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Variability, character association and path analysis for *Annona* yield and quality attributes

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Abstract

The knowledge of genetic variability among the genotypes for yield and quality attributes is the utmost requirement for any crop improvement work. The eighteen *Annona* genotypes of two species were studied for five leaves and fruit morphological attributes and twenty-nine components related to growth, yield and fruit quality. The experiment was arranged in a randomized block design in two replicates. A vast variability among the genotypes was revealed as seen based on the significant difference from ANOVA for all the quantitative traits. For morphological traits, genotypes showed variations for leaf shape, base and apex also for fruit shape and segmentation. The high magnitude of heritability and genetic advance as per cent mean was noted for most of the traits indicated presence of fixable genes and least influence of environment for inheritance. The results of the association analysis presented significant and positive association of fruit yield with growth and fruit morphology and fruit quality attributes at both genotypic and phenotypic levels. A strong influence of fruit traits and fruit quality related traits on yield observed owing to their positive and significant direct effects. The pulp/seed ratio, fruit weight, fruit per plant, total soluble solids, sugar content could be emphasize to discriminate the various *Annona* genotypes so as to utilize them for future hybridization programme to generate desirable genotypes for yield and quality.

Keywords *Annona*, character association, fruit quality, genetic variability, path analysis

Introduction

Fruits are the integral part of the human diet since long and their potential benefits on health are well-known. Owing to this, the consumption of fruits by human for nutrition has gained its importance now a day. The concentrations of various nutrients and chemicals compositions are important before deciding the fruits for consumption purpose [1]. *Annona* genus is member of *Annonaceace* family which is mostly known for its edible fruits. *Annona* being the family of primitive angiospermic plants of plantae kingdom, magnoliphyta division, magnoliopsida class [2]. *Annona squamosa* L. is cross pollinated crop with diploid chromosome number of 2n=14 and 16 whereas, *A. glabra* L., which act as tetraploid in nature (2n=28) [3-4]. *A. squamosa* L. generally referred as sugar apple, sweetsop or custard apple considered as key arid fruit crop in India [5]. *A. atemoya* Mabb, is a hybrid between

A. squamosa L. and *A. cherimola* Mill. having large and uneven to round fruits with better quality and possess few seeds [6]. The fruits of sugar apple appeared round to heart shape, tuberculate skin, sweet and low fibrous pulp with pleasant flavour and rich in protein, carbohydrate, minerals, fiber, fat, iron, calcium, phosphorus, Vitamin-C, thiamine and riboflavin [7]. The fresh fruits are used for preparing dried pulp powder as an ingredient of fermented liquors, drinks and ice-creams. The leaves and bark of stem possess selective acetogenins which is cytotoxic activity and potentially use for cancer treatment [8]. The individuals of the *Annona* species are severely affected by climate change [9]. The restriction of the broad spread growing area affects the heterozygosity of the population, resulting in a decline in population diversity. The genetic erosion due to inbreeding and genetic drift mainly resulted in endangerment of little isolated populations. The populations obtained from such single homozygous or heterozygous individuals has been narrow downed the genetic base of the population generated. Narrowing of the genetic diversity may result the absolute loss of the crop plants and affect the future crop improvement programme [10]. Looking to the global climate change, germplasm collection and evaluation emerged as one of the best tactics to reduce the genetic erosion of the *Annona* genotypes. This would help to discover the phenological divergence exists in accessions.

The breeding of *Annona* genotypes is important for its precocity of bearing, higher in flower to fruit set, better shelf life, symmetrical shape and yield. The important objectives of *Annona* are, prefer fruits without carpel projections, hold out bruising in transportation and other characters includes attractive skin colour, low number of seeds, pulp to seed ratio and sugar acid blend with good flavour [11]. Fruit ripening leads to reduction in fruit acids and the sugar content increases [12]. Total soluble solids include various soluble solids that are available in fruits. Apart from these solids, various organic acids and their quantity show a vital role in fruit flavour, sugar in osmotic adjustment and protection against stresses and determine the pulp sweetness [13]. These characteristics aid scientists to isolate the desirable genotypes for used in genetic enhancement. Several environmental and physiological factors correlated to the susceptibility to biotic stress, poor shelf life and quality attributes that are controlled by genes. The phenol content in fruit influenced by the geographical area, genotypic diversity, harvest and storage period and extraction techniques [14]. Compare to fruits of pomegranates and mango genotypes, Sri Lanka an *A. muricata* fruit showed low content of total phenol. The phenological and nutritional quality attributes changes with environmental variations and stages of fruit development for fruit length, fruit weight, total soluble sugar and acidity [15].

The value of genetic variability observe in population affects the genetic improvement and provides the basis for selection. Yet few efforts had been made to understand the genetic diversity of the *Annona* genotypes [16]. The study of genetic parameters related to fruit quality and yield attributing are major concern to any scientist working for genetic improvement of the crop [17]. The associations of various traits help us to understand the relationship of various traits. Very few reports are available for association of fruit quality attributes such as sugar, acid and phenol content of fruit and field observations it's yielding potential [18]. Usually, the association studies among quantitative traits are of great importance to breeders to separate elite traits for practicing selections.

The genetic, environmental and management practices before and after harvest influence the concentration of bioactive compounds of the fruits [19]. The information of direct and indirect effect of various traits on fruit yield would be utilized to isolate desirable genotypes from the diverse populations [16]. The current study also presents the proximate analysis of the various fruit related biochemical attributes and their association with the fruit yield which could be utilized for fruit quality enrichment. The improvement in trait can be made through direct selection are estimated by the availability of heritable variation. Selection which has been regarded as a powerful tool to improve a certain trait and the genetic gain is highly influenced by heritability of the trait [20]. The knowledge of only heritability does not imply to formulate the futuristic breeding strategies. Here, genetic advance with heritability help to decide the genetic control of the trait. Owing to these situations, the present research work was designed to understand the genetic divergence in various qualitative and numerical traits of *Annona* genotypes to improve yield and quality simultaneously by determining variance component, heritability, genetic advance, association studies and effects of independent traits on yield.

