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Evaluation of the Behavior of Cashew Genotypes against Anthracnose Disease Aggression in Agroforestry Farms in Northern 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 DD and DN managed the analyses of the study. Author OZF managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

As in all cashew producing areas, anthracnose causes enormous production losses in cashew agroforestry farms in Côte d'Ivoire. To overcome this problem, the use of anthracnose-resilient production plant material in cashew forest agrosystems is becoming a necessity for sustainable

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development. Thus, this study was carried out with the aim of evaluating the behavior of genotypes of cashew trees cultivated in peasant agroforestry systems in the north of Côte d'Ivoire. To do this, peasant agroforestry cashew orchards were prospected, cashew trees were marked, codified and geolocated. The incidence and severity of anthracnose were then assessed on the marked and geotagged cashew leaves, twigs, inflorescences and fruits. Descriptive analysis of the incidence and severity data revealed that more than 50% of the genotypes studied are resilient to anthracnose with an incidence on nuts in the order of 0.00 ± 5.75%. The ACP explained 52.96% of the total variability observed with the first two axes. The CAH made it possible to structure these genotypes into four groups. MANOVA showed that genotypes in groups 2 and 4 exhibited traits of resilience against anthracnose disease. Group 2 was characterized by a relative absence of disease in the fruits (0.00 ±0.00) and by very severe infections in the twigs (88.19 ± 2.98). Groups 4 were differentiated by low fruit infections (1.32±0.32) and low incidence on fruits (2.17±1.09). These results should help promote the agroecological management of anthracnose disease, enhance and intensify agroforestry practices in Côte d'Ivoire.

Keywords: Cashew genotypes; agroecology; agroforestry; ACP; anthracnose disease.

1. INTRODUCTION

Native to northeastern Brazil [1,2] the cashew tree *(Anacardium occidental L.)* was introduced by the Spanish and the Portuguese in the colonies of Africa and Asia [3,4,5]. Africa alone accounts for 55% of global cashew production [6]. West Africa, led by the Ivory Coast, is the newest and most dynamic production area in the world. Indeed, it provides 88% of African production [7]. In Côte d'Ivoire, the cashew tree was introduced in 1951 as a species for reforestation [8]. Thus orchards were created in the North of Côte d'Ivoire by the Technical Assistance Company for the Modernization of Agriculture in Côte d'Ivoire (SATMACI) and the Forestry Development Society (SODEFOR) in the 1960s [9]. These orchards were intended to fight against erosion and deforestation in the northern regions of Côte d'Ivoire.

Nowadays, the cashew tree has become a cash crop for this country agroforestry system as in Tanzania, Mozambique, Nigeria, Guinea Bissau and Benin [10,11,12,13]. Since 2015, Côte d'Ivoire has been the world's leading producer and exporter of raw cashew nuts [14] with a national production of 738,000 tonnes of raw cashew nuts marketed in 2018. Despite the importance of Ivorian cashew production, the average yield of Ivorian peasant orchards remains low, in the order of 350 to 500 kg / ha [15]. This low production is mainly due to the use of plant material from all sources combined with high pest pressure [15,16]. Indeed, these orchards are faced with attacks from diseases including anthracnose [17,18]. In Tanzania, anthracnose is one of the four diseases responsible for declining cashew yields [19]. In 2000, anthracnose in Brazil caused a drop in production of around 40% [20]. Based on this observation, the use of resilient cashew genotypes for the development of agroforestry operations would be the best agroecological management approach for parasites in order to permanently curb anthracnose disease. In addition, it would help build a more resilient, less costly and environmentally friendly farming system.

To achieve this, the authors propose to evaluate, at different stages of development, the behavior of cashew genotypes developed in an agroforestry system and to structure them according to the severity and incidence of anthracnose disease.

2. MATERIAL AND METHODS

2.1 Expérimentation Site

The peasant orchards of the departments of Korhogo, Sinématiali and Boundiali were the sites of the study. These departments are all 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. The vegetation consists of wooded savannah and the soils are ferralitic, moderately to strongly denatured [4].

2.2 Plant Material

The plant material used is composed of 30 genotypes of cashew trees 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 1).

