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THE RESULTS OF DETERMINING THE CAUSATIVE AGENT OF POWDERY MILDEW IN CUCUMBER CULTIVATION UNDER GREENHOUSE CONDITIONS IN MONGOLIA

GESTÃO ECOLÓGICA DO OÍDIO EM PEPINOS DE ESTUFA ATRAVÉS DA REGULAMENTAÇÃO AMBIENTAL NA MONGÓLIA

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Abstract
Powdery mildew is one of the most destructive diseases affecting greenhouse cucumber (Cucumis sativus L.) production in Mongolia, causing significant yield losses and increased management costs. The present study aimed to identify the causal agent of cucumber powdery mildew using morphological characteristics and molecular phylogenetic analysis. Cucumber leaf samples exhibiting typical powdery mildew symptoms were collected from greenhouse production systems in five climatically distinct regions of Mongolia.
Morphological examination revealed abundant mycelia and conidiophores bearing chains of ovoid to ellipsoid–ovoid conidia. Fibrosin bodies were consistently observed within conidia from all samples, indicating characteristics typical of Podosphaera xanthii. Molecular identification was performed using PCR amplification of the internal transcribed spacer (ITS) region with universal and species-specific primers. PCR results confirmed the presence of powdery mildew fungi, and species-specific amplification

Resumo
O oídio é uma das doenças mais destrutivas que afetam a produção de pepino (Cucumis sativus L.) em estufas na Mongólia, causando perdas significativas de rendimento e aumento dos custos de gestão. O presente estudo teve como objetivo identificar o agente causador do oídio do pepino utilizando características morfológicas e análise filogenética molecular. Amostras de folhas de pepino que apresentavam sintomas típicos de oídio foram coletadas de sistemas de produção em estufas em cinco regiões climaticamente distintas da Mongólia.
O exame morfológico revelou micélios abundantes e conidióforos com cadeias de conídios ovóides a elipsoidais-ovóides. Corpos de fibrosina foram observados consistentemente nos conídios de todas as amostras, indicando características típicas de Podosphaera xanthii. A identificação molecular foi realizada usando amplificação por PCR da região do espaçador transcrito interno (ITS) com primers universais e específicos para a espécie. Os resultados da PCR confirmaram a presença de fungos do oídio, e a amplificação específica para a espécie

identified P. xanthii as the predominant pathogen in three of the five sampled regions.
Phylogenetic analysis based on ITS sequences, conducted using the Maximum Likelihood method, demonstrated that the Mongolian isolates clustered within the Podosphaera xanthii clade together with reference sequences retrieved from GenBank. DNA sequences of representative isolates were deposited in the NCBI GenBank database under accession numbers MW939431, MW939432, and MW939433.
This study provides the first comprehensive morphological and molecular characterization of cucumber powdery mildew pathogens in Mongolia and confirms Podosphaera xanthii as the primary causal agent under greenhouse conditions. The findings contribute valuable baseline information for the development of effective disease management strategies and future epidemiological studies.

Keywords: PCR. Fungal disease. Podosphaera xanthii. DNA.

identificou P. xanthii como o patógeno predominante em três das cinco regiões amostradas.
A análise filogenética baseada em sequências ITS, realizada utilizando o método de máxima verossimilhança, demonstrou que os isolados da Mongólia se agruparam no clado Podosphaera xanthii juntamente com sequências de referência recuperadas do GenBank. As sequências de ADN de isolados representativos foram depositadas na base de dados NCBI GenBank sob os números de acesso MW939431, MW939432 e MW939433.
Este estudo fornece a primeira caracterização morfológica e molecular abrangente dos patógenos do oídio do pepino na Mongólia e confirma Podosphaera xanthii como o principal agente causal em condições de estufa. As descobertas contribuem com informações básicas valiosas para o desenvolvimento de estratégias eficazes de gestão de doenças e futuros estudos epidemiológicos.

