



MOLECULAR IDENTIFICATION OF ANTHRACHNOSE PATHOGEN (*COLLETOTRICHUM MUSAE*) IN BANANA FRUITS AND THE USE OF EXOPHYTIC AND ENDOPHYTIC FUNGI TO CONTROL THE PATHOGEN

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ABSTRACT

Banana rot disease is often found in Bali, especially bananas are the main means for completing religious ceremonies in Bali. Banana rot often spoils during storage or post-harvest. The results showed that the cause of banana rot disease was *Colletotrichum musae* with DNA fragments measuring 650 bp successfully amplified using universal primers ITS1/ITS4. The highest *in vitro* inhibition of exophytic fungi against pathogens was achieved by *A. niger*, *Neurospora sp.* and *Rhizopus sp.* each with an inhibitory power of 100%, the lowest was achieved by *Neurospora sp.* at the time of days after inoculation (DAI) by 50%. While the inhibition of endophytic fungi against pathogens was *Rhizopus sp.* with inhibition of 100% from 1 DAI to 4 DAI followed by *A. niger* at 100% at 3 and 4 DAI. The results of the *in vivo* inhibition of selected exophytic and endophytic fungi against pathogens were as follows: the highest inhibitory power was C (*Rhizopus sp.1*) of $94 \pm 5.48\%$, followed by treatment A (*A. niger* 1) of $92 \pm 8.37\%$, treatment B (*A. niger* 2) was $64 \pm 5.48\%$, treatment E (*Rhizopus sp. 2*) was $54 \pm 5.48\%$, and the least inhibition was treatment D (*Neurospora sp. 1*) by $44 \pm 5.48\%$.

KEYWORDS

Molecular identification, in vitro and in vivo inhibition, exophytes and endophytes, Colletotrichum musae



INTRODUCTION

Banana (*Musa paradisiaca* L.) is one of the most popular fruits in Bali. Bananas are usually harvested before ripening and stored in cold temperatures during transportation and marketing processes. Long-distance transportation and long-term storage in the market make bananas sensitive to disease (Thompson and Burden, 1995). Moreover, it is often found in traditional markets, many bananas are consumed for offerings.

Anthracoze caused by *Colletotrichum musae* (Berk. & Brief.) Arx. is the most important pathogen in injured ripe and green bananas (Meredith, 1960; Stover and Simmonds, 1987). Sometimes the fungus attacks the neck of the green radius when it is damaged by bending (Wardlaw, 1995). The lesions are sunken and covered with salmon-colored acervuli (Sutton and Waterston, 1970). Infection stimulates fruit ripening and lesions lengthen with ripening. On ripe fruit, sunken brown spots develop with orange acervuli (Stover and Simmonds, 1987).

Fruit quality can be decreased due to anthracnose disease, this is due to lack of plant care, and poor handling in the garden and during transportation which causes mechanical damage and provides the opportunity for infection for larger banana fruit rot microbes. Anthracnose attacks can occur in addition to pathogens entering through wounds as well as fruit being penetrated from the start of fruit on the tree (Faizal *et al.*, 2011). Some of the important consequences of the disease are (i) decreased nutritional value [2] (ii) contamination of foodstuffs by mycotoxins produced by pathogens (iii) toxic metabolites produced by diseased plant tissues in response to fungal attack (iv) bad taste. unacceptable associated with diseased material. Among the various factors responsible for banana postharvest losses, especially anthracnose caused by *C. musae*, is one of the main factors aimed at local as well as remote markets (Jeffries *et al.*, 1990).

I. MATERIALS AND METHODS

I.1. Place and time of research

The research was carried out in two places: 1) looking for sick and healthy fruit specimens from the Batubulan market and supermarkets. 2) Laboratory of Plant Diseases and Agricultural Biotechnology Laboratory. The research was carried out from April to August 2021.