2.3 Méthods

2.3.1 Orchard prospection and choice of genotypes

The prospecting was carried out in the peasant orchards of the departments of Sinématiali, Korhogo and Boundiali. It consisted in looking for genotypes all coming from high producer cashew tree (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 tree 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. [21] to conduct eco-geographic surveys and those of Diouf et al. [22] to carry out ethnobotanical surveys. During surveys, the incidence and severity of anthracnose diseaseon the populations of shea tree, cashew tree and mango tree were realized.

2.4 Statistical Analysis

Data were collected on each side of the North-South and East-West axes of the tagged cashew tree. These data focused on the incidence and severity of anthracnose disease in leaves, twigs, inflorescences and fruits.

2.4.1 Evaluation of the severity index (Is) of anthracnose disease

Severity was assessed every two weeks on the leaves, fruits and panicles of the ten (10) branches marked on either side of the N-S and E-W axes. The evaluation approach resulted in a visual rating scale ranging from 0 to 9 [23,24,25].

The anthracnose disease severity index was determined according to the formula of Kranz [26] cited by Dianda et al. [27] according to the following formula.

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

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).

2.4.2 Assessment of the incidence (Ic) of anthracnose disease

The incidence was determined as the ratio of the number of sick individuals to the total number of individuals observed as a percentage. The impacts were determined according to the following formula [28,29]:

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

A scale adapted to that used by Bhagwat et al. [30] for the discrimination of mango varieties infected with anthracnose allowed to qualify the level of incidence of anthracnose 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 (10) branches marked on each side of the N-S and E-W axes to be seen and carried by hand.

2.4.3 Statistical analysis of the data collected

Data entry and graphs were performed with Excel 2013 software. Statistica 7.1 software was used to perform descriptive analyzes of the data and tests of homogeneity of the means in the event of a significant difference. Multivariate tests such as principal component analysis (PCA), ascending hierarchical classification (CHA) and multiple analysis of variance (MANOVA) were carried out with Statitistica 7.1 software in order to discriminate genotypes in according to their behavior towards anthracnose.

Table 1. 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'

Table 2. Anthracnose disease severity index following the evolution of the cashew tree

	Vegetative stage		Flowering stage	Fruiting stage
Génotype	**(IsFe)**	**(IsRam)**	**(IsInflo)**	**(IsFr)**
SST	26,85±5,63abcde	46,29±4,45bcdefg	46,29±7,26abcde	0,00±0,00a
STSL	59,25±6,19ef	63,88±4,24efghij	50,92±11,33abcde	18,51±8,91abc
BKA	44,44±9,93bcdef	77,77±6,87hijk	81,48±6,19e	0,00±0,00a
SSS	55,55±4,96def	81,48±6,02ijk	67,59±9,55abcde	0,00±0,00a
SGYM	35,18±6,52bcdef	43,51±7,51bcdef	74,07±10,31cde	12,96±8,80abc
SFA	29,62±5,10abcde	81,48±8,80ijk	80,55±6,37e	9,25±5,30ab
BBY	24,07±5,67abcd	88,88±6,57jk	51,85±9,36abcde	0,00±0,00a
KOMC	20,37±6,02abc	74,07±3,70fghijk	40,74±4,68abcde	44,44±9,51cde
BAK	19,44±9,80abc	97,08±2,45k	69,44±8,57bcde	25,92±4,68abcd
KSCK	15,74±8,29abc	89,58±8,02jk	39,81±4,16abcde	0,00±0,00a
KLYN	46,29±11,53cdef	96,25±2,39k	42,59±7,81abcde	70,37±4,68e
SYD	36,11±10,11bcdef	90,41±4,97jk	60,18±14,65abcde	0,00±0,00a
KTYY	0,00±0,00a	94,16±4,50jk	62,96±4,68abcde	55,55±0,00de
KVSS	0,92±0,92a	75,00±8,08ghijk	77,77±5,73de	12,96±12,9abc
KBSD	11,11±0,00ab	95,00±2,50k	68,51±10,40abcde	0,00±0,00a
KBT	11,11±0,00ab	77,08±9,84ghijk	34,25±9,55abcd	0,00±0,00a
STSB	64,81±4,45f	42,59±6,67bcde	74,07±6,19cde	18,51±12,31abc
BKKY	21,37±1,17abc	31,48±5,30abcd	34,25±10,67abcd	0,00±0,00a
KKSN	11,11±0,00ab	55,5±4,05defghi	24,07±4,68a	0,00±0,00a
SWSZ	42,59 ± 8,80bcdef	46,29±3,41bcdefg	30,55±7,82abc	0,00±0,00a