Methodology

The experiment material was comprised of eighteen *Annona* genotypes namely Selection-1 to 15, Sindhan, Mammoth and Washington being *A. squamosa* L. and Island Gem belonging to *A. atemoya* Mabb. The genotypes were evaluated in randomized block design with two replications during *kharif* 2020 at Agroforestry Research Station, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India. The observations were recorded for five leaf and fruit morphological traits namely, leaf shape, lead base, leaf apex, fruit shape and skin segmentation. Apart from this, twenty-nine quantitative characters *viz*., plant height (m), plant spread (N-S) & (E-W) (m), flower size (cm), leaf length & breadth (cm), petiole length (cm), fruit length & width (mm), fruit diameter (cm), pulp, rind and seed weight (g), pulp & seed per cent, pulp/seed ratio, core length (cm), number of seed per fruit, fruit weight (g), number of fruit per plant, total soluble sugar (˚B), titrable acidity (%), TSS/TA ratio, reducing sugar, non-reducing sugar & total sugar per cent, ascorbic acid (mg/100g), phenol content (%) and fruit yield per plant (kg) were studied. Ten fruits per replication were taken for measuring the fruit quality attributes and average was worked out. Vegetative traits were measured at the end of fruiting season. Mean values of various traits taken for each genotype in all replications was utilized for statistical analysis for all the traits under study. The statistical method analysis was performed using software R programme as per the procedure explained by Popat et al., [21]. The corrlogram analysis was performed using Rstudio software [22]. The relative difference (RD) between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), was estimated by RD = (PCV − GCV/PCV) × 100.

Results and Discussion

The observations on various leaf morphology revealed that the genotype, Mammoth noted with lanceolate leaf shape, obtuse leaf base and acuminate leaf apex, Washington and Island Gem had elliptic leaf shape and rounded leaf base and apex. While, remaining showed ovate type of leaf, acute leaf base and apex. For fruit morphology, all the genotypes depicted cordate fruit shape except Island Gem (irregular shape) and Selection-7 and Selection-10 (rounded fruit shape). Among all the genotypes, only Island Gem reported smooth segmentation of the surface while remaining showed overlapping type. From the foregoing results it can be concluded that the leaf and fruit morphological traits showed wide range of variations. This might be due to influencing gene expression and genetic background of the genotypes.

The sugars and organic acid content in fruits would be expected to account for sweetness variations at least. The quantification of sugar and organic acid contents might be standard indices for evaluating flavour quality in fruit and vegetables [23]. Identification of such indices based on quality traits might be good scopes for the breeders need to isolate the genotypes for good flavour in *Annona*. The present study showed a wide range of variation for total sugars (17.79-23.70%), Titrable acidity (0.18 to 0.80%) and ascorbic acid (27.55-43.10 mg/100g) content. Similarly, TSS/TA ratio often used as a measure of sweetness of the fruit which being maximum of 153.09. The phenol content of the fruit has a wide range of 0.18 to 0.36 per cent among the accessions studied. The mean fruit yield varies from 2.75 to 33.30 kg with a mean of 17.27 kg. The genotype, Selection-9 recorded highest fruit yield per plant of 33.30 kg with 110 fruits per plant and 297.55 g average fruit weight. Whereas, the genotypes Island Gem recorded maximum pulp per cent (56.88) and the lowest seeds per fruit. Low seed weight with lesser seeds per fruits are the basis for selections based on seed traits. Seed weight also ranged from 4.45 to 14.60 g per fruit. Less accumulation photosynthetic in seed might has resulted in low seed weight in fruits. The edible portion of the fruit i.e. pulp content depend on the dimensions of the fruit. The pulp to seed ratio, pulp texture and flavour are the basis criterion for isolating superior fruiting trees. Minimum weight of the rind, a non-edible part in fruits is utmost criterion for choosing the superior genotypes. Fruit weight depends on the genetic makeup of the selected genotypes. The phenol content in fruit varied 0.18 to 0.36 %. Ma et al., [24] described variation in the total phenol content among mango accessions. While, total phenol content in pomegranates also varied at different location in Sri Lanka as reported by Amaratane et al., [25]. These morpho-biochemical analysis presented a wide range of variability among the genotypes. Also, the results of analysis of variance depicted significant difference among all the genotypes showing a vast amount of variability for all the quantitative traits in current research work (Table 1).

Table 1. Analysis of variance and genetic parameters for quantitative traits in *Annona*

SN.	Characters	Mean sum of squares			Range	GV	PV	GCV (%)	PCV (%)	
		Replication	Genotypes	Error						RD (%)
	Degree of freedom	1	17	17						
1	Plant height (m)	0.11	0.39**	0.05	5.14-6.89	0.17	0.19	6.62	7.05	6.10
2	Plant spread (N-S) (m)	0.04	0.58**	0.09	4.11-6.06	0.24	0.29	9.58	10.43	8.15
3	Plant spread (E-W) (m)	0.74	1.56**	0.23	3.88-6.62	0.66	0.78	15.27	16.57	7.85
4	Flower size (cm)	0.01	0.18**	0.05	2.55-3.50	0.06	0.09	8.61	10.18	15.42
5	Leaf length (cm)	0.01	3.35**	0.51	9.55-15.19	1.42	1.68	10.81	11.74	7.92
6	Leaf breadth (cm)	0.001	3.48**	0.08	3.68-8.88	1.70	1.74	25.60	25.89	1.12
7	Petiole length (cm)	0.01	0.55**	0.02	1.27-2.93	0.27	0.28	23.93	24.35	1.72
8	Fruit length (mm)	0.52	95.05**	18.68	54.99-84.75	38.18	47.52	8.28	9.24	10.39
9	Fruit width (mm)	33.81	79.16**	29.50	66.94-88.99	24.83	39.58	6.27	7.92	20.83
10	Fruit diameter (cm)	1.46	9.81**	1.41	19.25-27.73	4.20	4.91	8.23	8.90	7.53
11	Pulp weight (g)	20.28	1684.32**	60.55	57.58-162.04	811.88	842.16	23.07	23.49	1.79
12	Pulp per cent	0.001	20.86**	7.51	46.66-56.88	6.68	10.43	5.05	6.31	19.97
13	Rind weight (g)	0.44	1173.28**	73.90	42.25-132.85	549.69	586.64	21.98	22.70	3.17
14	Seed weight (g)	0.01	17.96**	1.06	4.45-14.60	8.45	8.98	27.33	28.17	2.98
15	Seed per cent	0.01	3.69**	0.16	1.69-7.91	1.76	1.844	29.24	29.90	2.21
16	Pulp/seed ratio	0.36	72.89**	2.33	8.34-33.75	35.28	36.44	46.53	47.29	1.61
17	Core length (cm)	0.04	0.56**	0.11	1.50-3.69	0.23	0.28	15.07	16.74	9.98
18	No. of seed per fruit	0.11	107.01**	6.84	12.60-40.80	50.08	53.50	25.29	26.14	3.25
19	Fruit weight (g)	23.78	5517.78**	129.23	105.10-297.55	2694.28	2758.89	21.54	21.80	1.19
20	No. of fruit per plant	4.69	1683.83**	66.81	11.00-110.00	808.51	841.92	42.25	43.11	1.99
21	Total soluble solids (ºB)	1.22	14.14**	3.06	18.39-28.32	5.54	7.07	9.23	10.42	11.42
22	Titrable acidity (%)	0.0001	0.05**	0.00	0.18-0.80	0.026	0.027	44.74	45.44	1.54
23	TSS/TA ratio	9.49	2240.44**	74.23	23.02-153.09	1083.11	1120.22	39.21	39.88	1.68
24	Reducing sugar (%)	1.52	2.86**	1.04	15.02-18.42	0.91	1.43	5.56	6.97	20.23
25	Non-reducing sugar (%)	1.05	1.32**	0.26	2.77-5.92	0.53	0.66	16.01	17.84	10.26
26	Total sugar (%)	0.01	4.59**	0.80	17.79-23.70	1.90	2.30	6.33	6.96	9.05
27	Ascorbic acid (mg/100g)	4.27	33.70**	11.14	27.55-43.10	11.28	16.85	9.70	11.86	18.21
28	Phenol (%)	0.0002	0.004**	0.01	0.18-0.36	0.0014	0.0019	16.44	19.45	15.48
29	Fruit yield per plant (kg)	0.28	145.83**	3.51	2.75-33.30	71.16	72.92	48.86	49.45	1.19

