Short Note

First Report of *Phytopythium vexans* (de Barry) Abad, de Cock, Bala, Robideau, Lodhi & Lévesque Causing Potato Tuber Rot in Indonesia

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ABSTRACT

*Phytopythium vexans* (de Barry) Abad, de Cock, Bala, Robideau, Lodhi & Lévesque was successfully isolated from soil of potato fields in Ngablak, Magelang. This research aimed to obtain knowledge of *P. vexans* potency as a pathogen on potatoes, and also morphologically and molecularly identify *P. vexans* compared to Oomycetes, *Phytophthora* and *Pythium*. Morphological identification was conducted by observing macroscopic colony pattern that grew on PDA medium for five days and microscopic observation on its hyphae, sporangia, papillate, and chlamydospore. Molecular identification was conducted using multigene analysis, ITS and LSU. The in vitro pathogenicity test was done by inoculating *P. vexans* inoculum to healthy potato leaves and tubers. Results of morphological observation showed that *P. vexans* had a stellate pattern, aseptate hyphae, ovoid shaped sporangium and completed with semipapillate. Chlamydospores were also found and often used for survival. This research revealed that the morphology characters of *P. vexans* were combination between the characteristics of *Pythium* and *Phytophthora*. Whereas, based on molecular analysis using ITS and LSU, *Phytopythium* spp. was more closely related to *Phytophthora* spp. rather than *Pythium* spp. The pathogenicity test of *P. vexans* showed that it could infect the flesh of potato tubers by showing a brown lesions symptom.

Keywords: ITS; LSU; oomycetes; potato; *Phytopythium*

INTRODUCTION

Potato (*Solanum tuberosum* L.) is an essential non-cereal staple food and is widely cultivated in more than 100 countries. The tubers contain high nutrients, including carbohydrates, protein, minerals, fiber, and vitamins (Zhang et al., 2017). In Indonesia, potato production centres area spread in the highlands across Sumatra and Java. Based on Central Statistics Agencies of Magelang Regency in 2018, Ngablak is one of the potato production areas located in Central Java that produced 44,540 quintals from 141 ha cultivated area (Badan Pusat Statistik Kabupaten Magelang, 2018). Nevertheless, pathogens and pests are still a severe potato production problem.

The most destructive soil-borne pathogen is *Phytophthora infestans* and is globally known as the causal agent of potato late blight. Millions of people died due of the Ireland-Irish famine (Hammond-Kosack, 2014). Another pathogen of potato production in Indonesia, *Pythium vexans*, was mentioned by Centre of Agriculture and Biosciences International. (1987). No further information was found about this pathogen, especially from potato production areas in Indonesia. Lévesque and de Cook (2008) have proposed a new genus called *Phytopythium* spp. based on the molecular analysis to separate the clade K from the *Pythium* genus, one of the clade K members is *Phytopythium vexans*.

In the last five years, *P. vexans* was first reported by many countries and also its destructive potential on various host plants, including dieback disease in Morocco (Jabiri et al., 2020), decline syndrome of kiwi in Italy (Prencipe et al., 2020), rot and collar rot of Kiwi in Turkey (Polat et al., 2017), and root rot...
on Mandarin (*Citrus reticulate* L. cv. Sainampueng) in Thailand (Noireung et al., 2020). Rapid and proper identification are required before controlling pathogens. The Internal Transcribed Spacer (ITS) region is the most common region of DNA used to identify Oomycetes. Nevertheless, due to the accurate comparison issues, Robideau et al. (2011) used a multigene analysis method using ITS, Cytochrome c Oxidase subunit I (COX1), and nuclear, large subunit (LSU) rDNA with 28S rDNA to define genus including *Pythium*, *Phytophthora*, and *Phytopythium* from Oomycetes. In Indonesia, especially in potato productions, studies about *Phytopythium* have not been conducted to our knowledge. Therefore it is essential to study *P. vexans* isolates based on molecular, morphology, and pathogenicity of this Oomycetia soil-borne pathogen found in potato production.