	Vegetative stage		Flowering stage	Fruiting stage
Génotype	**(IsFe)**	**(IsRam)**	**(IsInflo)**	**(IsFr)**
SDYN	42,59±8,32bcdef	22,22±7,02abc	35,18±10,89abcd	40,74±13,65bcde
SDYY	20,37±6,02abc	18,518±2,34ab	33,33±9,51abcd	0,00±0,00a
SLLC	16,66±3,79abc	11,11±0,00a	27,77±4,75ab	9,20±6,52ab
SYDN	20,37±3,41abc	50,00±8,48cdefgh	42,59±8,44abcde	0,00±0,00a
KCP1	40,37±9,85bcdef	83,55± 6,56ijk	63,25±3,55abcde	22,67±6,63abcd
KCP2	48,80±7,09cdef	88,88± 8,43jk	52,75±2,98abcde	0,00±0,00a
KCP3	48,11±11,45cdef	58,61±9,07defghi	38,21±11,02abcde	0,00±0,00a
KTY1	53,03±6,51def	93,83±4,33jk	43,50±12,63abcde	23,95±9,88abcd
KTY2	50,14±2,45cdef	86,64±3,22jk	36,94±9,34abcd	0,00±0,00a
KTY3	53,01±3,43def	63,92±6,50efghij	23,75±7,54a	33,17±13,77bcde
Average	32,31±5,58	67,5±5,54	50,31±8,02	13,27±3,92
P-value	0,000	0,000	0,000	0,000
CV(%)	17,27	8,21	15,94	29,54

The numbers assigned the same letters in the columns are not statistically different according to Turkey's HSD tests at the 5% level
CV: coefficient of variability; IsFe: severity index on leaves; IsRam: severity index on twigs; IsInflo: severity index on inflorescences; IsFr: severity index on fruits

3. RESULTS

3.1 Descriptive Profile of the Severity and Severity Index of Anthracnose Disease

The severity indices (Table 1 and Fig.1) revealed a strong variability between the genotypes. Infections range from medium to very severe, including severe infections. Mild severe infections (ranging from 11 to 25%) were observed in four genotypes, namely SLLC, SDYY, BKKY, and KKSN.

18 genotypes presented severe infections (between 25 and 50%); these are the genotypes SYDN, SST, SWSZ, KBT, SDYN, KSCK, KCP3, BBY, SGYM, KVSS, KTY3, KTY2, KBSD, KOMC, SYD, STSL, KCP2, and STSB.

Eight genotypes have presented very severe infections (> 50%); they are: the SFA; the BKA, the KCP1, the BAK, the KTYY, the SSS, the KTY1, and the KLYN.

3.2 Descriptive Analysis of the Incidence of Anthracnose Disease

Averages were taken with incidence data at each stage of the disease. The results showed variation between genotypes (Fig. 1). All trees all exhibited mean incidences greater than 25%; thus, eighteen (18) genotypes (KBT, KSCK, KBSD, SYD, KVSS, BBY, KTYY, BAK, KKSN, SST, KTY1, BKKY, SYDN, KCP3, KCP2, SDYY, SLLC, SWSZ) presented between 25 and 50%. The other twelve genotypes, namely; STSL, SSS, KOMC, SGYM, BKA, KLYN, SFA, KTY2, KTY3, KCP1, STSB, SDYN showed incidences of over 50%.

3.3 Principal Component Analysis (ACP) of the Incidence and Severity of Bacterial Disease

ACP was defined by the first two axes which explained 52.96% of the total variability observed (Figs. 3 and 4). The most eccentric variables of the factorial plane, and the most distant from the axes are those which expressed the strongest correlations of said axes. Axis 1, which expressed 29.49% of the total variability, was positively correlated with the severity index of anthracnose on twigs (IsRam) with the KTYY, KVSS, and BAK genotypes, and negatively correlated with the incidence of anthracnose on leaves (IcFe) with genotypes SDYN and STSB. Axis 2, expressing 23.47% variability, was positively correlated with incidence and severity index on fruits (IcFe and IsFe) with the KLYN genotype.