Palavras-chave: *PCR. Doença fúngica. Podosphaera xanthii. ADN.*

1 INTRODUCTION

Powdery mildew is caused by a taxonomically diverse group of obligate fungal pathogens classified within the order *Erysiphales* (phylum Ascomycota), encompassing approximately 500 species that collectively infect over 10,000 plant species worldwide (Braun et al., 2002; Takamatsu, 2004).

Cucurbits are significantly affected by chronic powdery mildew disease, which is caused by various species belonging to the order Erysiphales. This disease poses a substantial threat to cucurbit crops, as highlighted in research conducted by (McGrath, 1997). The disease is most commonly diagnosed by the appearance of superficial, powdery fungal growth forming pale white patches on aerial plant tissues, particularly leaves and stems (Perez-Garcia et al., 2009). When infection becomes severe, physiological stress symptoms develop, including leaf yellowing, deformation, and a noticeable reduction in canopy density, which collectively result in diminished fruit quality and yield performance (Keinath and DuBose, 2004; MT, 1996). Studies conducted worldwide indicate that *Podosphaera xanthii* is the most prevalent powdery

mildew species infecting cucurbit crops (DJ, 1994). This species is predominantly found in subtropical and tropical regions and is especially common in greenhouse cultivation systems. In contrast, *Golovinomyces cichoracearum* is more frequently reported in temperate and cooler climates under open-field conditions (Kvristková et al., 2005). Both pathogens may occur either individually or as co-infections on cucurbit hosts (Jahn et al., 2002; Kvristková et al., 2005; Lebeda et al., 2009). Accurate identification of cucurbit powdery mildew pathogens has long been challenging. The two principal species reported in the literature have frequently been misidentified and, in some cases, treated as synonymous (McCreight et al., 1987; Bhatti et al., 2021). This difficulty arises because both pathogens produce nearly identical disease symptoms on cucurbit hosts. Species discrimination is most reliable when the sexual (teleomorphic) stage is present, as diagnostic characters such as the structure of chasmothecia and the number and morphology of asci, ascospores, and appendages can be examined (Block and Reitsma, 2005: Hashmi et al., 2022). However, the sexual stage is rarely observed under field or greenhouse conditions, making routine diagnosis dependent on the asexual (anamorphic) stage. Despite this limitation, *Podosphaera xanthii* and *Golovinomyces* cichoracearum can be distinguished using several anamorphic traits. These include differences in conidial size and shape, the presence of fibrosin bodies, the morphology of immature conidial margins, and germ tube development. These morphological features provide essential criteria for reliable species identification when the teleomorph is absent. In 2022, world production of cucumbers and gherkins was 95 million tonnes, led by China with 82.0% of the total. The history of greenhouse farming in Mongolia dates back to 1955, when cucumbers were cultivated. Greenhouse cultivation in Mongolia will reach 355.7 hectares in 2022, an increase of 66.5 hectares or 23.0 percent from the previous year. 78.6% of greenhouse cultivation is done by households, and 21.4% by enterprises.

In 2020, 6.296.000 tons of crops were harvested from 399.1 hectares of greenhouses, in 2021, 4318.2 tons of crops were harvested from 289.2 hectares of land, and in 2022, 3595.6 tons of crops were harvested from 355.7 hectares. Plant diseases affect the growth and decline of this greenhouse crop and harvest.

Cucumber cultivation occupies about 70% of the total greenhouse area in Mongolia. More than 20 species of infectious diseases are damaging cucumber crops grown in greenhouses. According to studies conducted in Mongolia, more than 15

infectious diseases have been identified and recorded in greenhouse-grown cucumber (*Cucumis sativus* L.) crops. Classification of the causative microorganisms indicates that nine diseases are of fungal origin, two are bacterial, and three are viral. Yield losses in cucumber attributable to these diseases range from 8.5% to 35.0% annually (Uranchimeg.A et al 2023; ; Mushtaq et al., 2023). Occurrence of cucumber powdery mildew has been documented not only in the Ulaanbaatar region but also in Tuv, Bayan-Ulgii, Dornod, Dornogovi, Darkhan-Uul, Uvurkhangai, Umnugovi, Zavkhan, and Khovd provinces, indicating the widespread distribution of the disease in Mongolia. Surveys indicate that the disease prevalence in greenhouse cucumber production systems reaches up to 90%. The disease recurs annually, resulting in yield losses of 15–30% in cucumber crops, while in certain production unit's losses of up to 50–90% have been reported (A.Uranchimeg, 2025).

