Evaluation of the behavior of cashew genotypes with regard to bacteriosis in agroforestry farms in northern Côte d'Ivoire

ABSTRACT

Notwithstanding the inflows of currency for the populations who practice it, the cultivation of the cashew tree contributes to strengthening the forestry agrosystem in Côte d'Ivoire. However, this culture, with multiple interests, is confronted with attacks from parasites including bacterial disease. Bacterial disease causes extensive damage to vegetative organs as well as fruits and causes yield losses. The objective of this study is to assess the behavior of cashew genotypes in relation to the severity and incidence of bacterial blight in the context of agroforestry production in Côte d'Ivoire. To achieve this objective, 30 cashew trees from the agroforestry orchards of cashew trees, from the Korhogo, Sinématiali and Boundiali departments, have been selected and geolocated. The factor studied is the genotype, made up of 30 cashew genotypes, with 6 modalities. The data collected was subjected to a descriptive analysis, a PCA. Ascending hierarchical classification (CAH) and multivariate analysis completed the data analysis. The results obtained revealed three groups of cashew trees. Those of group three made up of twelve (12) genotypes, namely SYDN, SDYY, SDYN and KBSD coming from the departments of Sinématiali and Korhogo, were differentiated from the others by a weak infection in the nuts (8.67 ± 2.74). The development of these results could contribute to promoting agroecological management of bacterial disease, to enhance and intensify agroforestry practices in C. d'Ivoire.

Key words: cashew tree, agroforestry system, bacterial blight, incidence, severity

Introduction

The cashew tree (*Anacardium occidentale*) was introduced to Africa in the 16th century by Portuguese navigators (Bamba, 2018). Originally, this plant was developed in Côte d'Ivoire as a species for reforestation (Kouamé et al., 2016; Kouakou et al., 2018). Nowadays, the cashew tree has become a cash crop for this country and is among others developed there following an agroforestry system as in Tanzania, Mozambique, Nigeria, Guinea Bissau and Benin (Tandjiékpon et al., 2003; Dwomoh et al., 2008; Hammed et al., 2008; Yabi et al., 2013). As a result, this crop is experiencing tremendous development for the Ivory Coast (Lebailly et al, 2012) thanks to the marketing of cashew nuts (Djaha et al., 2014).

Even if the associated crops can be hosts of the bacterial disease (Hamza, 2010; Pruvost and Lionel, 2001) and present themselves as a potential source of natural inoculation of cashew

trees, this agricultural system associating the cashew tree with other crops on the same agricultural holding contributes to the reduction of the atmospheric carbon rate, promotes an environment conducive to agricultural and human development (Balogoun et al., 2014). 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) (Lebailly et al., 2012; Firca, 2018). Thus, Côte d'Ivoire has managed to rank first among cashew nut producing and exporting countries since 2015 with 702,510 tonnes of raw nuts (Conseille Coton Anacarde in Doukouré and Kodjo, 2018).

However, the average yield of orchards remains low (350 to 500 kg / ha) (Djaha et al., 2014) and lower quality nuts with an outurn of between 46 to 48 Ibs (Issaka, 2019) due to growing environment favoring the distribution of diseases including bacteriosis in farms. Which farms are characterized by unimproved planting material and in particular vulnerable to parasites including bacterial disease (caused by *Xanthomonas sp*.) Which causes enormous losses in production and product quality (Wonni et al., 2017; Dénis et al., 2017; Dénis et al. al., 2018). The management of these plagues raises several issues.

Indeed, producers have always practiced chemical control which is not only expensive but proves inaccessible, non-resilient and dangerous for the health of populations and for the environment (Paré, 2011; MINADER, 2017; Ducroquet et al., 2017). Therefore, knowledge of the determinants of the spread of bacteriosis in agroforestry farms and their agroecological management could sustainably curb the damage of bacteriosis. In addition, it would contribute to the establishment of a more resilient, less expensive and environmentally friendly agricultural system. It is with this in mind that the authors propose to identify the agromorphological determinants favoring the propagation of bacterial disease in cashew genotypes developed in an agroforestry system and to structure them.