I.2. Molecular identification

a. DNA Extraction

DNA extraction followed the procedure of Doyle and Doyle (1987), 0.2 g of pathogenic fungal mycelium samples were ground with liquid nitrogen and powdered fungal pathogens were put into Eppendorf tubes. Then 500 L of CTAB buffer and 50 L -mercaptoethanol were added, then mixed until homogeneous using a vortex. To lyse the cell wall, heating at a temperature of 70°C for 60 minutes where every 10 minutes is back and forth to speed up the lysis process.

Then cooled down to room temperature. Then 500 L of chloroform isoamylalcohol (24:1) was added to the tube and mixed until homogeneous by vortex and centrifuged at 12,000 rpm for 15 minutes. The supernatant obtained was transferred to a new Eppendorf tube by adding 500 L of sodium acetate, mixed until homogeneous by vortex and centrifuged again at 12,000 rpm for 10 minutes. The supernatant was transferred to an eppendorf tube and then 500 L of sodium acetate and isopropanol were added, mixed until homogeneous by vortex and

centrifuged again at 12,000 rpm for 10 minutes. The tube was shaken gently to bind DNA and incubated at -20°C for 30 minutes. The DNA threads obtained were precipitated by centrifugation for 10 minutes. The supernatant was discarded, the pellet was washed with ethanol (70%) then centrifuged at 8,000 rpm for 5 minutes. The ethanol was removed and the pellets were dried. The pellet was resuspended with 50 L of TE buffer and stored at -20°C for further use in the DNA amplification process.

b. DNA amplification

DNA amplification was carried out on a Thermo Cycle PCR machine. Amplification was carried out using universal primers to detect the internal transcribed spacer (ITS) region of ribosomal DNA (rDNA), namely forward primer ITS1 (5'-CTTGGTCATTTAGAGGAAGTAA-3') and reverse primer ITS4 (5'-TCCTCCGCTTATTGATATGC-3') with target size results. amplification was 490 bp (Doyle & Doyle, 1987). The DNA amplification reaction was carried out with a total volume of 25 L consisting of 1 L of DNA, 2.5 L of 10 x buffer and Mg²⁺, 0.5 L of 10 mM dNTP, 1 L of each primer, 12.5 L of Taq DNA (10 units/ L), and 9.5 L H₂O. The amplification conditions were divided into several stages, namely predenaturation at 94 C for 3 minutes, followed by 30 cycles of amplification, each cycle consisting of strand separation/denaturation of DNA at 94 C for 1 minute, primer attachment/annealing at 45 C for 1 minute, DNA synthesis at 72 C. for 2 minutes. Especially for the last cycle, the synthesis step is added for 10 minutes, then the cycle will end with a temperature of 4 C.

c. DNA electrophoresis

The amplified product was analyzed using Blued electrophoresis with 1% agarose gel (0.5xTris-Borate EDTA/TBE). Electrophoresis was carried out at 100 volts for 28 minutes and then the agarose gel was incubated in dye containing ethidium bromide (1%) for 15 minutes, then washed with H₂O for 10 minutes. The results of the electrophoresis were visualized with an ultraviolet transilluminator. The DNA bands formed on the electrophoresis results were documented with a digital camera.

d. DNA Sequence Analysis

The amplification product was sent to Macrogen (Singapore) for nucleotide sequencing. The tracing results were then analyzed using the basic local alignment search tool (BLAST) program with an optimization program to obtain DNA base sequences that have homology with DNA sequences found on the National Center for Biotechnology Information (NCBI) website. The nucleotide sequences obtained were then analyzed using ClustalW multiple alignment on Bioedit sequence alignment editor software version 7.0.5. Homology results close to 100% similarity categorized as the same species as the sample species.

I.3. Isolation of Endophytic and Exophytic Fungi

Isolation of endophytic fungi, plant parts such as fruit, leaves and stems were washed with sterile running water, then the plant parts were sterilized with 0.525% sodium hypochlorite for 3 minutes, and 70% alcohol for 2 minutes, then rinsed with sterile water for 1 minute. and then placed on PDA media (which was first given an anti-bacterial antibiotic, namely livoploxacin with a concentration of 0.1% (w/v). The fungus that emerged from the leaf pieces was transferred to a test tube containing PDA to be stored and classified by morphospecies.