*** and ** represents significance at 0.05 and 0.01 levels, respectively**

Genotypic, phenotypic variances GCV, PCV and their relative differences were presented in Table 1. Briefly, the result exhibited that genotypic variance varied from phenol content in fruits (0.0014) to fruit weight (2694.28). Similarly, for phenol content in fruits the least phenotypic variance was 0.0019 and fruit weight reported the maximum value of 2758.89. Superficially, the phenotypic variance is greater than its genotypic counter part. The magnitudes of phenotypic and genotypic variance showed low difference suggesting less environment influence and genotypic component being major part of the total variance. The variations of genotypic and phenotypic coefficients are the measure of simple variability among the different genotypes. The variation of GCV and PCV were classified as lower (< 10 %), moderate (10-20 %) and higher (>20 %) as given through

Shivasubramanian and Madhavamenon [26]. Looking to these criteria, the present research results presented that both GCV and PCV were low to high. Top most GCV and PCV values were calculated for fruit yield followed by pulp/seed ratio. The magnitudes of GCV and PCV were higher for fruit yield per plant (48.86 % and 49.45 %), pulp/seed ratio (46.53 % and 47.29 %), titrable acidity (44.74 % and 45.44 %), number of fruit per plant (42.25 % and 43.11 %), TSS/TA ratio (39.21 % and 39.88 %) seed per cent (29.24 % and 29.90 %), seed weight (27.33 % and 28.17 %), leaf breadth (25.60 % and 25.98 %), number of seed per fruit (25.29% and 26.14%), petiole length (23.93% and 24.35 %), pulp weight (23.07 % and 23.49 %), rind weight (21.98 % and 22.70 %), fruit weight (21.54 % and 21.80 %). High variation of genotypic and phenotypic coefficients suggested the presence of considerable value of variability further selection could be practiced due to the effect of additive genes. The pulp per cent reported the lowest estimates for GCV & PCV being 5.05 and 6.31 %. While, low estimates were observed plant height, plant spread (N-S), flower size, fruit length, fruit width, fruit diameter, pulp per cent, total soluble solids, reducing sugar, total sugar and ascorbic acid (Table 1). The coefficient of variation was low for both genotypic and phenotypic coefficients of variation which emphasizing on low variation among the genotype for the traits which indicated limited scope of selection for respective traits due to the high effect of environment for their inheritance. Largely, the selection could be practiced for the traits with high degree of desirable variation for fruitful results [27]. The relative difference (RD) is referred to as an estimation of the ratio of GCV in association with the respective PCV and the estimated RD values ranged from 1.12 % (Leaf breadth) to 20.83% for fruit width (Table 1). The traits with high difference in between the estimates of their PCV and GCV compared to other traits indicated presence of environmental effect for their variability and direct selection could not be beneficial for the improvement of such attributes. Contrary, the lower relative difference is signifying the variability due to effects of genes rather than environment which has a better response to selection. High GCV and PCV values were observed by Anuragi et al., [16] for petiole length. This result is in coherence with the reports of Ankita et al., [28] who founded higher magnitudes of PCV and GCV of pulp/seed ratio. The above fruit weight consequences were not in contradiction among Bhatnagar et al., [7] who found moderate values of GCV and PCV. The titrable acidity for above result was in discordant with Bhatnagar et al., [7] who obtained little values of GCV and PCV, Anuragi et al., [16] and depicted moderate values of GCV and PCV. The above results are not in contradiction with Anuragi et al., [16] and Nag et al., [5] for fruit yield per plant.

Broad sense heritability and Genetic advance as mean percent

The heritability is the resemblance between parents and their progeny, whereas the genetic advance as mean per cent provide the information about expected gain for particular characters after selection. Heritability is measurement of transmission of traits from one generation to other next generation and consistent performance of progeny in succeeding generation which depends on the magnitude of inherent part of variant. Broad sense heritability (h^2_b) can be represented as the ratio of genetic variance to total or phenotypic variance. It can be classified as lower (< 30%), moderate (30-60 %) and higher (>60%) as reported by Robinson [29]. The genetic advance for each traits were determined as per the procedure of Allard [30] and converted to genetic advance as per cent of mean (GAM) and then categorized as low (< 10%), moderate (10-20 %) and high (>30%) as per Johnson et al., [31]. High h^2_b along with GAM was recorded for plant spread (N-S) (84.23% and 23.30%), plant spread (E-W) (85.01% and 37.18%), leaf length (84.76% and 26.27%), leaf breadth (97.77% and 66.82%), petiole length (96.50% and 62.05%), fruit diameter (85.65% and 20.12%), pulp weight (96.41% and 59.79%), rind weight (93.70% and 56.16%), seed weight (96.11% and 70.00%), pulp/seed ratio (96.80% and 120.85%), core length (81.05% and 35.82%), number of seed per fruit (93.61% and 64.61%), fruit weight (97.56% and 56.19%), number of fruit per plant (96.03% and 109.30%), total soluble solids (78.36% and 21.56%), titrable acidity (96.95% and 116.30%), TSS/TA ratio (96.69% and 101.80%), non-reducing sugar (80.56% and 37.94%), ascorbic acid (66.94% and

