Full Length Research Paper

Inter-relations of growth and disease expression in pepper using principal component analysis (PCA)

E.A. Madu and M.I. Uguru*

Department of Crop Science, University of Nigeria, Nsukka.

Field reactions of 12 indigenous pepper lines (UNS_2, UNS_3, NSKY-LP, Atanukwu yola, Sombe, NSKY-SE, Tarugu, Tartasi, Dangarawa, Oshosho, NSKY-RW and a *Hybrid* between *Sombe a*nd NSKY-RW) for resistance to pepper veinal mottle virus (PVMV) were determined with principal component analysis (PCA). Genetically related genotypes tend to cluster, indicating that there is a significant genetic component to the underlying patterns of variations in growth and disease attributes. The PCA showed that the vegetative trait had high PRIN 1 value, thereby suggesting that the trait could be used to assign pepper genotypes into different agronomic groups. Similarly, the disease characters were the main determinants of PRIN 2 thus, implicating them as additional useful traits for classification of pepper lines.

Key words: Pepper, *Capsicum* spp., pepper veinal mottle virus, principal component analysis.

INTRODUCTION

Pepper, *Capsicum* species belongs to the family *Solanaceae*. There are both cultivated and wild species in the genus, *Capsicum*. *Capsicum frutescens* and *Capsicum annuum* are the two widely grown species in the tropics. *C. frutescens* is pungent while *C. annuum* is less pungent and mild (Uguru, 1996). Pepper is an important spice crop that is produced and consumed either fresh or processed (Sonago, 2003). It has both nutritive and medicinal values. It is rich in vitamins A and C (Yayock et al., 1988). However, its production is constrained by vast array of pathogenic organisms and insect pests. Of the disease organisms, the pepper veinal mottle virus (PVMV) is the most virulent. Its incidence can be very high at the end of the wet season (Alegbejo and Uvah, 1986). Incidence of this naturally occurring PVMV is of a serious concern because there is no cure for virus infection. Infection can result in loss of saleable produce from the plant. The development of resistant varieties is the most likely cost effective means of control of PVMV.

Wide variability exists particularly in vegetative characters and disease expression potentials in pepper accessions. The association between growth, yield and disease expression in pepper lines may determine if the pattern of quantitative and qualitative variation in vegetative and disease traits agree with agronomic groupings. Principal component analysis (PCA) may reveal relationship among the vegetative, yield and disease characters and determine how the Nigerian indigenous pepper lines vary in terms of all the variables considered together. This study was therefore, initiated to investigate the pattern of variations and the inter-relations of growth and disease expressions in the indigenous pepper genotypes using principal component analysis.

MATERIALS AND METHODS

Twelve *Capsicum* lines (UNS_2, UNS_3, NSKY-LP, Atanukwu yola, Sombe, NSKY-SE, Tarugu, Tartasi, Dangarawa, Oshosho, NSKY-RW and a hybrid between *Sombe* and NSKY-RW) were obtained from the Department of Crop Science, University of Nigeria, Nsukka (U.N.N.) pepper germplasm. The experiment was conducted at the

*Corresponding authors E-mail: maxokoye2001@yahoo.co.uk.

Table 1. Eigenvector values for principal components using disease and vegetative traits in 12 pepper lines at fruiting.

Trait	PC1	PC2	PC3
Infected	-0.18496	0.66457	-0.21162
Mosaic	-0.49622	0.34923	0.32921
Mosaic and Puckering	0.24253	0.45820	-0.47617
Normal	-0.48645	-0.44337	-0.29748
Puckering	0.28244	-0.17023	-0.58042
Total no of leaves	0.58680	-0.02980	-0.44126
Eigenvalue	1.990	1.863	1.578
% of total variation	33.17	31.04	26.29

Table 2. Eigenvector values for principal components using disease, yield and vegetative traits in 12 pepper lines at maturity.

Trait	PC1	PC2	PC3
Aborted	-0.42146	-0.15598	0.32184
Fruit no.	-0.32809	0.07351	0.47817
Fruit wt	-0.38915	0.17818	0.46354
Infected	-0.22252	0.43033	-0.15505
Mosaic and Puckering	-0.25569	-0.36197	-0.22863
Mosaic	0.04788	0.56959	0.06867
Normal	-0.41655	0.18113	-0.41073
Puckering	-0.29444	-0.49178	-0.04087
Total no of leaves	-0.43116	0.15237	-0.44889
Eigenvalue	3.019	1.908	1.661
% of total variation	33.55	21.09	18.46

