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Agromorphological Determinants Favoring the Spread of Anthracnose Disease in Cashew Agroforestry Farms in Côte d'Ivoire

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Authors' contributions

This work was carried out in collaboration among all authors. Author BKG designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors SS and DD managed the analyses of the study. Author NYCF managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Cashew cultivation faces several health problems. Among these problems, anthracnose causes extensive damage to twigs, leaves and fruits and causes loss of yield. The spread of this disease is thought to be determined by certain agromorphological features of the cashew tree. The objective

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of this study was to search for these agro-morphological determinants that influence the spread of anthracnose disease in agroforestry systems in Côte d'Ivoire. To achieve this objective, 30 cashew trees spread across 26 agroforestry cashew orchards in the Korhogo, Sinématiali and Boundiali departments were chosen and geolocated. The factor studied was the clone, consisting of 30 cashew genotypes, with 15 modalities. The collected data was subjected to descriptive analysis, correlation test, PCA and hierarchical ascending classification (CAH). The results showed that the wingspan, leaf area and size of cashew trees are determinants that promote the spread of anthracnose disease. Following this result, the CAH made it possible to screen the genotypes into three groups. These results could contribute to management of anthracnose disease in agroforestry, to enhance and intensify this cropping systems.

Keywords: Disease distribution; croping system; wingspan; leaf area; size; agroforestry system.

1. INTRODUCTION

The cashew tree is native to northeastern Brazil (Trevian et al., 2005) [1]. It was introduced by the Portuguese in the colonies of Africa and Asia [2,3] (Lautié et al., 2001). Africa alone accounts for 55% of world cashew production [4]. West Africa, led by Côte d'Ivoire, is the newest and most dynamic production area in the world. Indeed, it provides 88% of African production (Kouadio, 2018). The cashew tree is traditionally developed in Côte d'Ivoire by farmers following an agroforestry system, as in Tanzania, Mozambique, Nigeria, Guinea Bissau and Benin [5-8]. This crop then experienced a prodigious development for the Ivory Coast [9] thanks to the marketing of cashew nuts [3].

Notwithstanding the nature of a refuge plant for diseases that associated crops can present [10,11] and appear as a potential source of natural inoculation of cashew trees [12,13], the agroforestry system contributes to the reduction of the atmospheric carbon rate, promotes an environment conducive to agricultural and human development [14]. Consequently, this crop has aroused real enthusiasm which is reflected in the increase in the areas sown:1,350,000 ha in 2018 against 8,200 ha in 1970 [9,15].

The Ivory Coast has managed to occupy the first rank of cashew nut producing and exporting countries since 2015 with 702,510 tonnes of raw nuts [16]. However, the average yield of orchards remains low (350 to 500 kg/ha) [3] due to a growing environment favoring the distribution of diseases on farms, including anthracnose, caused by *Colletotrichum gloeosporioides*. These orchards are characterized by unimproved planting plant material and in particular vulnerable to pests as the anthracnose, which causes enormous production losses [17-19]. In Tanzania, anthracnose is one of the four diseases responsible for declining cashew yields (NARI, 2009). In 2000, anthracnose caused a drop in production of around 40% in Brazil [20].

The management of these plagues raises several issues. Indeed, chemical control is not only expensive but proves inaccessible for producers, non-resilient and dangerous for the health of populations and for the environment [21-23]. Therefore, the morphology of the host plant can make it more or less vulnerable. According to Calonnec [24] the agro-morphological parameters of the tree influence the dynamism of an epidemic within a crop. Thus, knowledge of the determinants of the spread of anthracnose in agroforestry operations and their agroecological management could sustainably curb the damage of anthracnose. In addition, it would contribute to the establishment of a more resilient, less expensive and environmentally friendly agricultural system.

It is in this perspective that the present study, first proposes to identify the agro-morphological determinants favoring the propagation of anthracnose disease in the cashew genotypes developed in an agroforestry system and secondly to structure these genotypes.