20.96%), phenol (71.45% and 36.68%) and fruit yield per plant (97.59% and 127.42%). Higher estimates of h^2_b and GAM point out the presence of additive gene. High value of h^2_b with moderate GAM was recorded for plant height (88.19% and 16.42%), flower size (71.62% and 19.24%), fruit length (80.35% and 19.60%), fruit width (62.73% and 13.12%), pulp per cent (64.02% and 10.66%), reducing sugar (63.56% and 11.69%), total sugar (82.65% and 15.20%) suggests the presence of fixable genes and less influence by environmental for the inheritance of characters (Figure 1). These traits can be beneficial for selection by fixing genes.

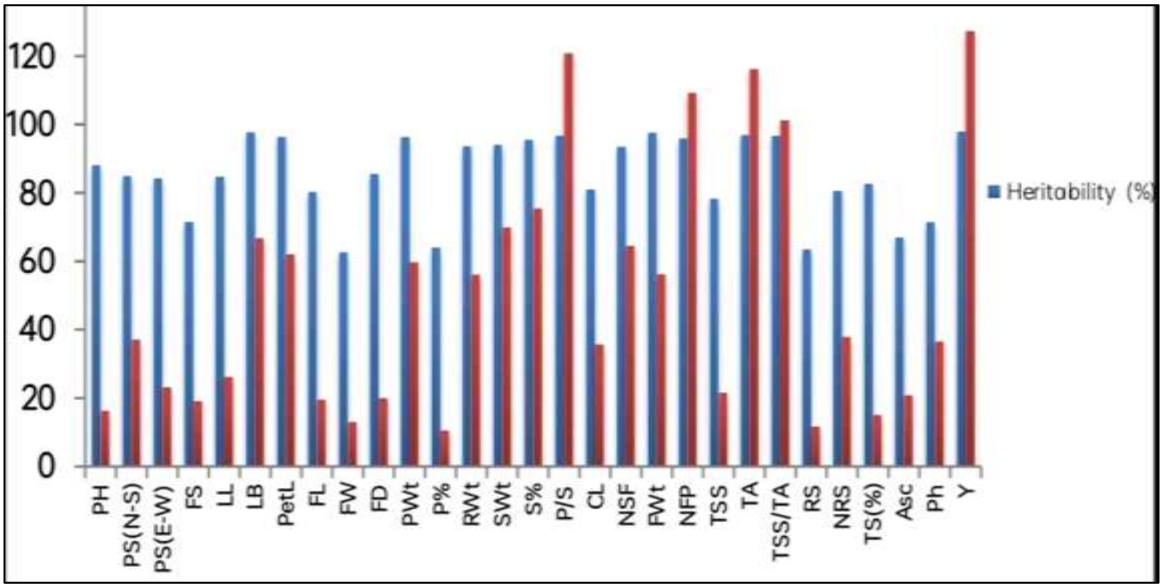

Figure 1. Heritability (%) and genetic advance as mean (%) of *Annona* genotypes

PH = Plant height
PS (N-S) = Plant spread (N-S)
PS (E-W) = Plant spread (E-W)
FS = Flower size
LL = Leaf length
LB = Leaf breadth
PetL = Petiole length
FL = Fruit length
FW = Fruit width
FD = Fruit diameter
PWt = Pulp weight
P% = Pulp per cent
RWt = Rind weight
SWt = Seed weight
S% = Seed per cent
P/S = Pulp/seed ratio
CL = Core length
NSF = Number of seed per fruit
FWt =Fruit weight
NFP = Number of fruit per plant
TSS = Total soluble solids
TA = Titrable acidity
TSS/TA = TSS/TA ratio
RS = Reducing sugar
NRS = Non-reducing sugar
TS (%) = Total sugar
Asc = Ascorbic acid
Ph = Phenol
Y = Fruit yield per plant

Higher GCV, in conjunction with high heritability and genetic advance, depicts a superior sign of selection rather than consideration for measuring unit. A potent selection could be realized when the effects of additive genes are sufficiently robust than the environmental effects [32]. High h^2_b couple with high GAM for leaf length and leaf breadth was also observed by Anuragi et al., [16]. These results are in contradiction with the revealed of Nag et al., [5] who depicted moderate heritability with the moderate genetic advance for leaf length. The results are not in similar with the finding of Nag et al., [5] who recorded moderate heritability coupled with high genetic advance for seed weight. The agreement result was also found with the Ankita et al., [3] who observed high heritability along with high genetic advance for number of seed per fruit. These findings were in accordance with Anuragi et al., [16] and Nag et al., [5] depicted higher heritability along with higher GAM for fruit yield.

Genotypic and phenotypic association matrix

The association analysis based on the relationship between two attributes showed genotypic association better than phenotypic counterpart, suggesting more genetic control than environment. The significant and positive genotypic (r_g) and phenotypic (r_p) association was established among fruit yield per plant and plant height (r_g= 0.66** and r_p= 0.60**), fruit length (r_g= 0.68* and r_p= 0.60**), fruit width (r_g= 0.81** and r_p= 0.61**), fruit diameter (r_g= 0.76** and r_p= 0.69**), pulp weight