**MATERIALS AND METHODS**

**Soil-Borne Pathogen Isolation**

The pathogen was isolated from soil of potato fields located at Ngablak, Magelang (7°23’57.386”S 110°23’52.242”E) in 2019. The isolation was conducted using the soil baiting method according to Purwantisari and Hastuti (2009) with modification. Apple cv. Manalagi were bored using 0.5 cm boring tool and filled with collected soil. Holes were closed with tips and preserved in a plastic box completed with wet cotton to keep the high moisture levels. It was incubated at room temperature for 3–4 days until brown lesions appeared. Test apples were cut at regions with both healthy and lesion portions, then cultured on Carrot Sucrose Agar, amended with Rifampicin 1000 ppm (20 ml/L), and incubated at 18°C in dark condition. After 5–6 days, the isolates that appeared were subcultured to PDA. In this research, we have found a unique culture with a papillate pattern named NG isolate and used for further studies.

**Morphological Observation**

Morphological observations were conducted based on the macroscopic and microscopic characteristics of the five-day-old NG isolate. Macroscopic observation described the pattern and color of the colony. Microscopic observation described the shape and size of sporangia, chlamydospore, hyphae from the isolate. Observations were conducted under a binocular microscope (Olympus X32). The results were compared to literatures for genus identification based on the morphological characteristics (Paul et al., 2006; Bridge et al., 2008; Santos, 2016; Bennett et al., 2017; Ho, 2018; Nam & Choi, 2019; Gómez-González et al., 2020; Shimelash & Dessie, 2020).

**In Vitro-Pathogenicity Test**

The pathogenicity test of *P. vexans* was conducted using the NG isolate and inoculated on healthy potato leaves and tubers. For the potato tuber, the pathogenicity test was conducted according to Gherbawy et al. (2019) with modification. Healthy potato tubers weighing 100–150 g were selected for this test. Potatoes were cut into 1 cm thick pieces. While for potato leaves, healthy leaves were sterilized in sodium hypochlorite solution for 3 minutes, rinsed using sterile distilled water three times, and dried under a laminar flow. The tubers and leaves were placed in a petri dish amended with a small ball of wet cotton to maintain the moisture inside. Then, an agar cut (± 1 cm²) with active mycelia from NG isolate was placed in the center of potato tubers and leaves for inoculation. Other treatments used different inoculum. The positive control was used a piece of potato leaves consisting of *P. infestans’* spores and the negative control used water agar. All treatments were incubated in the dark at 18°C for seven days.

**Molecular Identification**

The DNA extraction from five days-old NG isolates was carried out using Genomic DNA Mini Kit (Plant) Protocol (GeneAid, Australia) under the kit protocol. Internal transcribed spacer (ITS) and Large Subunit Ribosomal (LSU) were amplified using ITS1/ITS4 and UN-up28S40/UN-lo28S576B primers (Robideau et al., 2011). PCR reactions were performed in 25 μl mixture of 12.5 μl of 2x DNA Taq polymerase (MyTaq HS Red Mix; Bioline, London, United Kingdom), 9.5 μl miliQ sterile water, 1 μl of 0.08 lM each marker forward and reverse, and 1 μl of DNA template in T100 Thermal Cycler machine (Biorad, California, United States). The temperature adjustment on PCR cycling was based on Standard MyTaq HS Red Mix Protocol and annealing temperatures were set to
55°C for ITS and 51°C for LSU. The PCR products were evaluated on 1% agarose gel and run in 100 V for 30 min. Then, the gel was colored with ethidium bromide for 15 min and visualized under UV Transilluminator. Sequence analysis was carried out at 1st BASE, Malaysian service providers.

**Phylogenetic Analysis**

Phylogenetic analysis was constructed from NG isolate and consensus sequences from the previous research by Robideau et al. (2011). The consensus sequences were selected and explored as representatives from Oomycetes (Phytopythium, Pythium, and Phytophthora) using BLAST in Table 1. All sequences were aligned by ClustalW using MEGA X. The phylogenetic tree was constructed from ITS and LSU sequences by adjusting the Maximum Likelihood (ML) method with the Kimura 2-parameter model and tested by 1000 bootstrap replications.

**RESULTS AND DISCUSSION**

**Morphological Observation**

The morphological description of the P. vexans colony was described from five-day-old cultures growing on PDA. P. vexans colony, which was incubated at dark conditions and 18°C, was white, had thin mycelia, and stellate patterns. This Oomycetes colony grew fast, covering 9 cm of petri dish in 5 days, as shown in Figure 1. Further microscopic observation was conducted from this isolate, as shown in Figure 2. In Table 2, P. vexans’ characteristics were compared to Phytophthora, Pythium, and Phytopythium.

