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Genetic characterization of *Phytophthora colocasiae* isolates causing taro leaf blight (TLB) in the Sudanian climatic zone of Burkina Faso

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ABSTRACT

Taro leaf blight, caused by the oomycete *Phytophthora colocasiae*, represents a significant constraint to taro production in the Sudanian climatic zone of Burkina Faso. Effective and sustainable management of this disease necessitates a thorough understanding of the genetic diversity of the pathogen. This study aimed to characterize the genetic diversity of *Phytophthora colocasiae* through morphological and molecular analyses of isolates collected from multiple locations. A total of 44 isolates were evaluated using four morphological markers and nine molecular markers. Morphological assessment identified six distinct morphotypes based on colony growth characteristics, with isolates further categorized into three growth-rate classes. Molecular characterization revealed low genetic diversity within the pathogen population, as indicated by a Shannon diversity index of 0.4. Analysis of molecular variance (AMOVA) showed that genetic variation was predominantly distributed within populations, with minimal differentiation and low genetic distances between groups. These findings offer essential insights into the population structure of *Phytophthora colocasiae* and provide a foundation for the development of targeted management strategies to mitigate taro leaf blight in Burkina Faso.

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INTRODUCTION

Taro (*Colocasia esculenta*) is a critical food and cash crop for millions of households in tropical and subtropical regions. However, its production is significantly constrained by taro leaf blight, a devastating disease caused by the oomycete *Phytophthora colocasiae*. This pathogen is renowned for its high aggressiveness and capacity to cause substantial yield losses, which can exceed 50%, severely impacting food security and rural incomes (Hong *et al.,* 2021; Takor *et al.,* 2020; Manju et *al.,* 2017). The disease manifests as water-soaked circular lesions on leaf edges, which expand into necrotic areas with chlorotic margins, ultimately leading to the collapse of entire leaves (Bandyopadhyay *et al.,* 2011).

In Burkina Faso, particularly within the Sudanian climatic zone, taro leaf blight represents a growing threat due to favorable environmental conditions for the pathogen, including high humidity and warm temperatures. The socio-economic consequences of the disease are compounded by the pathogen's genetic variability, which facilitates rapid adaptation to control measures (Cécé *et al.,* 2024; Mishra *et al.,* 2010). Conventional management approaches, such as fungicide applications, have shown limited efficacy. Taro's waxy leaf surface reduces fungicide absorption, necessitating frequent and costly applications, while intensive fungicide use has been linked to the emergence of resistant pathogen strains (McDonald and Linde, 2002; Taggart *et al.,* 1999). Consequently, there is an urgent need for sustainable and integrated disease management strategies.

The deployment of resistant cultivars is a promising approach for managing *Phytophthora colocasiae*. However, the success of resistance-based strategies hinges on a thorough understanding of the pathogen's genetic structure and diversity. High genetic variability within pathogen populations increases the likelihood of resistance breakdown, highlighting the importance of monitoring both morphological and molecular variation (Padmaja *et al.,* 2017; Adomako *et al.,* 2018).

Modern molecular tools have proven instrumental in studying the genetic diversity of plant pathogens, providing insights into population structure, evolutionary dynamics, and adaptation potential. Techniques such as restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD), and single-nucleotide polymorphism (SNP) analysis have been extensively applied to *Phytophthora* species (Forster *et al.,* 2000; Ochwo *et al.,* 2002; Yang *et al.,* 2008). Notably, simple sequence repeat (SSR) markers are highly effective for detecting genetic variation due to their high sensitivity, reproducibility, and codominant inheritance (Acosta, 2007; Bindler *et al.,* 2007; Pervaiz *et al.,* 2009). While such methods have been applied to *Phytophthora colocasiae* populations in regions like Southeast Asia and India (Lebot *et al.,* 2003; Nath *et al.,* 2012, 2013, 2015), studies in Burkina Faso, remain scarce.

This study aims to bridge this knowledge gap by evaluating the genetic diversity of *Phytophthora colocasiae* populations in Burkina Faso through a combination of morphological and molecular approaches. The specific objectives are to:

a. Characterize the phenotypic variability of *Phytophthora colocasiae* isolates collected from different sites,
b. Assess the molecular diversity within *Phytophthora colocasiae* populations using SSR markers, and
c. Estimate genetic distances among isolates.

By integrating phenotypic and genetic analyses, this research seeks to provide critical insights into the population structure of *Phytophthora colocasiae* and establish a foundation for the development of effective and sustainable management strategies tailored to Burkina Faso's agricultural and environmental conditions.