(r_g= 0.52* and r_p= 0.51*), rind weight (r_g= 0.62** and r_p= 0.60**), seed weight (r_g= 0.80** and r_p= 0.77**), core length (r_g= 0.53* and r_g= 0.47*), number of seed per fruit (r_g= 0.65** and r_p= 0.61**), fruit weight (r_g= 0.61** and r_p= 0.60**), (r_g= 0.94** and r_p= 0.94**), total soluble solids (r_g= 0.71** and r_p= 0.65**), TSS/TA ratio (r_g= 0.75** and r_p= 0.73**), reducing sugar (r_g= 0.87** and r_p= 0.71**) and total sugar (r_g= 0.78** and r_p= 0.72**). The results signifies, the plant height, fruit length, fruit width, fruit diameter, pulp weight, rind weight, seed weight, fruit weight, number of seed per fruit and number of fruit per plant increase with the fruit yield per plant which desirable. While, positive and significant association fruit quality trait such as total soluble solids, TSS/TA, reducing sugar and total sugar with fruit yield specified the presence sugar content, taste, flavour and good quality pulp increase its demand for juice and ice-cream making market. Anuragi et al., [16] reported positive significant genotypic correlation of fruit length, fruit width, fruit weight and number of fruit per plant with fruit yield. A negative and significant association between fruit yield with leaf length, leaf breadth, petiole length and titrable acidity at both the levels. The negative and significant correlation between fruit yield with increasing titrable acidity which indicated ripe fruit makes the taste of fruits are sour indicated inverse association between these characters, it is useful to plant breeder in selection of superior genotypes from varied genetic population (Figure 2). These above result contradiction with Anuragi et al., [16] who obtained non-significant and negligible genotypic correlation between fruit yield per plant with number of seed per fruit.

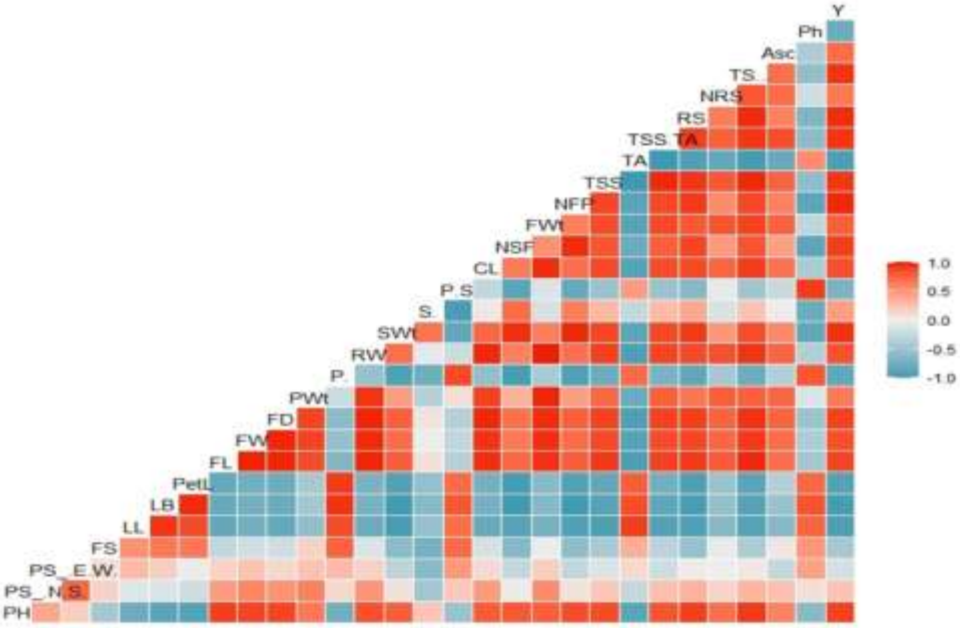

Figure 2. Genotypic correlogram analysis for *Annona* traits

Genotypic path analysis

Genotypic path coefficient analysis was as per by Dewey and Lu [33]. Path coefficient analysis aid to measure the degree and nature of direct and indirect effect of each trait on the dependent trait i.e., fruit yield. The cause of associations between fruit yield per plant with all the other twenty eight traits were measured based on genotypic associations. Path analysis based on genotypic correlation revealed petiole length (0.35), pulp per cent (0.96), seed per cent (0.80), pulp/seed ratio (0.31), number of seed per fruit (0.42), fruit weight (26.37), number of fruit per plant (0.77), reducing sugar (0.74) and non-reducing sugar (0.46) recorded positive direct effect on the fruit yield per plant in desirable direction and direct selection for these characters could be rewarding for yield improvement. However, negative direct effect on fruit yield was obtained for pulp weight (-16.44), rind weight (-9.45), seed weight (-1.67), titrable acidity (-0.54), TSS/TA ratio (-0.47) and total sugar (-0.84) which suggesting an inversely relationship with fruit yield per plant and revealed to the

Table 2. Genotypic path analysis showing direct and indirect effect of various traits on fruit yield

