Genetic dissimilarity, attributes association, and path analysis of sweet peppers

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ABSTRACT

The present investigation was conducted on genetic diversification, character connections, and their direct and indirect effects using 21 sweet pepper genotypes to identify superiors owing to develop variety (es) and/or utilizing the pertinent genotypes in hybridization program. It was found that, with the exception of fruit length (FL), all of the features had larger phenotypic coefficients of variation (PCV) than genotypic variation coefficients of variation (GCV), and the gap between PCV and GCV was rather small. Except for FL (24.98%) and seed number per fruit (24.76%), all traits had a high estimation of broad sense heritability of more than 75.00%, indicating significant improvement is possible employing standard selection procedures. High genetic advance as percentage of mean was observed for all the characters. Genotypic and phenotypic correlation analyses showed that there had a strong positive correlation for fruit yield per plant with fruit yield/plot and yield (t/ha) (r = 1.00**). In addition, the importance and close correlation of characters to enhance yield or to use as selection catalogs were demonstrated by the fact that the genotypic direct impacts utilized by the yield component traits were fairly bigger than their equivalent phenotypic effects.

1. INTRODUCTION

Sweet pepper (*Capsicum annuum* L.) is a solanaceous vegetable ($2n = 24$) and Bangladeshi people commonly known it as capsicum. This vegetable is popular in Bangladesh for its bright color, nutritional enrichment, and mouthwatering taste. It has a lot of Vitamin C and ascorbic acid (150–180 mg/100 g) and Vitamin A can make up to twelve percent of the total amount of pigments. It possesses anti-oxidant qualities and helps to prevent certain cancers, cardiovascular diseases, strokes, atherosclerosis, and cataracts [1]. The demand of sweet pepper is gradually increasing, and it might be a lucrative vegetable crop in Bangladesh. There is a need to find better germplasm because of the crop's demand as a high-value crop and its economic relevance owing to develop variety (es) and/or utilizing the relevant genotypes in hybridization program.

Several processes were included in the systematic breeding activities such as, accumulating genetic material, assessing variation in genes, creating genetic variations, making the right selection, and selecting the best genotypes for commercial sale [2,3]. Identifying efficient genotypes for direct use as varieties or as parent's incoming progress programs requires an estimation of many characteristics as a measure of genetic variability. A character's heritability estimate is useful to plant breeders because it indicates the degree to which a trait can be passed on from parents to offspring [4]. Similarly, genetic progress is valued since it reveals how much improvement in a character was achieved during a single round of selection. As a result, for any successful breeding operations selection of line should be done based on some genetical traits such as genetic variance and heritability genetic advance (GA) as percent of mean (GAM). [5-7]. Each breeding effort requires knowledge of the materials' inherent variability, as well as the degree of correlation among the different traits. Rapid and more emotive genetic development can result from using indirect selection in breeding operations, and correlation analysis makes this evaluation feasible by analyzing the amount and direction of the links among features [8,9]. Breeders have been using the path analysis method to generate effective techniques for choosing

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superior genotypes of various crops, such as tomato [10], peppers, and sweet peppers [11,12]. The availability of genetic variation in the crop is vital for the effectiveness of crop enhancement programs [13]. Even so, efforts to enhance the crop have mostly been hampered by a lack of sufficient knowledge on the genetic and inherent features of the plant.

To better develop new crop varieties, it is vital to learn about and know the genetic basis of economic features. Despite the potential for significant genetic improvement of sweet pepper, the lack of access to the necessary genetic information has resulted in significant progress being made in Bangladesh. Furthermore, no hybrid types resulting from gene recombination have been created in Bangladesh. Consequently, the aim of this study to measure genetic diversity, heritability, and genetic progress to promote breeding efforts for yield improvement; and to evaluate the correlations and the direct and indirect effects of the 14 yield and yield contributing characters by path analysis.

