0.24ns	-0.33**	-0.13ns
DM	0.54**	0.62**	1.00	0.29*	0.32**	0.66**	0.39**	-0.45**	-0.69**	-0.60**	-0.60**	-0.33**	-0.65**	0.55**	-0.33**	-0.47**	-0.28*
PH	0.37**	0.31**	0.26**	1.00	0.18ns	0.11ns	0.73**	0.07ns	0.04ns	0.03ns	0.00ns	0.06ns	0.09ns	0.13ns	0.14ns	0.09ns	0.20ns
CD	0.25**	0.18**	0.31**	0.20*	1.00	0.39**	0.41**	-0.23ns	-0.27*	-0.24ns	-0.23ns	0.07ns	-0.16ns	0.35**	-0.04ns	-0.01ns	0.28*
NPB	0.34**	0.47**	0.61**	0.12ns	0.37**	1.00	0.31*	-0.58**	-0.73**	-0.62**	-0.60**	-0.11ns	-0.63**	0.70**	-0.26*	-0.48**	-0.02ns
SD	0.38**	0.37**	0.31**	0.61**	0.36**	0.27**	1.00	-0.08ns	-0.06ns	-0.11ns	-0.16ns	0.10ns	-0.07ns	0.38**	0.07ns	0.09ns	0.26*
FPL	-0.24**	-0.32**	-0.39**	0.06ns	-0.19*	-0.52**	-0.09ns	1.00	0.59**	0.60**	0.52**	0.15ns	0.51**	-0.51**	0.35**	0.26*	0.19ns
FL	-0.27**	-0.41**	-0.64**	0.03ns	-0.25**	-0.69**	-0.05ns	0.56**	1.00	0.72**	0.67**	0.27*	0.80**	-0.66**	0.30*	0.62**	0.25*
FD	-0.24**	-0.40**	-0.56**	0.02ns	-0.22*	-0.59**	-0.09ns	0.57**	0.70**	1.00	0.84**	0.37**	0.79**	-0.70**	0.60**	0.47**	0.37**
FPT	-0.26**	-0.36**	-0.50**	0.11ns	-0.19*	-0.52**	-0.07ns	0.40**	0.58**	0.74**	1.00	0.38**	0.74**	-0.56**	0.49**	0.49**	0.44**
DFYP	-0.12	-0.17**	-0.32**	0.05ns	0.07ns	-0.10ns	0.09s	0.15ns	0.26**	0.37**	0.34**	1.00	0.57**	0.06ns	0.46**	0.43**	0.75**
FW	-0.26**	-0.42**	-0.61**	0.08ns	-0.15ns	-0.60**	-0.05ns	0.49**	0.77**	0.77**	0.64**	0.56**	1.00	-0.60**	0.54**	0.63**	0.52**
NFP	0.27**	0.37**	0.52**	0.12ns	0.31**	0.67**	0.34**	-0.48**	-0.65**	-0.68**	-0.49**	0.06ns	-0.58**	1.00	-0.40**	-0.30*	0.04ns
NSF	-0.09	-0.22**	-0.31**	0.14ns	-0.03ns	-0.25**	0.08ns	0.33**	0.30**	0.59**	0.43**	0.45**	0.52**	-0.40**	1.00	0.19ns	0.42**
TSW	-0.22*	-0.32**	-0.40**	0.09ns	0.03ns	-0.41**	0.06ns	0.23**	0.58**	0.46**	0.46**	0.40**	0.59**	-0.28**	0.17ns	1.00	0.47**
TFY	-0.06ns	-0.15ns	-0.25**	0.23**	0.23*	-0.02ns	0.25**	0.18*	0.23**	0.33**	0.42**	0.70**	0.49**	0.06ns	0.39**	0.41**	1.00

Note: ns= non Significance *and **=significant at 5% and 1% probability levels, respectively. DFL=days to 50 percent flowering, DFR= Days to 50 percent fruiting, DM = days to maturity, PH = plant height(cm), CD = canopy diameter(cm), NPB= Number of primary branches per plant, SD= Stem diameter(mm), FPL= Fruit pedicel Length(cm), FL= Fruit length(cm), FD= Fruit diameter(mm), FPT = Fruit pericarp thickness(mm), DFYP= Dry fruit yield per plant(g), FW= Average single fruit weight(g), NFP=Number of Fruit per plant, NSF= Number of seed per fruit, TSW= Thousand seed weight(g), TFY= Total fruit yield(tha^{-1}) .

Table 5. Estimates of direct (bold and diagonal) and indirect effect (off diagonal) of different characters on fruit yield of 64 hot pepper genotypes at genotypic level at Mereb Leke in, 2017/2018

