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Variability and association analysis of recombinant inbred lines (RILs) of monoecious x hermaphrodite ridge gourd [*Luffa acutangula* (L) Roxb]

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Abstract
Higher yield with required fruit size and quality are important traits defining the commercial importance of ridge gourd. Hermaphroditism is a crucial trait which serves as a source for developing gynoecious lines through breeding programmes. Thirty recombinant inbred lines (RILs) were selected for study which was derived from a cross between Arka Sujeet (monoecious) x Kasi Kushi (hermaphrodite).The objective of this study was to characterize the selected RILs for genetic diversity and to explore the association among the traits investigated. Characters under study includes node at which first female flower appear, days to first harvest, number of fruits per plant, fruit weight, fruit length, fruit girth, vine length and yield per plant. Analysis of variance was found significant among the population for all the characters. Results revealed that populations show higher heritability and genetic advance as percentage of mean in all the traits except number of fruits per plant. Correlation analysis showed that highest significant and positive correlation with yield trait was observed in number of fruits per plant (0.4010** and 0.2277**) followed by vine length (0.2599** and 0.2279**) and fruit weight (0.2297** and 0.2016**). From the Path analysis high direct and positive effect for yield was observed in number of fruits per plant (0.4858) followed by fruit girth (0.0692), vine length (0.0688) and fruit weight (0.0682). Hence such characters can be given more importance for enhancing the yield.

Keywords: Ridge gourd, RILs, heritability, genetic advance, association analysis

1. Introduction

Ridge gourd [*Luffa acutangula* (L) Roxb] is an indispensable crop among Cucurbitaceae family of vegetable crops. The medicinal and nutritive values of the crop make its value more intrinsic. The alleviative properties of ridge gourd are myriad. From the presence of antioxidant properties, dietary fibre content, vitamin A, vitamin C, vitamin B6, iron, magnesium and hypoglycemic nature it is evident that ridge gourd is an nutrient opulent crop. A glycoprotein was isolated from seeds of *L. acutangula*, which was found to be immunologically distinct from abortifacient proteins isolated from other members of the Cucurbitaceae family (Yeung *et al.* 1991) [27]. The luffaculin, a protein isolated from its seed, exhibited abortifacient, antitumor, ribosome inactivating and immunomodulatory activities (Ng *et al.* 1992) [18]. Another ribosome inactivating peptide isolated from seeds of ridge gourd designated luffangulin inhibited cell-free translation (Wang and Ng, 2002) [26]. Despite of its nutritive value, ridge gourd possess diversity in various aspects including morphological characters like fruit size and shape and sex forms. Knowledge of genetic diversity among existing cultivars of any crop is essential for long-term success in breeding program and to maximize the exploitation of the germplasm resources. Higher yield is the most pivotal character looking for, which in turn is a complex character which relies on many other traits involved. Several studies aids in untangling this complexity that leads to find plants with better performances. Genetic variation studies and Correlation analysis are one among them. Correlation analysis measures the degree of relationship between the variables that discloses the direct and indirect effects on major trait. For a successful planning of breeding improvement program, the analysis of variability among the traits and their association of a particular character in relation to yield and yield attributing traits would be greater importance (Methela *et al.* 2019 in ridge gourd; Ananthan and Krishnamoorthy, 2017 in ridge gourd) [15, 11].

There is a wide variability of sex forms in ridge gourd *viz.,* monoecious, andromonoecious, hermaphrodite and gynoecious. Hermaphrodite plants are important underutilized crop which is not yet commercialized. They bear in clusters unlike monoecious crop. Hermaphrodite plants play an important role in enhancing the antioxidant property of the vegetables.

