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Characterization of Bean Common Mosaic Virus (BCMV) strain Peanut Stripe Virus (PStV) associated with patchouli mottle disease in Indonesia

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Abstract. *Hartono S, Kandito A. 2024. Characterization of Bean Common Mosaic Virus (BCMV) strain Peanut Stripe Virus (PStV) associated with patchouli mottle disease in Indonesia. Biodiversitas 25: 3860-3867.* Patchouli (*Pogostemon cablin* Benth.) is an important commodity that is traded for its essential oil. Indonesia is the main producer of patchouli oil and provides 90% of the global oil trade. However, patchouli plantations face several constraints, especially plant diseases caused by viruses. Considering its economic importance, we conducted surveillance and detection of patchouli mottle disease (PMoD) in several patchouli plantations in Java. Leaves of infected plants exhibited symptoms of mosaic, mottling, and malformations. To confirm the presence of the virus, we collected the infected plants and mechanically inoculated it on healthy patchouli plants. This process involves applying the sap to healthy plants in a controlled manner to ensure that the symptoms observed in the field can be reproduced. Local lesions were produced on mechanically infected *Chenopodium amaranticolor* and *Gomphrena globosa*; systemic symptoms on *Cucurbita maxima, Vigna unguiculata, Nicotiana tabacum*, and *Nicotiana glutinosa*. Electron microscopic analysis of leaf-dip preparations from a symptomatic sample revealed flexuous viral particles sized approx. 750 nm long, identical to the *Potyvirus* virion. Molecular detection using RT-PCR and degenerate primers for *Potyvirus* produced 709 base pair amplicons, indicating positive results in our samples. Nucleotide sequencing data showed the sample was infected by Bean Common Mosaic Virus (BCMV) strain Peanut Stripe Virus (PStV), with high similarity to BCMV isolated from legume plants. To our knowledge, this is the first report of the natural occurrence of BCMV strain PStV on patchouli plants in Indonesia. Therefore, integrated pest management measures are needed to control the disease and reduce the economic impact of PMoD.

Keywords: BCMV, patchouli, patchouli mottle disease, PStV, RT-PCR

INTRODUCTION

Patchouli (*Pogostemon cablin* Benth.) is one of the main commodities for the global trade market, primarily valued for its essential oil, which is extensively used in the fragrance and pharmaceutical industries. The cultivation of patchouli is predominantly concentrated in tropical regions, with Southeast Asia being the primary production area. Notably, Indonesia accounts for approximately 90% of the world's patchouli supply, making it a critical player. The islands of Sumatra, Sulawesi, and Java are the primary cultivation zones, covering a combined planting area of 20,000 hectares and yielding an annual production of 2,600 tons of patchouli oil (Central Bureau of Statistics Indonesia 2023). Because of its economic significance and simple cultivation, patchouli was cultivated in Indonesia as a cash crop (Keumalasari et al. 2021).

However, the cultivation of patchouli faces several challenges, particularly from plant diseases caused by *Ralstonia solanacearum*, *Synchitrium pogostemonis*, and plant viruses (Miftakhurohmah et al. 2017; Sriwati et al. 2022; Zulfadli et al. 2023). Among these, Patchouli Mottle Disease (PMoD) caused by plant viruses stands out as a major concern due to its severe impact on plant health and oil yield. PMoD is characterized by symptoms such as mosaic patterns, leaf distortion, and stunted growth, leading to substantial reductions in both the quality and quantity of patchouli oil and patchouli alcohol content. The economic impact of PMoD is profound, with infected crops suffering significant yield losses (Miftakhurohmah et al. 2013). Given the extensive cultivation of Patchouli in Indonesia, these losses translate to significant economic detriments for farmers and the national economy. The propagation of patchouli through vegetative means, such as stem cuttings, exacerbates the spread of viral infections, as infected plant material can easily transmit viruses to healthy plants.

Previous studies have identified several viruses associated with PMoD, including members of the *Potyvirus*, *Fabavirus*, *Secovirus*, *Tobravirus*, *Necrovirus*, *Cucumovirus*, and *Potexvirus* genera (Zaim et al. 2013; Miftakhurohmah et al. 2017). There are several common species known to be associated with PMoD, including Patchouli Mottle virus (PatMoV), Patchouli Mosaic Virus (PaMV), Patchouli Yellow Mosaic Virus (PaYMV), Cucumber Mosaic Virus (CMV) and Bean Common Mosaic Virus (BCMV) strain PStV (Natsuaki et al. 1994; Zaim et al. 2013; Noveriza et al. 2016; Miftakhurohmah et al. 2017).