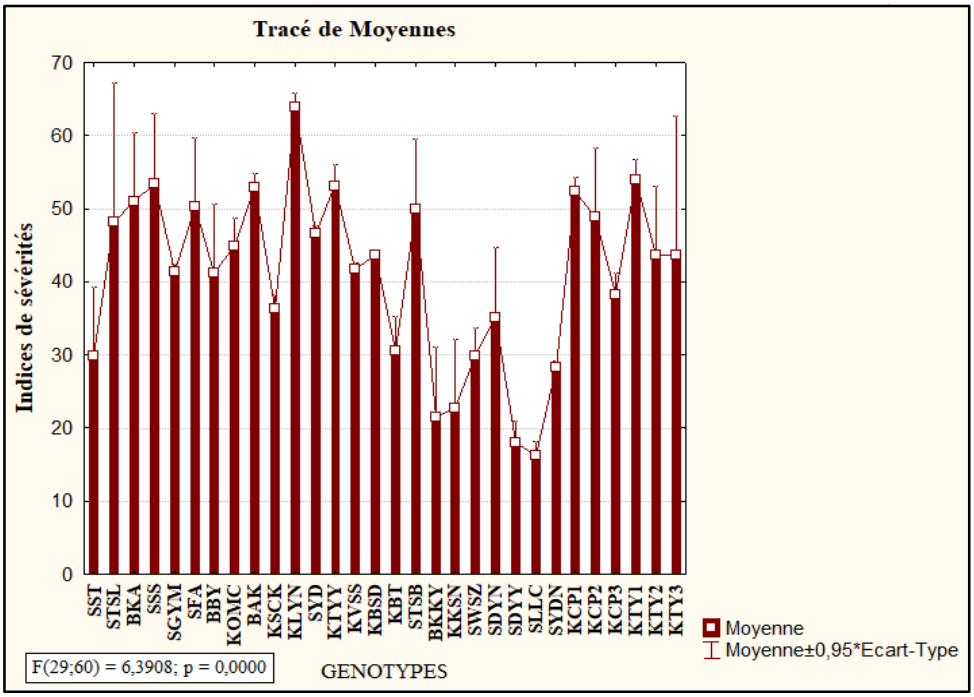

Fig.1. Histogram of anthracnose mean severity indices

Table 3. Incidence of anthracnose disease following the course of the cashew tree

	Vegetative stage		Flowering stage	Fruiting stage
Genotype	(IcFe)	(IcRam)	(IcInflo)	(IcFr)
SST	16,18±6,05abcde	76,25±7,46ab	86,12±3,84ghi	0,00±0,00a
STSL	22,96±3,91abcde	95,00±1,70cd	57,11±18,53bcdefghi	25,00±9,55ab
BKA	27,87±6,92bcde	85,00±7,24bc	92,68±4,08i	0,00±0,00a
SSS	23,01±6,63abcde	90,83±4,11c	86,95±8,72ghi	0,00±0,00a
SGYM	19,89±4,79abcde	90,00±1,11c	78,12±2,12efghi	16,07±7,59ab
SFA	6,43±1,88abc	88,75±4,90bcd	86,4±5,43ghi	30,55±16,33ab
BBY	9,32±4,44abcd	94,16±2,00cd	47,55±7,90abcdefgh	0,00±0,00a
KOMC	2,67±1,06ab	88,33±3,74bcd	60,97±8,78cdefghi	52,08±11,27b
BAK	1,84±0,85a	97,08±2,45cde	46,66±11,59abcdefg	20,15±10,90ab
KSCK	0,34±0,19a	89,58±8,02bcd	36,25±8,77abcde	0,00±0,00a
KLYN	31,81±11,27cde	96,25±2,39cde	33,5±10,82abcd	46,26±18,14ab
SYD	8,62±1,83abc	90,41±4,97c	33,41±9,14abcd	0,00±0,00a
KTYY	1,28±1,28a	94,16±4,50cd	40,83±7,06abcdef	23,33±10,54ab
KVSS	3,20±2,51ab	75,00±8,08ab	19,58±2,08abc	40,47±20,00ab
KBSD	17,30±1,64abcde	95,00±2,50cd	16,66±3,57ab	0,00±0,00a
KBT	19,23±1,98abcde	77,08±9,84abc	11,25±2,71a	0,00±0,00a
STSB	77,02±4,87g	97,08±2,45cde	90,41±6,78hi	16,36±8,38ab
BKKY	40,39±2,43ef	89,58±8,02bcd	56,66±13,71bcdefghi	0,00±0,00a
KKSN	29,91±3,17cde	96,25±2,39cde	48,75±5,46abcdefgh	0,00±0,00a
SWSZ	35,60±4,21e	90,41±4,97c	70,00±6,35defghi	0,00±0,00a
SDYN	63,67±5,21fg	94,16±4,50cd	95,83±2,71i	50,81±17,20b
SDYY	34,55±11,50de	75,00±8,08ab	84,16±6,79fghi	0,00±0,00a
SLLC	20,42±1,87abcde	95,00±2,50cd	64,75±9,05defghi	15,25±11,25ab
SYDN	23,94±2,38abcde	77,08±9,84abc	88,33±9,39ghi	0,00±0,00a
KCP1	43,15±2,27ef	76,06±9,12ab	63,41±9,14defghi	28±8,34ab
KCP2	52,14±1,57fg	95,25±2,39cd	47,85±7,05abcdefgh	0,00±0,00a
KCP3	2,87±1,08ab	70,16±4,50a	57,12±9,23bcdefghi	23,66±11,09ab
KTY1	3,9±2,51ab	78,74±7,24abc	85,63±9,39fghi	46,69±18,20ab
KTY2	32,24±1,57de	90,41±4,97c	90,03±7,8hi	0,00±0,00a
KTY3	63,3±8,33fg	96±7,20cd	40,83±7,06abcdef	15,25±11,25ab
Moyenne	24,50±3,67	88,13±5,11	60,59±7,50	14,99±6,33
P-value	0,000	0,02322	P= 0,000	P= 0,000
CV%	14,97	5,79	12,38	42,24