MATERIALS AND METHODS

Sampling

The study was conducted in the Sudanian climatic zone of Burkina Faso, focusing on the provinces of Houet, Kénédougou, and Comoé, which are

characterized by a high prevalence of taro leaf blight (Cécé *et al.,* 2024). Sampling took place between June and July 2023, covering nine distinct sites across these provinces. In Houet, samples were collected from Bama. In Comoé, two sites (Bérégadougou and Séréfédougou) were surveyed. Kénédougou, the most extensively sampled province, included six sites: Kourinion, Guéna, Mbié, Diéri, Lanfiéra, and Djolé. This selection of sites ensured a representative assessment of the pathogen across regions.

Sample collection

In each surveyed locality, five fields of taro approximately 6–7 months old were randomly selected for sample collection. From each field, five infected leaf samples were collected, targeting plants exhibiting blight symptoms at various stages of infection. Leaves were excised using disinfected scissors, ensuring that both healthy and symptomatic areas were included in each sample. The excised samples were placed in labeled collection bags to prevent moisture loss and contamination. Labels included critical information such as the collection date, GPS coordinates, locality name, and sample number (e.g., Field 1-Sample 1).

To maintain hygiene and avoid cross-contamination, scissors were disinfected with alcohol between collections. The samples were immediately stored in a cooler with ice to preserve their integrity during transportation to the Phytopathology Laboratory at Joseph KI-ZERBO University. Sampling was conducted in July 2023, coinciding with the primary cropping season when weather conditions (high humidity and warm temperatures) were conducive to disease development. Samples were collected from two taro varieties: the local variety Tabouchi and the exotic variety BL/SM/120.

Isolation of *Phytophthora colocasiae*

Taro leaf samples were processed to isolate *Phytophthora colocasiae* following established protocols (Padmaja, 2013). Initially, leaves were rinsed under running water to remove debris. Sections approximately 5 cm in length, containing both healthy and symptomatic tissue, were excised using a sterile scalpel. These sections were surface-sterilized by immersion in a 3% sodium hypochlorite solution for 1 minute to suppress the growth of saprophytic organisms. The sterilized sections were then rinsed thoroughly with distilled water for 2 minutes to remove residual bleach. Each section was placed in a Petri dish containing carrot-tomato agar medium, prepared using 156.5 g of tomatoes, 100 g of carrots, and 20 g of agar dissolved in 1000 ml of distilled water. Samples were plated in duplicate and incubated for three days. After the incubation period, tissue samples approximately 5 mm in size were excised from the junction of necrotic and healthy tissue using a sterile metal loop.

These tissue samples were subsequently subcultured onto fresh carrot-tomato agar medium, which is known to promote the growth of *P. colocasiae* (Kaboré, 2022). Identification of *P. colocasiae* was performed based on the morphological characteristics of its mycelia and sporangia, as described by Drenth and Sendall (2011).

Colony characterization of *Phytophthora colocasiae* isolates

The morphological characterization of *Phytophthora colocasiae* isolates was performed using mycelial discs obtained from three-day-old pure cultures. Discs were centrally placed on Petri dishes containing Potato Dextrose Agar (PDA) medium. Plates were incubated in darkness at 28 ± 2 °C, following a completely randomized design with three replicates per isolate. After an incubation period of 8 days, macroscopic characteristics of the colonies, including appearance, color, and mycelial growth rate, were recorded. The growth rate of the mycelium was calculated using the formula:

$$V = \frac{[(D1 - 0{,}4) + (D2 - 0{,}4)]}{N}$$

Where:

V: Fungal growth rate (cm/day)

D1: First colony diameter (cm)

D2: Second colony diameter perpendicular to D1D_1D1 (cm)

N: Number of days post-transfer of explant

0.4: Diameter of the initial explant (cm)

Genomic DNA isolation

Genomic DNA from *Phytophthora colocasiae* isolates was extracted using the Cetyltrimethyl Ammonium Bromide (CTAB) method, following the protocol described by Wu *et al.* (2001).