1-**Materials and methods**

1.1-Experimental sites

The peasant orchards of the departments of Korhogo, Sinématiali and Boundiali were the sites of the study. These departments were located in the north of the Ivory Coast. The climate there 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 with a dry wind from November to March. The average annual rainfall varies between 1000 and 1400

mm in these departments. The vegetation consists of wooded savannah. The soils are ferralitic, moderately to strongly denatured (Djaha et al., 2014).

1.2- Planting materials

The planting materials used in this study composed of 30 genotypes of cashew trees, collected from the peasant orchards of the departments surveyed (Korhogo, Sinématiali and Boundiali). The cashew trees of these peasant orchards have a planting period of 10 years and have the particularity of being developed, in an agroforestry system, in cultural association with the shea tree and the mango tree (Table I).

Table I : Different cashew genotypes and the geographic location of the 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'

1.3- Méthods

1.3.1- Orchard prospection and choice of genotypes

The prospecting was carried out in the peasant orchards of the departments of Boundiali, Korhogo and Sinématiali. It consisted in looking for genotypes all coming from high producers of cashew trees (between 20 and 50 kg), having a planting period of 10 years of age and developed in an agroforestry system which associates them with the mango tree and the shea tree. These trees populations were surveyed using the traveling inventory method

combined with the diagonals and medians 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. (1997) to conduct eco-geographic surveys and those of Diouf et al. (1999) 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.

1.3.2- Data collection

Data were collected on each site of the North-South and East-West axes of the tagged cashew trees. The data collection focused on the incidence and severity of bacterial blight in leaves, twigs and fruits.

1.3.2.1-Evaluation of the severity index (SI) of bacterial disease

Severity was assessed every two weeks on the leaves, fruits and panicles of the ten branches marked on either sites of the N-S and E-W axes.

The evaluation approach resulted in a visual rating scale ranging from 0 to 9 (Groth et al., 1999; Cardoso et al., 2004 in Silué et al., 2018).

The bacterial disease severity index was determined according to the formula of Kranz, (1988) cited by Dianda et al. (2018) according to the following formula.

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

Is : severity index; **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 (9).

1.3.2.2- Assessment of the incidence (Ic) of bactérial disease

The incidence was determined as the ratio of the number of infected individuals to the total number of individuals observed as a percentage. The impacts were determined according to the following formula (Aka et al., 2009 ; Zahri et al., 2014):

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

A scale adapted to that used by Bhagwat et al. (2015) for the discrimination of mango varieties infected with anthracnose allowed to qualify the level of incidence of bacterial disease. This six-grade scale (0-5) is defined as follows: 0 (no symptoms); grade 1 (1-10%: low incidence); grade 2 (11-20%: moderate incidence); grade 3 (21-30%: medium or intermediate incidence); grade 4 (31-50%: high incidence); grade 5 (> 50%: very high incidence).

This evaluation focused on ten branches marked on each side of the N-S and E-W axes to be seen and carried by hand.

1.3.3-Statistical analysis of the data collected

La saisie des données et les graphiques ont été effectués avec le logiciel Excel 2013. Le logiciel Statistica 7.1 a permis de faire les analyses descriptives des données et des tests d'homogénéités des moyennes en cas de différence significative. Les tests multi-variés tels que la classification ascendante hiérarchique (CHA) et l'analyse en composante principale (ACP) ont été effectuées avec le logiciel Statitistica 7.1.

2-Résults

2.1. Descriptive profile of the severity and severity index of bacterial disease

The mean severity indices presented in figure 2 revealed a strong variability between the genotypes. The infections range from moderate to very severe, including severe infections (Table II, Figure 1). Mild severe infections (between 11 and 25%) were observed in ten genotypes which are SST, KSCK, SYD, KVSS, KBT, STSB, KKSN, SDYN, SDYY and SYDN (Figure 1).

Nineteen genotypes presented severe infections (between 25 and 50%); these were SWSZ, KTY1, KTY2, KTY3, KCP1, KCP2, KCP3, STSL, BKA, SSS, SGYM, SFA, BBY, BAK, KLYN, KTYY, KBSD, BKKY, SLLC.