2 MATERIALS AND METHODS

2.1 Sample collection

Cucumber (*Cucumis sativus* L.) leaf samples exhibiting typical symptoms of white mold infection, including chlorotic lesions and grayish-white fungal growth on the leaf surface, were collected from greenhouse production systems located in different agro-climatic regions of Mongolia. Sampling was conducted in both urban and rural greenhouse facilities. The surveyed sites included sunny greenhouses in Songinokhairkhan district and Bayangol district, Ulaanbaatar City; an plastic film greenhouse in Sergelen soum, Tuv province; sunny greenhouses in Gurvan Tes soum, Umnugovi province; and sunny greenhouses in Ulgii soum, Bayan-Ulgii province. At each location, symptomatic leaves were randomly collected from multiple plants and transported to the laboratory for further analysis.

2.2 Morphological observation and DNA extraction

Conidia were obtained from cucumber (*Cucumis sativus* L.) leaf samples showing typical white mold symptoms. Conidial impressions were prepared from each sample and

examined under a light microscope for morphological characterization. Measurements of conidial size and shape were recorded, and the presence of fibrosin bodies within conidia was assessed as a diagnostic feature.

For molecular analysis, conidia were carefully collected directly from infected leaf surfaces into sterile 1.5 mL microcentrifuge tubes and stored at −20 °C until further processing. Conidia used for DNA extraction were obtained from samples collected in Songinokhairkhan district and Bayangol district, Ulaanbaatar City; an acrylic-film greenhouse in Sergelen soum, Tuv province; sunny greenhouses in Gurvan Tes soum, Umnugovi province; and sunny greenhouses in Ulgii soum, Bayan-Ulgii province.

Genomic DNA was extracted from conidia using a modified phenol–chloroform method. Briefly, liquid nitrogen was applied to the conidial mass, which was then thoroughly ground using a sterile plastic pestle. Subsequently, 700 µL of lysis buffer (50 mM Tris-HCl, pH 7.2; 50 mM EDTA, pH 7.2; 3% SDS; 1% β-mercaptoethanol) was added to each tube. The samples were mixed gently and incubated in a water bath at 40 °C for 1 h, followed by centrifugation at 12,000 × g for 10 min at 4 °C.

The supernatant containing genomic DNA was transferred to a new tube and mixed thoroughly with an equal volume (700 µL) of phenol/chloroform (1:1, v/v), then centrifuged at 12,000 × g for 10 min at 4 °C. The aqueous phase was transferred to a fresh tube, mixed with 500 µL of chloroform, and centrifuged again at 12,000 × g for 4 min at 4 °C.

For DNA precipitation, 500 µL of the aqueous phase was transferred to a new tube, followed by the addition of 50 µL of 3 M sodium acetate (NaOAc) and 500 µL of isopropanol. The mixture was incubated at −20 °C and centrifuged at 12,000 × g for 20 min at 4 °C. The resulting DNA pellet was washed with 500 µL of 70% ethanol and centrifuged at 12,000 × g for 20 min. After air-drying at room temperature for 10–15 min, the DNA pellet was resuspended in 50 µL of TE buffer (10 mM Tris-HCl, 1 mM EDTA; pH 8.0) and stored at −20 °C until PCR analysis.