research farm of the Department of Crop Science, University of Nigeria, Nsukka. Nursery seedlings were raised in a soil mixture of topsoil, poultry manure and riversand mixed at a ratio of 3:2:1 by volume, respectively. The experiment was a Randomized Complete Block Design (RCBD) with 3 blocks of 41.1 m x 2 m each. Each block was divided into 12 plots, each measuring 2.9 m x 2 m (5.8 m^2). A distance of 0.5 m was allowed between blocks and between plots. Well cured poultry manure was applied broadcast at the rate of 2.9 kg/plot (5 tonnes/ha) and worked thoroughly into the soil in each plot. Pepper seedlings were transplanted at four weeks after planting at a spacing of 60 cm inter row and 45 cm within row giving a plant population of 21 plants per plot. The pepper accessions were randomly assigned to each block. Plots were labeled accordingly. Weeding was manually done as and when necessary using a hoe. Data were collected at fruiting stage and at maturity stage on the total number of leaves per plant, number of normal leaves per plant, number of infected leaves per plant, number of leaves with mosaic, number of leaves with puckering, number of leaves with mosaic and puckering, number of aborted fruits per plant, number of fruits per plant, weight of fresh fruits (g) per plant. Principal component analysis was conducted using the traits evaluated to reveal patterns within the data matrix. PCA was performed using GENSTAT statistical package (Genstat, 1995). First and second principal components (PRIN) were plotted to enhance the dispersion of the 12 pepper genotypes, based on vegetative, yield and disease characters.
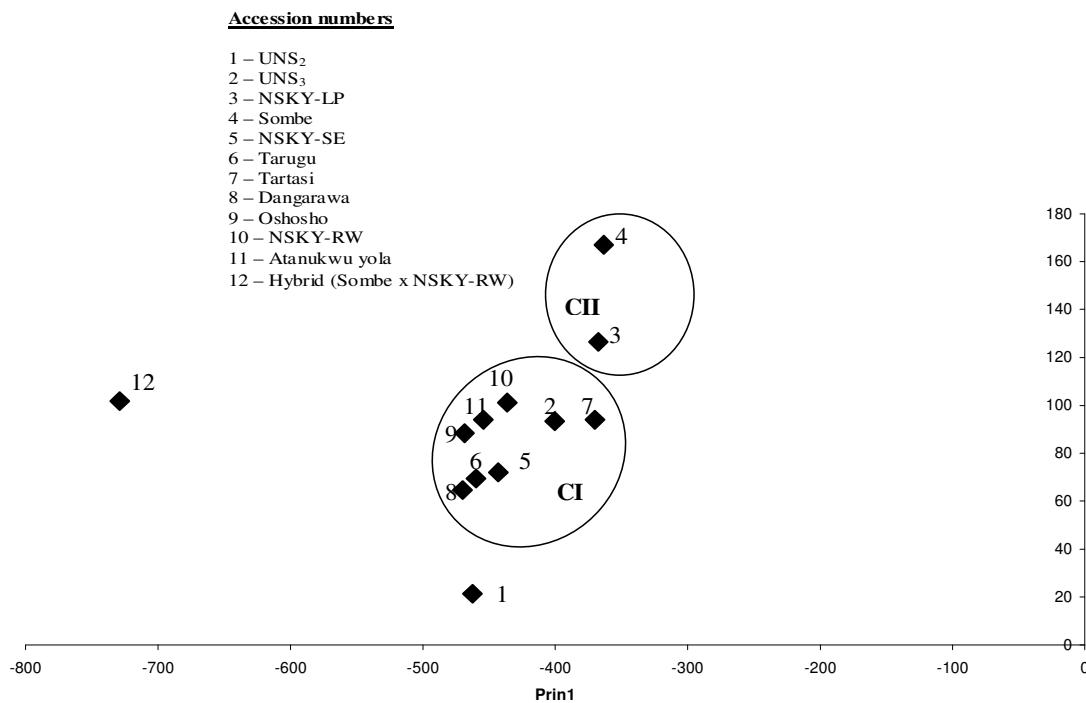
RESULTS AND DISCUSSION

Table 1 shows the result of the principal component analysis on data collected at fruiting stage. The PRIN 1 explained 33.17% of the total variance. The principal component is accounted for by the singular vegetative character (i.e. total number of leaves produced per plant). Only the hybrid (*Sombe* x *NSKY-RW*) has a high PRIN 1 score (Figure 1) while the rest accessions clustered at the centre of PRIN 1 suggesting moderate leaf production. PRIN 2 (infected leaves per plant) explained 31.04% of the total variation. Clusters 1 (*NSKY-LP,Tarugu, Dangarawa* and *NSKY-RW*) and Cluster III (*Tartasi Sombe* and *Oshosho*) had high and low PRIN 2 scores, respectively. The disease infection increased from zero to positive values along PRIN 2 axis. PRIN 3 contributed 26.29% of the total variance. Its loading was for leaf puckering. At the maturity stage (Table 2) the result of the PCA showed that the 3 principal components accounted for 73.10% of the total variance (i.e. 33.55%, 21.09% and 18.46%). PC1 was able to classify the lines basically on the vegetative characters (total number of leaves and number of normal leaves per plant). The hybrid (*Sombe* x *NSKY-RW)* produced more leaves (i.e., high PRIN 1 score) than the other lines (Figure 2). Along PRIN 2 axis the infectivity (number of infected leaves, number of leaves infected with mosaic and number of leaves infected with puckering) maintained a consistent increase. Cluster II (*Sombe and NSKY-LP)* was more susceptible to PVMV. UNS$_2$ had low PRIN 2 score. Yield characters affecting PC3 were total number of fruits per plant and fresh fruit weight.