Based on macroscopic observation results, the colony pattern of P. vexans was similar to Phytopythium, especially P. vexans from durian, which colony had patellate or stellate patterns (Santoso, 2016). Nam and Choi (2019) also isolated P. vexans on several media for 72 hours and resulting in different mycelial diameters, such as 35–40 mm on PDA, >70 mm on V8 medium and 55–60 mm on CMA (Corn Meal Agar). However, it did not change the pattern of the mycelial colonies. P. infestans had a radiate growth pattern on various mediums such as on lime bean agar (LBA), on Rye A and Carrot agar (AZ) (Gómez-González et al., 2020), as well as Pythium (Paul et al., 2006).

Based on microscopic observations, the seven-day-old culture of NG isolates showed hyphae sizes of 3.36–4.60 µm, was less than 5 µm and similar to Phytopythium. Comparison between Phytopythium to Phytophthora and Pythium, both would have a larger diameter of hyphae, 5–7 µm and 4–6 µm respectively (Ho, 2018). Further observations were conducted until the culture of P. vexans reached 30 days old and at 25°C, chlamydospore and sporangium were found. Chlamydospor is known as the survival structure.

<table>
<thead>
<tr>
<th>No.</th>
<th>Species</th>
<th>Isolate</th>
<th>Genebank Accesion Number</th>
<th>Genbank Accesion Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Phytium insidiosum</td>
<td>CBS 574.85</td>
<td>HQ643570</td>
<td>HQ665273</td>
</tr>
<tr>
<td>2</td>
<td>Phytium aphanidermatum</td>
<td>CBS 118.80</td>
<td>HQ643438</td>
<td>HQ665084</td>
</tr>
<tr>
<td>3</td>
<td>Phytium delinense</td>
<td>CBS 314.33</td>
<td>HQ643522</td>
<td>HQ665204</td>
</tr>
<tr>
<td>4</td>
<td>Phytopythium vexans</td>
<td>P3980</td>
<td>HQ261730</td>
<td>EU080487</td>
</tr>
<tr>
<td>5</td>
<td>Phytopythium vexans</td>
<td>CBS 119.8</td>
<td>HQ643400</td>
<td>HQ665090</td>
</tr>
<tr>
<td>6</td>
<td>Phytopythium litorale</td>
<td>CBS 122662</td>
<td>HQ643385</td>
<td>HQ665114</td>
</tr>
<tr>
<td>7</td>
<td>Phytopythium boreale</td>
<td>CBS 551.88</td>
<td>HQ643372</td>
<td>HQ665261</td>
</tr>
<tr>
<td>8</td>
<td>Phytopythium ostraeodes</td>
<td>CBS 768.73</td>
<td>HQ643395</td>
<td>HQ665295</td>
</tr>
<tr>
<td>9</td>
<td>Phytopythium vignae</td>
<td>P3019</td>
<td>HQ261724</td>
<td>EU079787</td>
</tr>
<tr>
<td>10</td>
<td>Phytophthora palmivora</td>
<td>CBS298.29</td>
<td>HQ643307</td>
<td>HQ665195</td>
</tr>
<tr>
<td>11</td>
<td>Phytophthora sojae</td>
<td>P3114</td>
<td>HQ261677</td>
<td>EU079794</td>
</tr>
<tr>
<td>12</td>
<td>Phytophthora infestans</td>
<td>P10650</td>
<td>HQ261589</td>
<td>EU079630</td>
</tr>
<tr>
<td>13</td>
<td>Phytophthora tentaculata</td>
<td>CBS 55296</td>
<td>HQ643365</td>
<td>HQ665264</td>
</tr>
<tr>
<td>14</td>
<td>Eurychauma dicksoni*</td>
<td>FI373</td>
<td>HQ643131</td>
<td>HQ665307</td>
</tr>
</tbody>
</table>

*outgroup
of pathogens in response to insufficient nutrients or unsuitable environment condition for optimum growth. The presence of chlamydospores from *P. infestans* Ic haplotype isolate collected from Ethiopia was found on rye and pea agar plates after 1 to 4 weeks of incubation of single cultures at 20°C in the dark (Shimelash & Dessie, 2020). Chlamydospore sizes of *Phytophthora* and *Pythium* were 20–25 µm and 40–70 µm, respectively (Bridge et al., 2008).

