First Report of Powdery Mildew Caused By *Podosphaera Xanthii* on *Ageratum Conyzoides,* in Indonesia

Siska Arie Santy Siahaan[1*], Jamjan Meeboon[2], Iman Hidayat[3], Kartini Kramadibrata[4], Arvita Netti Sihaloho[5], Ika Rosenta Purba[6]

[1,5]Department of Agrotechnology, Faculty of Agriculture, Universitas Simalungun. Jalan Sisingamangaraja Barat, Kel. Bah Kapul, Kota Pematangsiantar, 21142, North Sumatra, Indonesia
[2]Institute of Vegetable and Floriculture Science, National Agriculture and Food Research Organization (NARO), 360 Kusawa, Ano, Tsu, Mie 514-2392, Japan
[3]Research Center for Biology, Indonesian Institute of Sciences-LIPI, Jl. Raya Jakarta-Bogor KM 46, Cibinong 16911, West Java, Indonesia
[4]Indonesian Mycological Society (MIKOINA), Bogor Branch, Bogor, West Java, Indonesia
[6]Department of Urban and Regional Planning, Postgraduate Program, Universitas Simalungun. Jalan Sisingamangaraja Barat, Kel. Bah Kapul, Kota Pematangsiantar, 21142, North Sumatra, Indonesia
*Corresponding Author:
Email : siskasiahaan2023@gmail.com

Abstract.

Powdery mildew is one of the most common and important fungal diseases and may cause huge economic losses to crop yields worldwide. During survey of powdery mildews in 2011 and 2013, six samples of Ageratum conyzoides were collected from different regions in Indonesia, i.e. Bali, South Sumatera and West Java provinces. Anamorphic features revealed that the fungus belongs to the genus Podosphaera. Two sets of sequences of both ITS rRNA and 28S regions were obtained from the six samples. Phylogenetic analyses, including maximum parsimony (MP) and maximum likelihood (ML) were executed using MEGA7. The strength of internal branches of the resulting trees were tested with bootstrap analysis. Tree scores, including tree length, CI, RI and RC were also calculated. The phylogenetic analysis confirmed that the fungus belongs to the genus Podosphaera, forming a clade with the sequences from Podosphaera xanthii. This is the first report of powdery mildews on Ageratum conyzoides from Indonesia.

Keywords : *Anamorph; Erysiphales; Molecular Phylogeny and Plant Disease.*

I. INTRODUCTION

Powdery mildew is one of the most common and important fungal diseases on many economically important plants. It forms a white powdery film on the surface of plant leaves, stems, flowers, and fruits by producing quite large white mycelia and powdery spores like talcs. It is an obligate biotrophic ascomycetous fungi belonging to the order Helotiales comprising ca 900species belonging to 18 genera (Shirouzu et al., 2020). They are able to colonize approximately 10.125 plant species belonging to 205 families (Glawe, 2008; Bradshaw et al., 2024).Powdery mildews may cause extreme yield losses on some economically important plants and crops world-wide i.e. severe defoliation and reduction in size and number of fruits on chili (*Capsicum annuum* L.) caused by *Leveilulla taurica* in India (Bademiya and Ashtaputre, 2019), premature defoliation and drying on mungbean (*Vigna radiata* L.) caused by *Erysiphe polygoni* in India (Meena et al., 2022), reduction in cone yield and quality on hop (*Humulus lupulus* L.) caused by *Podosphaera macularis* in USA (Gent et al., 2014), poor fruit set and low yield on grapes (*Vitis vinifera*) caused by *Uncinula necator* in Pakistan (Uddin et al., 2022).There are very few reports regarding powdery mildews in Indonesia despite the rich diversity of plants. Most of those reports were mainly written based on the anamorphic features only, which sometimes were unreliable due to similarity among closely related species (Raciborski 1900, Palm 1921, Schwarz 1926, 1927, Schweizer 1928, Spaulding 1961, Reddy 1970, Hirata 1986 and Semangun 1992).