Bean Common Mosaic Virus (BCMV) is a member of the *Potyvirus* genus, which is recognized as a major pathogen of legume plants and sesame. BCMV is known for its extensive genetic diversity and the existence of multiple strains, each with specific host preferences and pathogenicity profiles (Zhou et al. 2014; Damayanti 2015; Li et al. 2024). Among the various strains of BCMV, the Peanut Stripe Virus (PStV) strain is particularly noteworthy. Initially considered distinct from BCMV, PStV has since been identified as a strain within the BCMV species. In 2009, BCMV-PStV was reported to be associated with PMoD in India, thus adding patchouli as one of the BCMV hosts (Singh et al. 2009; Bano and Khan 2023). Currently, BCMV is classified into serotype A and serotype B, and it is a key aspect of its genetic makeup. Serotype A, previously known as Bean Common Mosaic Necrotic Virus (BCMNV), comprises five strains, while Serotype B, formerly known as BCMV, boasts 26 strains, such as PStV, BIC, AzMV, US1-10, NL1-4, etc. (Worrall et al. 2015; Tang and Feng 2023; Li et al. 2024). The BCMV genome, like other Potyviruses, consists of a single-stranded, positive-sense RNA molecule approximately 10 kb in length. The genome encodes a large polyprotein processed into functional viral proteins by virus-encoded proteases. The 3' untranslated region (UTR) and polyprotein gene are critical for studying genetic variability and strain differentiation among BCMV isolates.

The polyprotein gene of BCMV encodes several functional proteins, including the coat protein (CP), helper component proteinase (HC-Pro), protease (NIa), and RNA-dependent RNA polymerase (RdRp/NIb) (Shen et al. 2020). These proteins are essential for viral replication, movement, and host interaction. The HC-Pro is particularly notable for suppressing host RNA silencing mechanisms, a key defense response in plants. HC-Pro region is also a hotspot for recombination among BCMV strains, which affects its pathogenicity (Feng et al. 2014). Variations in the HC-Pro coding region among BCMV strains can affect the virus's ability to counteract host defenses and establish infection (El-Sawy et al. 2014; Tang and Feng 2023).

Our survey in several pachouli plantations showed some plants exhibiting mosaic and mottle symptoms, resembling an infection of the virus; molecular analysis revealed that the patchouli samples were infected by BCMV-PStV. Considering the substantial economic implications and the critical need for effective disease management strategies, this study aims to characterize the Bean Common Mosaic Virus (BCMV) associated with PMoD in Indonesia. Although BCMV has been reported in other regions affecting various hosts, its association with PMoD in Indonesia had yet to be documented prior to this research.

This study presents the first occurrence of BCMV, specifically the PStV strain, in association with PMoD in Indonesia. Through molecular characterization, including sequencing of the 3' UTR and polyprotein gene regions, we aimed to elucidate the genetic relationships and diversity of BCMV strains affecting patchouli. The findings from this study significantly advance our understanding of the epidemiology and genetic variability of BCMV, contributing to a broader and deeper understanding of virus-host interactions and informing the development of effective disease management strategies.

MATERIALS AND METHODS

Sample collection

Patchouli plants exhibiting symptoms of mild to severe mottle, mosaic, thickened, or stunted leaf growth were collected from patchouli cultivation areas in Magelang, Central Java, and Sleman, Yogyakarta Province, Indonesia (Figure 1). The leaf samples were stored at -20°C for further experimental work. The experimental works consisted of three parts i.e. virus identification using electron microscopy, transmission assays, and pathogenicity test.