2.3 PCR amplification and molecular identification

PCR amplification of fungal genomic DNA was conducted using the universal internal transcribed spacer (ITS) primer pair PN23 (5′-

CACCGCCCGTCGCTACTACCG-3′) and PN34 (5′-TTGCCGCTTCACTCGCCGTT-3′), which has been widely applied for the detection of powdery mildew fungi (Bardin et al., 1999). Each PCR reaction was performed in a total volume of 25 μL, consisting of 12.5 μL of 2× DreamTaq PCR Master Mix (Thermo Scientific), 15 pM of each primer, 1 μL of genomic DNA template, and nuclease-free distilled water to volume. PCR amplification was carried out in a thermal cycler under the following conditions: initial denaturation at 93 °C for 5 min; 45 cycles of denaturation at 93 °C for 1 min, annealing at 55 °C for 1 min, and extension at 72 °C for 2 min; followed by a final extension step at 72 °C for 10 min. For species-level identification of *Podosphaera xanthii* and *Golovinomyces cichoracearum*, species-specific primer sets were employed. The primer pair S1 (5′-GGATCATTACTGAGCGCGAGGCCCCG-3′) and S2 (5′-CGCCGCCCTGGCGCGAGATACA-3′) was used to detect *P. xanthii*, whereas the primer pair G1 (5′-TCCGTAGGTGAACCTGCGGAAGGAT-3′) and G2 (5′-CAACACCAAACCACACACACGGCG-3′) was used for *G. cichoracearum*, following previously established PCR and multiplex PCR protocols (Hirata et al., 2000; Khodaparast et al., 2001).

2.4 Gel electrophoresis

PCR products (5 μL) were separated by electrophoresis on a 2% (w/v) agarose gel prepared in 1× TAE buffer. Gels were stained with ethidium bromide (0.5 μg mL^{-1}), and DNA bands were visualized and documented under ultraviolet (UV) illumination using a gel documentation system.

2.5 Phylogenetic analysis

Phylogenetic analysis was conducted to determine the genetic relationship of the cucumber powdery mildew isolates obtained in this study with previously reported reference strains. Internal transcribed spacer (ITS) region sequences generated from representative isolates were analyzed together with related ITS sequences retrieved from the NCBI GenBank database. Multiple sequence alignment was performed using the MUSCLE algorithm implemented in MEGA version 11.0. The alignment was manually

inspected, and poorly aligned regions at the 5′ and 3′ ends were trimmed to ensure equal sequence length for all taxa. The final alignment was used for phylogenetic tree construction. The best-fit nucleotide substitution model was determined using the "Find Best DNA Models (ML)" option in MEGA based on the Bayesian Information Criterion (BIC). Phylogenetic relationships were inferred using the Maximum Likelihood (ML) method with 1000 bootstrap replicates to assess branch support. Gaps and missing data were treated using partial deletion. The resulting phylogenetic tree was visualized and edited in MEGA, and bootstrap values greater than 50% were shown at the corresponding nodes.

3 RESULTS

3.1 Sample collection

In this study, cucumber leaf samples showing wilting symptoms were collected from five climatically distinct regions of Mongolia (Figure 1). Powdery mildew was observed at multiple developmental stages of cucumber plants throughout the growing season. In early spring, symptoms were predominantly detected in seedlings and recently transplanted plants, leading to rapid plant weakening and mortality (Figure 2a, b). During the second half of summer and continuing into autumn, disease symptoms were recorded across all growth stages, including both vegetative and reproductive phases (Figure 2c, d). Affected plants exhibited progressive wilting, reduced vigor, and impaired overall growth.

Figure 1

Sampling locations of Powdery mildew–infected cucumber plants collected from different greenhouse production systems in Mongolia.

Figure 2

Young cucumber plants infected with powdery mildew: (a) Sergelen soum, Tuv province, 3 June 2021; (b) Ulgii soum, Bayan-Ulgii province, 10 June 2022; (c) Gurvan Tes soum, Umnugovi province, June 2021; (d) Songinokhairkhan District, Ulaanbaatar City, November 2022.

3.2 Morphological characteristics of the causal agent of cucumber powdery mildew

Microscopic examination of infected cucumber leaves revealed abundant mycelia and conidiophores bearing chains of conidia, forming characteristic white powdery

colonies on the leaf surface. Species identification was based on the morphology of dry conidia, including conidial shape, size, and the presence of fibrosin bodies.

