Genetic Variability and Correlation Studies in Germplasm Collection of Aromatic Peppers (*Capsicum annum L.*) of Nigeria

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Abstract

Ten genotypes of Nigerian aromatic pepper (Capsicum annum L.) were studied using randomized complete block design. Data were collected on canopy spread, plant height, leaf area, number of branches per plant, nodes per plant, nodes per branch, main stem length and fresh fruit yield. The observed variations were partitioned into heritable and non-heritable components in order to identify characters for which selection will be most effective. The result obtained revealed that genotypes showed considerable variation for all the characters evaluated thus showing a wide scope for selection. Wide disparity in the estimates of genotypic variances was observed for most of the characters. The genotype by year interactions were also significant implying environmental influence on the characters measured. Significant correlation values were also obtained among the characters studied. Based on the moderate to high estimates of genotypic coefficient of variation, heritability and genetic advance coupled with the highly significant positive correlation values, selection for fresh fruit yield in aromatic pepper can be effective on two characters, the number of branches per plant and number of nodes per plant.

Key words: Genetic variability, Germplasm, Aromatic Peppers, *Capsicum annum*, Heritability

Introduction

Peppers are widely grown in the tropics primarily for their pungency, which results from the concentration of the alkaloid capsaicinoid (Bosland and Votava 2000). The fruits make an important contribution in the diet as they are good sources of vitamins A and C especially in the fresh state. Plant breeding has contributed to human welfare in various aspects of agriculture but of immense importance to human well being are those advances leading to improved quality of agricultural products (Allard 1960). *Capsicum annum* is cherished for its pungency and aroma and is therefore used for food flavouring on a commercial scale (Lewis et al 1972, Uzo 1982). Nsukka yellow pepper is highly aromatic and consumers place a high premium on it, a factor which makes it costly in the market (Nwankiti 1981). An increasing demand on natural flavour has been reported as consumers are becoming aware of the health implications of artificial flavourings (Anon 1996, Hoch 1997, Blenford 1998). There is therefore the need to assemble the aromatic peppers of Nigeria and characterize them to determine the extent of variation among the genotypes. This work was undertaken to study the genetic variability among the genotypes using suitable genetic parameters such as phenotypic and genotypic coefficient of variations and heritable estimates as a basis for starting an effective selection programme.

Materials and Methods

The experimental material consists of ten aromatic pepper genotypes namely: *Dangarawa, Tatase, Oshosho, Shombe Ntuenokpo, Tarugu* and four lines of high aroma Nsukka yellow pepper (*UNS*$_2$ *Nsky –1p, Nsky – se and Nsky –rw*). The genotypes were selected based on their aroma qualities. The experimental design was a randomized complete block design (RCBD) with three replication. The genotypes were grown in the rainy seasons of 2002 and 2003 under derived savanna ecological zone of Nigeria (Latitude 06^0 52'N and longitude 07^{0}' 24'E). Each block was divided into ten plots measuring 2.9 x 2m with a distance of 0.5m between plots.

The seedlings of the different accessions were raised in nursery. The nursery medium was mixed in a proportion of 3:2:1 of top soil, poultry manure and river sand respectively. The seedlings were transplanted after four weeks at a spacing of 60 cm x 45 cm inter and intra row respectively. Each plot received a dosage of 2.9 kg per plot of well cured poultry manure. This was applied broadcast and worked thoroughly into the soil three days before transplanting.

Data were collected from tagged plants on the architectural traits and yield. The mean values from the experimental plants in each plot were used to compute a combined analysis of variance. Genetic analysis was also done to determine the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), Heritability (H) and genetic advance (GA). The genotypic variance (δ^2g) was obtained as δ^2(g) =

$$\frac{Ms_{(g)} - \sigma_e^2 - r\sigma_{gy}^2}{ry} \quad \text{(Uguru 2005)}$$

While Phenotypic variance

$$\sigma^2_{(p)} = \sigma_g^2 + \frac{\sigma_e^2}{ry} + \frac{\sigma_{gy}^2}{y} \quad \text{(Uguru 2005)}$$

Where Ms(g) = Mean square for genotypes (variance due to genotypes)