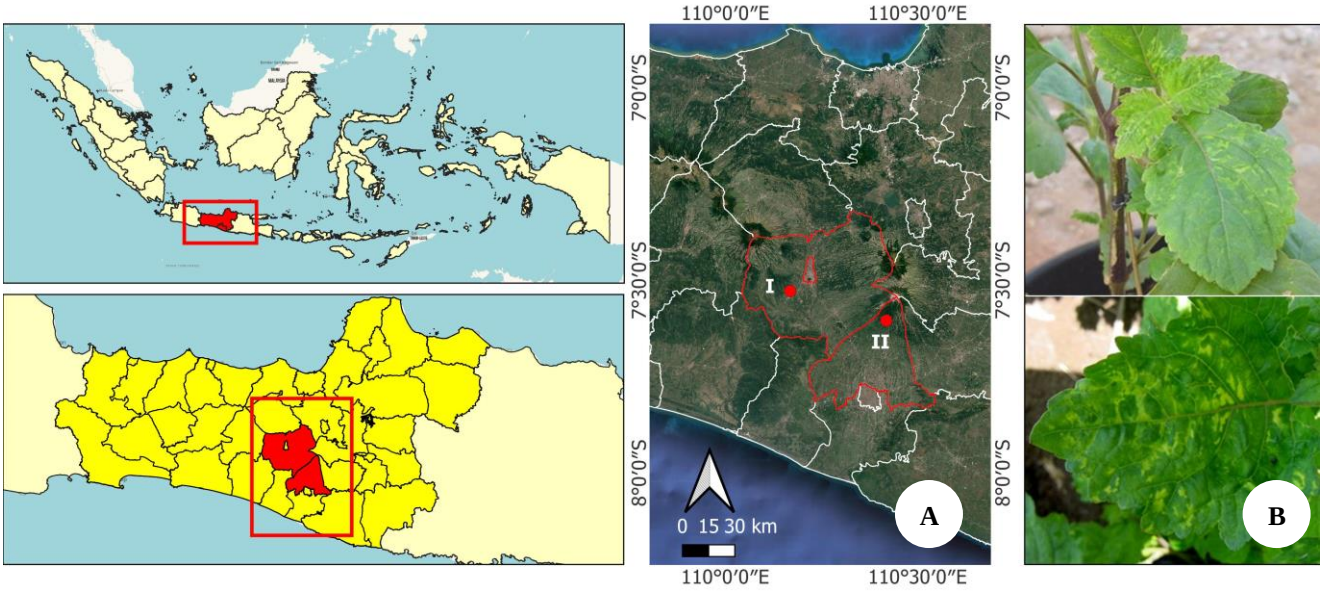

Figure 1. A. Sampling location and patchouli plants showed virus from Central Java and Yogyakarta, Indonesia. I: Magelang, Central Java, Indonesia, II: Sleman, Yogyakarta, Indonesia; B. Mottling symptoms

Virus identification

One square centimeter of symptomatic leaf tissue was ground in 100 µL of 0.1 M Tris-HCl, pH 7.4, with 10% sucrose with a sterilized mortar and pestle. The leaf extracts were transferred to collodion-coated grids and held for 1 min. After washing the grids with 30 drops of distilled water, grids were stained with 1% Phosphotungstic acid (PTA). Negatively stained specimens were viewed with a transmission electron microscope (JEM 1010 JEOL, Tokyo, Japan. Following the result of electron microscopy, we conducted a serological assay using a specific antibody of BCMV-PStV. The serological assay was performed following a previous study (Hartono et al. 2006).

RNA extraction and virus detection using RT-PCR

Fifty milligrams of dried sample were used for total RNA extraction. The sample was ground using a porcelain mortar and pestle without liquid nitrogen. The RNA extraction protocol was carried out using a Total RNA extraction kit for plants (Geneaid, Taiwan). Extraction steps are performed following manufacturer instructions. The total RNA is subsequently used as the template for cDNA synthesis. The cDNA synthesis was carried out using the RevertAid cDNA synthesis kit (ThermoFisher, US), according to the manufacturer's instructions protocol. Polymerase Chain Reaction (PCR) was carried out using MyTaq Redmix Polymerase (Bioline, Taiwan), molecular grade ddH_2O, forward primer, reverse primer, and cDNA templates. The reaction was carried out in a volume of 50 µL. Primers used were degenerate primers of *Potyvirus* from laboratory collection, namely PVY1 (5'-GTNTGGTGNATTGANATTGG-3') and oligo-dT. This primer pair amplified CP and 3'UTR of *Potyvirus*. The PCR program consisted of pre-denaturation at 95°C for 3 minutes, followed by 40 cycles of denaturation at 95°C for 1 minute, annealing at 50°C for 30 seconds, and extension at 72°C for 1 minute. The final extension was at 72°C for 10 minutes. The PCR product was subsequently visualized by agarose gel electrophoresis.