Since 2011, extensive surveys of powdery mildews were carried out in several regions of Indonesia. The determination of powdery mildew species of Indonesia is now carried out by using combination of molecular study (nucleotide sequences of the ribosomal DNA (rDNA) internal transcribed spacer (ITS)

region and 28S region) as well as by light and scanning electron microscope (Meeboon et al., 2012a, 2012b, 2013a, 2013b); Siahaan et al., (2015, 2016a, 2016b, 2016c). *Ageratum conyzoides* is a species native to Central and South America, belonging to the family Asteraceae. In Indonesia, this plant is considered a weed found along the roadsides and crop fields. During survey of powdery mildews in 2011, we collected two samples of *A. conyzoides* infected by powdery mildews from Bandung, West Java and one sample from Indralaya, South Sumatra. In 2013, we collected two more samples from Bandung, but from a different location from the first collection point and one sample from Bali. Identification of this fungus is crucial because this fungus could be a threat to economically important plants in the future.

II. METHODS

Fungal Collection and Morphological Observation

Samples used in this study were collected between 2011 and 2013 in Indonesia. These samples were deposited in Mie University Mycological Herbarium (MUMH, Tsu, Japan) and Herbarium Bogoriense (BO BRIN, Bogor, Indonesia) (BO Research Center for Biosystematics and Evolution, National Research and Innovation Agency (BRIN), Bogor, Indonesia (Table 1). Collection date, location, host plant species and accession numbers of the nucleotide sequences were given.In order to examine the asexual morph on the herbarium specimens, mycelial colonies on a small piece of infected leaf were rehydrated by the method described by Shin and La (1993). All specimens were examined using a light microscope (Axio Imager; Carl Zeiss, Göttingen, Germany) with phase contrast using 10×, 20× and 40× objectives. Thirty conidiophores and conidia were measured for each examined specimen. The size and shape of conidia; nature of conidiophores, e.g. size and shape of foot-cells, position of basal septa, shape and position of hyphal appressoria, position of germ tubes of conidia; and shape of appressoria on germ tubes of conidia (if found) were documented. For the rehydrated samples, the width of conidia was multiplied by Blumer's factor according to Braun and Cook (2012).

DNA extraction and PCR amplification

Whole-cell DNA was isolated from fresh or herbarium fungal specimens by the chelex method (Walsh et al., 1991; Hirata a nd Takamatsu, 1996). Mycelia were taken using a clean adhesive tape sized 5 x 5 mm, then put into 300 µl of 5% Chelex (Bio-Rad) in a 1.5 ml microcentrifuge tube. The chelex suspensions containing mycelia were incubated at 56^{o}C for 15 minutes.After mixing vigorously, the extracts were incubated in boiling water for 8 min, mixed using vortex for about 10-15 seconds and then boiled again for another 8 min. Thereafter, the extracts were centrifuged at 15,000 rpm for 5 min. Later, the supernatant was transferred onto a new tube and kept in -20^{0}C degrees until used for PCR amplification. The nucleotide sequences of the 5'-end of the 28S rRNA gene (including domains D1 and D2) and internal transcribed spacer (ITS) regions including the 5.8S rRNA gene were determined in this study. PCR reactions were conducted in a total reaction of 25 µl, including the following reagents:

H_2O 5.25 µl, 2x KOD buffer 12.5 µl; 2 mM of each deoxyribonucleotide triphosphate (dNTPs) 5 µl; two primers (Table 3.2) (20 pmol/µl) @ 0.375 µl, KOD FX Neo polymerase (1.0 unit/µl) 0.5 µl (*Toyobo, Japan)* and DNA 1 µl. PCR reactions were conducted under the following thermal cycling conditions in a thermal cycler SP (TaKaRa, Kyoto, Japan): an initial denaturing step at 94°C for 2 min; thermocycling for 40 cycles, where each cycle consisted of 10 sec at 98°C followed by 30 sec at 60°C for annealing. A positive and negative controls of template DNA were included for each set of reactions. The PCR product was subjected to preparative electrophoresis in 1.5% agarose gel in TBE buffer. The amplicons were sent to Solgent Co. Ltd (Daejeon, South Kores) for sequencing. New sequences determined in this study were deposited in DNA Data Base of Japan DDBJ under the accession numbers LC898138 – LC898139.