Exophytes can be carried out by spraying plant parts (fruit, leaves and stems). The washing water is collected, then in a tube, then taken, from a 1 ml tube it is grown into a PDA which has previously been filled with livoploxacin with a concentration of 0.1% (w/v).).

I.4. Identification of Endophytic and Exophytic Fungi

The stored endophytic and exophytic fungi were then grown in Petri dishes containing PDA and repeated 5 times. Cultures were incubated in the dark at room temperature ($\pm 27^{\circ}\text{C}$). Isolates were identified macroscopically after 3 days of age to determine colony color and growth rate, and microscopic identification to identify septa on hyphae, spore/conidia shape and sporangiophores. Fungal identification using reference book Samson *et al.*, 1981; Pitt and Hocking, 1997; Barnett and Hunter, 1998; and Indrawati *et al.*, 1999 and identification of actiomyceytes Miyadoh (1997).

I.5. Inhibitory Test of Endophytic and Exophytic Fungi Against Pathogens

The endophytic and exophytic fungi that were found were tested for their inhibition against the growth of pathogenic fungi using the dual culture technique (in one Petri dish, one pathogenic fungus was grown each flanked with two endophytic fungi). The inhibitory ability can be calculated as follows (Dollar, 2001; Mojica-Marin *et al.*, 2008):

$$\text{Inhibitory ability (\%)} = \frac{A - B}{A} \times 100$$

Where:
 A = Pathogen colony diameter in single culture (mm)
 B = Pathogen colony diameter in dual culture (mm)

I.6. Endophytic and Exophytic Fungal Prevalence

Determining the prevalence of endophytic and exophytic fungi was based on the frequency of endophytic and exophytic fungal isolates found in healthy fruit per Petri dish, divided by all isolates found times 100%. The prevalence of isolates will determine the dominance of endophytic fungi present in healthy mango fruit.

I.7. In Vivo Antagonist Test

In vivo antagonistic test of endophytic and exophytic fungi found by pricking fresh fruit with a spelden needle 10 times, then smeared with antagonistic fungal spores (spores of one Petri dish in 250 ml of sterile distilled water), then immersed in fungal spore suspension. pathogens. Endophytic and exophytic fungi found include:

A = antagonist treatment 1 (spore suspension 5×10^7)

B = antagonist treatment 2 (spore suspension 5×10^7)

C = antagonist treatment 3 (spore suspension 5×10^7)

D = antagonist treatment 4 (spore suspension 5×10^7)

E = antagonist treatment 5 (spore suspension 5×10^7)

K-P = control without pathogen

K+P = control with pathogen

All treatments were repeated 5 times. The experiment was designed with a randomized block design (RBD), and after the analysis of variance (ANOVA) was carried out, it was continued with the smallest significant difference test (SDT) at the 5% level. Attack parameters measured by the formulation: the number of stabs attacked by the fungus divided by the total number of punctures (20 x) times 100%.

II. RESULTS

II.1. Microscopic Identification of Pathogens

Symptoms at the end of the fruit appear small spots (anthracnose) which over time can coalesce to form larger spots (Figure 1A), then after being isolated and transferred to a Petri dish, white mycelium appears with a pink color in the middle. (Figure 1B), colonies growing on the fruit skin were transferred to a new Petri dish, the

mycelium appeared pink (Figure 1C), and when viewed under a microscope the conidia were small round (Figure 1D).