Sequence analysis

Nucleotide sequencing was conducted using the Direct Sanger Sequencing method with both forward and reverse primer. The nucleotide sequencing was further analyzed using BLAST (http://blast.ncbi.nlm.nih.gov/BLASTn). The alignment of nucleotide sequence data and phylogenetic tree diagram was constructed on MEGA v.11 software using the Neighbor-Joining method with 1000 bootstraps replication (Tamura et al. 2021). A pairwise nucleotide matrix was constructed in SDT v1.2 software (Muhire et al. 2014). Sequence subsequently deposited in the Genbank with accession number PP808493.

Pathogenicity test

To study the transmission of PMoD, we conducted a pathogenicity test using several methods i.e. mechanical inoculation, grafting, and vector transmission using aphids. The virus source was obtained from diseased patchouli plants and previously characterized by electron microscopy and serological assay as BCMV-PStV. The aphid used as a vector was laboratory collection and was identified by morphological characters as *Aphis gossypii* Glover 1877. All methods employed in pathogenicity tests were carried out in three biological replicates.

Diseased leaf samples from field observations were used for mechanical inoculation. Leaves were ground in a sterile mortar with 0.01 M phosphate buffer (pH 7.4), and the resulting plant sap was applied to test plants dusted with carborundum to facilitate infection. The test plants included *Pogostemon cablin*, *Chenopodium amaranticolor*, *Gomphrena globosa*, *Cucurbita maxima*, *Vigna unguiculata*, *Nicotiana tabacum*, and *Nicotiana glutinosa*. These inoculated plants were maintained in a controlled laboratory environment, and the appearance of local lesions was monitored daily for two weeks, starting seven days post-inoculation.

The grafting method involved attaching scions from diseased patchouli plants to healthy rootstock, facilitating the direct transfer of the virus. Vector inoculation was conducted by allowing *A. gossypii* to feed on diseased patchouli plants before transferring them to healthy patchouli plants to observe the transmission efficiency. For all methods, experiments were conducted with three biological replicates to ensure data reliability and reproducibility.

RESULTS AND DISCUSSIONS

Virus detection and electron microscopy

Patchouli samples exhibiting mosaic symptoms collected from the field were tested to detect viruses associated with patchouli. Detection results using the PVY1/oligodT primer pair revealed the presence of a 709 bp amplicon (Figure 2), indicating that the samples were positive for *Potyvirus* infection. Electron microscopy showed flexuous-shaped particles, identical to *Potyvirus* virions (Figure 3). These results showed that a member of *Potyvirus* infected patchouli samples.

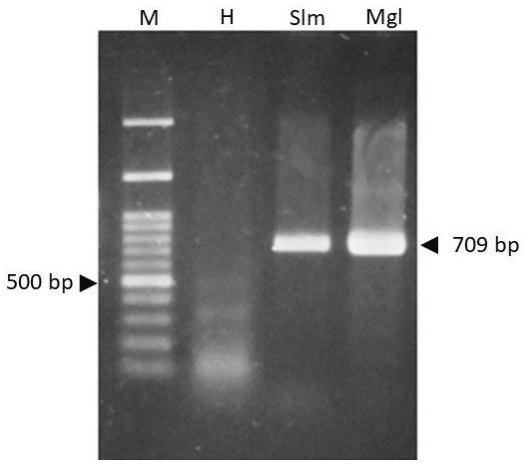

Figure 2. PCR visualization of *Potyvirus* detection on patchouli samples. H: Samples are healthy plants, Slm: Diseased plants from Sleman, Mgl: Magelang, M: 100 bp DNA ladder

Phylogenetic analysis

Based on sequencing data the virus associated with patchouli mottle disease was identified as BCMV strain PStV (Figure 4). This finding is consistent with reports of patchouli mosaic disease in India, also caused by BCMV strain PStV (Singh et al. 2009; Bano and Khan 2023).

Nucleotide sequence identity comparison of the CP region and 3' UTR regions of BCMV between the Indonesian and Indian isolates showed a high degree of similarity of more than 90%, indicating a close genetic relationship between these isolates. The pairwise homology based on the alignment of the CP region showed nucleotide identity >90%, indicating those isolates were considered as single species based on the demarcation criteria of potyvirids species (Inoue-Nagata et al. 2022) (Table 1). The PStV strain of BCMV has been identified as a significant pathogen affecting leguminous crops, with reports of its presence in several countries, including the USA, South Korea, India, China, and Indonesia. This strain is known for causing severe mosaic symptoms and yield losses in susceptible hosts (Singh et al. 2009). The high similarity in the polyprotein and 3' UTR sequences between the Indonesian and other PStV isolates indicates that this strain has a relatively stable genetic makeup, which could facilitate its spread across different regions and host plants (Li et al. 2024).