2. MATERIAL AND METHODS

2.1 Experimentation Site

The peasant orchards of the departments of Korhogo and Sinématiali of the Poro region and those of Boundiali of the Bagoué region were the places that hosted this study. These departments are located in the north of Côte d'Ivoire. In these regions, the climate is Sudanese and is marked by two seasons including a short rainy season which starts from May to October and a long dry season which extends from November to April. The wind is dry there from November to March. The average annual rainfall varies between 1000

and 1400 mm. The vegetation consists of wooded savannah. The soils are ferralitic, moderately to strongly denatured [3].

2.2 Plant Material

The plant material used consists of 30 genotypes of cashew trees from peasant orchards in the locality (Table 1). The cashew trees in these peasant orchards are 10 years old and have been developed in an agroforestry system, in cultural association with the shea tree and the mango tree. In this agroforestry system, the shea trees are arranged randomly, as the farmer found them, when the field is created. The mango trees, unlike the shea trees, represent protective hedges at the border and delimiting portions of the farm. The separation distances in this peasant system are not constant. These distances not only vary from one farm to another and in addition they are variable (2 meters to 10 meters) within the same farm.

2.3 Methods

2.3.1 Orchard prospection and choice of genotypes

The peasant orchards of the departments of Boundiali, Korhogo and Sinématiali were prospected to search for high-producing cashew genotypes (between 20 and 50 kg), 10 years old, developed in an agroforestry system that associates them with the mango tree and the shea tree. These tree populations were surveyed using the traveling inventory method combined with the diagonal and median method. Each tree or individual has been marked/ colored, numbered and geo-referenced using GPS. This approach was inspired by the strategies developed by Maxted et al. [25] to conduct eco-geographic surveys and those of Diouf et al. [26] to carry out ethnobotanical surveys. During surveys, the incidence and severity of bacteriosis on the populations of shea tree, cashew tree and mango tree were realized. Data related to agromorphological parameters were collected.

Table 1. Cashew genotypes and geographic locality of orchards

Locality 1: Boundiali		Locality 2: Korhogo		Locality 3: Sinématiali	
Genotypes	**Geographic Coordinates**	**Genotypes**	**Geographic Coordinates**	**Genotypes**	**Geographic Coordinates**
BKKY	N: 09°33.136’ O: 06°26.243’	KTY1	N: 09°29.984 O: 05°43.309’	KBSD	N : 09°35'154' O : 005°21'019
BBY	N: 09°27.798’ O: 06°29.779’	KTY2	N: 09°30.168’ O: 05°34.716’	KOMC	N : 09°36.505’ O : 005°20.710’
BKA	N: 09°38.382’ O: 06°21.127’	KTYY	N: 09°31.162’ O: 05°38.626’	KLYN	N : 09°36.354’ O : 005°20.627’
SST	N: 09°37.438’ O: 06°20.229’	KKSN	N: 09°31.674’ O: 05°38.783’	KT3	N : 09°33'721' O : 005°25'396
SYD	N: 09°24.467’ O: 06°21.871’	KKSS	N: 09°17.491’ O: 05°32.697’	BAK	N : 09°34'751 O : 005°25'302
SFA	N: 09°27.935’ O: 06°25.350’	KBT	N: 09°19.103’ O: 05°34.223’	SSS	N : 09°34.751' O : 005°28.030'
SWSZ	N: 09°31.733’ O: 006°25.921’	KSCK	N: 09°23.008’ O: 05°33.643’	STSL	N : 09°36.669’ O : 005°22'204’
SLLC	N: 09°32.295’ O: 006°30.356’	KC3	N:09°19.033’ O: 05°38.441’	SGYM	N : 09°29.800' O : 005°20.414'
SDYY	N: 09°28.861’ O: 06°32.693’	KCP2	N: 09°19.643’ O: 05°39.207’	SYDN	N : 09°33.345 O : 005°24.330'
SDYN	N: 09°39.932’ O: 06°29.327’	KCP1	N: 09°29.919’ O: 05°48.486’	STSB	N : 09°32.789' O : 005°23.864'

2.3.2 Data collection

For the sake of representativeness, data (agromorphological and phtopathological detailed below) were collected on 30 trees in the plots established in each yard.

On each of these trees, 10 branches were previously marked in the North-South (N-S) and East-West (E-W) axes. The marked branches are all located at breast height.

The data collected focused on the one hand on the height of the trees, the span, the circumference of the trunk, the leaf area, the number of main branches, the fruit load. In addition, was collected the incidence and severity of anthracnose disease on leaves, twigs and fruit.