Tableau II : Indice de sévérité de la bactériose suivant l'évolution de l'anacardier

	Stade Végétatif		Stade Fructification
Génotypes	**(IsFe)**	**(IsRam)**	**(IsFr)**
SST	26,25±2,52**ab**	11,09±2,43**a**	29,00±0,50**c**
STSL	59,05±6,15**efg**	13,35±3,25**ab**	52,01±5,31**e**
BKA	41,12±5,35**c**	17,17±2,21**abc**	44,00±0,30**de**

SSS	57,10±2,35**efg**	19,45±2,05**abc**	53,20±0,05**ef**
SGYM	43, 81±5,32**cd**	14,55±3,21**ab**	42,25±2,50**d**
SFA	67,24±2,30**fgh**	17,25±5,60**abc**	51,51±3,25**e**
BBY	39,25±3,45**bcd**	18,75±5,46**abc**	35,33±2,50**cd**
KOMC	80,51±0,22**g**	25,44±6,45**bc**	74,15±8,35**f**
BAK	39,25±5,60**bcd**	22,05±1,33**b**	35,23±2,35**cd**
KSCK	30,49±2,41**b**	16,15±5,12**ab**	20,50±0,30**b**
KLYN	65,29±10,25**fg**	30,25±8,45**c**	55,15±1,75**ef**
SYD	20,01±9,33**a**	10,25±4,33**a**	15,05±0,30**ab**
KTYY	40,50±1,30**c**	24,56±7,30**bc**	33,15±0,00**cd**
KVSS	30,03±0,15**b**	14,00±6,05**ab**	22,02±10,5**b**
KBSD	41,15±0,50**c**	25,10±0,50**bc**	33,00±1,05**cd**
KBT	31,51±0,30**b**	16,01±2,14**ab**	25,05±0,00**bc**
STSB	24,05±2,45**ab**	14,56±3,25**ab**	18,51±4,55**abc**
BKKY	41,12±0,33**c**	23,55±0,10**b**	32,01±0,20**c**
KKSN	31,00±0,00**b**	17,05±2,15**abc**	24,00±0,50**bc**
SWSZ	37,20 ± 5,20**bcd**	17,81±2,11**abc**	28,01±0,20**bcd**
SDYN	27,01±9,45**abc**	15,05±7,44**ab**	21,05±3,05**b**
SDYY	29,07±8,44**abc**	15,08±1,25**ab**	22,00±1,05**b**
SLLC	41,15±2,45**d**	25,00±0,33**bc**	33,00±1,75**c**
SYDN	33,01±1,95**cb**	10,50±9,35**a**	13,50±0,00**ab**
KCP1	57,05±5,52**efg**	23,77± 5,33**bc**	52,10±2,45**e**
KCP2	47,50±4,75**def**	31,25± 9,44**c**	30,55±0,05**c**
KCP3	58,51±15,65**efg**	26,25±4,33**bc**	35,73±8,50**cd**
KTY1	38,50±2,33**bcd**	20,75±9,55**b**	23,95±9,88**b**
KTY2	43,15±2,52**de**	25,55±4,33**bc**	24,50±0,75**bc**
KTY3	41,02±4,55**d**	25,15±2,33**bc**	33,00±7,33**cd**
Moyenne	**42,03±4,25**	**19,56±6,42**	**37,39±5,78**
P-value	**0,001**	**0,000**	**0,000**
CV(%)	**24,75**	**6,76**	**51,62**

Les chiffres affectés des mêmes lettres dans les colonnes ne sont pas statistiquement différents selon les teste HSD de Turkey au seuil de 5%.

CV : coefficient de variabilité ; **IsFe** : indice de sévérité sur feuilles ; **IsRam** : indice de sévérité sur rameaux ; **IsFr** : indice de sévérité sur fruits.