Phylogenetic analysis

Newly determined sequences were aligned with other sequences of the Erysiphaceae retrieved from DNA databases (DDBJ, EMBL, NCBI) using MUSCLE (Edgar 2004) implemented in MEGA7 (Kumar et al., 2016). Alignments were further manually refined using the MEGA7 program. Maximum parsimony (MP) and maximum likelihood (ML) methods were used in the molecular phylogenetic analyses of particular powdery mildews in this study. MP analyses were performed in PAUP* 4.b10 (Swofford 2002) with

heuristic search option using the tree bisection-reconstruction (TBR) algorithm with 100 random sequence additions to find global optimum tree. All sites were treated as unordered and unweighted, with gaps treated as missing data. Kishino-Hasegawa (KH) and Shimodaira-Hasegawa (SH) tests (Kishino and Hasegawa, 1989; Shimodaira and Hasegawa, 1999) were performed to determine whether a given dataset can significantly reject a constraint tree constructed based on a hypothesis. The strength of internal branches of the resulting trees was tested with bootstrap (BS) analyses using 1K replications with step-wise addition option set as simple (Felsenstein, 1985). BS values higher than 70% are given. Tree scores, including tree length, consistency index (CI), retention index (RI) and rescaled consistency index (RC) were calculated. The ML analysis was executed using MEGA7 (Kumar et al., 2016). In this analysis, partial deletion was set as gap/missing data treatment with coverage cut off was set 95%. The ML analysis was performed using the best evolutionary method determined respectively to the dataset used, and the initial tree for ML was set automatically. The strength of internal branches of the resulting tree was tested with bootstrap analysis using 1K replications (Felsenstein, 1985).

III. RESULT AND DISCUSSION

Result

Mycelium effused or patches, persistent to subevanescent; hyphae substraight to somewhat wavy, fairly uniform or sometimes irregular in width; **hyphal appressoria** indistinct, sometimes nipple shape, single; conidiophores erect, arising from the top of mother cell, single on a hyphal cell (78.3–) 84.4–168.2(–184) x (7.3–)8.8–12.2(–12.7) µm (average 121 x 10.5 µm), **foot-cells** cylindrical, (36.9–)41–65.7(–87.2) x (7.3–)8.8–12.2(–12.7) µm (average 52.7 x 10.5 µm), straight or occasionally slightly curved, sometimes