2. MATERIALS AND METHODS

2.1. Collection of Planting Materials and Design of the Experiment

The research, which employed 21 distinct genotypes of sweet pepper, took place at the research farm of the Horticulture Department of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh, from October 2018 to April 2019. These genotypes were gathered from the World Vegetable Center (AVRDC); Horticulture Research center at BARI; England and Siddique Bazar, Dhaka. The collection sources of the genotypes are shown in Table 1. This experiment was set up using Randomized Complete Block Design, with three replications. To accommodate 10 plants, each of the 63-unit plots was 2.5 m × 1.0 m and had 50 cm × 50 cm spacing. Each block received 21 different genotypes of sweet peppers at random. Five plants were chosen at random from every regimen and marked to record different data parameters. The observations were recorded from each genotype and replication for the characters of: days to first flowering, days to first harvest, harvest duration, fruit length (FL) in mm, fruit diameter in mm, pericarp thickness in mm, number of locule per fruit, number of seed per fruit, thousand seed weight, individual fruit weight in g, fruit number per plant, yield of fruit per plant in kg, yield of fruit per plot in kg, and yield of fruit in t/ha.

2.2. Statistical Analysis

Mean performance of the observed data statistically was analyzed by "Statistix 10" tool.

Table 1: Source of collection and identity of 21 sweet pepper genotypes.

S. No.	Accession No.	Source	S. No.	Accession No.	Source
1.	SP 01	AVRDC, Taiwan	12.	SP 12	England
2.	SP 02	AVRDC, Taiwan	13.	SP 13	England
3.	SP 03	AVRDC, Taiwan	14.	SP 14	England
4.	SP 04	AVRDC, Taiwan	15.	SP 15	England
5.	SP 05	AVRDC, Taiwan	16.	SP 16	England
6.	SP 06	AVRDC, Taiwan	17.	SP 17	HRC, BARI
7.	SP 07	AVRDC, Taiwan	18.	SP 18	HRC, BARI
8.	SP 08	AVRDC, Taiwan	19.	SP 19	HRC, BARI
9.	SP 09	HRC, BARI	20.	SP 20	HRC, BARI
10.	SP 10	HRC, BARI	21.	SP 21	HRC, BARI
11.	SP 11	Siddique Bazar			

*BARI has given accession number. HRC: Horticulture Research Center

2.3. Determination of Genetic Traits

Genotypic (σ^2g) and phenotypic (σ^2p) variances, GA, and GAM were measured based on the formula provided [14]; genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV) coefficients of variance, and heritability in broad sense (h^2_b) were determined according to Burton and Devane [15] and Allard [16], respectively. GCV and PCV were classified [17,18]; h^2_b and GAM were characterized [14].

2.4. Correlation Matrix

In this study, the correlation between the features was measured both at genotypic and phenotypic level following the process stated by Singh and Chaudhury [19].

2.5. Path Coefficient

The analysis of path coefficient was analyzed following the method narrated by Dewey and Lu [20]; this method is also narrated by Singh and Chaudhury [19] in which simple correlation standard were used. The correlation coefficient in path analysis is divided into two categories: direct and indirect effects of independent features on the dependent features.

3. RESULTS AND DISCUSSION

There is enough genetic variation in the germplasm to account for all the features, and plenty of space for development exists, as shown by the range of mean, which revealed large variances within genotypes for all the attributes [Table 2]. Previous researchers had found that both bell peppers and chili peppers had sufficient genetic diversity for several of the horticultural parameters evaluated [21-24]. In a component breeding strategy, the genotype with the highest mean performance for a given character might be used as a donor to further enhance that character. Individual fruit weight ranged from 59.40 g to 242.33 g. Similarly, the fruit yield (t/ha) and FL ranged from 17.90 mm to 54.31 mm and 50 mm to 182 mm, respectively which clearly indicated the prevailing variability likely for breeding owing to utilize in further improvement and selection of superior genotype(s).