SN.	Characters	PH	PS (N-S)	PS (E-W)	FS	LL	LB	PetL	FL	FW	FD	PWt	P%	RW	SWt
1	PH	-0.20	0.03	0.09	-0.004	0.02	-0.07	-0.23	-0.01	0.15	-0.05	-5.64	-0.50	-5.62	-0.45
2	PS (N-S)	-0.07	0.09	0.14	0.005	-0.008	-0.01	-0.06	-0.01	0.19	-0.03	-8.43	0.42	-3.58	-0.03
3	PS (E-W)	-0.09	0.07	0.20	-0.002	-0.06	0.02	-0.08	-0.008	0.14	-0.02	-3.66	0.20	-2.00	0.38
4	FS	0.02	0.01	-0.008	0.04	-0.04	0.05	0.11	-0.002	0.05	-0.01	-7.32	0.69	-1.68	0.37
5	LL	0.03	0.006	0.10	0.01	-0.12	0.08	0.18	0.02	-0.15	0.05	5.47	0.84	5.82	1.55
6	LB	0.12	-0.009	0.03	0.02	-0.09	0.11	0.29	0.01	-0.13	0.04	1.78	0.90	4.33	1.38
7	PetL	0.13	-0.01	-0.04	0.01	-0.07	0.09	0.35	0.01	-0.13	0.03	1.72	0.79	3.95	1.05
8	FL	-0.14	0.05	0.08	0.005	0.10	-0.07	-0.24	-0.02	0.21	-0.06	-13.47	-0.27	-9.03	-0.82
9	FW	-0.14	0.08	0.13	0.009	0.09	-0.07	-0.22	-0.02	0.21	-0.07	-15.97	-0.07	-10.04	-0.76
10	FD	-0.13	0.04	0.05	0.008	0.08	-0.06	-0.16	-0.02	0.21	-0.07	-13.73	-0.19	-9.13	-0.84
11	PWt	-0.07	0.05	0.04	0.02	0.04	-0.01	-0.04	-0.02	0.20	-0.06	-16.44	0.28	-8.68	-0.40
12	P%	0.10	0.04	0.04	0.03	-0.11	0.11	0.29	0.005	-0.02	0.01	-4.81	0.96	0.80	1.07
13	RWt	-0.12	0.04	0.04	0.007	0.08	-0.05	-0.14	-0.02	0.22	-0.07	-15.10	-0.01	-9.45	-0.73
14	SWt	-0.05	0.002	-0.04	-0.009	0.11	-0.09	-0.22	-0.009	0.10	-0.04	-3.98	-0.61	-4.22	-1.67
15	S%	0.03	-0.04	-0.08	-0.02	0.06	-0.06	-0.13	0.006	-0.10	0.02	9.45	-0.64	3.90	-1.04
16	P/S	0.02	0.01	0.07	0.02	-0.07	0.08	0.16	-0.002	0.03	-0.002	-7.04	0.67	-1.94	1.15
17	CL	-0.07	0.02	0.05	0.01	0.09	-0.04	-0.14	-0.02	0.17	-0.06	-13.05	-0.10	-8.20	-0.88
18	NSF	-0.10	-0.007	-0.02	-0.005	0.08	-0.10	-0.30	-0.01	0.07	-0.02	-0.41	-0.69	-2.42	-1.23
19	FWt	-0.09	0.04	0.04	0.01	0.06	-0.04	-0.10	-0.02	0.22	-0.06	-16.07	0.85	-9.26	-0.64
20	NFP	-0.13	-0.005	-0.02	-0.006	0.07	-0.09	-0.20	-0.009	0.11	-0.04	-3.63	-0.55	-3.69	-1.36
21	TSS	-0.12	0.003	-0.02	-0.009	0.11	-0.08	-0.18	-0.02	0.17	-0.04	-10.35	-0.49	-7.34	-1.23
22	TA	0.11	-0.02	0.02	0.002	-0.08	0.07	0.12	0.02	-0.17	0.05	11.04	0.36	7.54	1.06
23	TSS/TA	-0.08	0.02	-0.02	0.005	0.07	-0.06	-0.07	-0.02	0.16	-0.04	-10.41	-0.15	-6.13	-1.11
24	RS	-0.14	0.03	0.05	-0.02	0.09	-0.09	-0.26	-0.02	0.20	-0.06	-8.99	-0.41	-6.66	-1.53
25	NRS	-0.08	-0.04	-0.001	0.01	0.03	-0.02	-0.08	-0.02	0.13	-0.03	-7.92	-0.28	-5.90	-0.05
26	TS(%)	-0.15	0.008	0.04	-0.007	0.08	-0.08	-0.24	-0.02	0.21	-0.06	-10.65	-0.43	-7.90	-1.09
27	Asc	-0.08	0.02	-0.04	0.008	0.05	-0.02	0.07	-0.006	0.08	-0.03	-8.45	0.16	-3.85	-0.38
28	Ph	0.07	0.01	0.10	0.001	-0.04	0.07	0.13	0.003	-0.05	0.03	-2.62	0.54	0.05	0.96

Continued

Table 2. Genotypic path analysis showing direct and indirect effect of various traits on fruit yield (Continued)

SN.	Characters	S%	P/S	CL	NSF	FWt	NFP	TSS	TA	TSS/ TA	RS	NRS	TS(%)	Asc	Ph	Y
1	PH	-0.13	-0.03	-0.05	0.22	12.42	0.48	-0.13	0.30	-0.19	0.54	0.19	-0.64	0.08	0.07	0.66 **
2	PS (N-S)	-0.34	0.05	-0.04	-0.03	11.97	-0.04	-0.007	0.09	-0.10	0.23	-0.17	-0.07	0.05	-0.03	0.17 NS
3	PS (E-W)	-0.35	0.11	-0.04	-0.05	5.44	-0.10	0.02	-0.06	0.04	0.21	-0.003	-0.19	-0.04	-0.09	-0.02 NS
4	FS	-0.31	0.15	-0.04	-0.05	8.27	-0.11	0.05	-0.03	-0.06	-0.34	0.11	0.15	0.04	-0.006	0.10 NS
5	LL	-0.41	0.17	0.11	-0.26	-13.47	-0.43	0.19	-0.36	0.27	-0.57	-0.11	0.55	-0.08	-0.06	-0.56 *
6	LB	-0.41	0.23	0.04	-0.36	-8.19	-0.60	0.16	-0.32	0.23	-0.61	-0.10	0.59	-0.03	-0.11	-0.71 **
7	PetL	-0.30	0.14	0.06	-0.36	-7.39	-0.44	0.11	-0.19	0.09	-0.57	-0.10	0.58	0.04	-0.07	-0.51*
8	FL	-0.23	0.03	-0.12	0.21	23.93	0.37	-0.19	0.44	-0.33	0.64	0.32	-0.81	0.06	0.03	0.68 **
9	FW	-0.39	0.05	-0.11	0.15	27.36	0.42	-0.18	0.45	-0.35	0.70	0.28	-0.84	0.07	0.04	0.81 **
10	FD	-0.27	0.01	-0.12	0.11	24.32	0.41	-0.14	0.39	-0.30	0.63	0.18	-0.69	0.09	0.07	0.76 **
11	PWt	-0.46	0.13	-0.11	0.01	25.77	0.17	-0.13	0.36	-0.30	0.41	0.22	-0.54	0.10	-0.04	0.52 *
12	P%	-0.53	0.22	0.02	-0.31	2.35	-0.44	0.11	-0.20	0.07	-0.32	-0.13	0.37	0.03	-0.10	-0.34 NS
13	RWt	-0.33	0.06	-0.12	0.11	25.83	0.30	-0.17	0.43	-0.30	0.52	0.29	-0.70	0.08	0.001	0.62 **
14	SWt	0.50	-0.22	-0.08	0.31	10.11	0.63	-0.16	0.34	-0.31	0.68	0.01	-0.55	0.04	0.10	0.80 **
15	S%	0.80	-0.27	0.03	0.25	-12.36	0.34	-0.02	-0.009	-0.03	0.18	-0.18	0.05	-0.03	0.10	0.20 NS
16	P/S	-0.68	0.31	-0.02	-0.26	7.67	-0.44	0.03	-0.06	0.09	-0.24	0.15	0.04	-0.001	-0.15	-0.40 NS
17	CL	-0.17	0.05	-0.14	0.08	22.56	0.22	-0.13	0.32	-0.25	0.60	0.15	-0.63	0.05	0.02	0.53 *
18	NSF	0.47	-0.19	-0.03	0.42	4.45	0.56	-0.13	0.26	-0.20	0.44	0.08	-0.43	0.0007	0.11	0.65 **
19	FWt	-0.37	0.09	-0.12	0.07	26.37	0.26	-0.16	0.41	-0.32	0.50	0.25	-0.64	0.09	-0.009	0.61 **
20	NFP	0.35	-0.18	-0.04	0.31	9.05	0.77	-0.14	0.33	-0.29	0.62	0.12	-0.59	0.06	0.10	0.94 **
21	TSS	0.09	-0.04	-0.09	0.25	19.43	0.48	-0.21	0.61	-0.44	0.57	0.31	-0.76	0.11	-0.002	0.71 **
22	TA	0.01	0.03	0.08	-0.20	-20.12	-0.47	0.24	-0.54	0.43	-0.65	-0.29	0.78	-0.13	-0.004	-0.72 **
23	TSS/TA	0.06	-0.06	-0.08	0.18	17.85	0.48	-0.20	0.50	-0.47	0.55	0.23	-0.64	0.14	0.02	0.75 **
24	RS	0.19	-0.10	-0.12	0.25	17.68	0.64	-0.16	0.47	-0.35	0.74	0.12	-0.76	0.02	0.06	0.87 **
25	NRS	-0.31	0.10	-0.05	0.07	14.45	0.19	-0.15	0.34	-0.23	0.20	0.46	-0.56	0.10	-0.04	0.34 NS
26	TS(%)	-0.04	-0.01	-0.11	0.22	20.29	0.5	-0.19	0.51	-0.36	0.67	0.31	-0.84	0.07	0.02	0.78 **
27	Asc	-0.14	-0.001	-0.04	0.0002	12.61	0.26	-0.12	0.39	-0.36	0.09	0.23	-0.29	0.19	0.06	0.44 NS
28	Ph	-0.46	0.26	0.02	-0.26	1.38	-0.45	-0.002	-0.01	0.05	-0.23	0.09	0.09	-0.07	-0.18	-0.50 *