Conidia from all five sampling sites were ovoid to ellipsoid–ovoid in shape. Measurements of 100 conidia per sample showed that conidial length ranged from 24 to 51 µm, while conidial width ranged from 13 to 23 µm, depending on the sampling location (Table 1). Fibrosin bodies were consistently observed within conidia from all samples.

The presence of fibrosin bodies, together with the ovoid to ellipsoid–ovoid conidial shape and the formation of conidia in chains, is characteristic of *Podosphaera xanthii* and distinguishes this species from *Golovinomyces cichoracearum*, which typically lacks fibrosin bodies. Based on these morphological features, the powdery mildew pathogen infecting cucumber plants across all surveyed regions was identified as *Podosphaera xanthii*.

Figure 3

Morphological features of cucumber powdery mildew: (a) cucumber leaf surface extensively covered with powdery mildew colonies (15 February 2022); (b) chains of conidia produced on conidiophores of the cucumber powdery mildew pathogen (3 May 2022); (c) conidia showing internal fibrosin bodies characteristic of Podosphaera xanthii (3 May 2022).

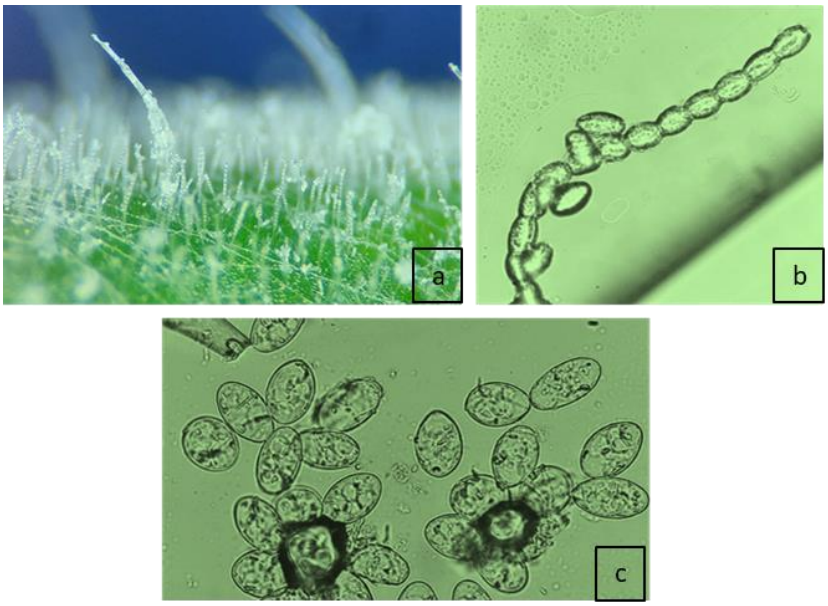


Table 1

Morphological characteristics of conidia of powdery mildew isolates from cucumber in Mongolia.

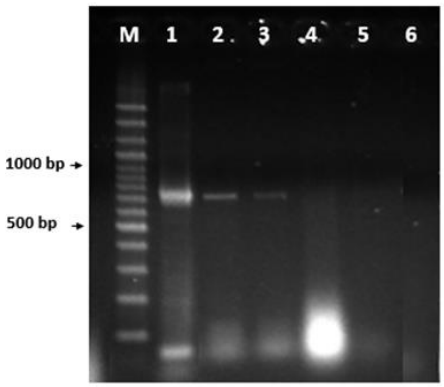
Points of sample	Shape of conidia, мкм (n=100)		Presence of fibrosin bodies
	length (L)	width (W)	
Songinokhairkhan district	28-51	15-23	+
Sergelen soum.Tuv	25-40	13-19	+
Ulgii soum. Bayan-Ulgii	26-48	14-22	+
Gurvan Tes soum. Umnugovi	24-45	14-20	+
Bayangol district	26-48	15-21	+