3.1. PCV and GCV

The coefficient of variation compares the corresponding levels of genetic variability. In addition, it assesses the probability of a positive advancement in selection [25]. For every character, the PCV was greater than the GCV, and the gap between these variations was little. Significant genetic variation was found for every character, with the exception of FL [Table 2]. The median of FL might significantly be affected by germplasm in case of fruit diameter of sweet pepper [26]. A smaller difference between coefficient of variation of both genotypic and phenotypic indicates that the environment has little impact (due to variation in soil fertility status or other unavoidable factors) according to [27-29]. The values of GCV ranged from 11.27% (for days to 1st flowering) to 40.95% (FL) and PCV from 12.76% to 81.95% for the same traits [Table 2]. Higher GCV values were recorded in individual fruit weight (38.05), FL (40.95), and seed number per fruit (38.05) followed by the number of fruits per plant (35.73), fruit yield per plant (31.29), per plot (31.24), yield ton per hectare (31.26), harvest duration (27.62), and fruit diameter (23.28). Higher PCV was also obtained from the same characters together with pericarp thickness. Other characters had moderate coefficient of variation in both PCV and GCV. When the PCV and GCV were large, it meant that there was a huge amount of variation to take advantage of in the breeding

Table 2: Calculation of mean-range, SE of mean, and different genetic parameters for 14 traits of sweet pepper genotypes.

Characters	Range	$(\bar{x}\,\bar{x})\pm SE$	Genetic parameters						
			σ^2g	σ^2p	GCV	PCV	h^2_b	GA	GAM
DFF	36–52	43.87±1.51	24.45	31.34	11.27	12.76	78.02	9.00	20.51
DFH	35–50	86.73±1.42	141.84	147.94	13.73	14.02	95.87	24.02	27.70
HDU	24.33–70	49.71±1.28	188.45	193.40	27.62	27.98	97.44	27.92	56.16
FL	50–182	99.53±1.42	1661.48	6652.05	40.95	81.95	24.98	41.96	42.16
FD	32.58–89	67.36±1.52	245.93	252.93	23.28	23.61	97.23	31.85	47.29
PT	3.82–8.19	6.31±0.212	1.52	1.65	19.49	20.34	91.84	2.43	38.48
LN	2–4	3.33±0.07	0.21	0.23	13.82	14.41	91.97	0.91	27.31
SNPF	24–128.98	71.40±3.08	738.29	2981.64	38.05	76.47	24.76	27.85	39.00
TSW	3.91–8.98	7.24±0.031	1.22	1.22	15.27	15.29	99.76	2.27	31.42
IFW	59.40–242.33	129.39±2.56	2423.57	2443.38	38.05	38.20	99.19	101.00	78.06
NFP	4.32–13.74	7.79±0.21	7.77	7.90	35.73	36.03	98.33	5.69	72.99
FYP	0.55–1.70	0.92±0.01	0.08	0.08	31.29	31.37	99.52	0.59	64.31
FYPP	4.66–10.62	7.36±0.08	5.30	5.32	31.24	31.31	99.55	4.73	64.21
FYTHA	17.90–54.31	29.47±0.35	84.84	85.23	31.26	31.33	99.55	18.93	64.24

DFF: Days to first flowering, DFH: Days to first harvest, HD: Harvest duration, FL: Fruit length (mm), FD: Fruit diameter (mm), PT: Pericarp thickness (mm), LN: Locule no. per Fruit, SNPF: Seed no. per fruit, TSW: Thousand seed weight (g), IFW: Individual fruit weight (g), NFP: No. of fruit per plant, FYP: Fruit yield per plant (kg), FYPP: Fruit yield per plot (kg), FYTHA: Fruit yield per ha. (ton): SE: Standard error, GVC: Genotypic coefficients of variation, PCV: Phenotypic coefficients of variation, GAM: Genetic advance as percent of mean

program by direct selection. The results again assure the judgment of researches in case of *C. annuum*, in fruit number per plant and fruit yield; in fruit weight; in fruit diameter, fruit weight and in number of fruit per plant; in FL; in fruit diameter, FL [5,21,25,30-32]. Moreover, moderate-to-low GCV and PCV estimates were observed by the traits pericarp thickness, thousand seed weight, duration of harvesting, and days to first flowering substantiating the variability in the studied genotypes.