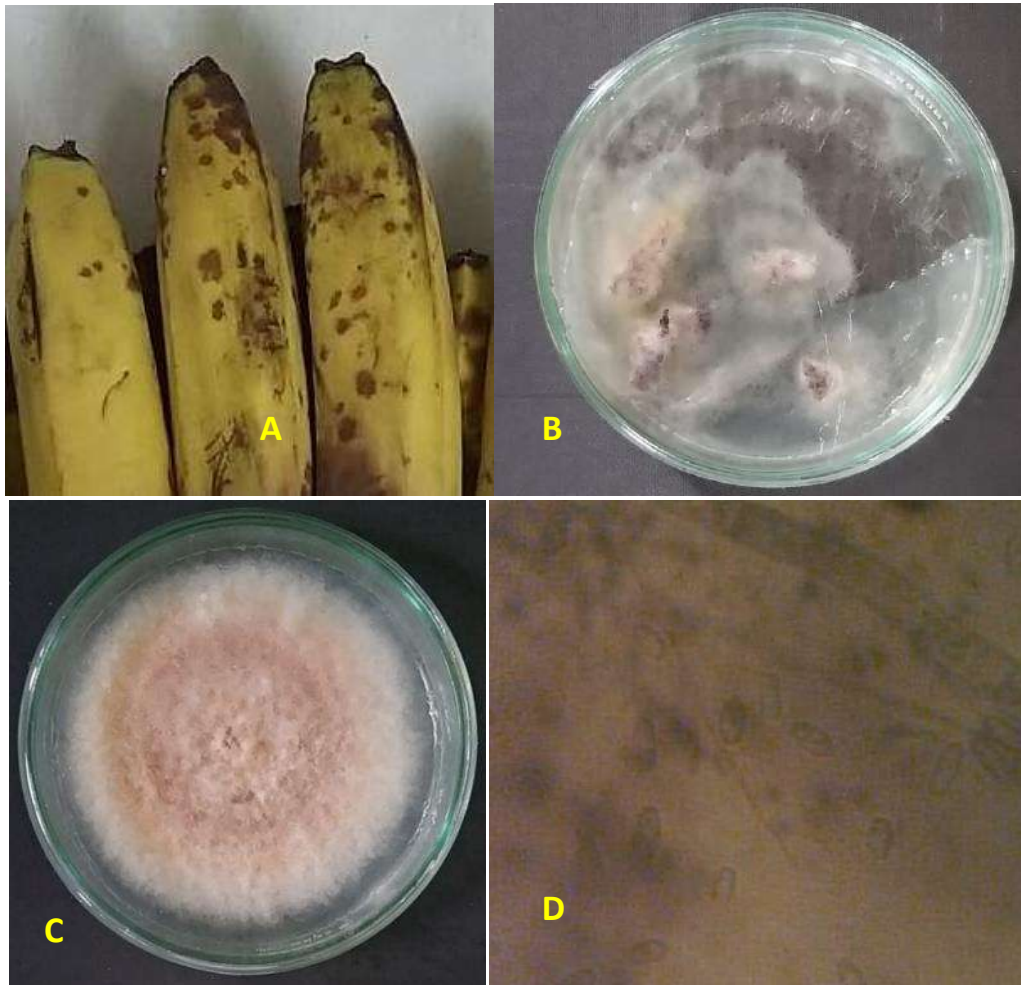


Figure 1. Symptoms of anthracnose (A), isolated pathogen (B), mycelium in Petri dishes (C, and conidia under a microscope (D), (s = symptom)

The results of the isolation of the pathogen obtained pink fungal mycelium colonies and very slow growth of 7 days to fill the Petri dish (Figure 1C) and the observations under the microscope showed conidia in large numbers of one-celled oval round shape (Figure 1D). After being investigated, it turned out that the pathogen was *C.musae*. Outcomes were identified based on reference pathogens according to Balendreset *al* (2020).

II. 2. Molecular Identification

Colletotrichum musae

DNA fragments measuring 650 bp were successfully amplified from 4 fungal samples using the universal primer ITS1/ITS4 (Figure 2). The amplified DNA sample was then used for the sequencing stage to determine the fungal species. Sequencing analysis confirmed that the fungus sampled was *Colletotrichum musae* with 98-100% homology to several *Colletotrichum musae* isolates in the genebank (Table 1). The phylogenetic tree of the pathogen (*Colletotrichum musae*) is shown in Figure 3).