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It is also evident that yield per plant was recorded higher in "monoecious x hermaphrodite" hybrids than "monoecious x monoecious" hybrids and "hermaphrodite x hermaphrodite" hybrids. Higher yield is due to the parental divergence for sex expression and fruiting habit (Pradip Karmakar *et al.* 2013) [10]. Studies have to be emphasized to explore the advantages of hermaphrodite ridge gourds into breeding program. Development of recombinant inbred lines is one such breeding programme which can be used as a tool to produce inbreds having commercial value. They are group of strains obtained from parental crosses which produces recombinants later inbred to produce isogenicity which will be a source for trait mapping and analysis. Such lines were developed and subjected for following study. The goal of this study was to characterize the selected RIL population for genetic variability and to infer the association of traits among the population.

2. Materials and methods
Thirty recombinant lines representing F_7 generation were used as experimental materials along with their parents. The population were derived from a cross between monoecious and hermaphrodite ridge gourd. Monoecious female parent used was Arka Sujeet developed from Indian Institute of Horticultural Research, Bangalore. On the other hand, hermaphrodite male parent used was Kasi Kushi developed from Indian Institute of Vegetable Research, Varanasi. Five plants were selected from each lines and were subjected to study. Experiment was conducted during kharif season of 2020 at Department of Horticulture College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. Seeds were sown in main field following randomized block design (RBD) with 3 replications in a spacing of 1.5 x 1.5 m. Characters recorded were node at which first female flower appear, days to first harvest, number of fruits per plant, fruit weight, fruit length, fruit girth, vine length and yield per plant.

2.1 Statistical analysis
The analysis of variance was performed as suggested by Panse and Sukhatme (1957). The 'F' calculated values were collated with the 'F' table value at 1% level of significance. Characters which possess significant differences among the genotypes were utilized for further analysis. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variations (GCV) were calculated according to formula given by Burton (1952) [3]. The magnitude of PCV and GCV were compared against the category suggested by Sivasubramanian and Menon (1973) [24]. PCV and GCV are recorded high (when the values ranges above 20%); moderate (10-20%) and low (<10%).
Heritability in narrow sense (h^2) was calculated as per procedures of Burton and Devane (1953) [4]. Heritability range obtained was compared with the category of low (0-30%); moderate (30-60%) and high (>60%) respectively.
Heritability is the variation due to genetic values (V_G) in the total variability or phenotypic variability (V_P). On the other side, narrow-sense heritability, $h^2 = V_A/V_P$, defines the total variability caused only due to additive genetic values (V_A).
Genetic advance was also estimated. The categories of genetic advance as percent of mean (GAM) were low (0-10%); moderate (10-20%) and high (20%) as suggested by Johnson *et al. (*1955) [8]. Genetic advance is the genotypic mean difference value between parental population and the selected

population. It measures the genetic gain of the selected population over the parental population which depends on magnitude of genetic variability of parental population, heritability of the character and selection intensity. It is estimated using the formula:

$$G.A. = \frac{\sigma^2 g}{\sigma^2 p}.K.\sigma p$$
$$= h^2.K.\sigma p \tag{1}$$

Where
K = Selection differential
h^2 = Heritability
When it is expressed as percentage of mean,

$$G.A.\,(\%) = \frac{\text{Genetic adavance}}{\overline{X}} \times 100 \tag{2}$$

The population was subjected to association studies which includes Correlation and path coefficient analysis. Correlation coefficient is a tool used to measure the degree and direction of relationship between two or more variables and it is denoted by '*r*'. Two variables are said to be related positive *i.e.,* increase in value of one variable increases the value of the other in same direction, when the correlation coefficient (r) is positive. When the correlation coefficient is negative, the variables are said to be negatively correlated. In such cases increase in one variable decreases the value of other variable.
Path coefficient analysis is the measure of direct and indirect effects of various independent variables over a dependent variable. It can be interpreted according to the classifications suggested by Lenka and Mishra (1973):
0.00-0.09 = Negligible effect
0.10-0.19 = Low effect
0.20-0.29 = Moderate effect
0.30-1.00 = High effect
>1.00 = Very high effect
Analysis was carried out in SPSS Software.