Prior to DNA extraction, each isolate was subcultured on carrot-tomato agar and incubated in the dark at 28 ± 2°C for 14 days. After incubation, fungal mycelium was scraped from the culture plates and transferred to 2 mL microcentrifuge tubes. Two grinding beads were added to each tube, and the fungal cells were lysed by vortexing for 10 minutes. To each tube, 600 µL of preheated CTAB extraction buffer (maintained at 60°C) was added, followed by brief vortexing to homogenize the mixture. The tubes were incubated in a water bath at 60°C for 30 minutes to facilitate cell lysis. After incubation, the tubes were cooled to room temperature for a few minutes. To remove cellular debris, 900 µL of chloroform-isoamyl alcohol (24:1) was added to each tube, and the mixture was gently inverted until it appeared milky. The samples were centrifuged at 13,000 rpm for 5 minutes at 25°C. The resulting supernatant, containing genomic DNA, was carefully transferred to new tubes. To further purify the DNA, 400 µL of chloroform-isoamyl alcohol was added to the supernatant, followed by centrifugation at 13,000 rpm for 2 minutes at 25°C. The supernatant was again transferred to fresh tubes, and DNA was precipitated by adding 350 µL of isopropanol. The tubes were incubated at -20°C for 1 hour and then centrifuged at 13,000 rpm for 5 minutes at 25°C. The supernatant was discarded, and the DNA pellet was air-dried on blotting paper at room temperature. The dried DNA pellet was dissolved in 50 µL of sterile distilled water and stored at -20°C for subsequent analyses.

Table 1. List of primers

N	Primer name	Primer sequence
1	TAT_66	F: TTGCTAAAGCGCAGATTACGC R: GTGTCTTACAGTGCTGCCATCCTACTC
2	CCT_4368	F: TCAGCGTGGGTATGTAGTCC R: GTGTCTTATGATGGTGACGCAGAGGAA
3	CTT_270	F: GCCACGAATAGACGACAGTC R: GTGTCTTGCAACTTTACCTGGGGTTGC
4	CTT_1936	F: TCTACTGTAACGTCCGTCGC R: GTGTCTTATCTCCAGTGCCGAAGAGTC
5	GCT_5986	F: CGCTTAGACTTGCGACTACG R: GTGTCTTTCCAGAAGACGGGAAACGAC
6	TCC_502	F: TCAGCGTGGGTATGTAGTCC R: GTGTCTTGCGTATTAAAGCGGACAGGG
7	CTA_421	F: CGCTTTGTTGAGTTGGACGA R: GTGTCTTTCCAATCCGATCACCACCAA
8	TAG_1296	F: ACAGCCATCCAACCATGTAA R: GTGTCTTACACTCACACCAAAGTAACGC
9	GA_106	F: GCTATTGTCTTACACAGACACG R: GTGTCTTGAAGCCCATCCACCTAATGG
10	TCC_1066	F: GCCACGAATAGACGACAGTC R: GTGTCTTGGGAAGCGACATGGAAGAAG
11	AGAC_2040	F: GATGGGAGAAAAAGGTGTCG R: GTGTCTTGAGATGTGCTCATCCCATTC

SSR-PCR amplification

The genomic DNA of *Phytophthora colocasiae* isolates was amplified using 11 simple sequence repeat (SSR) markers (Table 1). PCR amplifications were conducted according to the protocol described by Acosta (2007). Each 25 µL reaction mixture consisted of 10 µL of genomic DNA, 1 µL of the forward primer (3'), 1 µL of the reverse primer (5'), 4 µL of premix, and 9 µL of ultrapure water. The mixture was homogenized and loaded into PCR racks. Amplifications were performed in a TC-96/G/H (bD) thermocycler under the following conditions: an initial denaturation step at 94°C for 5 minutes, followed by 33 cycles of denaturation at 94°C for 40

seconds, annealing at the primer-specific temperature for 40 seconds, and extension at 72°C for 20 seconds. A final extension was carried out at 72°C for 10 minutes (Zhang *et al.*, 2023). The amplified products were resolved by electrophoresis on a 2% agarose gel. Visualization of the amplicons was achieved under ultraviolet light after staining the gel with ethidium bromide (0.5 µg/mL) for 1 minute. Photographic documentation of the bands was performed to record the results.

Data collection and analysis

Morphologically, the isolates were grouped together based on their colony types and diameter size. The Shannon-Wiener index, which evaluates both the richness and relative abundance of different morphological forms, was calculated using the following formula:

$$H = -\sum_{i=1}^{n} \text{pi} \ln(\text{pi})$$

Where:

H is the Shannon-Wiener index

n is the total number of different morphological forms

pi is the proportion of a morphological form

The amplified DNA fragments were scored as binary data, with the presence of bands recorded as "1" and the absence as "0." These binary matrices were used to assess the genetic diversity of *Phytophthora colocasiae* populations through several key parameters, including allelic richness, allelic frequency, Shannon index, and polymorphic information content (PIC). All diversity indices were calculated using GenALEX software.