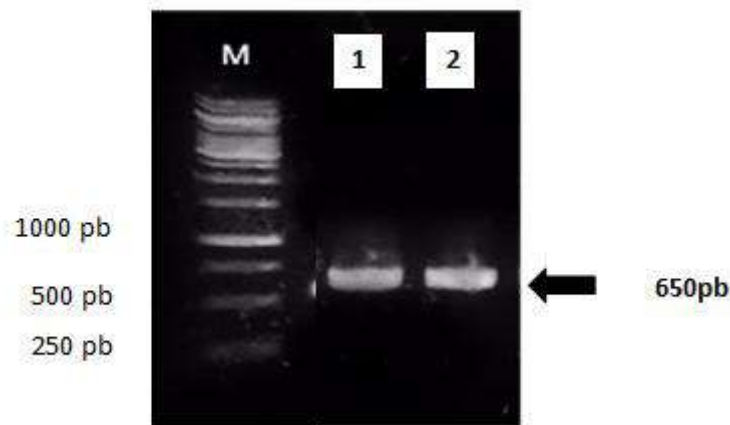


Figure 2. Visualization of amplified fungal pathogenic DNA using universal primers ITS1/ITS4 on 1% agarose gel. M: DNA marker (1kb ladder); Sample no. 1, and 2, (pathogen, *C. musae*)

II.3.Exophytic and Endophytic Fungus Populations

Exophytic fungi found in healthy fruit were *Aspergillus niger* as many as 2 isolates, *A. flavus* as many as 4 isolates, *Oidium sp.* a total of 4 isolates, *Nocardia asteroides* (Actinomycetes) as many as 2 isolates, *Nocardia sp.* (Actinomycetes) as many as 2 isolates, *Neurospora sp.* a total of 12 isolates and *Rhizopus sp.* A total of 18 isolates (Table 2). While the endophytic fungi found in healthy banana fruit were 6 isolates of *A. niger*, *Colletotrichum sp.* as many as 2 isolates, *A. flavus* as many as 2 isolates and *Rhizopus sp.* a total of 6 isolates (Table 2).

Table 1. Homology (%) of nucleotide sequences of *Colletotrichum musae* isolates with several isolates that have been reported in GenBank

Sikuen	<i>C. musae</i>	JX163232_MYS	MT351114_CHN	MK298312_AUS	MK087092_BRA	MH863550_CZH	MG386643_MYS	KX069828_AUS
<i>Colletotrichum musae</i>	ID	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
JX163232_ <i>C. musae</i> _MYS	100.0% ID		100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
MT351114_ <i>C. musae</i> _CHN	100.0%	100.0% ID		100.0%	100.0%	100.0%	100.0%	100.0%
MK298312_ <i>C. musae</i> _AUS	100.0%	100.0%	100.0% ID		100.0%	100.0%	100.0%	100.0%
MK087092_ <i>C. musae</i> _BRA	100.0%	100.0%	100.0%	100.0% ID		100.0%	100.0%	100.0%
MH863550_ <i>C. musae</i> _CZH	100.0%	100.0%	100.0%	100.0%	100.0% ID		100.0%	100.0%
MG386643_ <i>C. musae</i> _MYS	100.0%	100.0%	100.0%	100.0%	100.0%	100.0% ID		100.0%
KX069828_ <i>C. musae</i> _AUS	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0% ID	
KT582190_ <i>C. musae</i> _SRI	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
KM233233_ <i>C. musae</i> _COL	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
KC790969_ <i>C. musae</i> _IND	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
GQ369594_ <i>C. capsici</i>	91.3%	91.3%	91.3%	91.3%	91.3%	91.3%	91.3%	91.3%

Further phylogenetic analysis showed that *Colletotrichum musae* isolates formed one group with other isolates that had been registered in the genebank. As an out group isolate, *Colletotrichum capsici* (GQ369594) isolate was used (Figure 3).