The alignment of amino acid sequences in the coat protein (CP) region of BCMV isolates revealed high similarity among various isolates. However, significant genetic variations were observed among BCMV isolates from the same host species and across different geographical locations. Specifically, our BCMV-PStV isolates from patchouli in Indonesia (PP808493) exhibited the closest genetic relationship with BCMV isolates from *Arachis hypogaea* (peanut), *Glycine max* (soybean), and *Sesamum indicum* (sesame) from various regions. Notably, compared to several global isolates of BCMV-PStV, our Indonesian isolates displayed distinct amino acid differences (Table 2.)

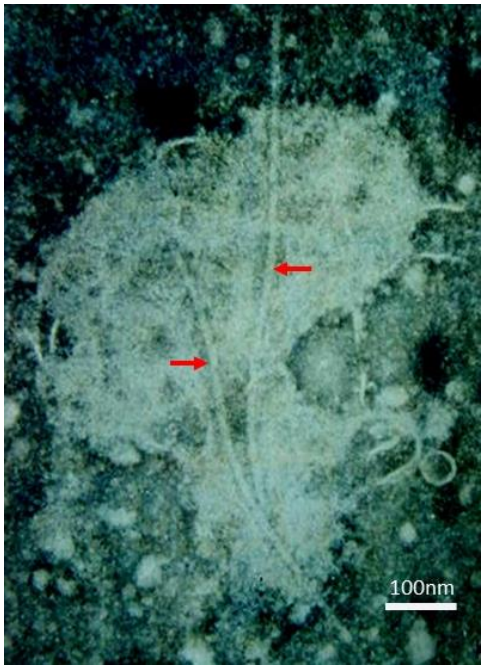

Figure 3. Electron microscopy showed *Potyvirus* particles. Flexuous particles were indicated with the red arrow. Bar represents 100nm length

Table 1. Identity percentage of BCMV-PStV isolate patchouli from Indonesia compared to global BCMV-PStV isolates

BCMV Isolates		Identity (%)	
Accession number	**Isolates**	**nt**	**aa**
MK069986	*Proteus vulgaris* Mexico	92.73	95.05
MF498886	*Proteus vulgaris* Iran	92.74	95.05
DQ666332	*Proteus vulgaris* Colombia	93.44	94.32
AY112735	*Proteus vulgaris* UK	93.09	95.05
AJ889245	*Arachis hypogaea* China	98.26	97.20
MH628437	*Arachis hypogaea* China	98.11	97.20
U34972	*Arachis hypogaea* USA	98.11	97.20
U05771	*Arachis hypogaea* USA	98.11	97.20
AF063222	*Arachis hypogaea* USA	96.22	92.85
AF200624	*Arachis hypogaea* Thailand	96.38	96.49
Z21700	*Arachis hypogaea* Australia	98.25	96.49
DN483753	*Arachis hypogaea* South Korea	98.11	97.20
KJ807812	*Glycine max* China	93.25	92.85
KJ807813	*Glycine max* China	98.26	97.20
KJ508092	*Glycine max* South Korea	98.11	96.49
KP903372	*Vigna angularis* China	93.39	95.77
AY575773	*Vigna unguiculata* Taiwan	93.37	93.59
MH568695	*Sesamum indicum* China	98.11	97.20
AJ851894	*Pogostemon cablin* India	95.55	94.32

Table 2. Amino acid translation showed genetic variation in the CP region of each BCMV-PStV isolate