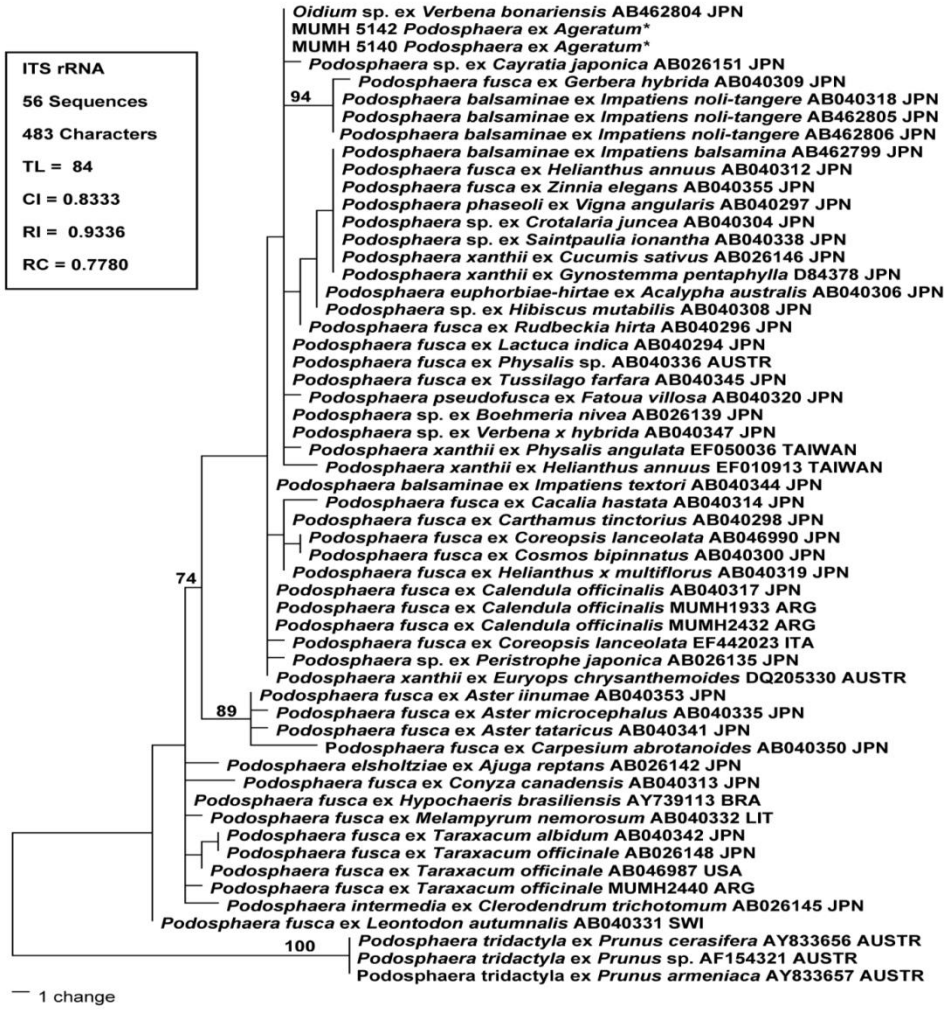

Fig 1. Phylogenetic analysis of the ITS rRNA gene sequences for two sequences of *P.xanthii* on *A. conyzoides* and sequences from *P. xanthii*.

This tree is one of the five equally parsimonious trees. Bootstrap (BS) value (≥ 70%) values by the maximum likelihood (ML) and maximum parsimony (MP) methods were shown on the respective branches. Samples retrieved in this study were marked with *(asterisks). constricted and swollen at bases, followed by 1–3 shorter cells, producing 2–7 conidia in chains with crenate edge, with a basal septum at the branching point of the mycelium; **conidia** ellipsoid-doliiform, sometimes cylindric, (21.8–)25.1–32.1 (–37.1) x (12.9–)14.3–18.3(–19.8) µm (average 28.7 x 16.6 µm), producing germination tube of *Fibroidium*-type, occasionally from terminal, alobatus.

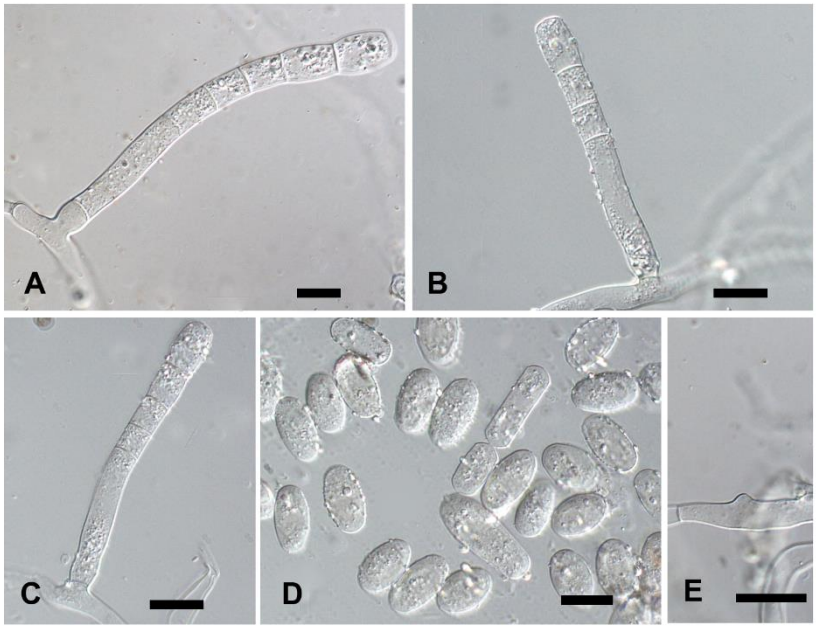

Fig 2. Anamorphic features of *Podosphaera xanthii* on *A. conyzoides*.
A–C. Conidiophores. D. Conidia. E. Germ tube. *Bars*: 20 µm.