Characters	DFL	DFR	DM	PH	CD	NPB	SD	FPL	FL	FD	FPT	DFYP	FW	NFP	NSF	TSW	rg
DFL	-0.08	0.06	-0.12	0.031	0.053	0.12	0.05	-0.03	0.06	0.04	-0.11	-0.06	-0.05	-0.006	-0.001	-0.04	-0.08
DFR	-0.06	0.08	-0.15	0.027	0.045	0.16	0.05	-0.05	0.09	0.07	-0.16	-0.08	-0.07	-0.008	-0.002	-0.06	-0.13
DM	-0.05	0.06	-0.21	0.019	0.066	0.20	0.04	-0.06	0.14	0.09	-0.22	-0.15	-0.10	-0.010	-0.003	-0.09	-0.28*
PH	-0.04	0.03	-0.06	0.065	0.037	0.03	0.08	0.01	-0.01	0.00	0.00	0.03	0.02	-0.002	0.001	0.02	0.20
CD	-0.02	0.02	-0.07	0.012	0.205	0.12	0.04	-0.03	0.05	0.04	-0.09	0.03	-0.03	-0.006	0.000	0.00	0.28*
NPB	-0.03	0.04	-0.14	0.007	0.080	0.31	0.03	-0.08	0.14	0.09	-0.22	-0.05	-0.10	-0.013	-0.002	-0.09	-0.02
SD	-0.04	0.04	-0.08	0.047	0.085	0.10	0.11	-0.01	0.01	0.02	-0.06	0.05	-0.01	-0.007	0.001	0.02	0.26*
FPL	0.02	-0.03	0.10	0.005	-0.047	-0.18	-0.01	0.13	-0.12	-0.09	0.19	0.07	0.08	0.009	0.003	0.05	0.19
FL	0.02	-0.04	0.15	0.003	-0.056	-0.22	-0.01	0.08	-0.20	-0.11	0.25	0.12	0.13	0.012	0.003	0.11	0.25*
FD	0.02	-0.04	0.13	0.002	-0.049	-0.19	-0.01	0.08	-0.14	-0.15	0.31	0.17	0.13	0.013	0.006	0.09	0.37
FPT	0.02	-0.04	0.13	0.000	-0.048	-0.18	-0.02	0.07	-0.13	-0.13	0.37	0.18	0.12	0.010	0.005	0.09	0.44**
DFYP	0.01	-0.01	0.07	0.004	0.014	-0.03	0.01	0.02	-0.05	-0.06	0.14	0.46	0.09	-0.001	0.004	0.08	0.75**
FW	0.02	-0.04	0.14	0.006	-0.034	-0.19	-0.01	0.07	-0.16	-0.12	0.27	0.26	0.16	0.011	0.005	0.12	0.52**
NFP	-0.02	0.03	-0.12	0.009	0.072	0.21	0.04	-0.07	0.13	0.10	-0.21	0.03	-0.10	-0.018	-0.004	-0.06	0.04
NSF	0.01	-0.02	0.07	0.009	-0.008	-0.08	0.01	0.05	-0.06	-0.09	0.18	0.21	0.09	0.007	0.010	0.04	0.42**
TSW	0.02	-0.03	0.10	0.006	-0.001	-0.15	0.01	0.04	-0.12	-0.07	0.18	0.20	0.10	0.006	0.002	0.18	0.47**

Residual effect = 0.50 *and ** = significant at 5% and 1% probability levels, respectively. DFL = days to 50% flowering, DFL = days to 50%fruiting, DM = days to maturity, PH = plant height (cm), CD = canopy diameter (cm), NPB = number of primary branches per plant**, SD = stem diameter (mm), FPL = fruit** pedicel length (cm), FL = fruit length (cm), FD = fruit diameter (mm), FPT = fruit pericarp thickness (mm), DFYP = dry fruit yield per plant (g), FW = average single fruit weight (g), NFP = number of fruit per plant, NSF = number of seeds per fruit, TSW = thousand seed weight (g) and rg = genotypic coefficient of correlation.

ISSN 2224-3208 (Paper) ISSN 2225-093X (Online) DOI: 10.7176/JBAH
Vol.9, No.13, 2019

Appendix 1. Mean values for phenological and morphological characters of 64 hot pepper genotypes evaluated at Mereb Leke in 2017/2018