To evaluate the genetic structure of *Phytophthora colocasiae* populations, an analysis of molecular variance (AMOVA) was conducted. Genetic relationships were further explored using a distance matrix-based factorial analysis, and a Neighbor-Joining dendrogram was constructed using Darwin software. Additionally, the genetic differentiation index (F_{ST}) was calculated with FSTAT v2.9.3.2, while Nei's minimum genetic distance between groups was computed using GenALEX.

RESULTS

Pathogen identification

A total of 44 isolates of *Phytophthora colocasiae* were successfully obtained from leaf samples collected across various farms within the Sudanian climate zone of Burkina Faso. The initial identification of these isolates as *Phytophthora colocasiae* was based on their mycelial and sporangial morphological characteristics.

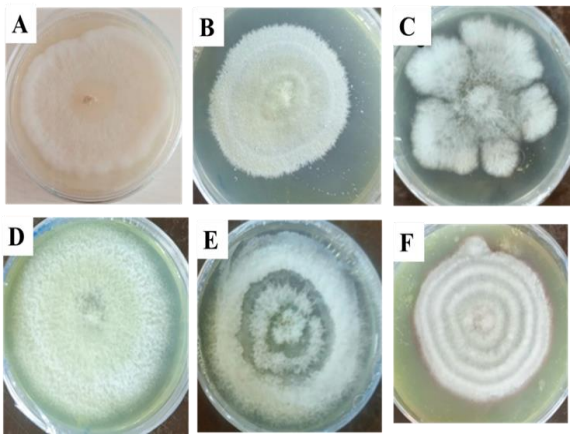

Fig. 1. Colonies morphologies of *Phytophthora colocasiae*

Morphological variation

The *Phytophthora colocasiae* isolates exhibited notable morphological diversity on PDA medium, with a diversity index of H = 1.29 (Fig. 1). No consistent correlation between isolate morphology and collection site was observed. Morphological variations were evident even among isolates from the same location, suggesting potential genetic diversity within the population. Based on colony characteristics, the isolates were categorized into six distinct morphotypes. Morphotypes A and B exhibited a cottony texture with concentric rings, though morphotype A was distinguished by a pinkish background. Morphotypes E and F displayed a spiral pattern, differing in spiral size: morphotype F had fine spirals, whereas morphotype E featured broader spirals. Morphotype D was characterized by a cottony texture, while morphotype C presented a petal-like appearance. In terms of pigmentation, 87.17% of the isolates formed white colonies, while the remaining isolates exhibited a pinkish hue. Among the

morphotypes, group D contained the highest number of isolates, whereas group E demonstrated the most vigorous growth performance (Fig. 2).

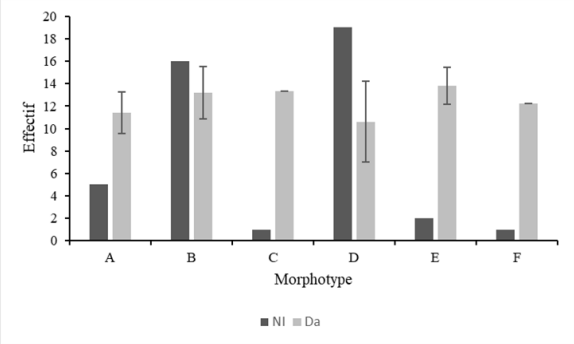

Fig. 2. Growth rate characteristics of *Phytophthora colocasiae* morphotypes

NI: Number of isolates per morphotype; Da: Morphotype growth rate

Genetic diversity of *Phytophthora colocasiae* isolates in the sudandian climate zone of Burkina Faso

Genetic diversity parameters of the collection of Phytophthora colocasiae

Nine out of the eleven molecular markers used in this study were selected for genetic analysis based on their polymorphism and high-quality amplification. Fig. 3 presents the amplification profile of the TCC_1066 marker tested across 44 *Phytophthora colocasiae* isolates. The genetic diversity parameters for the entire *Phytophthora colocasiae* population are summarized in Table 2. The average percentage of polymorphic loci was 96.67%, indicating a high level of genetic variability within the population. A total of 30 alleles were identified, with fragment sizes ranging from 55 bp to 600 bp. The number of alleles per locus varied among markers, with primers GCT_5986 and CTA_421 detecting 2 alleles, TAT_66 and TCC_1066 detecting 3 alleles, and CCT_4368, CTT_270, CTT_1936, TCC_502, and GA_106 detecting 4 alleles. The overall mean number of alleles per locus across the nine primers was 3.33.