Discussion

Tropical fungi have traditionally been under-researched and their taxonomic placement has been confounded, often misidentified with temperate fungi. Limkaisang et al., (2006) stated that the ecology and classification of the powdery mildew fungi on tropical trees are still uncertain, not only because of the limited number of researchers working on this fungal group in tropical regions but also the lack of teleomorphic state, which are necessary for species identification. Further, they stated that the identification of tropical powdery mildews fungi is mostly in their host plants and anamorphic state, which are not adequate to distinctly delimit the species. Furthermore, Arnold (2011) stated that the exploration of tropical fungi is thus limited by (i) the extensive training needed for sampling of complex tropical habitats, (ii) the paucity of newly trained systematics specializing in tropical mycology, and (iii) traditional difficulties in delineating species boundaries. Similarly, all these points suggest that the degree of exploration of powdery mildews in Southeast Asian countries is comparably low, undoubtedly due to a relatively small number of mycologists dealing with powdery mildews compared with Europe, North America and eastern Asia and also because sexual morph necessary for reliable identifications of species is mostly lacking in subtropical and tropical areas. There are very few reports regarding on powdery mildews in Indonesia.

These reports were mainly written based on the conventional taxonomical system, based on anamorph and not supported by molecular data. However, over the past decade, the exploration of powdery mildews in Indonesia is rapidly increasing. By combining morphological, molecular and host range data, eight new species have been reported from this country since 2012 (Meeboon et al., 2012a, 2012b, 2013a, 2013b); Siahaan et al., (2015, 2016a, 2016b, 2016c). These reports indicated that Indonesia has potentially many unique, undescribed and probably endemic powdery mildew species, playing an important role in providing additional information of the tropical powdery mildews, especially from Indonesia, for a better understanding of the geographical distribution and evolution of powdery mildews in the world. Therefore, the survey on the diversity of this group of fungi and its distribution in Indonesia should be carried out to

provide a comprehensive database of the fungi based on the current generic and/or species concept.The only information regarding powdery mildews on *Ageratum* in Indonesia was recorded by Aryuti and Rifai (1987) on *Ageratum houstonianum*, identified as *Oidium tabaci*. However, in their report, they did not provide any morphological or molecular information at all. Thus, the identification of this species is doubtful. Three powdery mildews species were reported on *A. conyzoides* in the world, i.e.

Erysiphe cichoracearum, *Oidium ageratii* and *Sphaerotheca fuliginea* (Amano, 1986; Braun, 1987). The morphology of the current fungus is mostly similar to the anamorphic state of *Sphaerotheca fusca* (≡ *Podosphaera fusca*). Braun et al., (2011) divided *P. fusca* to *P. fusca* and *P. xanthii* based on morphological and molecular characteristics. Recently, occurrence of powdery mildews on *Ageratum* were recorded from China (Mukhtar and Arend 2017), India (Thite et al., 2017) identified as *P. xanthii* and from Thailand (Meeboon et al., 2018), identified as *Golovinomyces* sp. Two sequences of the powdery mildew on *A. conyzoides* in this study were aligned with the data matrix of *Podosphaera* from the previous report (Takamatsu et al., 2010). The phylogenetic tree (MP tree) shown in Fig. 1 indicates that genus *Podosphaera* on *A. conyzoides* has a sequence identical with *Oidium* sp. on *Verbena bonariensis* and *Podosphaera fusca* on *Lactuca indica*, *Physalis* sp., *Tussilago farfara*, *Boehmeria nivea* and *Verbena x hybrida*, all identified as *Podosphaera xanthii*, confirming the identity of the fungus correspond with the anamorphic data. This is the first report of powdery mildew on *A. conyzoides* in Indonesia.

IV. CONCLUSION AND SUGGESTIONS

Podosphaera xanthii has a wide host range of mainly herbaceous plants, including the family of Asteraceae, Balsaminaceae, Cucurbitaceae, Fabaceae, Solanaceae and Verbenaceae. Some reports indicate that there were huge economic losses to crop yield, quality and value of economically important crops caused by this fungus (Afshan et al., 2025; Kelly et al., 2021). Annual loss of crop yield caused by plant disease are estimated to be more than 30% worldwide (Savary et al., 2019). Adequate knowledge of crop losses caused by disease is important for appropriate strategic and tactical management decisions.