2.3.2.1 Tree height

The height of the tree (HAr) was taken from the ground to the last leaf in height using a graduated ruler of length four meters (4 m).

2.3.2.2 Circumference of the trunk

The circumference of the trunk (CirTr) was measured by a tape measure at 5 cm from the ground.

2.3.2.3 Total leaf area

To evaluate the total leaf area (STF), 20 leaves were chosen at random from each plant of the different genotypes. On these leaves, the width and the length were measured then the SFT was determined according to the formula of Cornelissen et al. [27] below.

SFT = 0.86 × NF [0.91 × 3 (0.95 × L × w × π / 4)]

NF: Number of Leaves per tree (NF = 1); L: Length; l: width

2.3.2.4 Number of main branches

The number of branches (RPr) of trees of each genotype was determined by counting the main branches at the first branch level.

2.3.2.5 Tree spans North-South (Env N-S) and East-West (Env E-W)

The span of each tree was taken using a decametre in the North-South and East-West directions. The North-South wingspan was measured from the last leaf in the south to the last leaf in the north. For the East-West scale, it was taken from the last leaf in the East to the last leaf in the West.

2.3.2.6 Fruit load

The fruit load (ChFr) is the number of fruits present on a panicle. It was evaluated every two weeks by counting the fruits on the panicles of the ten branches.

2.3.2.7 Severity index of anthracnose disease

The severity was assessed on the twigs, leaves and fruits of each tree according to the rating scale of Cardoso et al. [28]. Severity was assessed using a visual rating scale ranging from 0 to 9 [28]; Grade 0: no symptoms; grade 1: 1-5%; grade 3: 6-10%; grade 5: 11-25%; grade 7: 26-50%; grade 9: > 50%. Scoring therefore consisted of assigning a percentage to diseased organs according to the distribution, intensity of symptoms and the number of organs affected. The summation of the severity scores at each branch marked in both directions of the tree was performed in order to obtain an average. The severity index (Is) of the observed diseases was determined according to the formula of Kranz [29] cited by Dianda et al. [30] below.

$$Is = \sum \left(\frac{Xi \times ni}{N \times Z}\right) \times 100$$

Is: Severity incident; **Xi:** severity i of the disease on the organ; **ni:** number of organ of severity i; **N:** total number of the organ observed; **Z:** highest severity scale.

2.3.2.8 Incidence of anthracnose disease

Anthracnose disease was diagnosed by the descriptions of symptoms made by Wonni I. et al. [18]; Massawe P. [31]; Afouda et al. [17]; Cardoso et al. [28]. The incidence (Ic) was determined by the ratio of the population of diseased individuals to the total population of individuals observed. The incidence (%) was assessed according to the following formula [32,33]:

$$Ic = \frac{\text{Number of organs attacked on the date of observation}}{\text{Total number of organs in the plot orbit}} \times 100$$

Ic : incidence

This assessment focused on forty branches per tree.

2.3.3 Statistical Analysis

Data entry was performed with Excel 2013 software. Statistica 7.1 software was used to perform descriptive analyzes. These analyzes were used to carry out the Pearson correlation test carried out with the SPSS 16.0 software to test the hypothesis according to which agromorphological parameters would be decisive in the propagation of the anthracnose disease in cashew tree culture. However, this hypothesis is verified, the ascending hierarchical classification (CAH), following the orientation of the principal component analysis (PCA) was carried out to structure individuals. Subsequently, the multivariate test completed these analyzes to characterize the homogeneous groups of individuals established by the CAH.

3. RESULTS

3.1 Determinants Influencing Anthracnose in Cashew Trees

3.1.1 Relationship between agromorphological and phytopathological parameters

The Pearson correlation test made it possible to detect 5 pairs of variables. These significant and positive correlations were detected between agromorphological parameters and incidence on the one hand, and between agromorphological parameters and severity on the other hand (Table 2). These were the correlations observed between the East-West wingspan and the severity index on the leaves (r = 0.75) and on the fruits (r = 0.67) on the one hand and on the other hand between the East-West wingspan and the incidence of anthracnose on the leaves (r = 0.76) and on the fruits (r = 0.57). The total leaf area (SFT) was correlated on the one hand both with the incidence on the leaves (r = 0.77), on the twigs (r = 0.69) and on the fruits (r = 0 , 54). On the other hand, the total leaf area (SFT) was correlated with both the severity index on leaves (r = 0.80) and on fruits (r = 0.67). Between the fruit load and the severity index on the fruits (r = 0.76) on the one hand and the incidence of anthracnose on the fruits (r = 0.59) on the other hand. These results showed that the incidence and severity of anthracnose are determined by east-west extent, leaf area, and fruit load.