BCMV isolates		Amino acid position in CP region														
Accession number	**Isolates**	**4**	**12**	**14**	**21**	**24**	**39**	**61**	**64**	**70**	**112**	**122**	**135**	**143**	**149**	**150**
MK069986	*P. vulgaris* Mexico	D	V	G	D	V	L	R	M	L	S	V	R	T	P	P
MF498886	*P. vulgaris* Iran	D	V	G	D	V	L	R	M	L	S	V	R	T	P	P
DQ666332	*P. vulgaris* Colombia	D	V	G	D	V	L	R	M	L	S	V	R	T	P	P
AY112735	*P. vulgaris* UK	D	V	G	D	V	L	R	M	L	S	V	R	T	P	P
AJ889245	*A. hypogaea* China	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
MH628437	*A. hypogaea* China	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
U34972	*A. hypogaea* USA	D	V	G	D	I	L	R	I	L	N	V	R	T	S	A
U05771	*A. hypogaea* USA	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
AF063222	*A. hypogaea* USA	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
AF200624	*A. hypogaea* Thailand	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
Z21700	*A. hypogaea* Australia	D	V	G	D	V	L	R	M	L	N	V	R	T	S	P
DN483753	*A. hypogaea* South Korea	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
KJ807812	*G. max* China	D	V	G	E	V	L	K	M	L	N	V	R	T	S	P
KJ807813	*G. max* China	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
KJ508092	*G. max* South Korea	D	V	G	D	V	L	R	M	L	N	M	R	T	S	A
KP903372	*V. angularis* China	D	V	G	D	V	L	R	M	L	N	V	R	S	S	P
AY575773	*V. unguiculata* Taiwan	D	V	G	D	V	L	K	M	L	S	V	R	T	S	P
MH568695	*S. indicum* China	D	V	G	D	V	L	R	M	L	N	V	R	T	S	A
AJ851894	*P. cablin* India	E	V	G	E	I	F	R	M	F	N	V	R	T	F	A
PP808493	*P. cablin* Indonesia	E	I	A	D	V	L	R	M	L	N	V	K	T	S	T