3. Results and discussion
Thirty RIL's along with their parents were evaluated for genetic variability which includes PCV, GCV, heritability and GAM. Results of analysis of variance were provided in Table 1. It is evident that all traits under study exhibit significant differences among genotypes at 1% level of significance. Highest level of variation was observed for fruit weight (30986.5378) followed by vine length (17736.0734), number of fruits per plant (380.6154), fruit length (192.7574), days to first harvest (176.2405), yield per plant (27.8086), fruit girth (10.9589) and node at which first female flower appear (3.4077).
The mean values of all the traits and their corresponding PCV, GCV, narrow sense heritability (h^2) and GAM are provided in Table 2. The magnitude of GCV ranged from 12.28 to 55.85. Highest GCV was observed for fruit weight (55.85) followed by fruit length (38.29) and yield per plant (24.99). Moderate GCV was observed for traits like number of fruits per plant (15.83), days to first harvest (15.66), node at which first female flower appear (13.63), vine length (13.32), and fruit girth (12.28). On the other hand PCV ranges from 12.85 to 58.19. Highest PCV was observed for fruit

weight (58.19), fruit length (39.61), number of fruits per plant (30.02) and yield per plant (27.37). Days to first harvest contributed a PCV range of 18.29, vine length with 13.88, node at which first female flower appear with 14.85, and fruit girth (12.85) possess moderate range of PCV. The values of phenotypic coefficient of variation (PCV) were slightly greater than the genotypic coefficient of variation (GCV). Hence it implies that there exists negligible role of environment over the expression of all the traits under study.

From the results, it is shown that characters like fruit weight, fruit length, number of fruits per plant and yield per plant have broader genetic base as they possess high magnitude of GCV and PCV. So they are most likely to be suitable for improvement through selection process. Estimates of GCV and PCV alone are not sufficient to obtain a conclusion regarding inheritability of the character. Therefore, the decision can be relied upon the extent of heritability of a trait.

Heritability (narrow sense) is the ratio of genotypic variance to the phenotypic variance. It estimates the magnitude of additive gene action upon the total variance. Similarly, heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (Johnson et al. 1955) [8]. Therefore the estimates of heritability combined with genetic advance as percentage of mean finds the nature of gene action in a particular trait and help breeders to select better breeding programme to improve the trait under study.

Magnitude of heritability ranges from 27.80% to 93.44%. Highest heritability was recorded for fruit length (93.44%)

followed by vine length (92.12%), fruit weight (92.08%), fruit girth (91.35%), node at which first female flower appear (84.21%), yield per plant (83.39%) and days to first harvest (73.31%). Low heritability was noticed in number of fruits per plant (27.08%) (Table2).

Genetic advance as the percentage of mean estimated for different characters was provided in Table 2. The values ranged from 17.20% to 110.39%. Number of fruits per plant (17.20%) recorded lowest GAM. Higher magnitudes of GAM were recorded for fruit weight (110.39%) followed by fruit length (76.25%), yield per plant (47.03%), days to first harvest (27.63%), vine length (26.33%), node at which first female flower appear (25.76%) and fruit girth (24.18%). These traits showed maximum GAM (>20%) as suggested by Johnson et al. (1955) [8]. This result was in accordance with Arunkumar et al. (2012) [2] in cucumber and Jat et al. (2014) [7] in kakri.

Characters like fruit weight, fruit length, yield per plant, days to first harvest, vine length, node at which first female flower appeared and fruit girth showed higher heritability accompanied with higher genetic advance as percentage of mean. Hence it is evident that heritability in these traits is due to additive gene action and hence in such characters, selection can be used as an effective breeding tool for improvement. Number of fruits per plant exhibited low heritability with low genetic advance as percentage of mean. Therefore, this trait is considered as highly environmental influenced and selection based on this trait will not be effective.