3.1.2 Structuring of variables and genotypes by principal component analysis (ACP)

The projection of the variables and individuals on the plane (Figs. 1 and 2) made it possible to illustrate the position of the variables and individuals with respect to the axes. Thus, axis 1, expressing 23.79% of the variability, was positively correlated with the severity index of anthracnose on twigs in the KVSS and KTYY genotypes. It was negatively correlated with total leaf area and east-west span with the KTY3 genotype.

Axis 2, which expressed 17.19% of the total variability, was positively correlated with the incidence of anthracnose on fruits with the KTY1 genotype. The incidence on inflorescences was negatively correlated with the genotypes SDYY and SWSZ.

3.1.3 Analysis of genotypes by Ascending Hierarchical Classification (CAH)

The Ascending Hierarchical Classification (CAH) made it possible to structure the genotypes studied into 4 groups (Fig. 3) according to the method of Ward (1963). The dendrogram carried out with the means of the 15 variables studied made it possible to identify 4 groups of genotypes. Group 1 contains 10 genotypes which are KVSS, KTYY, KLYN, KOMC, KBT, KBSD, BAK, SYD, KSCK, BBY. Group 2 is made up of 6 genotypes which are BKKY, STSB, SFA, SGYM, SSS, BKA. Group 3 includes KTY3, SLLC, SDYY (3 genotypes). Finally, group 4 is made up of 11 genotypes which are: KCP1, KCP2, KCP3, KTY1, KTY2, SDYN, STSL, SYDN, KKSN, SWSZ, SST.

Multiple analysis of variance (MANOVA) (Table 3) showed a significant difference between these groups (F> 3 or P <0.005). This significant difference was observed at the level of the East-West extent, of the total leaf area, of the incidence of disease on the inflorescences, the leaves and the twigs as well as at the level of the severity indices on the twigs and inflorescences.

Group 1 was distinguished by severe infections in the twigs (87.75 ± 2.84). Group 2 was characterized by trees with small leaves (157.46 ± 9.27) and low leaf disease incidences (12.57 ± 3.97). Group 3 was distinguished by trees with broad leaves (367.86 ± 10.21) and by strong incidences at the level of leaves (46.25 ± 15.39) and twigs (96.52 ± 0 , 28). Group 4 was also

characterized by trees with large leaves (280.29 ± 8.51), by a high incidence of the disease in the twigs (91.33 ± 1.83) and inflorescences (69, 79 ± 5.48).

Table 2. Correlation matrix between agromorphological and phytopathological parameters

	IcINFLO	IcFe	IcRam	IcFr	IsINFLO	IsFe	IsRam	IsFr
CirTr	-0,10	0,04	-0,03	0,15	-0,11	-0,12	0,22	0,18
EnvN-S	0,13	0,29	0,25	-0,06	-0,41	0,06	-0,25	-0,03
EnvE-O	-0,09	**0,76**	0,37	**0,57**	-0,26	**0,75**	0,04	**0,67**
HAr	0,35	-0,23	-0,11	0,09	0,10	-0,04	-0,02	0,08
RPr	-0,16	0,25	0,02	0,22	-0,07	-0,15	0,31	0,12
SFT	0,02	**0,77**	**0,69**	**0,54**	-0,24	**0,80**	-0,33	**0,67**
ChFr	0,13	0,09	0,12	**0,59**	-0,26	0,24	-0,28	**0,76**