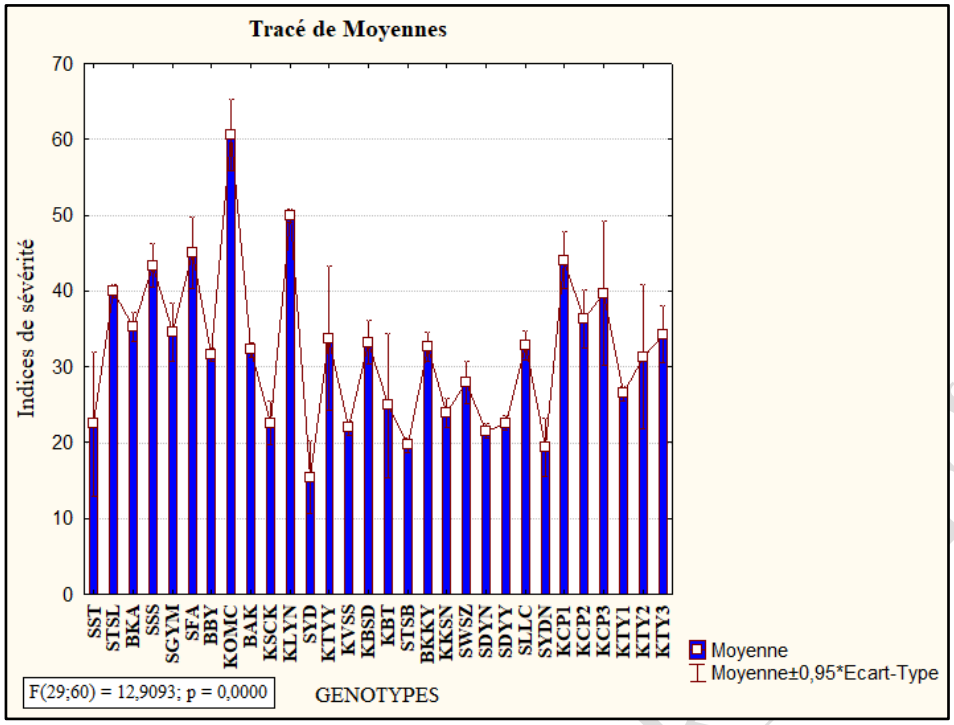


Figure 1: histogram of the means of the severity indices

2.2-Descriptive analysis of the incidence of bacterial disease

The histogram and the table of incidence values (Figure 2 and Table III) shows a significant difference between the genotypes (P <0.05). All trees exhibited mean incidences greater than 10%. Eight genotypes (STSL, BKA, SGYM, BBY, KBSD, SDYN, SDYY and SYDN) presented incidences of between 11 and 25%. Twenty genotypes, namely, SST, SSS, SFA, KOMC, BAK, KSCK, KLYN, SYD, KTYY, KVSS, KBT, STSB, BKKY, KKSN, SWSZ , SLLC, KCP3, KTY1, KTY2 and KTY3. Only KCP1 and KCP2 presented incidences greater than 50%.

Genotypes	Stade Végétatif (IcFe)	(IcRam)	Stade Fructification (IcFr)
SST	46,18±2,05**de**	28,25±3,33**cde**	40,00±5,01d
STSL	22,96±6,45**ab**	25,00±7,25**cd**	25,00±5,36**bc**
BKA	22,87±1,45**ab**	15,00±2,85**bc**	17,00±2,80**abc**
SSS	61,01±1,75**f**	10,83±5,11**b**	65,00±5,30**fg**
SGYM	19,89±8,65**a**	23,00±7,51**cd**	28,07±6,25**bcd**
SFA	50,43±0,45**e**	28,75±2,35**cde**	48,55±4,33**def**
BBY	19,32±5,74**a**	4,16±4,70**a**	20,00±2,90**b**
KOMC	68,67±3,35**fgh**	24,33±8,39**cd**	52,08±15,35**g**
BAK	40,84±1,73**d**	17,08±7,54**bcd**	45,15±9,20**de**
KSCK	63,34±5,27**fg**	23,58±6,45**cd**	43,00±7,50**de**
KLYN	66,81±12,45**fgh**	23,25±17,25**cd**	56,26±4,35**ef**
SYD	58,62±6,75**efg**	30,41±9,65**d**	50,00±7,85[e]
KTYY	56,28±11,55**efg**	34,16±8,45**de**	45,33±15,35**de**
KVSS	53,20±7,25**ef**	23,00±7,61**cd**	38,47±18,05**cde**
KBSD	35,30±9,61**cd**	19,00±13,50**bcd**	15,00±1,50**ab**
KBT	49,43±6,75**def**	34,58±4,56**de**	19,50±0,30**b**
STSB	36,02±3,69**cd**	28,08±5,11**cde**	17,36±5,71**abc**
BKKY	50,39±14,35**e**	39,58±9,45**e**	28,00±16,05**bcd**
KKSN	32,91±5,15**cd**	33,25±6,11**de**	16,00±0,50**ab**
SWSZ	39,60±7,43**cde**	40,41±8,35**e**	29,00±0,33**bcd**
SDYN	23,67±9,75**ab**	18,16±14,23**bcd**	10,81±6,45**a**
SDYY	24,55±7,30**ab**	21,00±9,25**c**	15,00±0,65**ab**