Table 1: Analysis of variance with respect to mean sum of squares (MSS) for yield characters in ridge gourd

S. No	Characters	Sources of variation		
		Replications	Treatments	Error
	Degrees of freedom (df)	2	31	62
1	Days to first harvest	3.9054	176.2405**	19.0671
2	Number of fruits per plant	53.3541	380.6154**	176.5693
3	Fruit weight (g)	454.9877	30986.5378**	863.5731
4	Fruit length (cm)	1.7951	192.7574**	4.4101
5	Fruit girth (cm)	0.4929	10.9589**	0.3352
6	Node at which first female flower appear	0.7217	3.4077**	0.2005
7	Vine length (cm)	2727.3492	17736.0734**	491.9260
8	Yield per plant (cm)	5.2707	27.8086**	1.7303

*,**- Significant at 5% and 1% level of significance

Table 2: Mean values of the populations and their corresponding phenotypic and genotypic coefficient of variability, heritability and genetic advance as percentage of mean

	DFH	NFP	FW	FL	FG	NFFA	VL	YP
Female	57.27	20.10	285.27	30.77	18.47	8.33	616.33	7.30
Male	56.93	46.43	38.36	16.86	14.53	6.33	598.57	16.33
1	38.47	69.03	327.73	16.07	14.13	7.17	645.99	12.23
2	37.47	66.17	264.13	14.47	15.00	6.13	643.54	11.17
3	46.93	57.83	270.80	16.33	17.80	7.30	607.77	10.03
4	46.37	71.33	198.03	17.80	16.90	7.40	618.36	12.13
5	47.17	70.03	250.73	20.03	17.33	6.10	619.45	12.87
6	49.93	35.27	101.07	9.63	13.47	9.07	505.11	7.63
7	53.23	46.87	142.27	14.53	14.90	8.70	465.83	9.63
8	58.13	37.43	94.20	15.20	15.23	9.10	437.16	9.87
9	57.90	33.60	67.50	9.63	12.83	8.83	431.41	5.97
10	60.27	38.03	53.53	9.70	13.07	8.33	457.23	8.23
11	35.00	69.67	37.33	31.07	14.07	5.90	480.31	7.40
12	36.00	54.33	62.33	32.73	16.17	7.10	560.08	13.90
13	42.67	57.33	68.33	28.33	13.17	6.13	628.41	9.30
14	45.67	57.00	226.67	35.33	18.20	8.13	589.77	10.13
15	57.67	58.33	284.00	25.83	14.90	8.57	499.10	17.67
16	54.67	48.67	308.33	30.13	18.20	7.20	539.33	7.73

17	46.33	53.33	98.33	30.03	12.17	8.93	620.54	12.03
18	50.67	57.00	85.33	36.30	15.07	7.50	641.63	11.87
19	44.00	59.00	227.00	19.47	13.93	8.80	652.14	10.73
20	36.67	53.00	286.00	15.13	18.10	6.43	590.73	15.60
21	40.00	53.33	196.33	14.90	14.90	6.87	469.44	13.57
22	45.67	53.00	235.33	24.63	14.27	7.93	443.97	14.93
23	43.33	53.67	264.33	11.93	16.90	8.83	665.20	15.73
24	34.67	52.33	294.33	28.77	18.00	7.17	608.53	11.90
25	43.33	44.67	63.33	11.20	12.70	9.03	468.97	12.57
26	47.00	51.00	87.33	20.37	15.73	6.97	653.83	10.93
27	47.33	51.67	43.33	16.57	17.73	8.63	565.53	14.87
28	37.00	48.00	315.67	17.77	13.03	6.10	612.80	15.90
29	39.00	46.33	163.33	15.67	15.10	6.53	624.67	15.50
30	42.00	53.00	301.00	24.93	14.23	7.20	653.13	11.77
GMean	46.21	52.08	179.42	20.69	15.32	7.59	569.21	11.79
F ratio	9.24	2.16	35.88	43.71	32.69	16.99	36.05	16.07
PV	71.46	244.58	10904.56	67.19	3.87	1.27	6239.98	10.42
GV	52.39	68.01	10040.99	62.78	3.54	1.07	5748.05	8.69
PCV	18.29	30.02	58.19	39.61	12.85	14.85	13.88	27.37
GCV	15.66	15.83	55.85	38.29	12.28	13.63	13.32	24.99
h^2	73.31	27.80	92.08	93.44	91.35	84.21	92.12	83.39
GA	12.77	8.96	198.08	15.78	3.70	1.95	149.89	5.55
GAM	27.63	17.20	110.39	76.25	24.18	25.76	26.33	47.03
S. E	2.52	7.67	16.97	1.21	0.33	0.26	12.81	0.76
C.D. (5%)	7.06	21.48	47.51	3.39	0.94	0.72	35.86	2.13
CV (5%)	9.45	25.51	16.38	10.15	3.78	5.90	3.89	11.15