The numbers assigned the same letters in the columns are not statistically different according to Turkey's HSD tests at the 5% level
CV: coefficient of variability; IcFe: impact on leaves; IcRam: incidence on twigs; IcMoy: average incidence; IcInflo: incidence on inflorescences; IcFr: impact on fruits

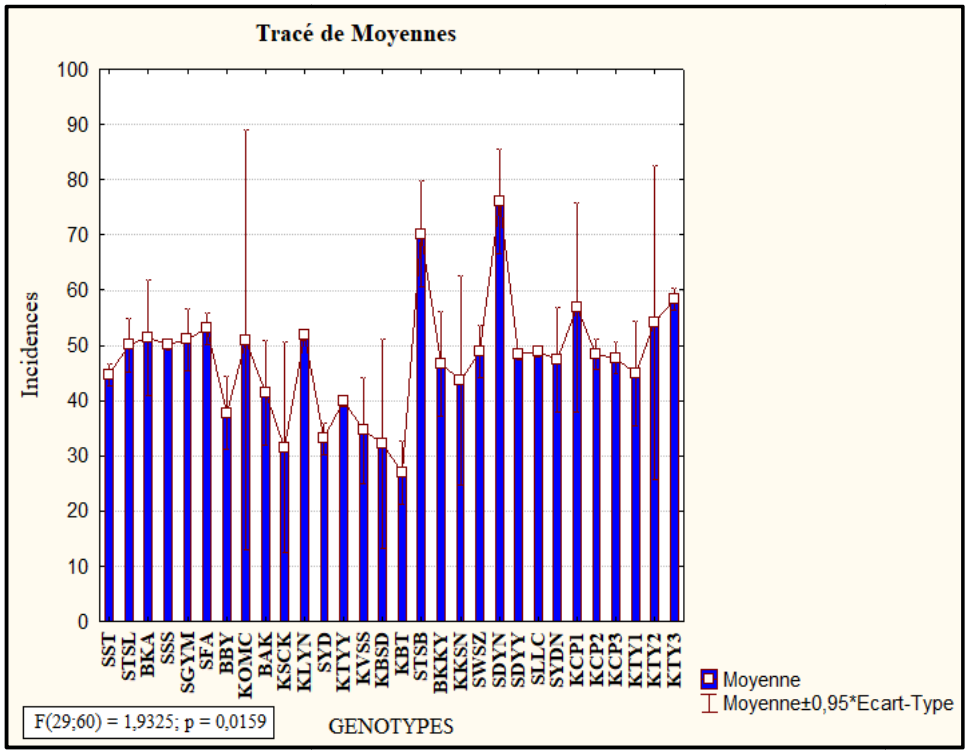

Fig. 2. Histogram of anthracnose mean incidences

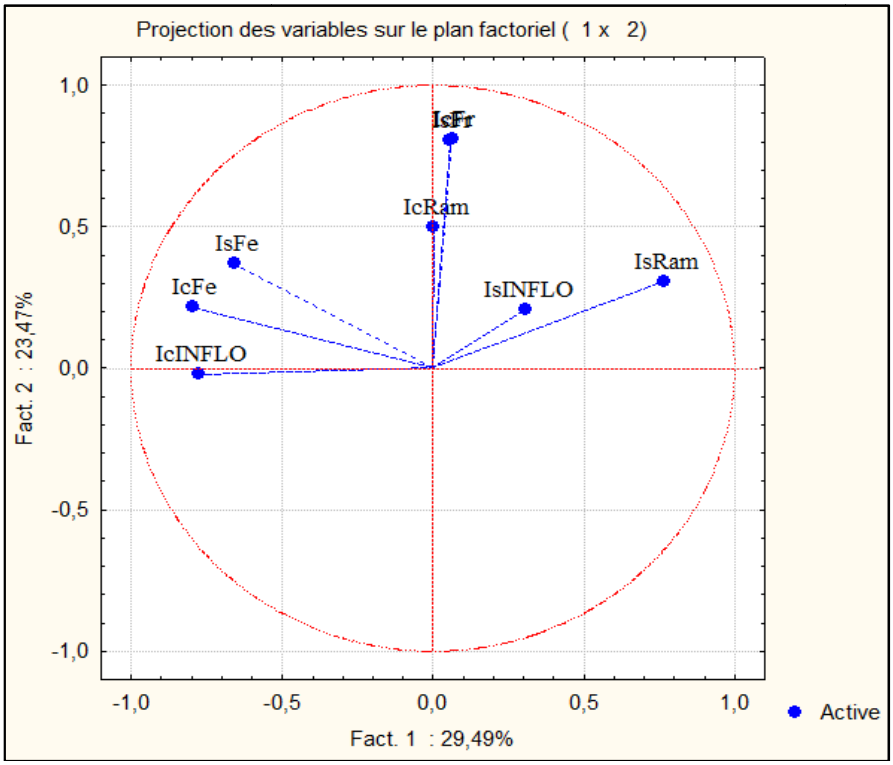

Fig. 3. Projection of the variables in the factorial plane

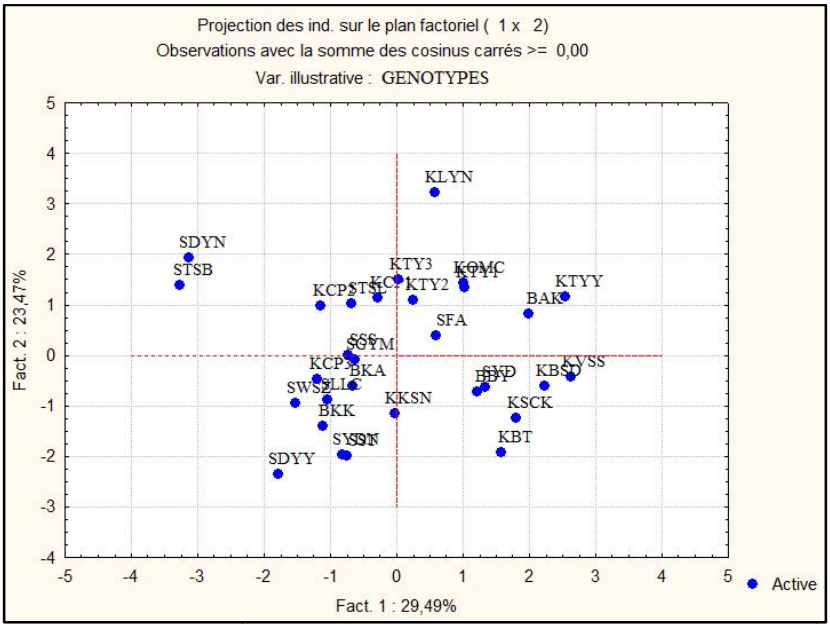

Fig.4. Projection of genotypes in the factorial plane

3.4 Structuring and Characterization of Genotypes by Ascending Hierarchical Classification (CAH) and Multiple Analysis of Variances (MANOVA)

The Ascending Hierarchical Classification (CAH) made it possible to structure the genotypes studied into 4 groups (Fig. 5) according to the method of Ward (1963). Group 1 containing six genotypes includes KVSS, KTYY, BAK, KLYN, KTY1 and KOMC. Group 2 consisted of five genotypes namely KBT, KBSD, KSCK, SYD and BBY. The third group with 12 individuals comprised the genotypes KCP1, SFA, SGYM, SSS, BKA, SDYN, STSB, KCP2, KCP3, KTY3, KTY2, STSL. Group 4 contained seven genotypes including SLLC, SDYY, KKSN, SWSZ, BKKY, SYDN, SST.