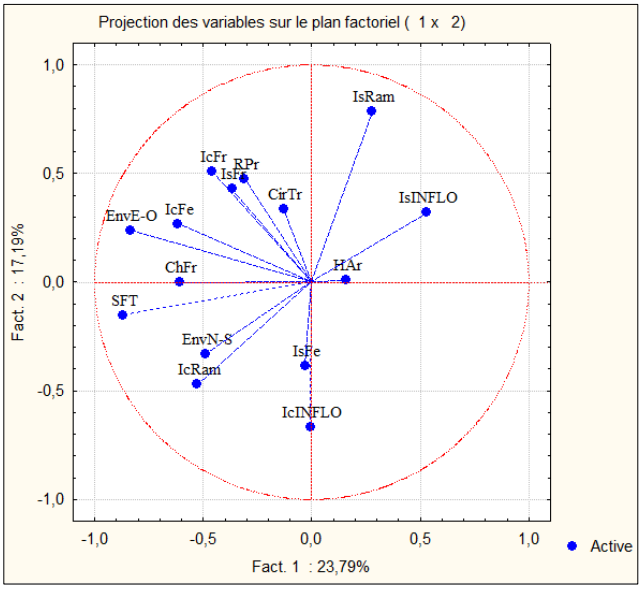

Fig. 1. Projection of the variables in the factorial plane

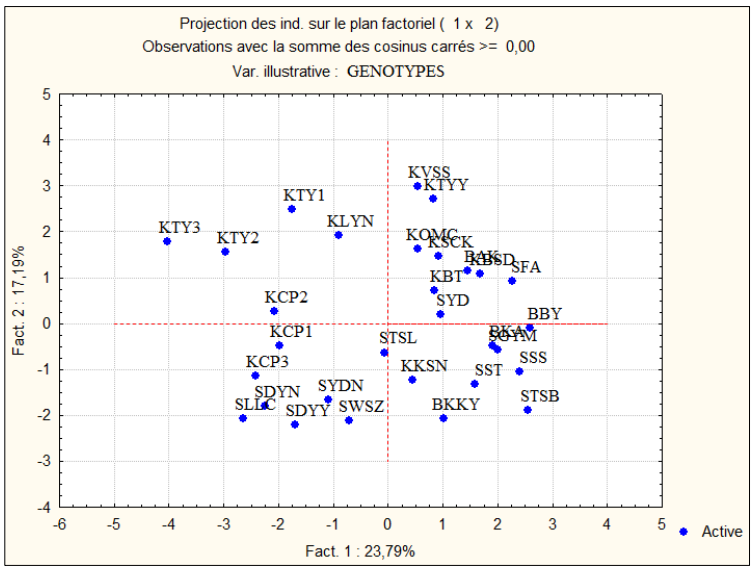

Fig. 2. Projection of individuals into the factorial plane

Table 3. Characteristics of groups generated by the CAH

	Groups				Statistics	
	GI	**GII**	**GIII**	**GIV**	**F**	**p**
CirTr	0,42±0,02**a**	0,42±0,03**a**	0,47±0,02**a**	0,41±0,014**a**	0,89741	0,455762ns
EnvN-S	5,20±0,17**a**	5,34±0,40**a**	6,13±0,13**a**	6,08±0,37**a**	2,01568	0,136388ns
EnvE-O	5,30±0,08**a**	4,377±0,32**ab**	3,77±0,62**c**	6,16±0,27**a**	**10,65527**	**0,000095s**
HAr	4,18±0,19**b**	4,37±0,31**b**	6,22±0,07**a**	3,12±0,16**c**	**5,23904**	**0,008304ns**
RPr	3,39±0,30**a**	3,05±0,25**a**	3,17±0,35**a**	3,62±0,26**a**	0,68429	0,569710ns
SFT	200,33±6,68**c**	280,46±9,27**b**	157,86±10,21**d**	367,29±8,51**a**	**70,34484**	**0,000000s**
ChFr	3,96±0,56**a**	3,75±0,75**a**	4,99±0,69**a**	3,97±0,64**a**	1,42369	0,258414ns
IcINFLO	64,66±4,88**c**	81,88±5,43**a**	31,47±14,14**d**	69,79±5,48**b**	**11,88806**	**0,000043s**
IcFe	22,99±5,87**b**	25,57±3,97**b**	12,25±15,39**c**	46,26±4,48**a**	**3,75718**	**0,062522s**
IcRam	83,78±1,99**b**	86,06±2,51**ab**	56,52±0,28**c**	91,33±1,83**a**	**5,08871**	**0,006638s**
IcFr	22,23±6,67**b**	15,49±5,15**c**	10,00±15,03**d**	29,44±5,95**a**	**7,34279**	**0,000622ns**
IsINFLO	54,81±4,74**b**	68,67±7,18**a**	37,85±7,47**c**	38,79±5,76**c**	**4,74867**	**0,009024s**
IsFe	18,51±4,57**b**	41,66±6,77**a**	21,82±3,47**b**	35,00±4,88**b**	**3,78737**	**0,00295s**
IsRam	87,75±2,84**a**	59,72±9,36**b**	36,95±22,24**c**	57,89±5,03**b**	**7,82056**	**0,0007s**
IsFr	20,92±8,48**b**	14,33±2,97**c**	7,19±3,71**d**	25,10±7,43**a**	**6,03655**	**0,002802ns**
Group size	**10**	**6**	**3**	**11**		