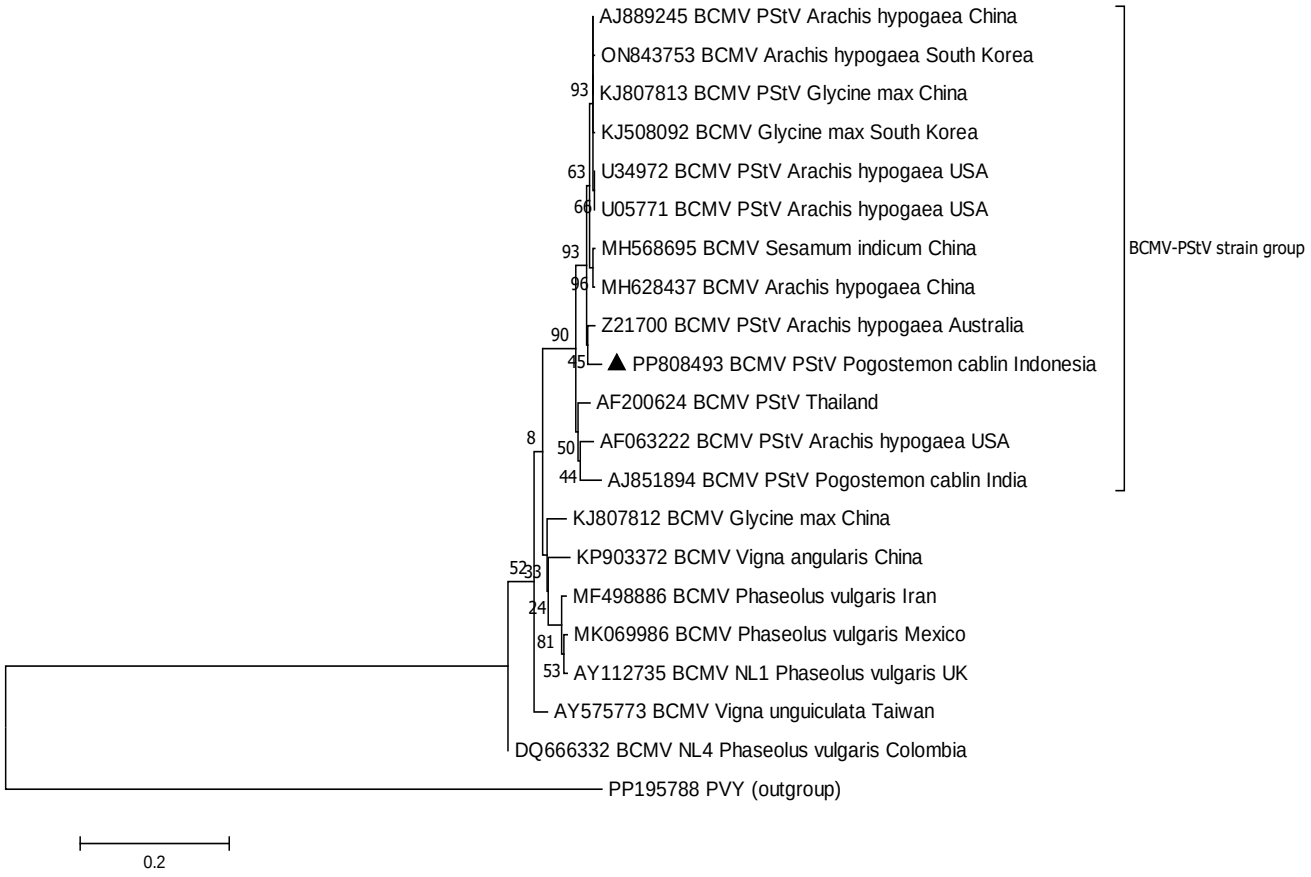

Figure 4. Phylogenetic analysis based on CP region and 3-UTR showed that the virus associated with PMoD in Indonesia was considered BCMV and belongs to the strain PStV group. The sample is indicated with a black triangle. Numbers on the node represent bootstraps support value and do not describe the nucleotide identity

The coat protein plays a crucial role in the infection and transmission of potyviruses, including BCMV. Variations in the CP region can influence the host range and transmission modes (Martínez-Turiño and García 2020). These genetic differences may impact the pathogenicity of BCMV isolates on different hosts, potentially altering their virulence and ability to infect new plant species. Previous studies have demonstrated that genetic diversity among BCMV isolates can affect the virus interaction with host plants, resulting in varied pathogenicity levels (Zhou et al. 2014).

Pathogenicity test

Mechanical inoculation of BCMV-PStV from patchouli to fifteen indicator plants revealed that the virus isolates could only infect *C. amaranticolor*, *G. globosa*, *N. tabacum*, *V. unguiculata*, and *C. maxima*. Interestingly, mechanical inoculation of the BCMV-PStV from patchouli to patchouli did not result in symptom expression, indicating that mechanical transmission of the virus from patchouli may not occur (Table 3). These facts suggest that BCMV-PStV, while associated with patchouli (family Lamiaceae), can also infect some species from the families Amaranthaceae, Solanaceae, Cucurbitaceae, and Fabaceae. Previous studies also suggest that BCMV might have a broader host range than initially known, including Pedaliaceae, Zingiberaceae, and Orchidaceae (Bhadramurthy and Bhat 2009; Zhou et al. 2014; Larrea-Sarmiento et al. 2020). Mechanical inoculation against several Solanaceae and Fabaceae species in this study showed that the virus was only infectious against certain species. The results showed that the virus infects *N. tabacum* var. *Samsun* and *N. glutinosa*, but did not infect *N. tabacum* var *Burley 21* and *N. glauca*. These findings indicate the possible specific host range of BCMV-PStV. This is in line with the findings of BCMV-PStV research on soybeans in China (Zhou et al. 2014)

To further confirm the transmission methods of BCMV-PStV, we conducted virus transmission tests from symptomatic patchouli to patchouli using four methods: mechanical inoculation, grafting, cuttings, and *A. gossypii* vector transmission (Table 4). Transmission tests from patchouli to patchouli were successful, with 100% transmission rates through grafting and cuttings. In comparison, vector transmission using *A. gossypii* resulted in a transmission rate of 66.67%. Meanwhile, mechanical inoculation of BCMV from patchouli to patchouli results in 0% transmission rates. These findings indicated that both vegetative propagations and vectors are effective pathways of viral transmission and could potentially trigger an epidemic of PMoD. Thus, the development of virus-free planting materials and vector management in field conditions are essential as a backbone for developing disease management.

Discussion

Several viruses are associated with patchouli, including Patchouli yellow mosaic virus (PatYMoV), Patchouli mottle virus (PatMoV), Patchouli mild mosaic virus (PMMV), and BCMV. These viruses negatively impact patchouli production, causing reductions of up to 50% both in patchouli oil and patchouli alcohol content. Additionally, viruses in patchouli pose a potential epidemiological threat, as patchouli is vegetatively propagated through stem cuttings.