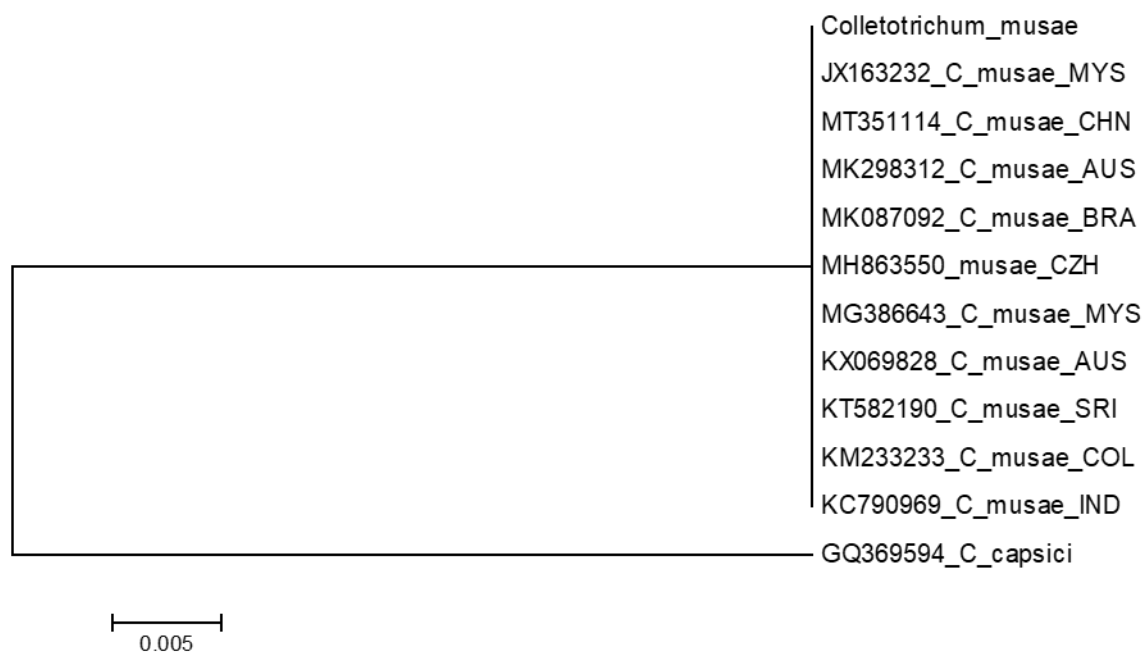


Figure 3. Phylogenetic analysis of *Colletotrichum musae* isolate based on partial nucleotide sequence alignment of DNA-A using Mega 6.06 (Neighbor Joining Algorithm with 1,000 bootstraps replicates)

II.4. In Vitro Inhibitory Test

The highest inhibitory power of exophytic fungi against pathogens (*C.musae*) was achieved by *A. niger*, *Neurospora* sp. and *Rhizopus* sp. each with an inhibitory power of 100%, the lowest was achieved by *Neurospora* sp. at the time of DAI by 50% (Table 3). While the inhibition of endophytic fungi against pathogens is *Rhizopus* sp. with an inhibition of 100% from 1 DAI to 4 DAI followed by *A. niger* at 100% at 3 and 4 DAI (Table 4).

Table 3. Observations of the inhibitory power of exophytes against pathogens (*Colletotrichum musae*)

No.	Name of exophytic microbes	2 DAI (%)	3 DAI (%)	3 DAI (%)	5 DAI (%)
1	<i>A. niger</i> 1	-	62	100	100
2	<i>A. niger</i> 2	100	100	100	100
3	<i>Oidium</i> sp.1	-	-	-	-
4	<i>Nocardia asteroides</i> 1 (Actinomycetes)	-	-	-	-
5	<i>A. flavus</i> 1	-	-	-	-
6	<i>Nocardia</i> sp.1 (Actinomycetes)	-	-	-	-
7	<i>Neurospora</i> spp.1-6	100	100	100	100
8	<i>A. flavus</i> 2	-	-	-	-
9	<i>Oidium</i> sp. 2	-	-	-	-
10	<i>Oidium</i> sp.3	-	-	-	-
11	<i>Nocardia asteroides</i> 2 (Actinomycetes)	-	-	-	-
12	<i>A. flavus</i> 3	-	-	-	-
13	<i>Nocardia</i> sp.2 (Actinomycetes)	-	-	-	-
14	<i>Neurospora</i> sp.	-	-	-	-
15	<i>Neurospora</i> sp. 8	50	67	75	83
16	<i>Neurospora</i> spp. 9-12	-	-	-	-
17	<i>A. flavus</i> 4	-	-	-	-
18	<i>Oidium</i> sp. 4	-	-	-	-
19	<i>Rhizopus</i> spp. 1-18	100	100	100	100