Numbers assigned the same letters on the lines are not statistically different (Turkey's HSD test at the 5% threshold). ***ns:*** *not significant,* ***s:*** *significant,* ***p:*** *probability,* ***F:*** *Fisher*

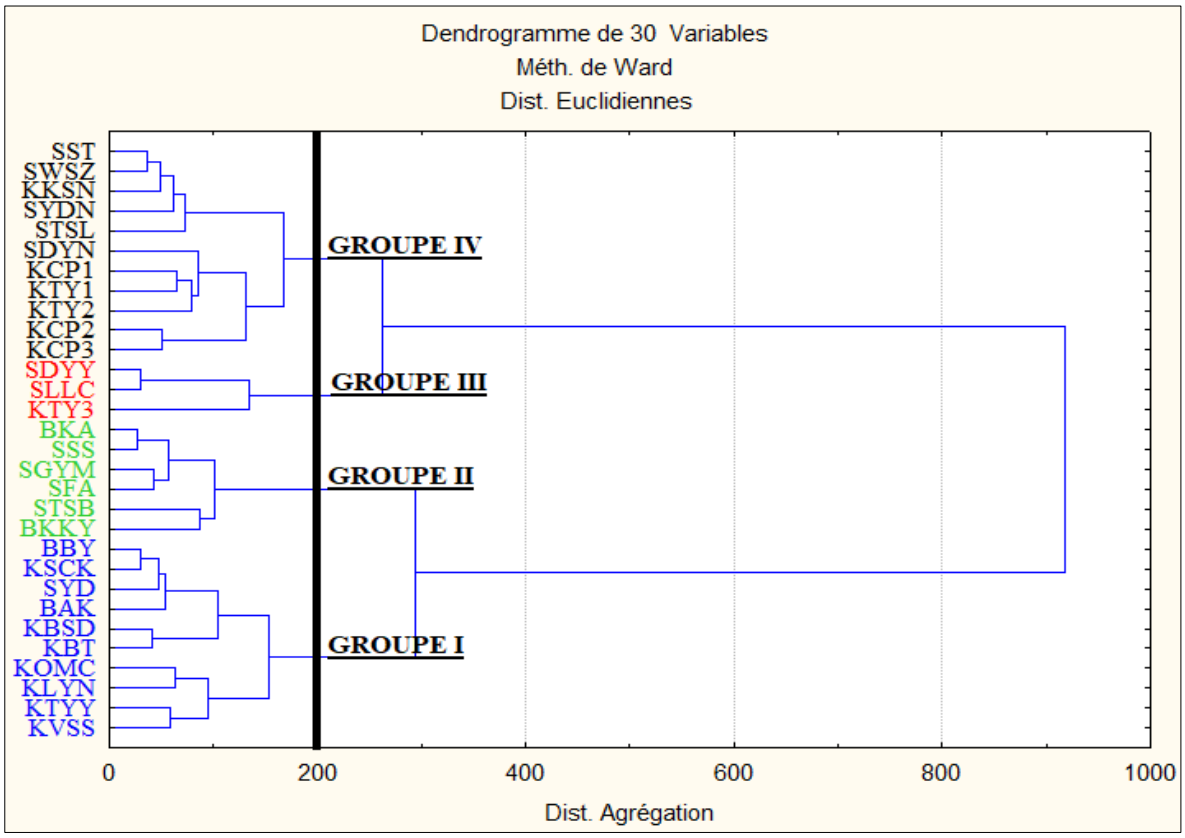

Fig. 3. Dendrogram showing the different groups of individuals by the CAH

4. DISCUSSION

The summary analysis of the results of the Pearson and ACP correlation test demonstrated that the North-South, East-West spans and leaf area are determinants that influence the level of incidence and the severity of the anthracnose disease. Establishing this correlation between these agro-morphological parameters and the severity index and incidence would explain that genotypes of large leaf areas as well as the East-West scope and significant fruit loads would favor an environment of severities and high incidences of anthracnose. Agro-morphological parameters would determine the degree of sunshine inside the canopy. Indeed the surface development of the leaves constitutes a cover for the twigs vis-à-vis the sun, creating a shade which will favor the manifestation of the disease.

This observation is confirmed by Bréda et al. [34]; according to them, all phenomena, such as radiation, precipitation and atmospheric deposition, are closely linked to the degree of closure of the plant cover and its leaf surface. In fact, a fairly pronounced development of the wingspan would reduce the porosity of the canopy to the sun and, under the effect of shade, would create a microclimate which would favor the manifestation of Calonnec [24]. This assertion was evoked by the studies of Zahavi and Reuveni [35] claiming that the light available inside the canopy would depend on the amount of light intercepted by the crown of the trees and therefore on the architecture of the plants used. However, as Poorter [36] argued, UV (Ultraviolet) rays reduce the germination of spores and the growth of mycelium in powdery mildew.

In addition, the positive correlation observed between the total leaf area and the incidence of anthracnose on leaves and fruits. This would attest to the close relationship between the leaves and the fruit. Indeed, the fruits are covered by the leaves; the closeness of these two organs can be detrimental for two-tier leaves. First, at the level of the interception of solar rays; This observation is also supported by studies by Calonnec [24] showing that solar radiation affects the survival of the spores of many fungi. Then, in terms of the dispersion of the spores, it should be noted that bringing the organs together would facilitate the dispersion of the spores between the organs. This result can be confirmed by