$\sigma^2(e)$ = Environmental variance

$\sigma^2(gy)$ = Interaction (genotype x year) variance

r = replications y = year

Table 1: Range, mean, mean square values (MS) coefficient of variation and variance ratios VR of the architectural traits and the yield

Character	Range	Mean±SE	MS (g)	MS(gxy)	MS(e)	CV (g)	VR (g)	VR(gxy)
Canopy diameter	24.89-35.08	30.81±0.7	60.75	28.41	29.27	25.3	2.08^{ns}	0.97^{ns}
Plant height	22.03-46.07	30.18±0.51	286.31	62.64	15.54	56.07	18.43***	4.03***
Leaf area	15.40-29.70	25.03±0.43	107.03	68.09	11.09	41.33	9.65***	6.14***
No. of branches	37.04-88.64	61.33±4.4	2773	1811	1189	76.01	1.83^{ns}	1.52^{ns}
Nodes/branch	11.33-18.23	16.24±0.31	24.56	11.08	5.58	30.52	4.40***	1.97^{ns}
Nodes/main stem	18.42-28.99	24.06±0.27	68.79	48.77	4.3	34.47	15.96***	11.3***
Nodes/plant	177.63-339.27	228.57±8.1	17642.0	3887	4012	58.11	4.40***	0.97^{ns}
Main stem length	14.95-28.95	20.88±0.45	101.05	54.78	12.6	48.14	8.13***	4.5***
Fresh fruit yield	1714.56-6695.56	4147.09±22.97	2.3x10^{7}	1.56x10^{7}	1.31x10^{7}	115.64	1.75^{ns}	1.19^{ns}

**** = very highly significant (p=0.001); n.s = not significant*

Table 2: Correlation coefficient estimated among the traits measured in the study

	Plant height	Leaf area	No. of branches/plt	No. of Nodes/branch	No. of nodes main stem	No. of nodes/plant	Main stem length	Fresh fruit yield
Canopy Spread	.55**	.33^{ns}	.76**	.50**	.43**	.78**	.56**	.67**
Plant height		.45**	.64**	.22^{ns}	.55*	.48**	.84**	.45*
Leaf area			.13^{ns}	.57**	.51**	.31^{ns}	.54**	.15^{ns}
No of branches/plt				.28^{ns}	.43*	.83**	.74*	.78**
No of nodes/branch					.38**	.32^{ns}	.28^{ns}	.17^{ns}
No of nodes on main stem						.48**	.51**	.30^{ns}
No of node/plant							57*	.82**
Main stem length								.53*

Table 3: Estimates of the genetic parameters for the traits studied

Character	Phenotypic variance	Genotypic variance	Genotype x year variance	Phenotypic coefficient of variation	Genotypic coefficient of variation	Genotype X year coefficient of variation	Heritability in broad sense %	Genetic advance
Canopy Spread	10.30	5.46	-0.09	10.42	7.58	-ve	53.01	8.28
Plant height	47.74	13.81	15.7	22.89	12.31	13.13	28.93	7.33
Leaf area	17.8	6.49	19.0	16.86	10.18	17.42	36.46	7.65
No of branches/plt	462.16	160.33	207.33	35.05	20.65	23.48	34.69	14.76
No of nodes/branch	4.09	2.26	1.84	12.64	9.25	8.29	55.12	10.55
No of nodes/main stem	11.46	3.34	14.82	14.07	7.59	16.00	29.10	4.54
No of nodes/plt	18289.84	13755	-41.67	46.87	46.02	-ve	96.46	79.49
Main stem length	16.84	7.71	14.21	19.66	13.30	18.05	45.79	12.55
Fresh fruit yield	3831666.67	1.225x10^{6}	8.4 x 10^{5}	47.20	26.69	221	31.97	17. 6

The genotypic coefficient of variation (GCV) was estimated from

$$\frac{\sqrt{\sigma^2_{(g)}}}{X} \times \frac{100}{1} \quad \text{(Burton 1952)}$$

Where $\sigma^2_{(g)}$ is as above and $\bar{x}$ is the mean value for any trait under consideration.