Meanwhile, Bennett et al. (2017) reported that no chlamydospore were observed from *Phytopythium* spp. In this study, *P. vexans* chlamydospore diameters was 15.79 µm. *P. vexans* produced ovoid-shaped sporangia and completed with semipapillate. This papillate makes the *P. vexans* to be excluded from *Phytium* sp. Only *Phytophthora* and *Phytopythium* were completed with papillate (Ho, 2018). Both *Phytophthora* and *Phytopythium* have different mechanisms for
Table 2. List of characteristic differences of *Phytophthora infestans*, *Pythium*, *Phytopythium vexans*, and NG isolate

<table>
<thead>
<tr>
<th>Characteristics</th>
<th><em>Phytophthora infestans</em></th>
<th><em>Pythium</em></th>
<th><em>Phytopythium vexans</em></th>
<th>NG isolate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony Pattern</td>
<td>radiate</td>
<td>radiate</td>
<td>stellate or patellate</td>
<td>stellate</td>
</tr>
<tr>
<td>Hyphae diameter</td>
<td>5–7μm</td>
<td>4–6μm</td>
<td>Up to 5 μm</td>
<td>3,36–4,60 μm</td>
</tr>
<tr>
<td>Sporangia shape</td>
<td>lemon-shaped</td>
<td>globose</td>
<td>globose, ovoid, ellipsoid, lemoniform, and obpyriform</td>
<td>ovoid</td>
</tr>
<tr>
<td>Sporangia size (Length and width)</td>
<td>60.5 μm and 31.7 μm</td>
<td>15–55 μm in diameter</td>
<td>7–28 μm and 5–22 μm.</td>
<td>16.78 μm and 12.59 μm</td>
</tr>
<tr>
<td>Chlamydospore size</td>
<td>20–25 μm</td>
<td>40–70 μm</td>
<td>not observed</td>
<td>15.79 μm in diameter</td>
</tr>
<tr>
<td>Papillate</td>
<td>semipapillate</td>
<td>absence</td>
<td>papillate</td>
<td>semipapillate</td>
</tr>
</tbody>
</table>

1) Paul et al. (2006); 2) Bridge et al. (2008); 3) Santoso (2016); 4) Bennett et al. (2017); 5) Ho (2018); 6) Nam & Choi (2019); 7) Gómez-González et al. (2020); 8) Shimelash & Dessie (2020).

zoospore discharge. In this case, *Phytophthora infestans* produces lemon-shaped sporangia and are completed with semipapillate. The zoospore was released from the papillate (Shimelash & Dessie, 2020). After being reclassified as a new genus, *Phytopythium* known for the morphologically and discharged of zoospore characteristic were intermediate between *Phytophthora* and *Pythium* (Ho, 2018). The sporangia size of *P. vexans* was 16.78 μm in length and 12.59 μm in width. This sporangia size was smaller than ones of *Phytophthora* with a length of 60.5 μm and a width of 31.7 μm (Gómez-González et al., 2020). The sporangia of *Pythium*, with a globose shape, was 15–55 μm in diameter with an average of 32.6 μm (Paul et al., 2006).

Based on all of the morphological descriptions of *P. vexans*, this species had morphological characteristics between *Phytophthora* and *Pythium*.

**In Vitro-Pathogenicity Test**

The pathogenicity test was conducted for seven days, and the final result showed that no lesion symptoms appeared on potato leaves inoculated with *P. vexans*. The appearance was the same as the control inoculated with water agar (Figure 3). Nevertheless, it was different from healthy leaves inoculated with a small cut of leaves consisted of *P. infestans* sporangia. The color of the leaves turned black. The infected leaves appearance changes into water-soaked and die. On the lower surface of leaves, *P. infestans* could sporulate to whitish color (Schumann & D’Arcy, 2000 as cited in Ristaino et al., 2018).

The observation was also done on potato tuber. *P. vexans* inoculated onto potato tubers showed the brown lesion surrounded the inoculum from a cut of mycelium. The brown lesion appeared rotten but dried. Furthermore, the control treatment where healthy tubers were inoculated with a small cuts of potato leaves with sporangium of *P. infestans* resulted in soft rot on tubers. Nevertheless, the control of potato tubers inoculated with water agar did not show any lesion symptoms, and the tubers were still in good condition.