Genetic diversity parameters of morphological groups

The analysis of qualitative morphological traits facilitated the classification of *Phytophthora colocasiae* isolates into six distinct morphotypes. Genetic diversity parameters were subsequently assessed within these morphotypic groups to explore potential genetic structuring. Table 3 provides details on the size and composition of each group. Due to insufficient sample sizes (fewer than five isolates), morphological groups C, E, and F were excluded from the genetic diversity analysis.

Table 2. Genetic diversity of the nine (09) primers tested on the 44 isolates

Locus	Band size (bp)	Na	Ne	I	He	PIC (%)	%P (%)
TAT_66	250-500	3	1.22	0.32	0.18	96.95	96.67
CCT_4368	100-400	4	1.67	0.59	0.41	68.03	96.67
CTT_270	100-350	4	1.31	0.38	0.23	91.32	96.67
CTT_1936	150-500	4	1.71	0.59	0.42	49.38	96.67
GCT_5986	250-300	2	1.43	0.43	0.28	90.81	96.67
TCC_502	150-350	4	1.24	0.33	0.19	94.58	96.67
CTA_421	90-100	2	1.05	0.09	0.04	49.90	96.67
GA_106	55-300	4	1.51	0.50	0.33	78.62	96.67
TCC_1066	200-600	3	1.33	0.38	0.24	91.27	96.67
Mean		3,33	1.39	0.40	0.26	78.98	96.67

Na: total number of alleles, Ne: effective number of alleles, He: expected heterozygosity, PIC: polymorphism information content, I: Shannon diversity index, P: polymorphic loci rate.

The results presented in Table 4 reveal the levels of genetic diversity among the three *Phytophthora colocasiae* morphotypes. Morphotype D exhibits the highest genetic diversity, followed by morphotype B. Specifically, morphotype D shows an effective number of alleles of 1.47, an expected heterozygosity of 0.30, and a polymorphic loci percentage of 90%. In contrast, for morphotype B, these values are 1.33 for the effective number of alleles, 0.23 for expected heterozygosity, and 76.67% for the polymorphic loci percentage. Conversely, morphotype A displays the lowest genetic diversity levels among the three morphotypes.

Table 3. Morphotype composition

Morphotype	Count	Isolates
A	5	Dj1, Dj2, Dj3, Dj4, S1
B	16	Dj5, Di1, Di2, Di3, Di4, Di5, L1, L2, L3, L4, G1, G5, M3, Ba2, Ba3, Ba4
D	19	G2, G3, G4, M1, M2, M4, M5, K1, K2, K3, K4, K5, B1, B2, B3, B4, B5, S4, S5

Table 4. Genetic diversity parameters of morphological groups

M	N	Na	Ne	I	He	%P	%PIC
A	5	0.87	1.23	0.22	0.18	40	84.63
B	16	1.57	1.33	0.35	0.23	76.67	79.35
D	19	1.83	1.47	0.44	0.30	90	72.75

M: Morphotype; N: Number of isolates; Na: Number of different alleles per locus in the population; Ne: Effective number of alleles; I: Shannon diversity index; He: Expected heterozygosity; PIC: Polymorphism information content; P: Percentage of polymorphic loci.

Table 5. Inter-population genetic differentiation

	Nei's minimum distance			Fst differentiation index		
M	A	B	C	A	B	C
A	0			0		
B	0.031	0		0.026^{NS}	0	
D	0.090	0.049	0	0.055^{NS}	0.013^{NS}	0

M: Morphotype; NS: Not significant

Table 6. Results of molecular variance analysis

Source	df	SS	MS	Est. Var.	Variation%
Inter-population	2	14.80	7.40	0.29	7
Intra-population	37	145.05	3.92	3.92	93
Total	39	159.85		4.21	100

df: degree of freedom; SS: sum of squares; MS: mean square; Est.Var: estimated variance

Table 7. Composition of groups obtained using the Neighbour-Joining method

Group	Count	Isolates
I	22	Dj4, Di4, Di5, L5, G1, G2, G3, M2, M5, K1, K2, K3, K4, K5, B1, B3, S1, S2, S5, Ba1, Ba2, Ba3
II	22	Dj1, Dj2, Dj3, Dj5, Di1, Di2, Di3, L1, L2, L3, L4, G4, G5, M1, M3, M4, B2, B4, B5, S3, S4, Ba4