3.2. Heritability, GA, and GAM

Heritability measures the amount of genotypic diversity in a population, and this is primarily responsible for selection's ability to alter the population's genetic make-up [33,34]. Except for FL (24.98%) and seed quantity per fruit (24.76%), the estimated values of broad sense heritability were greater than 75.00% for all variables, suggesting significant improvement is possible utilizing standard selection approaches. In general, a high level of heritability in broad sense suggested that a significant part of phenotypic variance was caused by genotypic variance and was less impacted by the environment. Hence, selection based on this trait is worthy for improvement of a crop. Expression of a character with high heritability helps the breeder in easy selection of parents keeping aside the other related traits for selection [5,18]. Researchers determined that the number of days to 50.00% blooming, FL, fruit diameter, fruit weight, and total yield in *C. annuum* had high estimates of heritability [30,35-37].

The GA as percentage was greater for all the characters [Table 1] but greater in case of single fruit weight (78.06%), fruit number per plant (72.99%), fruit yield per plant (64.31%), per plot (64.21%), and ton per hectare (64.24%), harvest duration (56.16%), fruit diameter (47.29%), and FL (42.16%). Consistent findings were found in the present study with those of yield per plant [38]; for days to 50% flowering, number of fruits per plant, fruit diameter, FL and yield/plant in chili [18]. There is a lot of opportunity for improvement in future breeding program if estimated heritability is high as well high GA [39].

Hence, the lines have sufficient genotypic variation for individual fruit weight, number of fruits/plant, yield/plot, yield (t/ha), fruit diameter, and harvest duration due to high PCV, GCV, and heritability and high GA as a percent of mean, demonstrating amplification of genes and less impact of environment on the above characteristics.

3.3. Genotypic and Phenotypic Correlation Matrix

Understanding the association between yield and its economically significant constituent is essential for breeding program. It offers the benefits of enough choices, or the ability to play many characters simultaneously in advance generations. The linking of genes or pleiotropy of genes is responsible for the correlations between pairs of characters. As a result, direct selecting for yield could not be productive. Since correlation studies aid in successful selection throughout the plant improvement program, it is important to have a strong foundation in this area [40].

The associations among different characters are presented in Tables 3 and 4. Genotypic and phenotypic correlation analyses showed that there had a strong positive correlation for fruit yield per plant with fruit yield/plot and yield (t/ha) (r = 1.00**) [41]. Number of fruits per plant also had a positive association with fruit yield. Moreover, corresponding results observed [1,40,42]. A moderate but significant correlation was observed among pericarp thickness with individual fruit weight (r = 0.515), fruit yield/plant, yield/plot, and yield (t/ha) (r = 0.633**) followed by harvest duration with the same characters (r = 0.533**) at both the level. Most of the traits were strongly linked to the number of days until the first flowering, but the number of days until the first harvest was positively (r = 0.770**) linked. Similar findings were reported by Sharma *et al.* [1]. Alternatively, substantial but negative was exhibited with harvest duration and fruit yield. This result indicated that the delay in flowering was associated with shorter harvesting duration and reduced yield/plant, yield/plot, and yield (t/ha). Both genotypic and phenotypic correlation results revealed that FL showed a negative association in most of the cases but positively correlated with seed number per fruit (r = 0.310*,

0.306*). On the other hand, fruit diameter had a positive correlation in most of the cases and this trait is thought to be one of the major contributors to yield of bell pepper as has been reported [23]. FL was negatively associated with fruit diameter (r = –0.508**) and pericarp thickness (r = –0.649), which indicated that more FL reduced fruit diameter and pericarp thickness. Thus, yield components showed multiple relationships, which can help researchers choose high-yielding genotypes. The higher magnitude of positive effects for fruit diameter, pericarp thickness, fruit yield/plant, yield/plot, and yield (t/ ha) indicated true, positive, and significant association.