REFERENCES

[1] Afshan, N. S., Jabeen, M., Akbar, A., Khalid, M., Saleem, A., Altaf, R., Afzal, S., Fiaz, M., Khalid, A. N. (2025). Geographic distribution and genetic diversity of *Podosphaera xanthii* in Pakistan. ***Asian Journal of Plant Pathology*** 19(1):81–95.https://doi.org/10.3923/ajpp.2025.81.95

[2] Amano (Hirata), K. (1986). Host range and geographical distribution of the powdery mildew fungi. Japan Scientific Societies Press, Tokyo

[3] Arnold, A. E., Maynard, Z., Gilbert, G. S., Coley, P.D., Kursar, T. A. (2000). Are tropical fungal endophytes hyperdiverse. Ecology Letter 3: 267–274.https://doi.org/10.31046/j.1461-0248.2000.00159.x

[4] Aryuti, T., Rifai, M. A. (1987). Marga-marga jamur embun tepung di Indonesia. Floribunda 1(3): 9–12.

[5] Bademiyya, S. I., Ashtaputre, S. A. (2019). Estimation of yield loss due to powdery mildew of chilli caused by *Leveillula taurica* (Lev.) Arn. ***International Journal of Pure & Applied Bioscience*** 7(1): 323–326.

[6] http://dx.doi.org/10.18782/2320-7051.7347

[7] Bradshaw, M., Boufford, D., Braun, U., Moparthi, S., Jellings, K., Maust, A., Pandey, B., Slack, S., Pfister, D. (2024). An in-depth evaluation of powdery mildew hosts reveals one of the world's most common and widespread groups of fungal plant pathogens. Plant Disease 108:576–581.

[8] https://doi.org/10.1094/PDIS-07-23-1471-RE

[9] Braun, U. (1987). A monograph of the Erysiphales (powdery mildews). Beihefte zur Nova Hedwigia 89: 1–700.

[10] Braun, U. (2011). The current systematic and taxonomy of powdery mildews (Erysiphales): an overview. Mycoscience 52:210–212.https://doi.org/10.1007/S10267-010-0092-1

[11] Braun, U., Cook, R. T. A. (2012). Taxonomic manual of the Erysiphales (powdery mildews). CBS Biodiversity series No. 11. CBS-KNAW Fungal Biodiversity Centre, the Netherlands.

[12] Edgar, R. C. (2004). MUSCLE: Multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research 32: 1792–1797. https://doi.org/10.1093/nar/gkh340

[13] Felsenstein, J. (1985). Confidence limits on phylogenetics: an approach using the bootstrap. Evolution 39: 783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

[14] Gent, D. H., Grove, G. G., Wolfenbarger, S. N., Woods, J. L. (2014). Crop damage caused by powdery mildew on hop and its relationship to late season management. Plant Pathology 63: 625–639.https://doi.org/10.1111/ppa.12123

[15] Glawe, D. A. (2008). The powdery mildews: A review of the world's most familiar (yet poorly known) plant pathogens. Annual Review of Phytopathology 46: 27–51. https://doi.org/10.1146/annurev.phyto.46.081407.104740

[16] Hirata, T., Takamatsu, S. (1996). Nucleotide sequence diversity of rDNA internal transcribed spacer extracted from conidia and cleistothecia of several powdery mildew fungi. Mycoscience 37:265–270. https://doi.org/10.1007/BF02461299

[17] Kelly, L. A., Vaghefi, N., Bransgrove, K., Fechner, N. A., Stuart, K., Pandey, A. K., Sharma, M., Nemeth, M. A., Liu, S., Tang, S.R., Nair, R. M., Douglas, C. A., Kiss, L. (2021). One crop disease, how many pathogens? *Podosphaera xanthii* and *Erysiphe vignae* sp. nov. identified as the two species that cause powdery mildew of mungbean (*Vigna radiata*) and Black gram (*V. mungo*) in Australia. Phytopathology 111(7): 1193–1206. https://doi.org/10.1094/PHYTO-12-20-0554-R

[18] Kishino, H., Hasegawa, M. (1989). Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in Hominoidea. ***Journal of Molecular Evolution*** 29: 170–179. https://doi.org/10.1007/BF02100115

[19] Kumar, S., Stecher, G., Tamura, K. (2016). MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0. for bigger datasets. *Molecular Biology and Evolution* 33: 1870–4.