The traits contributing to the first principal component (PC1) at fruiting was the total number of leaves. At maturity stage, the first principal component axis was also determined by the total number of leaves, and the number of normal leaves. PC1 accounted for most of the variation in the data collected, suggesting that the pepper genotypes were separated on the basis of leafiness. Thus the hybrid (*Sombe* x *NSKY-RW)* with high PRIN 1 score was evidently endowed with profuse leaf produc-
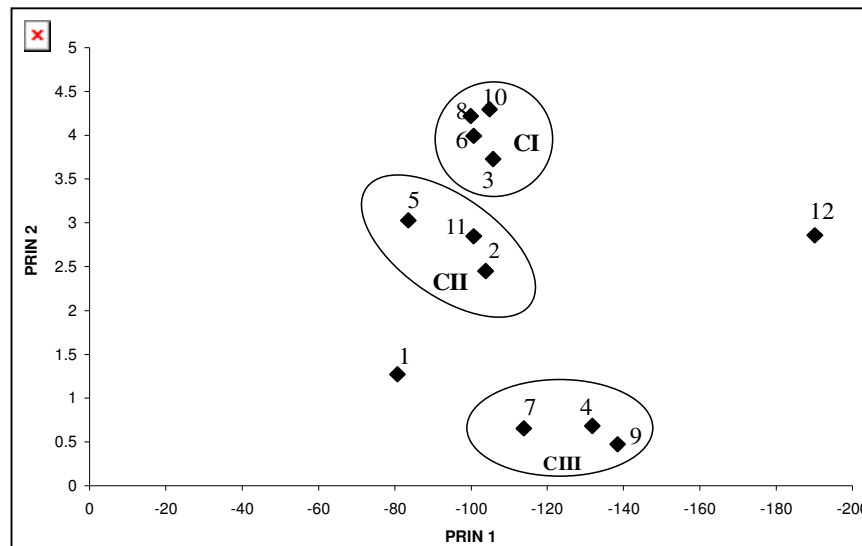
Figure 1. Plot of first (PRINI) and second (PRIN 2) principal components of vegetative and disease characteristics of 12 pepper accessions at fruiting stage.

Accession numbers

1 – UNS$_2$
2 – UNS$_3$
3 – NSKY-LP
4 – Sombe
5 – NSKY-SE
6 – Tarugu
7 – Tartasi
8 – Dangarawa
9 – Oshosho
10 – NSKY-RW
11 – Atanukwu yola
12 – Hybrid (Sombe x NSKY-RW)

Figure 2. Plot of first (PRIN I) and second (PRIN 2) principal components of vegetative and disease characteristics of 12 pepper accessions at maturity.

tion. Variation in PRIN 2 was primarily accounted for by the total number of infected leaves at fruiting. At maturity the contributor to PRIN 2 were the number of infected leaves, mosaic infection and the degree of leaf puckering. Hence, *NSKY-LP, Tarugu, Dangarawa* and *NSKY-RW* had high PRIN 2 scores at the fruiting stage. *Sombe and NSKY-LP* had high PRIN 2 score at maturity. The pepper

genotypes were grouped mainly into three classes at fruiting and two classes at maturity according to the pattern of variation as determined by PCA, which reflected the leaf production and disease tolerance potentials. Accessions in cluster 1 at fruiting were chiefly characterized by moderate leaf production and suscepti-bility to infection. They include *NSKY-LP, Tarugu,*

Dangarawa and *NSKY-RW*. Cluster II had accessions that are intermediate with respect to leafiness and level of infection. They comprise *NSKY-SE, Atanukwu yola and UNS₂.* Cluster II (*Tartasi, Sombe,* and *Oshosho*) had accessions that were resistant with moderate leaf production potentials. At maturity, accessions in clusters I and II produced leaves moderately. Genotypes in cluster I appear to be moderately tolerant to mosaic and puckering disorders, while cluster II produced accessions that were susceptible. *NSKY-LP* and *Sombe* fell within this group. Some of the genotypes were grouped together in a cluster. The cluster revealed the pattern of relatedness among the lines. This may be understood by this principle that genotypes strongly associated in the same group may share some underlying biological relationship (Iezzoni and Pritts, 1991). *UNS₃, NSKY-SE* and *Atanukwu yola* were grouped together in clusters II and I at fruiting and at maturity, respectively. This may be because they have a common origin i.e. belonging to the same species, *Capsicum fruitescens* (Udo et al., 2005). The hybrid (*Sombe* and *NSKY-RW)* showed better agronomic quality with respect to growth and disease tolerance potentials over other genotypes. The first principal component (PC1) explains the greatest portion of total variability in any principal component analysis (Iezzoni and Pritts, 1991). On this premise, it is reasona-ble to classify the pepper accessions based on the vegetative trait. This trait consistently affected all the major principal components (PC1). Similarly, the disease characters were the main determinants of PRIN 2, thus implicating them as additional useful traits for the classification of the pepper lines.

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