Table 3. Mechanical transmission of BCMV-PStV to several indicator plants

Test plants	Symptoms	
	Early observation	Advanced observation
Chenopodium amaranticolor	Chlorotic spot	Necrotic spot
Gomphrena globosa	Necrotic spot	Necrotic spot
Nicotiana tabacum	Vein clearing	Mosaic
Nicotiana tabacum var. *Samsun*	Vein clearing	Mosaic
Nicotiana tabacum var. *Burley 21*	-	-
Nicotiana glutinosa	Vein clearing	Mosaic
Nicotiana glauca	-	-
Physalis floridana	-	-
Tetragonia expansa	-	-
Vigna unguiculata	Vein clearing	Mosaic
Cucurbita maxima	Malformation	Malformation
Phaseolus radiatus	-	-
Vicia faba	-	-
Datura stramonium	-	-
Pogostemon cablin	-	-

Table 4. BCMV-PStV transmission by several methods

Methods	Number of plants		Transmission rate (%)
	Inoculated	Infected	
Mechanical inoculation	3	0	0
Grafting	3	3	100
Cutting	3	3	100
Aphis gossypii vector	3	2	66.67

Patchouli mottle disease (PMoD) represents a significant challenge in patchouli cultivation due to its severe impact on plant health and yield. Symptoms of PMoD include mosaic patterns, leaf distortion, and stunted growth, which collectively reduce the quality and quantity of patchouli oil (Miftakhurohmah et al. 2013). Potyviruses, such as BCMV, are known to be highly transmissible and can spread rapidly within and between fields through mechanical means and insect vectors like aphids and whiteflies *Bemisia tabaci* (Gilbertson et al. 2015; Rinika et al. 2023). The high propagation rate of these viruses necessitates vigilant monitoring and robust disease management practices to mitigate their spread and impact.

The 3' UTR of BCMV plays a crucial role in viral replication and translation. Comparisons of the 3' UTR sequences between different BCMV strains have revealed significant variations, which can influence the virus's ability to infect various host plants and its virulence. In this study, the 3' UTR sequence of the Indonesian BCMV patchouli isolate was compared to the Indian isolate, showing a high degree of nucleotide sequence identity. This close genetic relationship suggests a potential common origin or recent divergence of these strains, highlighting the need for cross-regional studies to understand the movement and evolution of BCMV (Inoue-Nagata et al. 2022).

Although BCMV was initially believed to be associated exclusively with the Fabaceae family, recent studies and our findings from this research demonstrate that BCMV actually possesses a broader host range. This range includes not only Fabaceae but also extends to other plant families such as Pedaliaceae, Orchidaceae, and Zingiberaceae. Specifically, BCMV has been identified in sesame (*S. indicum*, family Pedaliaceae), vanilla (*Vanilla planifolia*, family Orchidaceae), and ginger (*Zingiber officinale*, family Zingiberaceae) (Bhadramurthy and Bhat 2009; Zhou et al. 2014; Larrea-Sarmiento et al. 2020).

In addition, BCMV and its strains pose a broader agricultural threat due to their ability to infect a wide range of agricultural crops. The economic implications of BCMV infections are substantial, as they can lead to significant reductions in crop yield and quality. Understanding the genetic diversity and evolutionary dynamics of BCMV is crucial for developing effective control measures such as resistant crop varieties. Previous studies suggested the development of a resistant variety is the most effective way to manage the disease caused by BCMV and closely related viruses (Wu et al. 2018; Liu et al. 2021).

Effective management of PMoD requires the development of specific strategies within an integrated pest management (IPM) framework. These strategies include the use of virus-free planting materials, resistant cultivars, and control of insect vectors. Breeding for resistance, on the other hand, demands a deep understanding of the virus genome and its interactions with the host plant (Revers and García 2015). Developing virus-free material is particularly crucial, as it will suppress the initial inoculum. Notably, virus-resistant patchouli has been successfully developed using a transgenic approach by the coat protein precursor gene of *Potyvirus* (Swamy and Sinniah 2016). In a practical context, using virus-free material and developing resistant cultivars emerge as the most suitable solutions to managing potyviruses (Kakareka et al. 2021).

In conclusion, the identification of BCMV-PStV as a causal agent of patchouli mosaic disease in Indonesia underscores the need for continued research and surveillance to manage viral diseases in patchouli. This study contributes to the broader understanding of virus-host interactions and provides additional data on viruses infecting patchouli as a basis for developing effective disease control strategies. Further research should focus on the development of resistant patchouli cultivars and the implementation of comprehensive IPM practices to ensure the sustainability of patchouli cultivation.

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