Usually, the genotypic correlation coefficient's intensity was less than the equivalent values of phenotypic correlation coefficients. It also showed that the genotypic correlation coefficients were typically greater than the corresponding phenotypic correlation coefficients, showing that the characteristics were inherently associated and more desirable for breeding [Tables 3 and 4].

Similarly, for characteristics examined using chili genotypes, found that the magnitude of the genotypic correlation coefficients was often larger than the phenotypic correlation coefficients [43,44]. Again, noted intrinsic relationships between different features were demonstrated by a greater genotypic correlation coefficient than phenotypic ones in Ethiopian Capsicums [30,45]. The lack of significant variation between genotypic and phenotypic correlation [Tables 3 and 4] suggests that different types of environmental factors were not highly influential on these traits. Hence, it is exposed to select genotypes that proving better in the case of yield attributing characters as fruit yield [46-49].

3.4. Path Coefficient Analysis

Path coefficient analysis delivers the ability to categorize the overall correlations into the direct and indirect impacts of various features on yield. The path coefficients were calculated to get information for fourteen yield-contributing character connections. The direct and

Table 3: Genotypic correlation matrix of selected traits for 21 sweet pepper genotypes.

Traits	DFF	DFH	HD	FL	FD	PT	LN	SNPF	TSW	IFW	NFP	FYP	FYPP
DFH	0.770**												
HD	–0.789**	–0.874**											
FL	0.109 NS	–0.123 NS	–0.143 NS										
FD	–0.458**	–0.394**	0.489**	–0.508**									
PT	–0.700**	–0.481**	0.687**	–0.649**	0.717**								
LN	–0.262*	–0.028 NS	0.101 NS	–0.417**	0.602**	0.284*							
SNPF	0.019 NS	–0.027 NS	0.039 NS	0.310*	–0.370**	–0.240 NS	–0.233 NS						
TSW	–0.216 NS	–0.049 NS	0.064 NS	0.205 NS	–0.004 NS	–0.017 NS	0.354**	0.000 NS					
IFW	–0.550**	–0.540**	0.513**	–0.004 NS	0.800**	0.515**	0.308*	–0.151 NS	0.210 NS				
NFP	0.138 NS	0.324**	–0.209 NS	–0.015 NS	–0.670**	–0.130 NS	–0.336**	0.205 NS	0.162 NS	–0.662**			
FYP	–0.628**	–0.470**	0.541**	–0.090 NS	0.432**	0.664**	0.103 NS	–0.071 NS	0.393**	0.625**	0.118 NS		
FYPP	–0.627**	–0.471**	0.540**	–0.088 NS	0.430**	0.663**	0.099 NS	–0.070 NS	0.391**	0.624**	0.119 NS	1.000**	
FYTHA	–0.627**	–0.471**	0.541**	–0.088 NS	0.430**	0.663**	0.099 NS	–0.070 NS	0.390**	0.624**	0.119 NS	1.000**	1.000**

**and *reported at 1% and 5% level of significance respectively. NS reported non-significant. DFF: Days to 1st flowering. DFH: Days to 1st harvest, HD: Harvest duration, FL: Fruit length (mm), FD: Fruit diameter (mm), PT: Pericarp thickness (mm), LN: Locule no., SNPF: Seed no. per fruit, TSW: 1000 seed weight, IFW: Individual fruit weight (g), NFP: Number of fruit per plant, FYP: Fruit yield per plant, FYPP: Fruit yield per plot, FYTHA: Fruit yield ton per hectare

Table 4: Phenotypic correlation matrix of selected traits for 21 sweet pepper genotypes.