SLLC	35,42±7,45**cd**	32,00±8,50**de**	20,25±5,33**b**
SYDN	23,94±11,5**ab**	17,08±7,55**bcd**	14,00±8,44**ab**
KCP1	71,15±6,75**g**	56,06±13,45**fg**	48,16±12,51**def**
KCP2	80,14±15,20**h**	55,25±8,33**fg**	35,00±10,87**cd**
KCP3	62,87±9,45**f**	40,16±8,20**e**	43,66±12,33**de**
KTY1	63,9±17,66**fh**	25,74±9,44**cd**	46,69±20,33**de**
KTY2	58,24±12,05**efg**	33,41±10,32**de**	35,00±15,23**cd**
KTY3	46,3±12,55**de**	23,51±12,30**cd**	39,25±12,44**d**
Moyenne	**45,38±14,21**	**27,60±7,25**	**33,55±10,62**
P-value	**0,001**	**0,025**	**P= 0,000**
CV%	**17,97**	**6,08**	**45,13**

Table III : Incidence of bacterial disease following the course of the cashew tree

Les chiffres affectés des mêmes lettres dans les colonnes ne sont pas statistiquement différents selon les teste HSD de Turkey au seuil de 5%.

CV : coefficient de variabilité ; **IcFe** : indice de sévérité sur feuilles ; **IcRam** : indice de sévérité sur rameaux ; **IcFr** : indice de sévérité sur fruits.