Dj: Djolé; Di: Diéri; L: Lanfiéra; G: Guéna; Ba: Bama; K: Kourinion; M: Mbié; S: Séréfédougou; B: Bérégadougou

Table 8. Results of molecular variance analysis

Source	df	SS	MS	Est. Var.	Variation %
Inter-population	1	12.32	12.32	0.38	9
Intra-population	42	165	3.93	3.93	91
Total	43	177.32		4.31	100

df: degree of freedom; SS: sum of squares; MS: mean square; Est.Var: estimated variance

Table 9. Inter-population differentiation

	Nei minimum distance		Fst differentiation index	
Group	Group 1	Group 2	Group 1	Group 2
Group 1	0		0	
Group 2	0.033	0	0.141^{NS}	0

Nei's minimum genetic distances and genetic differentiation indices are low among the three morphotypes, preventing clear distinction between them (Table 5). According to molecular variance analysis (AMOVA), genetic diversity is predominantly distributed within populations (93%), while differentiation among

populations accounts for only 7% (Table 6). These findings indicate low genetic differentiation among the three morphological groups.

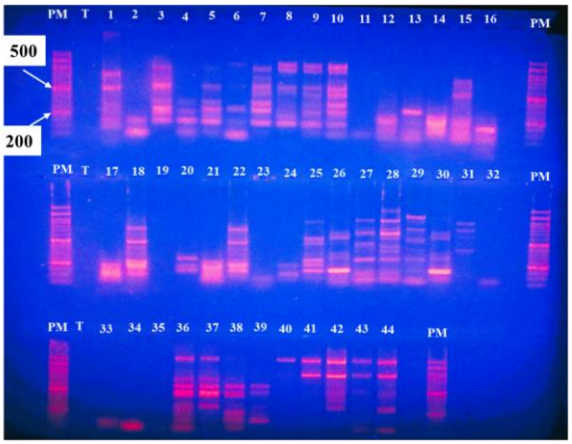

Fig. 3. Migration profile of marker TCC_1066
PM: molecular weight

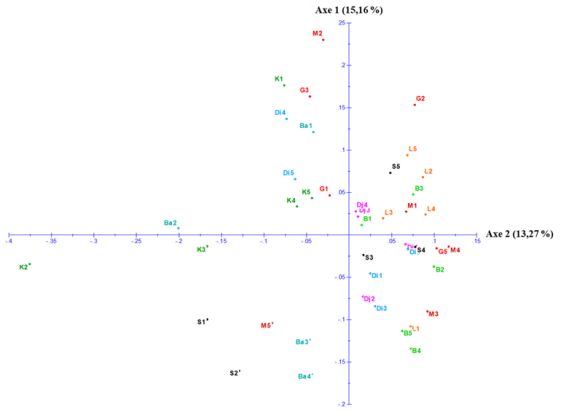

Fig. 4. Structure of the 44 isolates based on factorial analysis of the distance table using the dissimilarity matrix of the 09 SSR markers
Dj : Djolé ; Di : Diéri ; L : Lanfiéra ; G : Guéna ; Ba : Bama ; K : Kourinion ; M : Mbié ; S : Séréfédougou ; B : Bérégadougou

Analysis of genetic diversity structure using the Neighbour-Joining method

The Factorial Analysis of Distance Tables (FADT) elucidated the relationships among isolates from various localities (Fig. 4) and the associations between the identified morphotypes (Fig. 5). In the 1/2 plane, the FADT demonstrated a dispersed distribution of isolates and morphotypes, with no clear structuring, particularly along axis 2. This pattern indicates a low level of genetic variability within the analyzed *Phytophthora colocasiae* population.

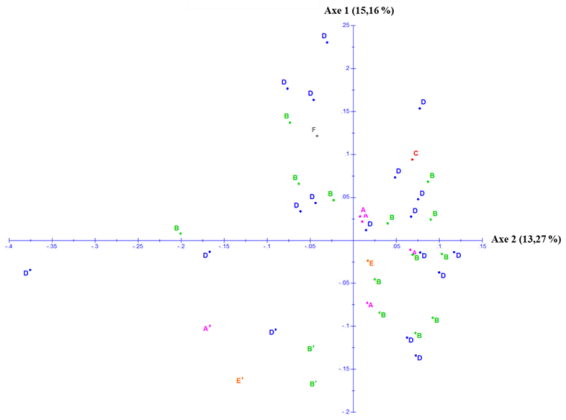

Fig. 5. Structure of 44 isolates highlighting morphological groups based on factorial analysis on distance table