Traits	DFF	DFH	HD	FL	FD	PT	LN	SNPF	TSW	IFW	NFP	FYP	FYPP
DFH	0.651**												
HD	–0.698**	–0.856**											
FL	0.093 NS	–0.124 NS	–0.139 NS										
FD	–0.403**	–0.382**	0.478**	–0.501**									
PT	–0.613**	–0.438**	0.645**	–0.621**	0.665**								
LN	–0.241 NS	–0.036 NS	0.110 NS	–0.401**	0.580**	0.252*							
SNPF	0.018 NS	–0.040 NS	0.039 NS	0.306*	–0.366**	–0.236 NS	–0.207 NS						
TSW	–0.190 NS	–0.050 NS	0.065 NS	0.204 NS	–0.004 NS	–0.017 NS	0.342**	0.001 NS					
IFW	–0.489**	–0.530**	0.509**	–0.002 NS	0.787**	0.486**	0.301*	–0.148 NS	0.209 NS				
NFP	0.120 NS	0.315*	–0.207 NS	–0.015 NS	–0.657**	–0.119 NS	–0.327**	0.203 NS	0.160 NS	–0.662**			
FYP	–0.557**	–0.460**	0.533**	–0.090 NS	0.425**	0.633**	0.101 NS	–0.069 NS	0.392**	0.621**	0.122 NS		
FYPP	–0.555**	–0.460**	0.533**	–0.087 NS	0.423**	0.633**	0.096 NS	–0.068 NS	0.389**	0.620**	0.123 NS	1.000**	
FYTHA	–0.555**	–0.460**	0.533**	–0.088 NS	0.423**	0.633**	0.096 NS	–0.068 NS	0.389**	0.620**	0.123 NS	1.000**	1.000**

DFF: Days to 1st flowering, DFH: Days to 1st harvest, HD: Harvest duration, FL: Fruit length (mm), FD: Fruit diameter (mm), PT: Pericarp thickness (mm), LN: Locule no., SNPF: Seed no. per fruit, TSW: 1000 seed weight, IFW: Individual fruit weight (g), NFP: Number of fruit per plant, FYP: Fruit yield per plant, FYPP: Fruit yield per plot, FYTHA: Fruit yield ton per hectare

indirect effects at genotypic and phenotypic level of all characteristics on yield were calculated and are presented in Tables 5 and 6, respectively.

Through the path analysis, it was observed that the higher amount of direct effect on fruit yield was employed by yield per plot (1.00) following individual fruit weight (0.004), pericarp thickness (0.004), number of fruits per plant (0.002), days to first flowering (0.002), locule number (0.002), and FL (0.001) whereas fruit yield per plant (–0.012), fruit diameter (–0.004), 1000 seed weight (–0.001), seed number per fruit (–0.001), and days to first harvest (–0.001) depicted negative direct effects and also negative indirect effects days to first flowering, days to first harvest, FL, and seed number per fruit on yield though the magnitude is relatively was low. Thus, FL, fruit number per plant, and pericarp thickness could be the most important yield components of sweet pepper which could be taken into account in the selection procedure for yield improvement while the opposite results were found in yield/plant (0.00125) and fruit diameter (0.00071) at

phenotypic level. The direct consequence of fruit number per plant and FL on yield could be considered as major yield component of sweet pepper [50]. Furtehrmore, the number of fruits per plant has a direct effect on the yield of hot peppers [12]. The highly predictable factor influencing chili fruit yield was the number of fruits per plant [51]. While the direct effect of harvest duration on yield was positive, the indirect effect was amplified by fruit diameter, suggesting that the latter plays a role in the selection process for improving sweet pepper yield. FL and fruit breadth demonstrated a direct beneficial influence on fruit yield with modest magnitudes on hot chili yield [52]. Phenotypic path analysis supported additional effects comparable to those observed in genotypic path analysis [Table 6]. The analysis revealed the existence of a positive direct effect of fruit yield per plant (0.00125), number of fruits per plant (0.00085), individual fruit weight (0.00024), pericarp thickness (0.00003), FL (0.00019), fruit diameter (0.00071), etc. on fruit yield. Furthermore, supporting the significance and strong

Table 5: Estimates of genotypic immediate effects (bold and crosswise) and long-term effects (oblique) of characters in favor of other independent characters on yield of 21 sweet pepper genotypes.