No.	Genotypes	DFL	DFR	DM	PH	CD	NPB	SD
1	Acc-1	65^{g-m}	72^{i-p}	113.5^{p}	60^{a-e}	39.5^{a-j}	5.75^{n-s}	16^{ab}
2	Acc-2	68^{c-k}	79^{a-g}	126^{b-g}	52.8^{c-m}	41.1^{a-g}	11^{a-d}	13.2^{c-j}
3	Acc-3	70.5^{a-h}	79.5^{a-f}	122.5^{d-l}	66.5^{a}	40.5^{a-h}	6.3^{k-p}	14.9^{a-e}
4	Acc-4	64^{i-n}	74^{e-o}	116^{m-p}	46.3^{j-o}	40.2^{a-i}	11^{a-d}	12.65^{d-m}
5	Acc-5	74^{a-c}	81^{a-d}	133^{a}	59.5^{a-f}	40.4^{a-h}	11.75^{ab}	14.4^{a-f}
6	Acc-6	71^{a-g}	82.5^{ab}	128.5^{a-c}	54.3^{c-m}	34.9^{j-o}	9.8^{a-g}	13.5^{c-h}
7	Acc-7	65^{g-m}	77.5^{b-j}	126.5^{b-f}	53.3^{c-m}	38.3^{b-l}	7.2^{h-o}	13^{c-l}
8	Acc-8	68.5^{c-k}	77.5^{b-j}	127.5^{a-d}	60.7^{a-d}	42.9^{ab}	10^{a-f}	15.25^{a-c}
9	Acc-9	75.5^{ab}	80^{a-e}	130.5^{ab}	60^{a-e}	37.7^{c-m}	11.6^{ab}	13.85^{a-g}
10	Acc-10	69.5^{b-j}	81^{a-d}	123.5^{d-k}	55.4^{b-l}	37.6^{d-m}	10.9^{a-e}	14.4^{a-f}
11	Acc-11	69.5^{b-j}	76.5^{b-l}	113.5^{p}	54.8^{b-m}	33.1^{m-o}	5.6^{n-s}	13.05^{c-k}
12	Acc-12	67^{d-m}	78^{b-i}	127^{b-e}	57.3^{a-h}	42^{a-d}	11.8^{a}	11.1^{h-o}
13	Acc-13	65^{g-m}	74.5^{e-n}	117.5^{l-p}	51.5^{d-m}	33.85^{l-o}	5.4^{n-s}	11.7^{g-o}
14	Acc-14	73^{a-d}	78^{b-i}	129^{a-c}	53.5^{c-m}	42.3^{a-c}	11.5a-c	15^{a-d}
15	Acc-15	70.5^{a-h}	77.5^{b-j}	126^{b-g}	54.1^{c-m}	43.3^{a}	6.3k-p	13.3^{c-j}
16	Acc-16	65.5^{f-n}	74.5^{e-n}	121.5^{e-m}	56.2^{b-j}	36.45^{g-o}	4.8o-s	12.9^{c-m}
17	Acc-28336	70^{b-i}	79^{a-g}	127^{b-e}	58.4^{a-g}	39.3^{a-j}	9.2b-i	12.8^{d-n}
18	Acc-230800	68.5^{c-k}	77^{b-k}	121.5^{e-m}	56.1^{b-k}	39.2^{a-j}	9c-j	12.25^{f-o}
19	Acc-28337	66^{f-n}	77^{b-k}	120.5^{g-m}	54.3^{c-m}	35.6^{i-o}	3.6rs	12.75^{d-n}
20	Acc-229699	65.5^{f-n}	75.5^{c-m}	124.5^{c-i}	54.6^{c-m}	36.9^{f-o}	11.8a	12.75^{d-n}
21	Acc-212912	70.5^{a-h}	78.5^{a-h}	120^{h-n}	60.1^{a-e}	41^{a-g}	8.4e-m	14.9^{a-e}
22	Acc-9097	61^{m-o}	72^{i-p}	123.5^{c-k}	37.1^{o}	39^{a-k}	6.3k-p	11^{i-o}
23	Acc-9084	57.5^{o}	68^{op}	122.5^{d-l}	53.5^{c-m}	36^{h-o}	8.8d-k	12.65^{d-m}
24	Acc-229697	68^{c-k}	77^{b-k}	124^{c-j}	50.1^{e-m}	32.4^{o}	9.7a-h	11.75^{g-o}
25	Acc-212913	64^{i-n}	71.5^{j-p}	119.5^{i-o}	55.8^{b-k}	41.5^{a-e}	3.9q-s	13.9^{a-g}
26	Acc-229700	66.5^{e-m}	78.5^{a-h}	125.5^{b-h}	50.9^{d-m}	33.5^{m-o}	8.7d-l	13.35^{c-i}
27	Acc-8995	70.5^{a-h}	77^{b-k}	128.5^{a-c}	52.8^{c-m}	39.1^{a-j}	11^{a-d}	12.6^{d-n}
28	Acc-9085	67.5^{d-l}	75^{d-m}	120^{h-n}	46.3^{j-o}	35.1^{j-o}	6.6^{j-p}	10.75^{k-o}
29	Acc-230798	64^{i-n}	71.5^{i-p}	116.5^{l-p}	47.6^{h-m}	35.1^{k-o}	3.7^{rs}	11^{i-o}
30	Acc-230799	72.5^{a-e}	79^{a-g}	126^{b-g}	52.7^{c-m}	38.9^{a-k}	7.8^{f-n}	11.8^{g-o}
31	Acc-236436	67^{d-m}	77.5^{b-j}	125.5^{b-h}	55.5^{b-l}	33.2^{m-o}	5.25^{n-s}	12.2^{f-o}
32	Acc-229698	62.5^{k-o}	70.5^{l-p}	118^{k-p}	49.5^{f-m}	35^{j-o}	3.6^{rs}	12.25^{f-o}
33	Acc-229701	63.5^{j-o}	71^{k-p}	117^{l-p}	37.5^{no}	37.5^{d-n}	9.7^{a-h}	10.4^{no}
34	Acc-237528	71^{a-g}	80^{a-e}	127.5^{a-d}	47.1^{h-m}	35.2^{j-o}	9.7^{a-h}	10.9^{j-o}
35	Acc-9102	64.5^{h-m}	72.5^{h-p}	124.5^{c-i}	59.4^{a-g}	35^{j-o}	6.7^{i-p}	13.65^{b-g}
36	Acc-9094	71.5^{a-f}	76.5^{b-l}	122.5^{d-l}	50.4^{d-m}	34.4^{k-o}	7.05^{i-p}	12.25^{f-o}
37	Acc-9098	63.5^{j-o}	78^{b-i}	127.5^{a-d}	54^{c-m}	37.6^{d-m}	8.6^{d-l}	12.9^{c-m}
38	Acc-9104	63.5^{j-o}	77.5^{b-j}	127^{b-e}	45.7^{k-o}	41.6^{a-e}	10.5^{a-e}	12.25^{f-o}
39	Acc-9099	70.5^{a-h}	79^{a-g}	128.5^{a-c}	46.8^{i-o}	35.1^{j-o}	8.7^{d-l}	12.75^{d-n}
40	Acc-9082	67^{d-m}	74^{e-o}	119^{i-p}	52^{c-m}	36.1^{h-o}	5.25^{n-s}	12.5^{e-n}
41	Acc-9101	67^{d-m}	71.5^{j-p}	122^{d-l}	57.3^{a-h}	43.1^{a}	7.7^{f-n}	13.35^{c-i}
42	Acc-9086	70^{b-i}	80^{a-e}	129^{a-c}	52.7^{c-m}	42.5^{ab}	7.3^{g-o}	13.2^{c-j}
43	Acc-229696	73^{a-d}	82.5^{ab}	127.5^{a-d}	55.3^{b-m}	36.6^{g-o}	7.7^{f-n}	13.6^{c-g}
44	Acc-9106	66^{f-n}	80^{a-e}	122.5^{d-l}	51.8^{d-m}	35.55^{i-o}	8.7^{d-l}	12.35^{f-n}