DAI = days after inoculation

Table 4. Observations of endophytic inhibition against pathogen B (*Colletotrichum musae*)

No.	Name of endophytic fungi	1 DAI (%)	2 DAI (%)	3 DAI (%)	4 DAI (%)
1	<i>A. niger</i> 1	40	54	100	100
2	<i>Colletotrichum</i> sp. 1	-	-	-	-
3	<i>A. niger</i> 2	10	38	100	100
4	<i>A. flavus</i> 1	-	-	-	-
5	<i>A. niger</i> 3	40	54	63	70
6	<i>A. niger</i> 4	-	-	-	-
7	<i>Colletotrichum</i> sp. 2	-	-	-	-
8	<i>A. niger</i> 5	50	71	78	83
9	<i>A. flavus</i> 1	-	-	-	-
10	<i>A. niger</i> 6	-	-	-	-
11	<i>Rhizopus</i> spp. 1-5	100	100	100	100

II.5. In Vivo In Vivo Inhibition Test

In vivo inhibition between selected exophytic and endophytic fungi with pathogen B (*C. musae*) was as follows: C (*Rhizopus* sp.1) had the highest inhibitory power of $94\pm 5.48\%$, followed by treatment A (*A. niger* 1) was $92\pm 8.37\%$, treatment B (*A. niger* 2) was $64\pm 5.48\%$ %, treatment E (*Rhizopus* sp. 2) was $54\pm 5.48\%$, and the smallest inhibitory power was treatment D (*Neurospora* sp. 1) was $44\pm 5.48\%$ (Table 5).

Table 4. Inhibition of selected exophytic and endophytic fungi against pathogen B (*Colletotrichum musae*) in vivo

Treatment	Replication					Average	Notation	
	I	II	III	IV	V		5%	1%
K-P	100	100	100	100	100	100	F	F
K+P	0	0	0	0	0	0	A	A
A	100	100	90	80	90	92 ± 8.37	E	E
B	70	60	70	60	60	64 ± 5.48	D	D
C	100	90	100	90	90	94 ± 5.48	E	E
D	50	40	50	40	40	44 ± 5.48	B	B
E	60	50	60	50	50	54 ± 5.48	C	C

Information: A = *Aspergillus niger* 1 (exophytic fungus), B = *A. niger* 2 (exophytic fungus), C = *Rhizopus* sp. 1 (endophytic fungi), D = *Neurospora* sp. 1 (exophytic fungi), and E = *Rhizopus* sp. 2 (endophytic fungi)

III. DISCUSSION

Exophytic and endophytic fungi found in healthy grapes are exophytic fungi, including *Neurospora* sp. as many as 2 isolates, Actinomycetes as many as 12 isolates, and *A. flavus* as many as 15 isolates, while the endophytic fungi were *A. flavus* as many as 5 isolates and *Aspergillus* sp. as many as 2 isolates (Sudarma *et al.* 2019). Likewise, in healthy mangoes, 6 isolates of *A. flavus* exophytic herbs were found, 6 isolates of *A. niger*, *Nucordia* sp. (Actinomycetes) as many as 6 isolates, *Rhizopus* sp. as many as 8 silat and *Streptomyces* (Actinomycetes) as many as 4 isolates (Sudarma *et al.*, 2020).