Heritability in broad sense was obtained as the ratio of the genotypic variance ($\delta^2 g$) and the phenotypic variance expressed in percentage $\frac{\sigma^2_g}{\sigma^2_p} X \frac{100}{1}$ (Allard 1960).

The expected genetic advance (%) was calculated from the formula by Johnson et al (1955) and which was also used by Okoye and Ene-obong (1992) and Adebola et al (2001)

$$\text{Thus} \quad GA = K\left(100\frac{\sqrt{\sigma^2_{(g)}}}{X}\right)\left(\frac{\sigma^2_g}{\sigma^2_p}\right)$$

Where K = 2.06 for 5% selection intensity (Johnson, *et al* 1955; Adebola *et al* 2001).

Results and Discussion

The range, mean, mean square values for genotypes, genotype X year interactions and error, coefficients of variation and variance ratios are presented in Table 1 and the correlation coefficient estimates among the traits evaluated are presented in Table 2. Table 3 shows the estimate of the genetic parameters among the characters. The analysis of variance revealed very highly significant differences (p = 0.001) among the ten genotypes in six out of the nine characters studied while four characters showed a highly significant genotype X year interactions.

The canopy spread ranged from 24.89 – 35.08 with a mean of 30.81± o.7 and a standard deviation value of 7.79. This seems to indicate the existence of a less bushy to a more bushy type with profuse growth and branching. There seems to be greater proportion of the profuse type as is validated by the highly significant positive correlations of 0.76** and 0.78** between the canopy spread and the number of branches per plant and number of nodes per plant, respectively. Plant height ranged from 22.03 – 46.07 with a mean of 30.18 ± 0.15 and a standard deviation value of 16.92. This implies the existence of short and tall genotypes. Taller genotypes may have the advantage of ease of picking as pepper is manually harvested. Taller plants had taller primary shoots (main stem length) the values ranging from 14.95 – 28.95 and a mean of 20.88 ± 0.45. Plant height had a significant positive correlation value of 0.84** with primary shoot length. Taller plants with longer primary shoots had more leaves at the main stem as is shown by a highly significant positive correlation value of 0.51** of main stem length to number of nodes on the main stem.

The number of branches per plant ranged from 37.04 – 88.64 with a mean value of 61.33 ± 4.4 and a standard deviation value of 26.62. This shows that some genotypes had profuse branching habit. The number of branches per plant is an important yield component as the flower bearing pedicels are produced at the branch nodes. Profuse branching is a useful agronomic trait to fresh fruit yield considering its highly significant correlation value of 0.78** with fresh fruit yield. Increased fresh fruit yield can be selected via number of branches per plant, canopy spread and number of nodes per plant based on their high correlation values with fruit yield. However it is important to note that some of these characters have large non-genetic components as was shown in the estimates of the genetic components (Table 3).

Estimate of components of genetic variance and coefficients of variation for the different characters revealed that the phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation in all characters. This indicates that all the characters had to some degree interacted with the environment. This is also supported by the significant genotype x year interactions. This finding is in agreement with the result obtained in African yam bean (Okoye and Ene-obong, 1992), Castor plant (Uguru 2000) and Kola (Adebola *et al*, 2001). The number of branches per plant and number of nodes per plant had high genetic components as shown by the genotypic variance of 160.33 and 13755, GCV of 20.65 and 46.02 respectively, while number of branches had moderate heritability value of 34.69, number of nodes per plant had a high heritability value of 96.46. These two characters also had the highest values for genetic advance. These in addition to their very high positive correlation values with fresh fruit yield make these parameters useful agronomic tools for the improvement of fresh fruit yield in *Capsicum annum* genotypes. The moderate heritability and low genetic advance as observed in other characters suggest that the variability in these traits were mainly due to non-additive gene action and hence there is a limited scope for selection with respect to these characters. The variations due to year were larger than those due to genotype and genotype X year interaction for fruit yield. This seems to suggest that some degree of selection for wide adaptability in traits measured occurred in this genetic material grown at Nsukka.

The study showed that improvement in yield through direct selection can be done via selecting for higher number of branches and nodes per plant.

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