Journal of Biology, Agriculture and Healthcare www.iiste.org
ISSN 2224-3208 (Paper) ISSN 2225-093X (Online) DOI: 10.7176/JBAH
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Appendix 1. (Continued)

No.	Genotypes	DFL	DFR	DM	PH	CD	NPB	SD
45	Acc-9007	70^{b-i}	77.5^{b-j}	129^{a-c}	60.8^{a-c}	35.9^{h-o}	8.6^{d-l}	14^{a-g}
46	Acc-9107	71.5^{a-f}	76.5^{b-l}	126^{b-g}	52.7^{c-m}	37^{e-o}	5^{o-s}	12.05^{f-n}
47	Acc-28334	64.5^{h-m}	70.5^{l-p}	122.5^{d-l}	50.7^{d-m}	33.9^{l-o}	4.6^{p-s}	13.2^{c-j}
48	Acc-48	61.5^{l-o}	67.5^{p}	117^{l-p}	47.7^{h-m}	37.25^{e-n}	3.6^{rs}	10.55^{m-o}
49	Acc-49	63.5^{j-o}	67.5^{p}	114.5^{n-p}	45.3^{l-o}	39^{a-k}	3.5^{s}	10.75^{k-o}
50	Acc-229694	65.5^{f-n}	74.5^{e-n}	117^{l-p}	56.2^{b-j}	37.5^{d-n}	3.5^{s}	13.55^{c-g}
51	Acc-51	68^{c-k}	74.5^{e-n}	119.5^{i-o}	57.5^{a-g}	33.3^{m-o}	3.6^{rs}	12.75^{d-n}
52	Acc-52	66.5^{e-m}	77^{b-k}	121.5^{e-m}	47.3^{h-m}	37.5^{d-n}	3.4^{s}	11.85^{g-o}
53	Acc-9093	62.5^{k-o}	68.5^{n-p}	119^{i-p}	54.1^{c-m}	32.95^{no}	6.4^{l-q}	11.6^{g-o}
54	Acc-229692	67^{d-m}	73.5^{f-p}	118.5^{j-p}	51.6^{d-m}	36.2^{h-o}	3.9^{q-s}	12.3^{f-n}
55	Acc-55	65^{g-m}	69.5^{m-p}	117^{l-p}	52.5^{c-m}	37^{e-o}	4^{q-s}	12.3^{f-n}
56	Acc-56	68.5^{c-k}	71.5^{j-p}	116.5^{l-p}	56.1^{b-k}	35.55^{i-o}	5.5^{n-s}	11.6^{g-o}
57	Acc-57	64^{i-n}	72.5^{h-p}	114^{p}	47.2^{h-m}	36^{h-o}	3.5^{s}	10.6^{l-o}
58	Acc-58	69^{c-j}	73^{g-p}	119.5^{i-o}	51.6^{d-m}	37.5^{d-n}	3.5^{s}	12.3^{f-n}
59	Acc-59	75.5^{ab}	81.5^{a-c}	130.5^{ab}	59.6^{a-f}	43.4^{a}	10.1^{a-f}	16.05^{a}
60	Acc-23880	63.5^{j-o}	72.5^{h-p}	120^{h-n}	49^{g-m}	35.6^{i-o}	5.9^{m-s}	10.9^{j-o}
61	Acc-61	60.5^{no}	70.5^{l-p}	118^{k-p}	44.9^{m-o}	36^{h-o}	3.6^{rs}	9.85^{o}
62	Acc-62	62.5^{k-o}	74^{e-o}	120^{h-n}	56.8^{a-i}	33.3^{m-o}	3.95^{q-s}	11.95^{g-n}
63	Acc-63	76.5^{a}	84.5^{a}	126^{b-g}	65^{ab}	37.4^{d-n}	6.2^{l-r}	13.7^{a-g}
64	Acc-64	66^{f-n}	76.5^{b-l}	121^{f-m}	62.3^{a-c}	35^{j-o}	3.6r^{s}	13.7^{a-g}
	Mean	62.27	75.68	122.6	53.29	37.38	7.1	12.7
	CV (%)	3.8	3.3	2	7.8	5	15	7.7