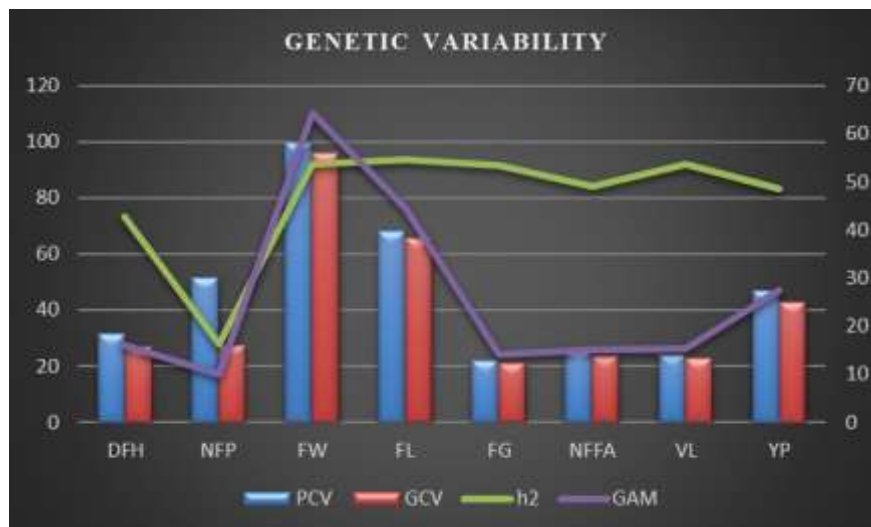|	
DFH- Days to first harvest	FG- Fruit girth (cm)
NFP- Number of fruits per plant	NFFA- Node at which first female flower appear
FW- Fruit weight (g)	VL-Vine length (cm)
FL- Fruit length (cm)	YP- Yield per plant (kg)

Fig 1: Graph representing the PCV, GCV, heritability (h^2), genetic advance as percentage of mean (GAM) for eight quantitative traits

3.1 Association analysis

Correlation coefficient is a tool which is used to find out the degree and direction of relationship between two or more variables. In plant breeding, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. On the other hand, Path coefficient analysis measures the direct and indirect contribution of various independent characters on a dependent character. According to the results obtained from Table 3 and 4, following discussions have been made.

Positive and significant correlation is observed between days to first harvest and node at which first female flower appear at both genotypic and phenotypic level (0.5838 and 0.4576). There is a significant and negative correlation observed for days to first harvest with number of fruits per plant (-0.8208 and -0.3223), fruit weight (-0.2756 and -0.2154), vine length (-0.4228 and -0.3401) and yield per plant (-0.3343 and -0.2689). It was evident that there exists no correlation between days to first harvest with fruit length and fruit girth. Number of fruits per plant is significantly and positively correlated with fruit weight (0.3118) at genotypic level, fruit length (0.2945) at genotypic level, vine length (0.5219 and 0.2612) and yield per plant (0.4010 and 0.2277). It is significantly and negatively correlated with node at which first female flower appear at both genotypic and phenotypic level (-0.6387 and -0.3693). Similar results of positive correlation with yield were observed for fruit size and number of fruit with fruit yield by Rakesh and Todd (2011) in watermelon. Number of fruits per plant has no correlation

with fruit girth.