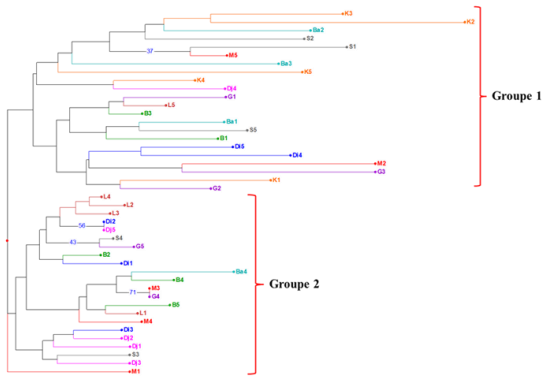

Fig. 6. Hierarchical representation of the 44 *Phytophthora colocasiae* isolates built from the dissimilarity matrix using the Neighbour-Joining method
Dj: Djolé; Di: Diéri; L: Lanfiéra; G: Guéna; Ba: Bama; K: Kourinion; M: Mbié; S: Séréfédougou; B: Bérégadougou

Fig. 6 and 7 illustrate the genetic structuring of 44 *Phytophthora colocasiae* isolates using the Neighbor-Joining method. Fig. 6 represents the structure based on localities, while Fig. 7 depicts the structuring according to morphotypes. The dendrogram analysis identifies two distinct genetic groups: Group 1, associated with provenance criteria (A), and Group 2, linked to morphotype criteria (B), each comprising 22 isolates (Table 7).

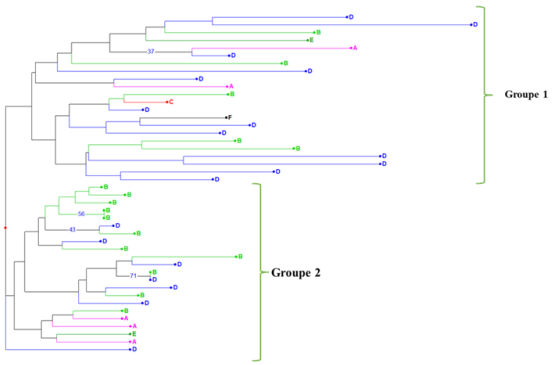

Fig. 7. Hierarchical representation of the 44 *Phytophthora colocasiae* isolates highlighting the different morphological groups constructed from the dissimilarity matrix using the Neighbour-Joining method

Group 1 predominantly consists of isolates from Kourinion (100%), with substantial contributions from Bama (75%), Guéna and Séréfédougou (60% each), and lower proportions from Bérégadougou, M'Bié, and Diéri (40% each), as well as Lanfiéra and Djolé (20% each).

Morphologically, this group is primarily dominated by morphotype D (54.54%). Group 2 mainly includes isolates from Lanfiéra and Djolé (80%), with significant contributions from M'Bié, Bérégadougou, and Diéri (60% each), and smaller proportions from Guéna and Séréfédougou (20% each). Morphologically, this group is predominantly characterized by morphotype B (50%).

These findings suggest a clustering pattern of isolates that does not strictly align with geographic origin or morphotype, indicating a more complex genetic structuring within the analyzed population.

The molecular analysis of variance (Table 8) indicates low inter-population diversity (9%) and high intra-population diversity (91%) between the two groups. Moreover, the genetic differentiation parameters are low, making it challenging to clearly distinguish them (Table 9). However, an *Fst* value of 0.141 was observed between the groups, suggesting moderate genetic differentiation.

DISCUSSION

Understanding the genetic diversity of plant pathogens is essential for developing sustainable and effective disease control strategies (Martin and English, 1997). In Burkina Faso, taro leaf blight, caused by the oomycete *Phytophthora colocasiae*, leads to significant economic losses, mirroring its impact in other affected regions worldwide. This study aimed to assess the genetic diversity of *Phytophthora colocasiae* in Burkina Faso using two complementary approaches: morphological variation analysis and molecular diversity assessment.

Morphological analysis of colonies on PDA medium revealed substantial variation among *Phytophthora colocasiae* isolates, independent of their geographic origin. This observation suggests that morphological differences are not necessarily linked to collection sites. Similar findings have been reported in studies conducted in India and the Pacific (Lebot *et al.,* 2003; Mishra *et al.,* 2010; Nath *et al.,* 2013, 2016; Adomako *et al.,* 2019). However, these results contrast with those of Akshara *et al.* (2017), who found no morphological variation among their isolates. This discrepancy could be attributed to differences in sampling methods; while Akshara *et al.* (2017) used isolates from a single leaf with multiple blight spots, the present study analyzed isolates from multiple infected taro leaves.