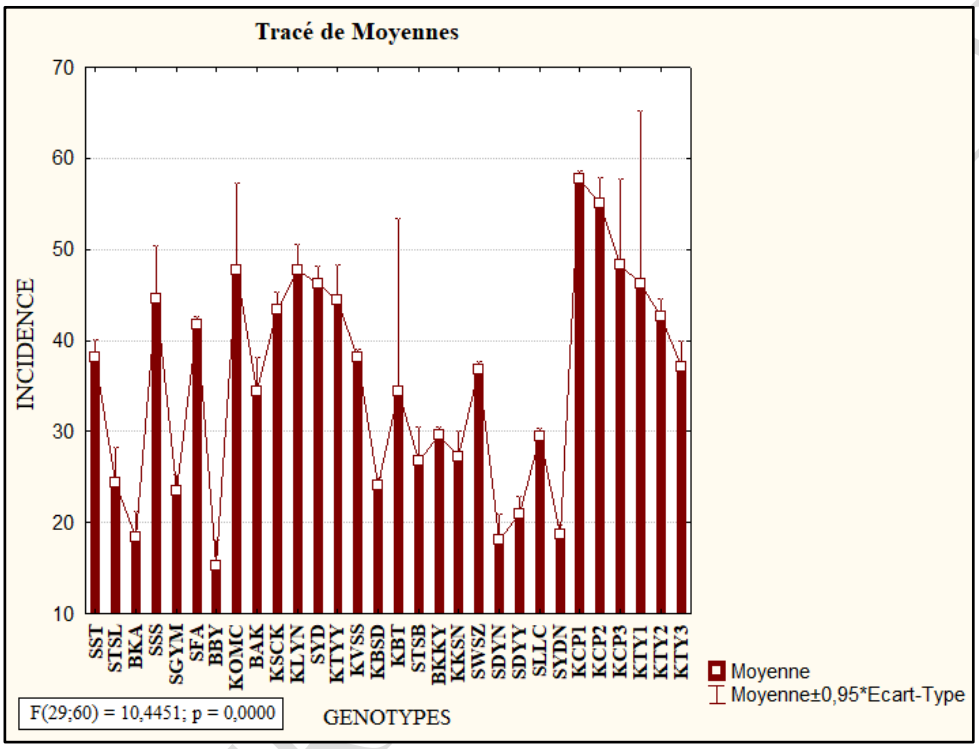
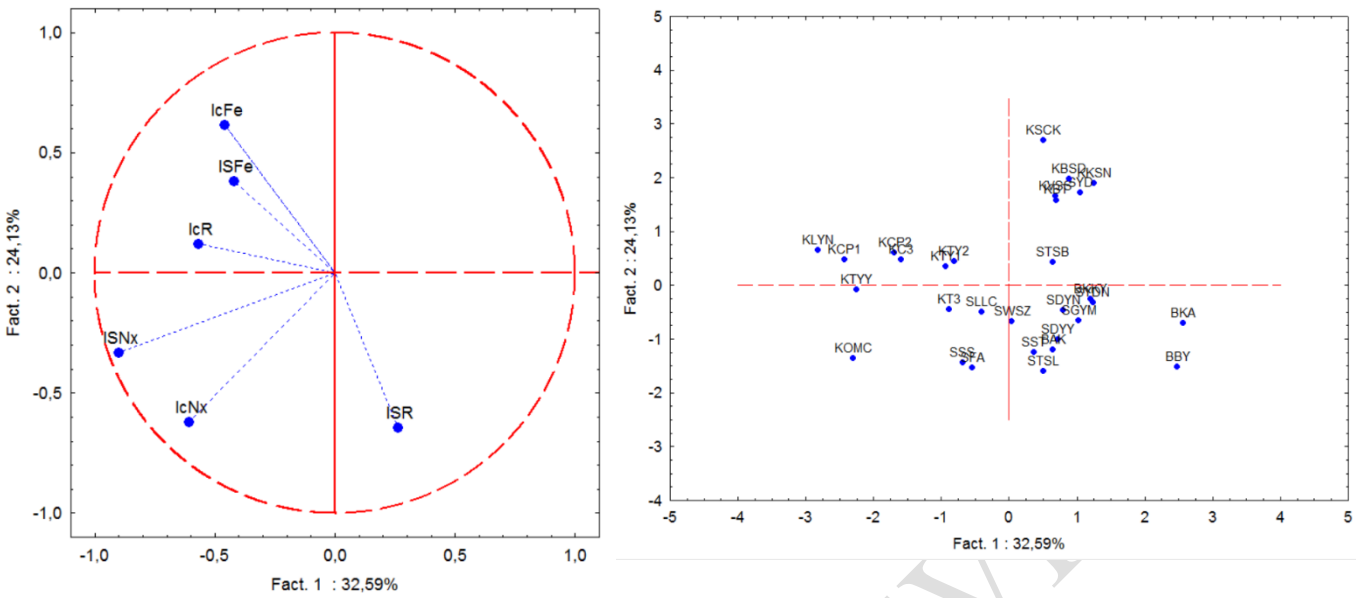


Figure 2: histogram of mean incidence values

2.3. Principal component analysis (PCA) of the incidence and severity of bacterial disease

Principal component analysis PCA was defined by the first two axes which explained 56.72% of the total variability observed. Axis 1 which returned 32.59% of the variability was defined on the negative side by the bacterial disease Severity Index on Walnuts (ISNx) with the KOMC. Axis 2 explained 24.13% of the observed variability. This axis was formed on the positive side by the incidence of bacterial disease on leaves (IcFe) and on the negative side by the incidence of bacterial disease on walnut (IcNx) and the severity index of bacterial disease on twigs (ISR) with the SFA and STSL genotypes.



A **B**

Figure 3: Projection of variables (A) and genotypes (B) in the factorial plane 1 and 2

2.4- Structuring and characterization of genotypes by Ascending Hierarchical Classification (AHC) and multiple analysis of variances (MANOVA)

The Ascending Hierarchical Classification (CAH) made it possible to structure the genotypes studied into 3 groups (Figure 4) according to the method of Ward (1963).