Calonnec [24] who specifies that in the environment, the main effect of tree architecture on the process of spore dispersal is the distance between the organs.

The structuring by CAH of the 30 genotypes studied and their characterization by multiple analysis of variances suggested that the group 3 genotypes, in this case KTY3, SDYY and SLLC representing 10% of the total number, presented trees of a significantly low East-West span, a significantly high tree height with a significantly low leaf area. These agromorphological characters could explain the low severity indices and the low incidence of anthracnose on the fruits. Indeed, according to Arraiano et al. [37] Plant morphology influences the manifestation of an epidemic by making the host plant more or less vulnerable. The great heights of the trees would not favor the transport of spores or germs taking place by splashing. Indeed, the work of Simón et al. [38] corroborated by those of Arraiano et al. [37], high plant heights may reduce the incidence and severity of disease. These authors state that taller plants are characterized by increased distances between the upper leaves and the lower leaves which are most often the main source of inoculum. Also, the increased distance of plants from the ground would result in a limitation of the amount of spores occurring by splashing.

Moreover, this distribution could explain the fact that each cashew tree genotype has its own specific characters that would allow it to react specifically to the aggression of the pathogen. Thus, each individual would have a specific resistance mechanism enabling him to react to an aggression against his aggressor [39,40]. In this context, the structuring of the cashew tree diversity into 3 groups would indicate that the genotypes of group 3 having recorded low severities and incidence on nuts would be more tolerant to attacks by the causative agent of anthracnose.

5. CONCLUSION AND PERSPECTIVES

The present study finds that the total leaf area, the east-west wingspan and the height of the tree are determinants of the spread of anthracnose.

The Ascending Hierarchical classification coupled with multivariate analysis made it possible to screen the genotypes into four groups. Group 3, consisting of genotypes KTY3, SDYY and SLLC, was distinguished by low severity and incidence of anthracnose on nuts. These genotypes of cashew trees exhibit better resilience for agroecological crop protection. In a context of reducing greenhouse gas emissions to fight climate disturbances, these cashew trees could help to enhance and intensify agroforestry cropping systems.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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