Given that *Phytophthora colocasiae* reproduces both sexually and asexually, the observed morphological variation may primarily stem from asexual reproduction mechanisms, particularly random mutations. These mutations, often neutral, serve as the main source of variation in oomycetes (Goodwin, 1997) and can sometimes lead to spontaneous phenotypic changes (Silvar *et al.,* 2006). Additionally, chromosomal rearrangements such as translocations, deletions, and duplications may contribute to the observed diversity, particularly in asexually reproducing pathogens.

While morphological variation provides insights into genetic diversity, it is often influenced by environmental factors, necessitating the use of

molecular markers. In this study, SSR markers were employed to overcome the limitations of morphological analysis. SSRs are neutral, highly polymorphic, and codominant, making them suitable for evaluating genetic diversity, even among closely related populations.

The SSR markers used demonstrated a high polymorphic information content (PIC) of 78.98%, underscoring their effectiveness. Despite this, overall genetic diversity was relatively low, as reflected by a Shannon index of 0.4. The number of alleles detected was also lower than that reported in *Phytophthora colocasiae* populations from Japan (Zhang *et al.,* 2023).

This difference may stem from the limited number of isolates in this study and variations in sample origin. Factorial analysis of distance tables (FADT) revealed no significant genetic structuring, as isolates clustered independently of collection sites and morphological groups. These findings align with those of Nath *et al.* (2013). Genetic structuring using the Neighbor-Joining method identified two distinct groups. Molecular analysis of variance (AMOVA) further confirmed that most genetic variation exists within groups rather than between them (91% and 93% for groups based on genetic and morphological classifications, respectively). Additionally, genetic distances and differentiation parameters between groups were low, further supporting a lack of strong genetic structuring. These findings are consistent with those of Zhang *et al.* (2023), who reported genetic homogeneity among *Phytophthora colocasiae* populations in Japan. However, they contrast with studies in India, Southeast Asia, and the Pacific (Lebot *et al.,* 2003; Mishra *et al.,* 2010; Nath *et al.,* 2012, 2015, 2016; Adomako *et al.,* 2019), which reported significant genetic diversity within the pathogen. The discrepancies may be attributed to regional differences in *Phytophthora colocasiae* populations, sampling strategies, or the genetic markers used.

Several factors could explain the low genetic diversity observed in *Phytophthora colocasiae* populations in Burkina Faso. One possibility is that the pathogen population is regionally constrained, limiting genetic divergence. The study area is characterized by a relatively homogeneous climate, and many collection sites are geographically close. Additionally, taro is cultivated predominantly as a monoculture (Cécé *et al.,* 2024), exposing *Phytophthora colocasiae* to uniform host selection pressures. This cultivation practice limits interactions between the pathogen and genetically diverse host plants, potentially reducing opportunities for genetic diversification. Furthermore, the absence of chemical control methods in Burkina Faso may contribute to the low genetic diversity observed. Chemical treatments often drive pathogen evolution by selecting for resistant strains through mutation-driven adaptations. In contrast, the absence of such pressures may promote genetic stability within the population.

Understanding the genetic diversity of *Phytophthora colocasiae* is critical for effective disease management. The low genetic diversity observed in Burkina Faso presents an opportunity for targeted control strategies, particularly through host resistance breeding. Since genetic variability within the pathogen is limited, breeding programs could focus on selecting taro varieties with resistance to the prevalent *Phytophthora colocasiae* strains.

While vertical resistance may offer immediate benefits, prioritizing horizontal resistance is recommended for long-term disease management. Horizontal resistance is more durable and less susceptible to pathogen adaptation (Burdon *et al.,* 2014; Brown, 2015). Integrating resistant cultivars with sustainable agricultural practices could help mitigate the impact of taro leaf blight in Burkina Faso while limiting the emergence of new pathogen strains.

CONCLUSION

This study provides important insights into the genetic diversity of *Phytophthora colocasiae* in

Burkina Faso. Morphological and molecular analyses indicate low genetic variability, with no clear structuring based on geography or morphotype. Several factors, including regional constraints, monoculture practices, and the absence of chemical control measures, may contribute to this limited diversity. Despite these findings, continued surveillance using diverse molecular markers and expanded sampling strategies is recommended to capture potential variations and guide sustainable disease management strategies.

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