Traits	DFF	DFH	HD	FL	FD	PT	LN	SNPF	TSW	IFW	NFP	FYP	FYPP	Yield
DFF	**0.002**	–0.001	0.000	0.000	0.002	–0.003	–0.001	0.000	0.000	–0.002	0.000	0.007	–0.633	–0.627
DFH	0.002	**–0.001**	0.000	0.000	0.002	–0.002	0.000	0.000	0.000	–0.002	0.001	0.006	–0.475	–0.471
HD	–0.002	0.001	**0.000**	0.000	–0.002	0.003	0.000	0.000	0.000	0.002	0.000	–0.006	0.545	0.541
FL	0.000	0.000	0.000	**0.001**	0.002	–0.002	–0.001	0.000	0.000	0.000	0.000	0.001	–0.089	–0.088
FD	–0.001	0.000	0.000	0.000	**–0.004**	0.003	0.001	0.000	0.000	0.003	–0.001	–0.005	0.434	0.430
PT	–0.002	0.000	0.000	0.000	–0.003	**0.004**	0.001	0.000	0.000	0.002	0.000	–0.008	0.669	0.663
LN	–0.001	0.000	0.000	0.000	–0.003	0.001	**0.002**	0.000	0.000	0.001	–0.001	–0.001	0.100	0.099
SNPF	0.000	0.000	0.000	0.000	0.002	–0.001	0.000	**–0.001**	0.000	–0.001	0.000	0.001	–0.071	–0.070
TSW	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	**–0.001**	0.001	0.000	–0.005	0.394	0.390
IFW	–0.001	0.000	0.000	0.000	–0.004	0.002	0.001	0.000	0.000	**0.004**	–0.001	–0.007	0.630	0.624
NFP	0.000	0.000	0.000	0.000	0.003	0.000	–0.001	0.000	0.000	–0.003	**0.002**	–0.001	0.120	0.119
FYP	–0.001	0.000	0.000	0.000	–0.002	0.003	0.000	0.000	0.000	0.003	0.000	**–0.012**	1.000	1.000
FYPP	–0.001	0.000	0.000	0.000	–0.002	0.003	0.000	0.000	0.000	0.003	0.000	–0.012	**1.000**	1.000

DFF: Days to 1st flowering, DFH: Days to 1st harvest, HD: Harvest duration, FL: Fruit length (mm), FD: Fruit diameter (mm), PT: Pericarp thickness (mm), LN: Locule no., SNPF: Seed no. per fruit, TSW: 1000 seed weight, IFW: Individual fruit weight (g), NFP: Number of fruit per plant, FYP: Fruit yield per plant, FYPP: Fruit yield per plot, FYTHA: Fruit yield ton per hectare

Table 6: Estimates of phenotypic immediate effects (bold and crosswise) and long-term effects (oblique) of characters in favor of other independent characters on yield of 21 sweet pepper genotypes.