4. DISCUSSION

Multiple analysis of variance (MANOVA) (Table 1) showed a significant difference between these groups (F> 4 or P <0.005). This significant difference was observed in the incidence of anthracnose on inflorescences, leaves and fruits and the level of severity indices on twigs, leaves and fruits.

Thus, group 1 was characterized by the highest incidences of disease (30.39 ± 6.72) and severe infections in the fruits (39.28 ± 10.20). Group 2 was characterized by an absence of disease in the fruits (0.00 ± 0.00) and by very severe infections in the twigs (88.19 ± 2.98). Group 3 was distinguished by higher incidences on inflorescences (73.33 ± 5.85) and relatively strong incidences on the leaves (34.28 ± 6.51). Group 4 was differentiated by low fruit infections (1.32 ± 0.32) and low incidence on fruits (2.17 ± 1.09).

The results of the descriptive analysis revealed that anthracnose disease affects all 30 genotypes observed. Just like Silué et al. [25] pointed out, the disease was diagnosed at the vegetative stage on leaves, at the flowering stage on inflorescences and at the fruiting stage on fruits. In addition to this result, which is similar to that of Silué et al. [25], the present study noted that anthracnose disease affected young, leafless twigs. Even though all genotypes have contracted anthracnose disease, there is a diversity in the level of severity and incidence depending on the genotype and stage of development of the genotype. This diversity in expression of anthracnose disease could be explained by 52.96% of the total variability observed in the analysis of the principal components of diversity. These results are similar to those of Banganingwa [31] who also highlighted differences in severity depending on the cassava cultivars used, in the face of cassava mosaic. Likewise, Mestries et al. [32] revealed differences in severity between

Table 4. Descriptive analysis of the different groups of cashew trees formed by the CAH

	Groupes				Statistics		
Variables	GI	GII	GIII	GIV	F	P-value	significance
IcINFLO	48,51±8,78ab	29,02±6,64a	73,33±5,85b	71,25±5,86b	7,94785	0,000636	oui
IcFe	12,73±5,10a	10,96±3,39a	34,28±6,51b	28,71±3,33ab	4,10453	0,016443	oui
IcRam	88,46±3,03a	89,25±3,21a	89,39±1,60a	85,65±3,50a	0,41766	0,741802	non
IcFr	30,39±6,72b	0,00±0,00a	27,01±5,33b	2,17±1,09a	8,83639	0,000331	oui
IsINFLO	60,63±6,28c	50,92±6,31b	52,95±7,53b	34,12±2,98a	2,53973	0,078354	non
IsFe	21,65±6,95a	19,62±4,75a	43,41±4,36b	22,61±3,77a	5,65316	0,004044	oui
IsRam	84,97±3,93c	88,19±2,98c	62,59±5,87b	37,03±6,41a	14,98363	0,000007	oui
IsFr	39,28±10,20c	0,00±0,00a	24,79±5,00b	1,32±0,32a	8,71107	0,000362	oui
Number	6	5	12	7			

The numbers assigned the same letters on the lines are not statistically different depending on the test HSD of Turkey at the 5% threshold

IcFe: impact on leaves; IcRam: incidence on twigs; IcMoy: average incidence; IcInflo: incidence on inflorescences; IcFr: impact on fruits; IsFe: severity index on leaves; IsRam: severity index on twigs; IsMoy: average severity index; IsInflo: severity index on inflorescences; IsFr: severity index on fruits