***P<0.05, ** P <0.01, NS= Non-Significant**

quality of the *Annona* genotypes has negative effect on fruit yield (Table 2). Very low residual value (-0.00062) suggested that factors influencing the fruit yield were included in the present study. Similar results direct effect of high and positive for number of fruit per plant on fruit yield were founded by Anuragi et al., [16].

Conclusion

The present research work strongly resolved the study of genetical parameters and association between the fruit quality and field observations including fruit yield. An achievement in genetic improvement of any crop depends on the available genetic variability for selection of superior genotypes. Narrow genetic base is the bottleneck in any breeding work. Climate change also affected the crop diversity by genetic erosion. To bred for ensuring the food and nutrition for increasing population, genetic variability in any crop play a vital role. Knowledge about the available germplasm, its conservation and utilization in breeding is required. Hence, characterization of the available germplasm for morphological and biochemical traits became prerequisite. Such genetical studies revealed the vast genetical aspects for using these various landraces, indigenous and exotic germplasm to be utilized and to develop the breeding strategies. The study reported considerable genetic variability among *Annona* genotypes for twenty-nine traits. High magnitudes of h^2_b and GAM was computed for all the traits except plant height, flower size, fruit length, fruit width, pulp per cent, reducing sugar and total sugar which suggested the presence of the fixable genes and less environmental influence indicated great chance of selection for genetic improvement. The significant and positive association was found between fruit yield and plant height, fruit length, fruit width, fruit diameter, pulp weight, rind weight, seed weight, core length, number of seed per fruit, fruit weight, number of fruit per plant, total soluble solids, TSS/TA ratio, reducing sugar and total sugar at both genotypic and phenotypic levels. The traits namely, petiole length, pulp per cent, seed per cent, pulp/seed ratio, number of seed per fruit, fruit weight, number of fruit per plant, total soluble solids, reducing sugar and non-reducing sugar are important with direct positive effect on fruit yield. These set of traits could be utilized as an index for practicing selection for improvement fruit yield and quality attributes. The superior genotypes for various morphological and biochemical traits could be utilized to generate the superior segregants in single cross progenies and selection can be practiced by combining desirable genes from both the parents.

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References

[1] T. G. Albuquerque, F. Santos, A. Sanches-Silva, M. B. P. P. Oliveira, A. C. Bento and H. S. Costa **(2016)**. Nutritional and phytochemical composition of *Annona cherimola* Mill. fruits and by-products: potential health benefits. Food Chem., **193:** 187-195.

[2] Digital herbarium of crop plants **(2016)**. Dept. of Crop Botany, Bangabandhu Sheikh Mujibur Rahman Agricultural University. Available online: http://dhcrop.bsmrau.net/custard-apple/ (accessed on 19th June, 2021).

[3] M. C. Ankita, D. A. Peerjade, D. Satish, K. Hipparagi and A. M. Nadaf **(2019)**. Studies on genetic variability, heritability and genetic advance in custard apple (*Annona squamosa* L.) genotypes. J. Pharmacogn. Phytochem., **8:** 795-797.

[4] D. R. Thakur and R. N. Singh **(1965)**. Studies on pollen morphology, pollination and fruit set in some Annona. Indian J. Hortic., **22:** 10-18.

[5] J. L. Nag, N. Shukla and A. Qureshi **(2018)**. Characterization of custard apple (*Annona squamosa* L.) genotypes in northern bastar of Chhattisgarh, India. Int. J. Curr. Microbil. App. Sci., **7:** 1700-1707.

[6] H. Anuragi, H. L. Dhaduk, S. Kumar, J. J. Dhruve, M. J. Parekh, and A. A. Sakure **(2016)**. Molecular diversity of Annona species and proximate fruit composition of selected genotypes. 3 Biotech., **6:** 204. doi: 10. 1007/s13205-016-0520-9.

[7] P. Bhatnagar, J. Singh, M. C. Jain and B. Singh **(2012)**. Evaluation of landraces of custard apple (*Annona squsmosa* L.). Plant Arch., **12:** 1045-1048.