Means followed by the same letter in the same column are not significantly different. CV (%) = coefficient of variation, DFL = days to 50% flowering, DFR = days to 50% fruiting DM = days to maturity, PH = plant height (cm), CD = canopy diameter (cm), NPB = number of primary branches per plant, SD = stem diameter (mm)

Appendix 2. Mean performance for fruit yield and fruit characteristics of 64 hot pepper genotypes evaluated at Mereb Leke in, 2017/2018

No.	Genotypes	FPL	FL	FD	FPT	FW	NFP	NSF	TSW	DFYP	MFY	UNMY	TFY
1	Acc-1	4.05^{a-g}	16.75a	23.25^{d-f}	2.3^{a-g}	6.6^{a-c}	26^{j-m}	136.5^{n-p}	6.55^{a-d}	128.5^{e}	3.25^{c-d}	0.125^{qr}	3.38^{bc}
2	Acc-2	2.67^{o-t}	6.2^{o-u}	11.21^{x}	1.7^{k}	2.41^{p-u}	53.15^{ab}	105.3^{wx}	5.8^{c-j}	106^{i-l}	2.67^{c-j}	0.24^{e-m}	2.91^{c-j}
3	Acc-3	4.1^{a-f}	11^{e-j}	29.4^{ab}	2.3^{a-g}	6.3^{a-d}	19.25^{o-r}	221^{b}	6.45^{a-e}	167.5^{ab}	3.855^{ab}	0.41^{a}	4.27^{a}
4	Acc-4	2.8^{n-t}	7.52^{no}	18.72^{k-m}	2.3^{a-g}	2.95^{k-r}	34.6^{e}	188^{d}	5.8^{c-j}	168^{ab}	4.34^{a}	0.21^{i-r}	4.55^{a}
5	Acc-5	3.4^{g-n}	4.56^{v-x}	15.14^{p-v}	1.85^{h-k}	2.185^{q-u}	55.5^{a}	111^{u-w}	5.7^{d-j}	105.5^{i-l}	2.85^{c-h}	0.29^{c-i}	3.14^{c-f}
6	Acc-6	2.32^{t}	5.08^{s-x}	15.11^{o-v}	1.7^{k}	3.7^{h-m}	44.3^{c}	147.4^{j-m}	6.5^{a-d}	143^{cd}	2.465^{c-m}	0.16^{l-r}	2.63^{c-n}
7	Acc-7	3.73^{d-j}	11.2^{d-i}	15.36^{o-t}	1.82^{i-k}	2.92^{k-r}	29.3^{f-k}	118.8^{s-v}	6^{b-i}	83.5^{o-q}	1.9^{i-o}	0.13^{p-r}	2^{j-o}
8	Acc-8	3.05^{k-r}	4.39^{wx}	12.01^{v-x}	1.95^{f-k}	2.235^{q-u}	50.9^{ab}	138.5^{m-o}	5.9^{b-j}	102.5^{j-l}	2.88^{c-h}	0.2^{i-r}	3.1^{c-g}
9	Acc-9	2.65^{o-t}	6.49^{o-t}	14.06^{p-x}	1.85^{h-k}	2.205^{q-u}	31.5^{e-h}	116.5^{t-v}	4.6^{l-p}	63.5^{t-v}	2.02^{h-n}	0.25^{e-l}	2.27^{f-o}
10	Acc-10	3.25^{i-o}	10.25^{h-l}	12.4^{t-x}	1.9^{g-k}	1.55^{u}	52.9^{ab}	110^{u-w}	5.1^{h-n}	118.5^{e-h}	2.56^{c-l}	0.14^{o-r}	2.7^{c-m}
11	Acc-11	4.25^{a-e}	14.5^{b}	23.1^{d-f}	2.25^{b-h}	6.325^{a-d}	23.4^{l-p}	145.5^{k-n}	6.6^{a-d}	126.5^{e}	2.64^{c-j}	0.12^{r}	2.8^{c-l}