3.3 PCR amplification and molecular identification

Conidia isolated from all five samples were ovoid to ellipsoid–ovoid in shape, and fibrosin bodies were consistently observed within the conidia, supporting preliminary morphological identification of the powdery mildew pathogen. This study represents the first molecular identification of cucumber powdery mildew pathogens from five different regions of Mongolia using PCR-based methods. Genomic DNA was successfully extracted from all samples, with DNA concentrations varying among locations. The measured DNA concentrations were 131.6 ng μL^{-1} for Umnugovi, 128.6 ng μL^{-1} for Bayangol district, 191.3 ng μL^{-1} for Sergelen soum, Tuv province, 102.7 ng μL^{-1} for Songinokhairkhan district, and 343.6 ng μL^{-1} for Bayan-Ulgii. Initial PCR amplification was performed using the universal ITS primer pair PN23/PN34 to confirm the presence of powdery mildew fungi in infected cucumber leaf samples from all five study sites. Clear amplification products were obtained from samples collected in Songinokhairkhan district, Tuv Province, and Bayan-Ulgii province, whereas no visible bands were detected for samples from Gurwan tes soum, Umnugovi Province and Bayangol district (Figure 4).

Figure 4

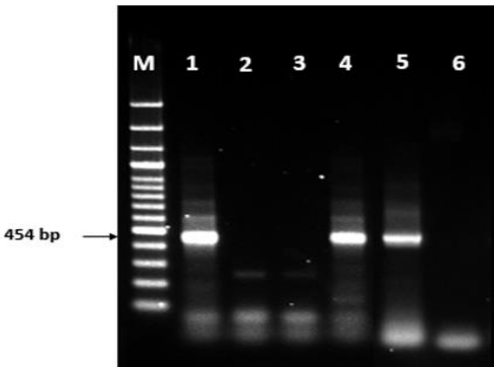
PCR amplification of powdery mildew fungal DNA using the universal ITS primer pair PN23/PN34. Lane M: 100 bp DNA ladder; lane 1: Songinokhairkhan district; lane 2: Tuv province; lane 3: Bayan-Ulgii province; lane 4: Umnugovi province; lane 5: Bayangol district; lane 6: negative control.



To further identify the fungal species responsible for cucumber wilt disease, multiplex PCR was conducted using species-specific primer pairs S1/S2 and G1/G2, targeting *Podosphaera xanthii* and *Golovinomyces cichoracearum*, respectively. Amplification products corresponding to *P. xanthii* were detected in samples from Songinokhairkhan district, Sergelen soum, Tuv province, and Ulgii soum, Bayan-Ulgii province, while no amplification was observed with primers specific to *G. cichoracearum* (Figure 5).

Figure 5

Species-specific PCR amplification of cucumber powdery mildew pathogens using primer pairs S1/S2 (Podosphaera xanthii) and G1/G2 (Golovinomyces cichoracearum). Lane M: 100 bp DNA ladder; lane 1: Songinokhairkhan District; lane 2: Gurwan tes soum. Umnugovi province; lane 3: Senjit-Oyu; lane 4: Sergelen soum. Tuv province; lane 5: Bayan-Ulgii Province; lane 6: negative control.



Based on the combined results of morphological observation and molecular analysis, the predominant powdery mildew pathogen affecting greenhouse-grown cucumbers in Mongolia was identified as *Podosphaera xanthii*. PCR products from three representative samples identified as *P. xanthii* were subjected to DNA sequencing. The obtained sequences were deposited in the NCBI GenBank database under accession numbers MW939431.1, MW939432.1, and MW939433.1, confirming the molecular identity of the pathogen.