[8] A. Hisham, C. Sunitha, U. Sreekala, L. Pieters, T. De Bruyne, H. Van den Heuvel and M. Claeyes **(1994)**. Reticulacinone, an acetogenin from *Annona reticulata*. Phytochem., **35:** 1325-1329.

[9] J. S. Strijk, D. D. Hinsinger, M. M. Roeder, L. W. Chatrou, T. L. P. Couvreur, R. H. J. Erkens, H. Sauquet et al., **(2021)**. Chromosome-level reference genome of the soursop (*Annona muricata*): A new resource for Magnoliid research and tropical pomology. Mol. Ecol. Resour., **21:** 1608-1619.

[10] T. Begna (2021). Effects of crop evolution under domestication and narrowing genetic bases of crop species. Open J. Plant Sci., **6:** 049-054.

[11] G. M. Vinay, T. Sakthivel and H. L. Priyanka **(2017)**. Recent advances in *Annona* breeding: A review. Int. J. Pure Appl. Biosci., **2:** 1168-1181.

[12] P. Chaimanee and O. Suntornwat **(1994)**. Changes in Carbohydrate Content During Fruit Ripening m A New Approach of Teaching of Carbo- hydrate Chemistry in Biochemistry Course. Biochem. Educ., **22:** 0307-4412.

[13] H. L. Priyanka, T. Sakthivel, K. S. Shivashankar, M. R. Dinesh and G. M. Vinay **(2019)**. Biochemical profiling of *Annona* species and *Annona atemoya* varieties. Int. J. Chem. Stud., **7:** 257-261.

[14] N. Babbar, H. S. Oberoi, D. S. Uppal and R. T. Patil **(2011)**. Total phenolic content and antioxidant capacity of extracts obtained from six important fruit residues, Food Res. Int., **44:** 391-396.

[15] K. H. Jnapika, C. Sarvamangala, H. S. Kulapati, S. G. Gollagi, G. R. Sanjeevvaraddi and P. Basavaraj **(2019)**. Morphological characterization of *Annona* species under northern dry zone of Karnataka. Int. J. Chem. Stud., **7:** 2107-2122.

[16] H. Anuragi, B. T. Jain, H. L. Dhaduk, and S. Kumar **(2017)**. Genetic association studies for fruit yield and its components and qualitative phytochemical screening in promising *Annona* genotypes. Res. J. Agric. Sci., **8:** 222-227.

[17] B. D. Singh **(2019)**. Plant Breeding: Principle and Methods. Eleven revised edition, Kalyani Publishers, New Delhi.

[18] J. L. Nag, P. Singh and A.Tiwari **(2020)**. Correlation and path coefficient analysis of fruit yield and quality related traits of custard apple (*Annona squamosa* L.). Indigenous accessions from Northern Bastar of Chhattisgarh. Int. J. Chem. Stud., 8: 3056-3060.

[19] B. Manochai, P. Ingkasupart, S. H. Lee and J. H. Hong **(2018)**. Evaluation of antioxidant activities, total phenolic content (TPC), and total catechin content (TCC) of 10 sugar apple (*Annona squamosa* L.) cultivar peels grown in Thailand. Food Sci. Technol., 38: 294-300.

[20] M. M. H. Khan, M. Y. Rafii, S. I. Ramlee, M. Jusoh, A. Mamun **(2020)**. Genetic variability, heritability, and clustering pattern exploration of bambara groundnut (*Vigna subterranean* L. Verdc) accessions for the perfection of yield and yield-related traits. Biomed Res. Int., Article ID 2195797, doi: 10.1155/2020/2195797.

[21] R. Popat, R. Patel and D. Parmar **(2020)**. Variability: genetic variability analysis for Plant Breeding Research. R package version 0.1.0. Available at: https://cran.r-project.org/web/packages/variability/variability.pdf.

[22] R Studio Team **(2020)**. RStudio: Integrated Development for R. RStudio, PBC. Boston, MA: RStudio Team.

[23] T. M. M. Malundo, R. L. Shewfelt, G.O. Ware and E. A. Baldwin **(2001)**. Sugars and acids influence flavor properties of mango (*Mangifera indica*). J. Am. Soc. Hort. Sci., **126:** 115-121.

[24] X. Ma, H. Wu, L. Liu, Q. Yao, S. Wang, R. Zhan and S. Xing et al., **(2011)**. Polyphenolic compounds and antioxidant properties in mango fruits. Sci. Hortic., **129:** 102-107.

[25] D. I. M. Amararatne, W. A. P. Weerakkody and J. A. L. P. Jayakody **(2012)**. Bioactive properties of fruit juice of Promegrante (*Punica granatum*) grown in dry regions of Sri Lanka. Trop. Agric. Res., 23: 370-375.

[26] S. Shivasubramanian and P. Madhavamenon **(1978)**. Genotypic and phenotypic variability in rice. Madras Agric., **60:** 1093-1096.

[27] N. M. Fakuta, I. F. Ojiekpon, I. B. Gashua and O. C. Ogunremi **(2015)**. Quantitative genetic variation in gum arabic (*Acacia senegal* (L) Willd) provenances. Am. J. Plant Sci., **6:** 2826-2831.

[28] M. C. Ankita, D. A. Peerjade, D. Satish, K. Hipparagi and A. M. Nadaf **(2019)**. Studies on genetic variability, heritability and genetic advance in custard apple (*Annona squamosa* L.) genotypes. J. Pharmacogn. Phytochem., **8:** 795-797.

[29] H. F. Robinson **(1966)**. Quantitative genetics in relation to breeding on the central of mendalism. Indian J. Genet., **26:** 171-187.

[30] R. W. Allard **(1960)**. Relationship between genetic diversity and consistency of performance in different environment. Crop Sci., **1:** 127-133.

[31] H. W. Johnson, H. F. Robinson and R. E. Comstock **(1955)**. Estimates of genetic and environmental variability in soyabean. Agron. J., **47:** 314-318.

[32] M. G. Usman, M. Y. Rafii, M. R. Ismail, M. A. Malek and M. Abdul Latif **(2014)**. Heritability and genetic advance among chili pepper genotypes for heat tolerance and morphophysiological characteristics. Sci. World J., Article ID 308042 doi: 10.1155/2014/308042.

[33] D. R. Dewey and K. H. Lu **(1959)**. A correlation and path analysis of components of crested wheat grass seed production. Agron. J., **51:** 515-518.