12	Acc-12	2.67^{o-t}	4.41^{wx}	12.89^{s-x}	1.85^{h-k}	2.21^{q-u}	31.25^{e-i}	109.5^{vw}	4.2^{n-p}	87^{o-q}	2.37^{d-m}	0.22^{h-n}	2.59^{c-n}
13	Acc-13	2.75^{n-t}	8.23^{mn}	16.03^{o-r}	1.94^{f-k}	2.75l-s	26.3^{i-m}	110.2^{u-w}	5.35^{f-m}	54.5^{v}	1.63^{m-o}	0.16^{l-r}	1.78^{n-p}
14	Acc-14	2.52^{r-t}	5.25^{t-x}	12.94^{s-x}	1.75^{jk}	2.51^{n-u}	43.15^{cd}	94^{y}	5.4^{e-l}	86^{o-q}	2.56^{d-l}	0.24^{f-n}	2.79^{c-k}
15	Acc-15	3^{l-s}	7^{n-p}	12.6^{t-x}	1.8^{i-k}	2.38^{p-u}	42.6^{cd}	105.3^{wx}	6.7^{a-d}	82^{p-s}	1.865^{j-o}	0.23^{f-n}	2.095^{i-o}
16	Acc-16	4.2^{a-f}	9.15^{lm}	19.72^{g-l}	2.45^{a-d}	4.82^{fg}	32.6^{e-g}	158.1^{g-i}	6.1^{b-h}	150^{c}	3.84^{ab}	0.225^{f-p}	4.1^{ab}
17	Acc-28336	4.2^{a-f}	4.4^{wx}	13^{r-x}	1.7^{k}	3.175^{k-r}	41.1^{cd}	143^{k-n}	4.7^{k-p}	128^{e}	2.415^{d-m}	0.16^{l-r}	2.58^{c-n}
18	Acc-230800	2.75^{n-t}	6.55^{o-s}	11.94^{wx}	1.9^{c-k}	3.395^{j-p}	24.3^{l-n}	118.7^{s-v}	6^{b-i}	78.5^{q-s}	2.49^{c-m}	0.175^{j-r}	2.7^{c-n}
19	Acc-28337	3.73^{d-j}	7.03^{n-p}	18.9j-n	2.13^{c-j}	3.75^{h-l}	19^{o-r}	173.9^{e}	4.9^{j-p}	83.5^{o-q}	2.42^{d-m}	0.15^{m-r}	2.57^{c-n}
20	Acc229699	3.25^{i-o}	4.165^{wx}	23.8^{de}	2.36^{a-f}	3.58^{h-m}	42.9^{cd}	149.9^{i-l}	4.1^{op}	159.5^{b}	3.07^{b-f}	0.125^{qr}	3.19^{c-e}
21	Acc212912	4.25^{a-e}	9.56^{j-m}	31^{a}	2.7^{a}	6.82^{ab}	19.6^{n-r}	231^{a}	6.8^{a-c}	163^{ab}	4.16^{a}	0.33^{a-e}	4.49^{a}
22	Acc-9097	4.5^{a-c}	6.38^{o-u}	16.8^{l-q}	1.9^{g-k}	1.815^{s-u}	17.9^{qr}	101.1^{w-y}	5.7^{d-j}	61.5^{uv}	2.125^{g-n}	0.125^{qr}	2.25^{f-o}
23	Acc-9084	2.53^{q-t}	5.25^{s-x}	11.91^{wx}	1.75^{jk}	1.61^{tu}	42^{cd}	125.2^{rs}	5.1^{h-n}	82.5^{o-r}	1.9^{i-o}	0.23^{f-n}	2.13^{h-o}
24	Acc-229697	3.8^{d-j}	4.95^{v-x}	14.91^{o-w}	2^{e-k}	1.82^{s-u}	52^{ab}	93^{y}	4^{p}	83.5^{o-q}	2.125^{g-n}	0.315^{b-f}	2.44^{d-o}
25	Acc-212913	3^{l-s}	9.5^{k-m}	18.63^{k-n}	2.35^{a-f}	5.98^{b-d}	49.9^{b}	118.3^{s-v}	7.2^{a}	172.5^{a}	4.18^{a}	0.14^{n-r}	4.32^{a}
26	Acc-229700	3.57^{f-m}	5.45^{q-x}	11.855^{wx}	1.7^{k}	2.23^{q-u}	54.9^{a}	128.1^{p-s}	5.4^{e-l}	160^{b}	2.425^{c-m}	0.22^{g-q}	2.7^{c-n}