Various fungi have been present on the leaf surface, among these fungi have been tested for their fungitoxicity against *Aternariabrassicae* which causes leaf spot disease in cabbage. Colony interaction showed that *Trichoderma viride* and *Aspergillus flavus* gave maximum suppression for the inhibition of the fungus *A. brassicae* (Yadav *et al.*, 2011). The potential of the phylloplane fungus *Sarpgandha* (*Rauwolfia serpentina*) as a biocontrol agent was screened for antagonistic activity against *Alternaria alternata* in vitro, causing leaf spot on *Rauwolfia serpentina*. The antagonist culture filtrate was examined under "with cells" and "cell-free" conditions and showed that *T. piluliferum* (79.50) was equivalent to *T. harzianum* ISO-1(76.80) followed by *T. harzianum* ISO-2 (64.02), *P. sublateralium* (59.00) and *A.niger* (50.00). Meanwhile, *C. cladosporioides* showed minimum suppression (13.10) (Thkur and Harsh, 2016).

The phylloplane of the plant *Psidium guineense* was examined for fungal diversity in three months. A total of 17 fungal species were identified and one mycelium was sterile. Among them, most of the microorganisms grew in May and the least were found in March and January. *Cladosporium cladosporioides*, *Gliocladium viride*, *Mucor racemosus*, *Penicillium chrysogenum* and sterile mycelium were found to be dominant among all species. The highest number of species was obtained from the month of May. The Shannon diversity index is maximum in May. Simpson high dominance index in May and high evenness in March. Thus the results showed that the monthly variation was not significant in fungal species in the leaves of *P. guineense* (Saha et al., 2013).

Potential of endophytic fungi isolated from healthy cocoa pods to control *Phytophthora palmivora* in vitro and in vivo. Endophytic fungal isolates were classified based on the morphological characteristics of their culture and reproductive structure. All isolates found were tested to inhibit *P. palmivora* by double culture method, and the 10 best isolates were continued for separate pod tests. Then, the five best isolates (*Aspergillus*4, *Aspergillus*5, *Aspergillus*6, *Fusarium*6, *Ramichloridium* sp.) were evaluated for their ability to reduce *P. palmivora* in cocoa seedlings and plants in the field. *Aspergillus*, *Fusarium*, and *Ramichloridium* showed maximum activity against *P. palmivora* in multiple culture assays, pods, and seedlings. However, when these five isolates were applied in the field, they did not suppress disease progression (Simamora et al., 2021).

Endophytes are asymptomatic fungal or bacterial microorganisms found in almost all reported living plant species. They are plant-associated microbes that form symbiotic associations with their host plants by colonizing internal tissues, which makes them valuable for agriculture as a tool in improving crop performance. Many endophytic fungi produce secondary metabolites like auxins, gibberellins etc which help in the growth and development of their host plants. Some of these compounds are antibiotics that have antifungal, antibacterial and insecticidal properties, which strongly inhibit the growth of other microorganisms, including plant pathogens (Dutta et al., 2014).

CONCLUSION

The results showed that the cause of banana rot disease was *Colletotrichum musae* with DNA fragments measuring 650 bp successfully amplified using universal primers ITS1/ITS4. The highest in vitro inhibition of exophytic fungi against pathogens was achieved by *A. niger*, *Neurospora* sp. and *Rhizopus* sp. each with an inhibitory power of 100%, the lowest was achieved by *Neurospora* sp. at the time of days after inoculation (DAI) by 50%. While the inhibition of endophytic fungi against pathogens was *Rhizopus* sp. with an inhibition of 100% from 1 DAI to 4 DAI followed by *A. niger* at 100% at 3 and 4 DAI. The results of the in vivo inhibition of selected exophytic and endophytic fungi against pathogens were as follows: the highest inhibitory power was C (*Rhizopus* sp.1) of 94±5.48%, followed by treatment A (*A. niger* 1) of 92±8.37%, treatment B (*A. niger* 2) was 64±5.48% %, treatment E (*Rhizopus* sp. 2) was 54±5.48%, and the least inhibition was treatment D (*Neurospora* sp. 1) by 44±5.48%.

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