[20] Limkaisang, S., Cunnington, J. H., Liew, K. W., Salleh, B., Sato, Y., Divarangkoon, R., Fangfuk, W., To-anun, C., Takamatsu, S. (2006). Molecular phylogenetic analyses reveal close relationship of powdery mildew fungi on some tropical trees with *Erysiphe alphitoides*, an oak powdery mildew. Mycoscience 47: 327–335. https://doi.org/10.1093/molbev/msw054

[21] Meeboon, J., Hidayat, I., Kramadibrata, K., Nurcahyanto, D., Siahaan, S. A. S., Takamatsu, S. (2012a). *Cystotheca tjibodensis* (Erysiphaceae, Ascomycota): rediscovery in Java after 90 years and first finding of anamorph. Mycoscience 53: 386–390. https://doi.org/10.1007/S10267-011-0176-6

[22] Meeboon, J., Hidayat, I., Takamatsu, S. (2012b). *Erysiphe javanica* sp. nov., a new tropical powdery mildew from Indonesia. Mycotaxon 120: 189–194. https://dx.doi.org/10.5248/120.189

[23] Meeboon, J., Hidayat, I., Takamatsu, S. (2013a). *Pseudoidium javanicum*, a new species of powdery mildew on *Acalypha* spp. from Indonesia. Mycoscience 54: 183–187. https://doi.org/10.1016/j.myc.2012.08.006

[24] Meeboon, J., Hidayat, I., Takamatsu, S. (2013b). *Setoidium castanopsidis*, a new species of anamorphic *Cystotheca* (Ascomycota, Erysiphales) from Indonesia. Mycoscience 54: 274–278.

[25] https://doi.org/10.1016/j.myc.2012.10.004

[26] Meeboon, J., Kokaew, J., Takamatsu, S. (2018). Notes on powdery mildews (Erysiphales) in Thailand V. *Golovinomyces*. Tropical Plant Pathology 43(3): 202–217. https://doi.org/10.1007/s40858-017-0201-1

[27] Meena, N. K., Trivedi, A., Kumar, S., Jatwa, T. K., Meena, S. C. (2022). Survey and surveillance to observe occurrence and severity of powdery mildew of mungbean (*Vigna radiata* L.) growing areas around Udaipur region. ***The Pharma Innovation Journal*** 11(2): 960–963.

[28] Mukhtar, I., Arend, F. P. (2017). First report of *Podosphaera xanthii* causing powdery mildew on *Ageratum conyzoides* in China. Plant Disease 101(8), p.1553. https://doi.org/10.1094/PDIS-03-17-0448-PDN

[29] Palm, B. T. (1921). Een gevaar voor de tabakscultuur in Deli. Bull Deli Proefstat te Medan–Sumatra, Indonesia RAM 1:275

[30] Raciborski, M. (1900). Parasitische Algen und Pilze Javas. Teil I. Batavia (Djakarta). Bot Inst zu Buitenzorg, Indonesia

[31] Reddy, D. B. (1970). List of diseases of important economic crop plants of Indonesia. Techn Docum., FAO Plant Prot Comm S. E. Asia and Pacific Region No. 74

[32] Savary, S., Willocquet, L., Pethybridge, S. J., Esker, P., McRoberts, N., Nelson, A. (2019). The global burden of pathogens and pests on major food crops. Nature Ecology and Evolution (3)430–439.