Group 1 was made up of nine genotypes (KCP1, KCP2, KCP3, KTY1, KTY2, KTY3, KLYN, KTYY and SLLC. Group 2 also contained nine genotypes namely KOMC, SFA, SSS, KBT, KVSS, the SST, SWSZ, BAK, and BKK.

The third group with 12 individuals comprised the genotypes SYD, KSCK, KBSD, KKSN, BBY, BKA, SGYM, STSL, SDYY, SYDN, STSB and SDYN.

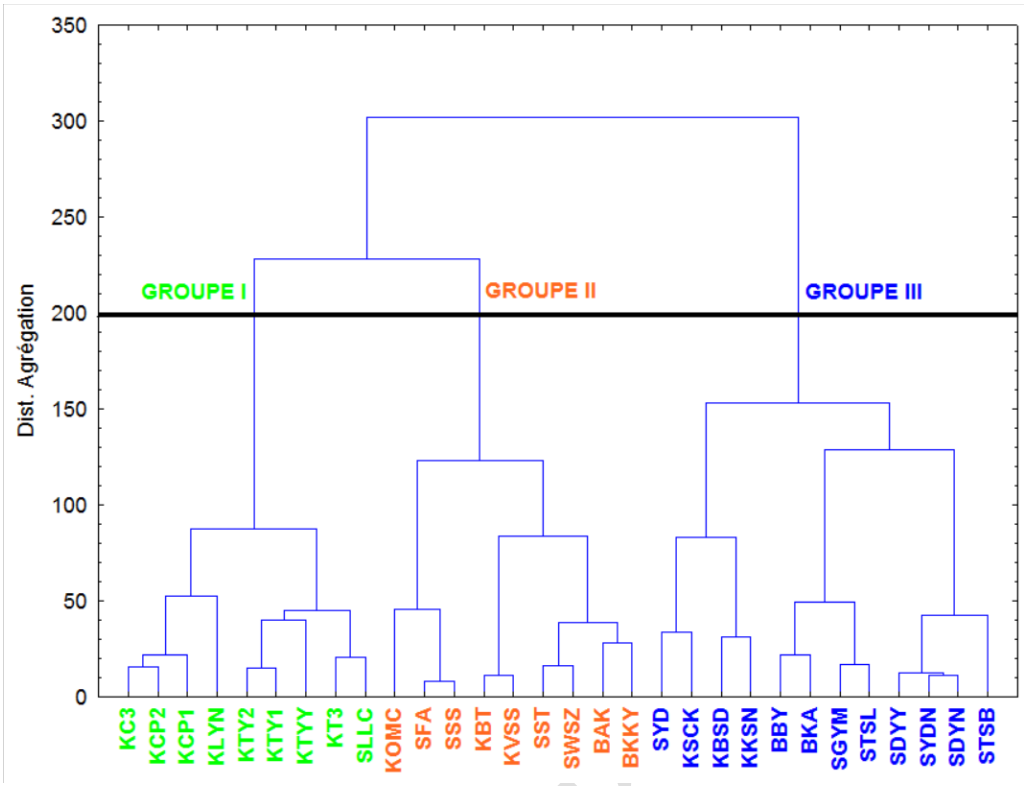


Figure 4: Structuring of groups of cashew trees by the Ascending Hierarchical Classification (CAH)

1.5. Characteristics of the groups obtained

Multiple analysis of variance (MANOVA) (Table IV) showed a significant difference between these groups (F> 4 or P <0.005). This significant difference was observed in the incidence of bacterial disease on twigs, leaves and nuts and the level of severity indices in nuts.