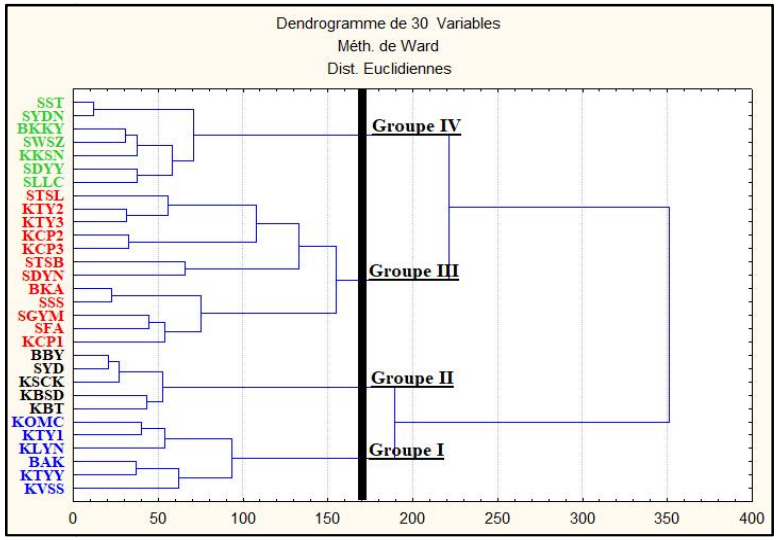

Fig.5. Dendrogram of genotypes

sunflower varieties with respect to phoma. Thus, the total variability at axis 1, which expressed 29.49%, was positively correlated with the severity index of anthracnose on twigs (IsRam) with the genotypes KTYY, KVSS and BAK negatively correlated with the incidence of anthracnose on leaves (IcFe) with the genotypes SDYN and STSB. In addition, axis 2, which produced 23.47% of the variability, was positively correlated with the incidence and severity index on fruits (IcFe and IsFe) with the KLYN genotype. These results clearly illustrate a strong diversity in the behavior of genotypes towards anthracnose disease and could explain the fact that cashew anthracnose is the most important disease due to its high presence in orchards. cashew farmers in Côte d'Ivoire. These results also corroborate those of Wonni et al. [18] who reveal that anthracnose is a serious disease in all cashew producing areas. These authors noted in their study of cashew tree diseases in Burkina Fasso that anthracnose is the predominant disease in orchards. This diversity of behavior is explained by the fact that each genotype has intrinsic capacities, in terms of passive and active defense mechanisms, which would allow to defend against aggression [33]. These defense mechanisms can therefore differ from one plant to another, which would lead to a variation in severity and incidence depending on the behavior of the genotypes. This result is in agreement with those of Désanlis [34]. Indeed, this author showed during his study of fungal diseases of sunflower in France that the defense mechanisms put in place during an attack could differ from one genotype to another. Thus, the incidence on inflorescences, incidence on leaves, severity index on twigs, incidence on fruits, severity index on fruits and severity index on inflorescences have were the most discriminating in the behavior of the genotypes observed. These results join those of Chetouhi, [35] and, Benhamou and Rey [36] on the differential behavior of genotypes which would be dependent on the effectiveness of the defense mechanisms that are phytoalexins and phytoanticipins brought into play by the plant. Thus, this differential screening revealed that group 1 is characterized by the highest incidences of disease (30.39 ± 6.72) and severe infections in the fruits (39.28 ± 10.20). Group 2 was characterized by a relative absence of disease in the fruits (0.00 ± 0.00) and by very severe infections in the twigs (88.19 ± 2.98). Group 3 was distinguished by higher incidences on inflorescences (73.33 ± 5.85) and relatively strong incidences on the leaves (34.28 ± 6.51). Finally, group 4 was differentiated by weak infections in fruits (1.32 ± 0.32) and by weak incidences on fruits (2.17±1.09). According to Lecompte [37], the distribution of these genotypes in these four groups is attributable to the different levels of their intrinsic resistance.

5. CONCLUSION

In short, the diagnosis of anthracnose made it possible to demonstrate a diversity of behavior of the 30 genotypes studied. The structuring of these genotypes revealed four categories of genotypes according to their behavior at the different stages of their development. Thus, this study made it possible to structure and characterize these genotypes into four groups. Group 2 genotypes (BBY, SYD, KSCK, KBSD and KBT) and group 4 genotypes (SST, SYDN, BKKY, SWSZ, SDYY and SLLC) exhibited resilience against anthracnose disease. Group 2 was characterized by a relative absence of disease in the fruits and by very severe infections in the twigs. Group 4 cashew trees showed low fruit infections and low fruit incidence. These results could promote the agroecological management of anthracnose disease, enhance and intensify agroforestry practices in cashew cultivation in Côte d'Ivoire.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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