Journal of Biology, Agriculture and Healthcare
ISSN 2224-3208 (Paper) ISSN 2225-093X (Online) DOI: 10.7176/JBAH
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No.	Genotypes	FPL	FL	FD	FPT	FW	NFP	NSF	TSW	DFYP	MFY	UNMFY	TFY
27	Acc-8995	2.55^{p-t}	4^{x}	12.82^{t-x}	1.85^{h-k}	2.45^{p-u}	43.65^{cd}	176^{e}	5.2^{g-m}	99^{l-n}	2.14^{g-n}	0.38^{a-c}	2.52^{c-o}
28	Acc-9085	3.2^{j-p}	4.5^{wx}	11.86^{wx}	1.75^{jk}	2.31^{q-u}	45.3^{c}	120^{r-u}	4.9^{j-p}	127.5^{e}	1.825^{j-o}	0.115^{r}	1.94^{k-p}
29	Acc230798	3.94^{b-h}	10.73^{f-k}	27.75^{bc}	2.35^{a-f}	3.935^{g-k}	18.5^{p-r}	142.35^{k-n}	6.3^{a-f}	72.5^{r-t}	1.73^{k-o}	0.115^{r}	1.845^{l-p}
30	Acc-230799	2.95^{m-t}	5.3^{r-x}	14.93^{o-w}	1.95^{f-k}	2.24^{q-u}	31.6^{e-h}	95.5^{y}	5.2^{g-m}	100^{k-n}	1.675^{l-o}	0.16^{l-r}	1.79^{m-p}
31	Acc-236436	3.02^{l-r}	6.45^{o-u}	17.64^{k-o}	2.69^{a}	2.61^{m-u}	33.8^{ef}	99.3^{xy}	6.3^{a-f}	87^{o-q}	2.29^{f-m}	0.16^{l-r}	2.45^{e-o}
32	Acc-229698	3.35^{h-n}	12.2^{d-f}	23.25^{d-f}	2.35^{a-f}	4.35^{f-j}	15.1^{r}	142.5^{k-n}	6.3^{a-f}	138^{d}	2.78^{c-i}	0.115^{r}	2.9^{c-j}
33	Acc-229701	3.05^{k-r}	4.05^{wx}	12.1^{u-x}	1.85^{h-k}	2.125^{r-u}	52.25^{ab}	126.7^{q-s}	4.9^{j-p}	126^{e}	2.56^{c-l}	0.21^{h-r}	2.77^{c-k}
34	Acc-237528	2.29^{t}	4.93^{u-x}	15.12^{o-u}	2.05^{d-k}	2.36^{p-u}	30.3^{e-j}	144.5^{k-n}	4.4^{l-p}	56^{v}	1.7^{l-o}	0.35^{a-d}	2.04^{j-p}
35	Acc-9102	3.9^{c-i}	6.1^{o-v}	16.96^{l-p}	1.95^{f-k}	2.435^{p-u}	26.9^{h-m}	151.2^{i-k}	4.3^{m-p}	64^{t-v}	0.7^{p}	0.13^{p-r}	0.83^{q}
36	Acc-9094	2.3^{t}	6.9^{n-q}	19.23^{i-m}	1.8^{i-k}	2.63^{m-t}	24.5^{k-n}	150.3^{i-l}	4.7^{k-p}	98^{l-n}	2.08^{h-m}	0.165^{l-r}	2.25^{f-o}
37	Acc-9098	3^{l-s}	5.3^{r-x}	11.84^{wx}	1.85^{h-k}	2.22^{q-u}	39^{d}	123.5^{r-t}	5.4e-l	80.5^{q-s}	1.71^{k-o}	0.35^{a-d}	2.1^{i-p}
38	Acc-9104	2.75^{n-t}	5.2^{s-x}	15.19^{o-u}	1.8^{i-k}	2.31^{q-u}	28.2^{g-l}	110.8^{u-w}	4.9^{j-p}	79^{q-s}	2.065^{h-n}	0.265^{d-j}	2.33^{e-o}
39	Acc-9099	3.1^{k-r}	4.3^{wx}	12.2^{u-x}	1.8^{i-k}	2.235^{q-u}	22.1^{m-q}	150.4^{i-l}	4^{p}	64^{t-v}	1.395^{n-p}	0.26^{d-k}	1.66^{op}
40	Acc-9082	3.95^{b-h}	6.8^{o-r}	21.75^{e-j}	2.1^{d-k}	2.72^{l-s}	24^{l-o}	139^{m-o}	5.3^{f-m}	89.5^{n-q}	2.53^{c-l}	0.175^{j-r}	2.71^{c-l}
41	Acc-9101	3.19^{j-q}	4.3^{wx}	12.84^{t-x}	1.75^{jk}	2.245^{q-u}	42.9^{cd}	170.1^{ef}	4.1^{op}	84^{o-q}	2.555^{c-l}	0.155^{l-r}	2.71^{c-l}
42	Acc-9086	4^{a-h}	5.4^{r-x}	17.82^{k-o}	1.99^{e-k}	2.57^{m-u}	42.2^{cd}	137.9^{m-p}	4.1^{op}	99^{l-n}	2.4^{d-m}	0.39^{ab}	2.79^{c-k}
43	Acc229696	2.35st	4.18^{wx}	12.79^{s-x}	1.75^{jk}	2.71^{l-s}	42.5^{cd}	99.7^{xy}	4.3^{m-p}	92^{m-p}	2.1^{g-n}	0.31^{b-g}	2.41^{d-o}
44	Acc-9106	4.04^{a-g}	6.51^{o-t}	16.54^{m-q}	1.95^{f-k}	2.235^{q-u}	32^{e-g}	138.9^{m-o}	4.4^{l-p}	71.5^{s-u}	2.1^{h-m}	0.13^{p-r}	2.21^{g-o}
45	Acc-9007	3.69^{d-k}	4.22^{wx}	15.9^{n-s}	1.75^{jk}	2.495^{n-u}	31.3^{e-i}	156^{h-j}	5^{i-o}	115^{f-i}	2.035^{h-n}	0.37^{a-c}	2.4^{d-o}
46	Acc-9107	4.6^{ab}	10.97^{e-k}	23.88^{de}	2.25^{b-h}	3.21^{k-q}	16.6^{r}	128.9^{o-r}	5.2^{g-m}	82.5^{o-r}	2.41^{d-m}	0.125^{qr}	2.53^{c-o}
47	Acc-28334	4.25^{a-e}	14.7^{b}	25.24^{cd}	2.4^{a-e}	6^{b-d}	19.6^{n-r}	186.8^{d}	5.7^{d-j}	120^{e-h}	2.6^{c-k}	0.125^{qr}	2.73^{c-l}
48	Acc-48	4.25^{a-e}	11.4^{d-i}	25.18^{cd}	2.57^{ab}	5.77^{c-e}	19^{o-r}	200.9^{c}	5.7^{d-j}	121.5^{e-g}	2.57^{c-l}	0.13^{p-r}	2.7^{c-m}