The aggressiveness of *P. infestans* might be lethal for foliage and tubers of potato and tomato. This may cause this pathogen to be one of the most destructive pathogen in the potato field in the world. *Pythium* is also known as a saprophyte and opportunistic organism (Pegg et al., 2015). Kilany et al. (2015) reported that 60% of genus *Pythium* caused damping-off in the nurseries and was challenging to control due to its wide host range and ability to survive for long terms in soil. In Indonesia, Santoso (2016) reported two pathogens that attacked durian orchard, *Phytophthora palmivora* and *P. vexans*. In Indonesia, *P. vexans* were reported to infect durian and cause bumps to appear on the trunk. In another case in Australia, Vawdrey et al. (2005) reported there were 13 durian orchards that were
attacked by *P. palmivora* and *P. vexans*. Further experiments were conducted on the glasshouse trials and showed that healthy durian plants inoculated with *P. vexans* caused damage to the root and decreased the efficiency of the root to absorb the nutrient. *P. vexans* also can survive in wet or dry soil conditions. *P. vexans* is well known for causing root rot and damping-off on many ornamental plant pathogens (Yang & Hong, 2016).

This experiment revealed that *P. vexans* in Indonesia also infected potatoes with brownish blotches on tubers. It is the first reported pathogen from *Phytopythium* that could infect potatoes. After other Oomycetes like *P. infestans* known as a famous destructive pathogen on potatoes, *Phytophthora erythroseptica* as the causal agent of pink rot, and *Pythium ultimum* as the causal agent of the leak (Thompson et al., 2007) were already reported. Potato tubers are plant parts with high economic and nutritious values for daily consumption. Unfortunately, it has a low tolerance for pathogen presence in tubers. The tubers infection by a soil-borne pathogen can lead to economic loss to farmers. Until nowadays, there is no effective management available to control the soil-borne pathogen on potatoes (Lazarovits et al., 2008).

Phylogenetic Analysis

In 2008, Lévesque and de Cock proposed the Clade K of *Pythium* dispersed from the *Pythium* family due to the molecular analysis using ITS, Large Subunit (28S) ribosomal *Cytochrome Oxidase I* (COI) known as *Phytopythium*. Therefore NG isolate was amplified using ITS and LSU, and the single band showed at 850 bp and 650 bp. Phylogenetic analyses were constructed using sequences from ITS and LSU amplification. Based on Figure 4, we concluded that the NG isolate from this experiment had the highest similarity with *P. vexans* CBS 119.8. Based on ITS, LSU, and COI markers, the phylogenetic tree showed that *Phytopythium* spp. were more closely related to *Phytophthora* spp. rather than with *Pythium* spp. This result was similar to Robideau et al. (2011). The sequences of NG isolate from ITS and LSU are registered in GeneBank.

Figure 3. *In vitro* pathogenicity test on healthy potato leaves (A–C) and tubers (D–F); the materials were inoculated with water agar, negative control (A, D); *Phytopythium vexans* (B, E); and small cut of potato leaves infected by *Phytophthora infestans*, positive control (C, F) (→: inoculum)
with accession number as follow MW898226 and MW911663. This phylogenetic tree showed that Pythium, Phytopythium, and Phytophthora came from the same ancestor. The evolution is responsible for the differences in phylogenetic identification due to those organisms’ additional or missing genes (Rujirawat et al., 2018).

CONCLUSION

Since the separation of Pythium clade K was proposed by Lévesque and de Cock (2008), numerous Phytopythium reports have been published, especially in identifying and reporting the disease in various plants. This research revealed that even the morphology of P. vexans is between Pythium and Phytophthora. However, the phylogenetic cluster showed that P. vexans are more closely related to the Phytophthora spp. rather than Pythium spp. This article is the first report of P. vexans found in the potato field in Indonesia. The pathogen infecting the tuber raised our concern about the soil-borne pathogen on potatoes. Further study is needed to understand Phytopythium better, especially in potato agricultural practices.

LITERATURE CITED


Figure 4. Phylogenetic analysis of NG Isolate Maximum likelihood phylogeny from multigene analysis ITS and LSU sequence alignment with 1000× bootstrap; Eurychasma dicksonii F1373 is used as an outgroup