Traits	DFF	DFH	HD	FL	FD	PT	LN	SNPF	TSW	IFW	NFP	FYP	FYPP	Yield
DFF	**0.00045**	–0.00028	–0.00008	0.00002	–0.00028	–0.00002	0.00000	0.00000	0.00002	–0.00012	0.00010	–0.00070	–0.55418	–0.555
DFH	0.00029	**–0.00043**	–0.00010	–0.00002	–0.00027	–0.00001	0.00000	0.00000	0.00000	–0.00013	0.00027	–0.00057	–0.45947	–0.460
HD	–0.00031	0.00037	**0.00011**	–0.00003	0.00034	0.00002	0.00000	0.00000	–0.00001	0.00012	–0.00018	0.00067	0.53191	0.533
FL	0.00004	0.00005	–0.00002	**0.00019**	–0.00035	–0.00002	0.00001	–0.00001	–0.00002	0.00000	–0.00001	–0.00011	–0.08732	–0.088
FD	–0.00018	0.00017	0.00005	–0.00009	**0.00071**	0.00002	–0.00001	0.00002	0.00000	0.00019	–0.00056	0.00053	0.42192	0.423
PT	–0.00028	0.00019	0.00007	–0.00012	0.00047	**0.00003**	0.00000	0.00001	0.00000	0.00012	–0.00010	0.00079	0.63138	0.633
LN	–0.00011	0.00002	0.00001	–0.00007	0.00041	0.00001	**–0.00001**	0.00001	–0.00003	0.00007	–0.00028	0.00013	0.09593	0.096
SNPF	0.00001	0.00002	0.00000	0.00006	–0.00026	–0.00001	0.00000	**–0.00005**	0.00000	–0.00004	0.00017	–0.00009	–0.06826	–0.068
TSW	–0.00009	0.00002	0.00001	0.00004	0.00000	0.00000	0.00000	0.00000	**–0.00009**	0.00005	0.00014	0.00049	0.38870	0.389
IFW	–0.00022	0.00023	0.00006	0.00000	0.00056	0.00001	0.00000	0.00001	–0.00002	**0.00024**	–0.00056	0.00078	0.61851	0.620
NFP	0.00005	–0.00014	–0.00002	0.00000	–0.00046	0.00000	0.00000	–0.00001	–0.00001	–0.00016	**0.00085**	0.00015	0.12259	0.123
FYP	–0.00025	0.00020	0.00006	–0.00002	0.00030	0.00002	0.00000	0.00000	–0.00004	0.00015	0.00010	**0.00125**	0.99817	1.000
FYPL	–0.00025	0.00020	0.00006	–0.00002	0.00030	0.00002	0.00000	0.00000	–0.00004	0.00015	0.00010	0.00125	**0.99822**	1.000

DFF: Days to 1st flowering, DFH: Days to 1st harvest, HD: Harvest duration, FL: Fruit length (mm), FD: Fruit diameter (mm), PT: Pericarp thickness (mm), LN: Locule no., SNPF: Seed no. per fruit, TSW: 1000 seed weight, IFW: Individual fruit weight (g), NFP: Number of fruit per plant, FYP: Fruit yield per plant, FYPP: Fruit yield per plot, FYTHA: Fruit yield ton per hectare

connection of characteristics to increase yield or to utilize as selection indicators was the degree of genotypic direct effects produced by these yield component characters being considerably larger than their corresponding phenotypic impacts. The outcome also showed that attributes such as seeds per fruit, 1000 seed weight, and fruit width had negative consequences both directly and indirectly through other characters, which could have led to the conclusion that these traits could not be employed to increase sweet pepper output. The positive significant association of fruit number per plant, fruit weight, length, and diameter with yield in pepper [25]. The results were in conformity with the research findings in *C. annuum* [11,31,37]. According to a path coefficient study, selecting for FL, fruit weight, and fruit per plant will increase sweet pepper productivity overall.

4. CONCLUSION

The results from this study exhibited that the significant variability among all the genetic parameters such as genotypic and phenotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2_b), and GAM based on yield and yield contributing parameters, with a few notable exceptions (FL and seed no. per fruit) indicating effective exploitation by direct selection. In addition, it was found that the traits that contributed to yield had a strong positive correlation ($r = 1.00^{**}$) and greater genotypic (1.00) direct impacts than their phenotypic effects. Moreover, it can be said that using the appropriate genotypes in future breeding programs, there is sufficient scope for developing variety(s).

5. ACKNOWLEDGMENT

6. AUTHORS' CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agreed to be accountable for all aspects of the work. All the authors are eligible to be an author as per the International Committee of Medical Journal Editors (ICMJE) requirements/guidelines.

7. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

8. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

9. DATA AVAILABILITY

All generated and analyzed data are included in this research paper.

10. PUBLISHER'S NOTE

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