49	Acc-49	4.3^{a-d}	12.5^{c-e}	25.1^{cd}	2.4^{a-e}	7.1^{a}	15.2^{r}	142.3^{l-n}	6^{b-i}	144^{cd}	2.865^{c-h}	0.2^{i-r}	3.1^{c-g}
50	Acc-229694	4.27^{a-e}	13.78^{bc}	24.56^{de}	2.35^{a-f}	6.19^{a-d}	17.6^{qr}	139.3^{mn}	6.9^{ab}	112^{g-j}	2.92^{c-h}	0.115^{r}	3.03^{c-h}
51	Acc-51	3.9^{c-i}	12.5^{c-e}	29.45^{ab}	2.55^{a-c}	5.32^{d-f}	18.75^{pr}	166.4^{e-g}	6.3^{a-f}	105.5^{i-l}	2.14^{g-n}	0.16^{l-r}	2.3^{e-o}
52	Acc-52	3.2^{j-p}	12.65^{cd}	19.4^{h-m}	2.21^{b-i}	4.37^{f-j}	15.6^{r}	142.8^{k-n}	5.4^{e-l}	82.5^{o-r}	1.1^{op}	0.115^{r}	1.2^{pq}
53	Acc-9093	3.625^{e-l}	11.32^{d-i}	20.54^{f-k}	2.15^{b-j}	6.27^{a-d}	24.1^{l-o}	145^{k-n}	6.8^{a-c}	140.5^{cd}	3.34^{bc}	0.115^{r}	3.43^{bc}
54	Acc-229692	3.84^{c-j}	12.45^{c-e}	18.92^{j-n}	2.2^{b-i}	3.175^{k-r}	27.9^{g-l}	125.4^{r-t}	6.8^{a-c}	81.5^{p-s}	2.795^{c-i}	0.17^{k-q}	3^{c-i}
55	Acc-55	4.65^{a}	11.68^{d-h}	22.43^{d-g}	2.25^{b-h}	4.585^{f-h}	19^{o-r}	152^{i-k}	5.4^{e-l}	93^{m-o}	2.47^{c-m}	0.12^{r}	2.59^{c-n}
56	Acc-56	4.02^{a-g}	11.6^{d-h}	22.35^{d-h}	2.2^{b-i}	4.98^{ef}	14.85^{r}	138^{m-p}	6.7^{a-d}	100^{k-n}	2.22^{f-n}	0.14^{n-r}	2.36^{d-o}
57	Acc-57	3.95^{b-h}	11.27^{d-i}	21.97^{e-i}	2.25^{b-h}	5.79^{c-e}	14.75^{r}	174.4^{e}	6.5^{a-d}	167.5^{ab}	3.1^{b-f}	0.165^{l-r}	3.26^{b-d}
58	Acc-58	3.925^{c-h}	9.93^{i-l}	19.75^{g-l}	2.2^{b-i}	4.47^{f-i}	18.3^{p-r}	161.4^{f-h}	6.9^{ab}	138.5^{d}	2.83^{c-h}	0.14^{n-r}	2.97^{c-i}
59	Acc-59	2.42^{r-t}	5.62^{r-w}	13.7^{q-x}	1.8^{i-k}	2.61^{m-u}	53.5ab	139^{m-o}	6.2^{a-g}	125^{ef}	2.49^{c-m}	0.3^{c-h}	2.78^{c-k}
60	Acc-23880	3.86^{c-i}	11.18^{d-i}	22.2^{d-h}	2.15^{b-j}	4.58^{f-h}	15.2^{r}	135.3^{n-q}	6.6^{a-d}	112.5^{g-j}	2.515^{c-m}	0.125^{qr}	2.64^{c-n}
61	Acc-61	2.9^{n-t}	11.85^{d-g}	22.68^{d-g}	2.3^{a-g}	6.7^{a-c}	16.2^{r}	145.4^{k-n}	5.7^{d-j}	161^{b}	2.995^{c-g}	0.16^{l-r}	3.16^{c-f}
62	Acc-62	4.5^{a-c}	12.05^{d-f}	18.48^{k-n}	2.2^{b-i}	6.1^{b-d}	19.6^{n-r}	140.5^{l-n}	6.6^{a-d}	105^{i-l}	3.245^{b-e}	0.165^{l-r}	3.41^{bc}
63	Acc-63	4^{a-h}	10.4^{g-l}	13.27^{r-x}	2.05^{d-k}	3.46^{j-o}	30.6^{e-j}	128.4^{p-s}	4.4^{l-p}	110^{h-k}	2.43^{c-m}	0.125^{qr}	2.56^{c-o}
64	Acc-64	3.94^{b-h}	10.28^{h-l}	19.71^{g-l}	1.95^{f-k}	3.5^{i-n}	19.25^{o-r}	137.9^{m-p}	5.7^{d-j}	80^{q-s}	2.35^{e-m}	0.185^{j-r}	2.54^{c-o}
	Mean	3.5	8	18	2.1	3.6	31	139.1	5.6	107.3	2.48	0.19	2.67
	CV (%)	7.8	7.8	7.1	8.3	11.9	6.9	3.1	7.8	4.2	14.6	19.7	13.8

Means followed by the same letter in the same column are not significantly different.CV (%) = coefficient of variation, FPL = fruit pedicel length (cm), FL = fruit length (cm), FD = fruit diameter (mm), FPT = fruit pericarp thickness (mm), FW = average single fruit weight (g), NFP = number of fruits per plant, NSF = number of seeds per fruit, dry fruit yield per plant (g), MFY = marketable fruit yield (t ha^{-1}), UNMFY = Unmarketable fruit yield (t ha^{-1}), TFY = total fruit yield (t ha^{-1}).

Acknowledgements: The authors are highly grateful to TARI (Tigray Agricultural Research Institute) for funding this research and Axum Agricultural Research Center for provision of experimental fields and logistics for this study

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ISSN 2224-3208 (Paper) ISSN 2225-093X (Online) DOI: 10.7176/JBAH
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