[33] https://doi.org/10.1038/s41559-018-0793-y

[34] Schwarz, M. B. (1926). Meeldauw van tabak en *Physalis minima*. Indische Culturen (Teysmannia) 11:238–239 RAM 5: 634

[35] Schwarz, M. B. (1927). *Oidium verbenae* nov. sp.: Meeldauw van *Verbena laciniata*. Indische Culturen (Teysmannia), 12: 470–471 RAM 7:32

[36] Schweizer, J. (1928). Over Erysiphaceen (meeldauwschimmels) van Java. Arch v Rubbercult Nederl Indie 12: 323–343

[37] Semangun, H. (1992). Host index of plant diseases in Indonesia. Gadjah Mada University Press, Indonesia.

[38] Shimodaira, H., Hasegawa, M. (1999). Multiple comparison of log-likelihoods with the applications to phylogenetic inference. Molecular Biology and Evolution 16: 1114–1116. https://doi.org/10.1093/oxfordjournals.molbev.a026201

[39] Shin, H. D, La, Y. J. (1993). Morphology of edge lines of chained immature conidia on conidiophores in powdery mildew fungi and their taxonomic significance. Mycotaxon 66: 445–451.

[40] Shirouzu, T., Takamatsu, S., Hashimoto, A., Meeboon, J., Ohkuma, M. (2020). Phylogenetic overview of Erysiphaceae based on nrDNA and MCM7 sequences. Mycoscience 61:249–258. https://doi.org/10.1016/j.myc.2020.03.006

[41] Siahaan, S. A. S., Hidayat, I., Kramadibrata, K., Meeboon, J., Takamatsu, S. (2015). *Phyllactinia poinsettiae* sp. nov.: a new species of powdery mildew on poinsettia from Indonesia. Mycoscience 56: 580–583. https://doi.org/10.1016/j.myc.2015.05.005

[42] Siahaan, S. A. S., Hidayat, I., Kramadibrata, K., Meeboon, J., Takamatsu, S. (2016a). *Erysiphe baliensis* and *E. sidae*, two new species of anamorphic Erysiphe (powdery mildew) from Indonesia. Mycoscience 57: 35–41. https://doi.org/10.1016/j.myc.2015.08.001

[43] Siahaan, S. A. S., Hidayat, I., Kramadibrata, K., Meeboon, J., Takamatsu, S. (2016b). *Bauhinia purpurea*, *Durio zibethinus* and *Nephelium lappaceum*: additional hosts of the asexual morph of *Erysiphe quercicola*. Mycoscience 57: 375–383. https://doi.org/10.1016/j.myc.2016.06.001

[44] Siahaan, S. A. S., Hidayat, I., Kramadibrata, K., Meeboon, J., Takamatsu, S. (2016c). *Podosphaera perseae-americanae*, a new powdery mildew species on *Persea americana* (avocado) from Indonesia. Mycoscience 57: 417–421. https://doi.org/10.1016/j.myc.2016.07.004

[45] Spaulding, P. (1961). Foreign Diseases of Forest Trees of the World: An Annotated List. USDA Agriculture Handbook 197:1–361

[46] Swofford, D. L. (2002). PAUP*: Phylogenetic analysis using parsimony (*and other methods), version 4.0a150. Sinauer, Sunderland, MA. https://doi.org/10.1111/j.0014-3820.2002.tb00191.x

[47] Takamatsu, S., Niinomi, S., Harada, M., Havrylenko, M. (2010). Molecular phylogenetic analyses reveal a close evolutionary relationship between *Podosphaera* (Erysiphales: Erysiphaceae) and its rosaceous hosts. Persoonia 24: 38–48. https://doi.org/10.3767/003158510X494596

[48] Thite, S. V., Kore, B. A., Camacho-Tapia, M., Tovar-Pedraza, J. M. (2017). First report of *Podosphaera xanthii* causing powdery mildew on *Ageratum conyzoides* in India. ***Journal of Plant Pathology*** 99(2): 533–543. https://doi.org/10.3767/003158510X494596

[49] Uddin, M., Tareen, J. K., Ahmed, F., Adnan, F., Bazai, M.J., Fareed, S. R., Kakar, H. (2022). Powdery mildew a disease of grapes and the fungicide mode of action: a review. Biosight 03(02): 38–52. https://doi.org/10.46568/bios.v3i2.78

[50] Walsh, P.S., Metzger, D.A., Higuchi, R. (1991). Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. Biotechniques 10: 506–513.