Thus, group 1 was characterized by a high incidence of bacterial disease on the leaves (50.98 ± 3.96) and severe infections in the nuts (45.13 ± 4.01). Group 2 was characterized by a high incidence of disease in the twigs (81.1 ± 3.21) and by severe infections in the twigs (47.58 ± 5.82). Group 3 was differentiated from the others by a weak infection in the nuts (8.67 ± 2.74)

Table IV: Descriptive analysis of the different groups of cashew trees formed by the CAH

	GROUPES			STATISTIQUES		
Variables	I	II	III	F	P value	Significativité
IcR	64,77 ± 5,89^{b}	81,1 ± 3,21^{c}	33,23 ±5,03^{a}	25,7	P < 0,0001	OUI
IcFe	50,98 ± 3,96^{c}	20,02 ± 1,74^{b}	33,36 ± 5,72^{b}	10,34	P < 0,001	OUI
IcNx	20,37 ± 1,22^{b}	14,03 ± 3,28^{ab}	10,12 ± 2,92^{a}	3,62	P < 0,05	OUI
ISR	28,10 ± 2,93^{a}	47,58 ± 5,82^{a}	38,89 ± 6,59^{a}	2,62	P > 0,05	NON
ISFe	36,28 ± 3,29^{a}	34,45 ± 4,70^{a}	29,91 ± 3,97^{a}	0,69	P > 0,05	NON
ISNx	45,13 ± 4,01^{c}	21,71 ± 6,76^{b}	8,67 ± 2,74^{a}	17,04	P < 0,0001	OUI
Effectifs	9	9	12	13,95	P < 0,0001	OUI
Pourcentage (%)	30	30	40			

Discussion

Analysis of the data on the severity of bacterial disease showed a significant difference between the genotypes. This difference testifies to the existence of great diversity within the genotypes of peasant orchards. In fact, three classes of genotypes were obtained with the severity data. The presence of bacterial disease symptoms in all trees would show the sensitivity of these genotypes to virulent strains of *Xanthomonas sp*, and the existence of a microclimate favorable to the development of the pathogen according to the "triangle of diseases" described by Nasraoui (2008) . According to the author, the development of a disease in the plant requires the presence of three components (the host plant, the pathogen and a favorable environment).

The climate would have impacted the occurrence of bacterial disease, making the plant vulnerable while promoting the dissemination and germination of spores. In fact, this study began at a period corresponding to strong variations in temperature which would have caused physiological instability in these genotypes. This instability would have predisposed the immune system of these plants which recordrded strong severities. These results were in accordance with Cardoso et al. (2004) who showed that temperature variations create physiological instability in plants and make them more vulnerable to attack.

In addition, this variation in severity in these genotypes would be linked to the difference in their defense mechanisms. According to Desanlis (2013) the defense mechanisms put in place by a plant against a pathogen differ from one genotype to another. Indeed each genotype has intrinsic characteristics allowing it to resist it’s attacker. Thus, slightly infected genotypes

have defense mechanisms that allow them to react more quickly to aggression and to limit the progression of the infection (Gascuel, 2014; Cazaux, 2009).

In general, this first level of defense is easily avoided by the pathogen. As for the defense mechanisms induced, they result from an initial recognition between the pathogen and the host plant. It can be general or specific ( ). In this category, we can distinguish some of the so-called "non-host" mechanisms that provide all host plants with a first level of immunity against all species of a pathogen. On the other hand, so-called "host" mechanisms which provide a particular host with specific immunity against a reduced number of pathogens of a species (Gascuel, 2014; Desanlis, 2013 and Cazaux, 2009).

The ACP performed showed that 3 variables (incidence of bacterial disease on leaves and twigs, severity index on twigs) out of the six studied contributed the most to the total variability. The CAH carried out made it possible to classify the genotypes studied into four groups of phytopathological diversity (incidence and severity index). This screening confirms the phenotypic diversity observed within these genotypes.

Conclusion

The present study notes the existence of a strong phenotypic diversity within the genotypes studied. The diagnosis of bacterial disease revealed a strong variation in incidence and severity depending on the genotypes and the organ attacked.

The hierarchical ascending classification made it possible to screen the studied genotypes into three groups on the basis of the mean values of incidence and severity index. Thus, group 1 (made up of 9 genotypes) was characterized by a high incidence of bacterial disease on the leaves (50.98 ± 3.96) and severe infections in the nuts (45.13 ± 4.01) . Group 2 (9 genotypes) was characterized by a high incidence of disease in the twigs (81.1 ± 3.21) and by severe infections in the twigs (47.58 ± 5.82). Group 3 (composed of 12 genotypes) differentiated from the others by a weak infection in the nuts (8.67 ± 2.74).

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