Likewise, significant and positive correlation for fruit weight was observed with fruit girth (0.4305 and 0.4040), vine length (0.3843 and 0.3707) and yield per plant (0.2297 and 0.2016). Similar findings were observed for fruit weight by Shah and Kale (2002) [23] in ridge gourd.

Fruit length shows positive correlation with fruit girth (0.2723 and 0.2533) at both genotypic level and phenotypic level and vine length (0.2681 and 0.2415). It has no correlation with yield per plant. Fruit length had significant negative correlation with node at which first female flower appear (-0.2135). Correlation of fruit girth with fruit weight (0.4305 and 0.4040), fruit length (0.2723 and 0.2533) and vine length (0.2926 and 0.2803) was found positive and significant. It has no correlation with days to first harvest, node at which first female flower appear, number of fruits per plant and yield per plant.

Significant and positive correlation was recorded for node at which first female flower appears with days to first harvest (0.5838 and 0.4576). It is negatively correlated with other traits like number of fruits per plant (-0.6387 and -0.3693), fruit length (-0.2135) and yield per plant (-0.2157).

Vine length has significant and positive correlation with number of fruits per plant (0.5219 and 0.2612), fruit weight (0.3843 and 0.3707), fruit length (0.2681 and 0.2415), fruit girth (0.2926 and 0.2803), yield per plant (0.2599 and 0.2279). It was negatively correlated with days to first harvest (-0.4228 and -0.3401) and node at which first female flower appear (-0.3969 and -0.3516). Significant and positive correlation for yield per plant was observed with traits like number of fruits per plant (0.4010 and 0.2277), fruit weight (0.2297 and 0.2016) and vine length (0.2599 and 0.2279). Similar finding was also observed by Kumar et al (2013) [13] in sponge gourd. Fruit weight showed significant positive correlation with yield at genotypic level (0.2297). Node at which first female flower appears (-0.2157) and days to first harvest (-0.3343 and -0.2689) showed significant negative correlation with the yield trait.

Table 3: Correlation among eight characters in the population

		DFH	NFFP	FW	FL	FG	NFFA	VL	YP
DFH	G	1.00	-0.8208**	-0.2756**	-0.1405^{NS}	-0.0531	0.5838**	-0.4228**	-0.3343**
	P	1.00	-0.3223**	-0.2154*	-0.1205	-0.0166	0.4576**	-0.3401**	-0.2689**
NFP	G		1.00	0.3118**	0.2945**	0.0984	-0.6387**	0.5219**	0.4010**
	P		1.00	0.1433	0.1498	0.0880	-0.3693**	0.2612*	0.2277*
FW	G			1.00	0.0882	0.4305**	-0.1965	0.3843**	0.2297*
	P			1.00	0.0753	0.4040**	-0.1769	0.3707**	0.2016*
FL	G				1.00	0.2723**	-0.2135*	0.2681**	-0.0712
	P				1.00	0.2533*	-0.1975	0.2415*	-0.0629
FG	G					1.00	-0.1378	0.2926**	0.0901
	P					1.00	-0.1398	0.2803**	0.0544
NFFA	G						1.00	-0.3969**	-0.2157*
	P						1.00	-0.3516**	-0.1774
VL	G							1.00	0.2599*
	P							1.00	0.2279*
YP	G								1.00
	P								1.00

**. Correlation is significant at the 0.01 level.

*.Correlation is significant at the 0.05 level.

From the results of table 4 it was evident that, positive and direct effect on yield was observed in characters like number of fruits per plant (0.4858), fruit weight (0.0682), fruit girth (0.0692), and vine length (0.0866). Similar findings were observed by Karthick et al. (2019) in cucumber. Direct negative effect was observed in days to first harvest (-0.040), node at which first female flower appear (0.0697) and fruit length (-0.2367). Days to first harvest has positive indirect effect with fruit length (0.0333) and node at which first female flower appear (0.0407). Number of fruits per plant had very high positive direct effect with yield (0.4858). It was also indirectly and positively correlated through fruit weight (0.0213), fruit girth (0.0068), vine length (0.0359) and yield per plant (0.4010) respectively.

Fruit weight had direct positive effect with yield but it was positively indirectly correlated through number of fruits per plant (0.1515), fruit girth (0.0298), and vine length (0.0264). Fruit length has positive direct effect with yield accompanied with positive indirect effect with number of fruits per plant (0.1431), fruit weight (0.0060), fruit girth (0.0188) and vine length (0.0184). Fruit girth though it possess direct positive effect with yield (0.0692) and it had positive indirect effect with yield through number of fruits per plant (0.0478), fruit weight (0.0294) and vine length (0.0201).

Node at which first female flower appear has positive indirect effect with days to first harvest (0.0245) and fruit length (0.0505). it had negative indirect effect through number of fruits per plant (-0.3103), fruit weight (-0.0134), fruit girth (-0.0095) and vine length (-0.0273).Vine length has positive indirect effects with traits like number of fruits per plant, fruit weight and fruit girth. Similar results were also reported by Mehta et al. (2009) [14] in muskmelon.

From the results of path coefficient analysis it is concluded that number of fruits per plant possesses higher positive direct effect with the yield followed by other traits like, fruit girth, vine length and fruit weight. Hence these traits can be given more importance for direct selection in the process of enhancing the yield of the crop.

Table 4: Path coefficient analysis for direct and indirect effects of population for yield and its related attribute

	DFH	NFP	FW	FL	FG	NFFA	VL	YP
DFH	-0.0420	-0.3987	-0.0188	0.0333	-0.0037	0.0407	-0.0291	-0.3343
NFP	-0.0344	0.4858	0.0213	-0.0697	0.0068	-0.0445	0.0359	0.4010
FW	-0.0116	0.1515	0.0682	-0.0209	0.0298	-0.0137	0.0264	0.2297
FL	-0.0059	0.1431	0.0060	-0.2367	0.0188	-0.0149	0.0184	-0.0712
FG	-0.0022	0.0478	0.0294	-0.0645	0.0692	-0.0096	0.0201	0.0901
NFFA	0.0245	-0.3103	-0.0134	0.0505	-0.0095	-0.0697	-0.0273	-0.2157
VL	-0.0177	0.2535	0.0262	-0.0635	0.0202	-0.0277	0.0688	0.2599

Residue= 0.1018

4. Conclusions

From the results of the analysis, it is concluded that there is a significant variability among the population (RILs and the parents). Out of eight characters studied, higher magnitude of GCV and PCV were observed for fruit weight, fruit length, number of fruits per plant and yield per plant. Minimal difference between the phenotypic and genotypic coefficient of variation concludes that there is a less influence of environment over the expression of the traits. Hence such characters can be given mere importance during crop improvement programmes. Since all the characters except number of fruits per plant showed higher heritability (narrow sense) accompanied with high genetic advance as percentage of mean, the traits are highly amenable for selection as the heritability occurring in traits is due to the additive gene action. Analysis of Correlation coefficient shows that positive and significant correlation of dependent variable (yield) was observed for number of fruits per plant, fruit weight and vine length. Likewise, fruit length, number of fruits per plant and vine length possess direct and positive effect with yield per plant is confirmed with the results of path analysis. Hence such characters can be considered during breeding programmes for better enhancement of crop yield.

5. References

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