3.4 Phylogenetic Analysis

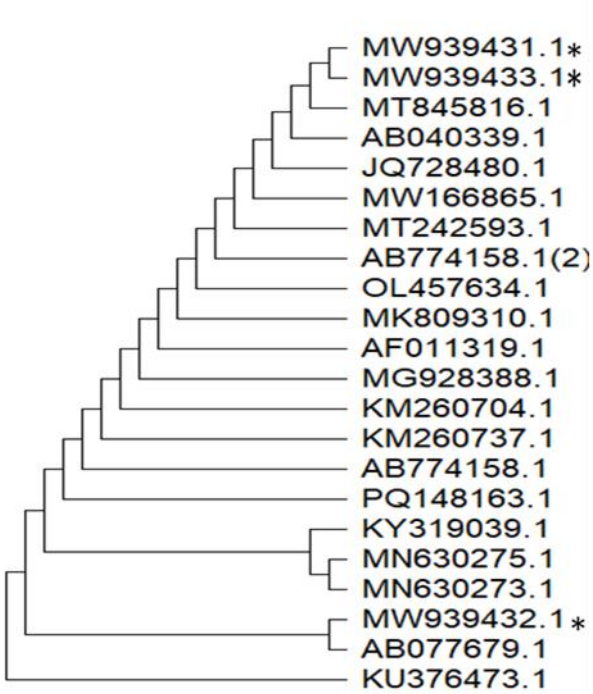
Phylogenetic analysis based on ITS region sequences revealed the genetic relationships between cucumber powdery mildew isolates obtained in this study and reference sequences retrieved from GenBank (Figure 6). The Maximum Likelihood tree showed that the Mongolian isolates clustered within the *Podosphaera xanthii* clade.

Two isolates, MW939431.1 and MW939433.1, grouped closely together and formed a well-supported subclade with previously reported *P. xanthii* reference sequences, including MT845816.1, AB040339.1, and JQ728480.1, indicating a high degree of sequence similarity. Another isolate, MW939432.1, clustered separately within

the same major *P. xanthii* lineage, suggesting minor intraspecific genetic variation among the Mongolian isolates. All Mongolian isolates were clearly separated from more distantly related reference sequences and formed a coherent group with authenticated *P. xanthii* sequences from different geographic origins. No clustering with non-*Podosphaer*a powdery mildew species was observed. These results confirm that the cucumber powdery mildew isolates analyzed in this study belong to the species *Podosphaera xanthii*.

Figure 6

Maximum Likelihood phylogenetic tree constructed from ITS region sequences of cucumber powdery mildew Podosphaera xanthii isolates, with bootstrap values (1000 replicates) indicated at branch nodes.



4 DISCUSSION

Powdery mildew is a major constraint to cucumber production worldwide, particularly under greenhouse conditions where temperature fluctuations and high humidity favor disease development. In Mongolia, greenhouse cucumber cultivation has expanded rapidly; however, information on the causal agents of cucumber powdery mildew has remained limited and, in some cases, inconsistent. Early studies reported

Erysiphe cichoracearum and *Sphaerotheca fuliginea* as causal agents (Puntsag, 1964; Byambajav, 1992), while later work identified *S. fuliginea* as predominant (Saran, 1999). Because these studies relied mainly on morphological observations and did not clearly describe diagnostic methods, the taxonomic identity of cucumber powdery mildew pathogens in Mongolia has remained uncertain.

Under Mongolian climatic conditions, cucumber production is primarily conducted in protected cultivation systems with one or two cropping rotations per year. These systems create microclimatic conditions that may strongly influence pathogen development and species composition. Because powdery mildew fungi exhibit overlapping morphological traits, molecular approaches are essential for reliable identification. Molecular phylogenetic analysis based on ITS sequences has been widely applied to resolve host specificity and species boundaries among powdery mildew fungi (Hirata et al., 2000).

In the present study, morphological examination revealed ovoid to ellipsoid–ovoid conidia containing fibrosin bodies in all samples. The presence of fibrosin bodies is a diagnostic feature of the Oidium stage of *Podosphaera xanthii* and allows differentiation from *Golovinomyces cichoracearum*, which typically lacks this characteristic (Reifschneider et al., 1985). Although variation in conidial size was observed among isolates, such variability is considered common within *P. xanthii* populations and is likely influenced by environmental conditions rather than species-level differences.

PCR-based molecular identification supported the morphological results. Universal ITS primers confirmed the presence of powdery mildew fungi, whereas species-specific primers identified *P. xanthii* as the predominant pathogen in three of the five sampled regions. Occasional non-specific amplification using universal primers has been reported previously and highlights the importance of species-specific primers for accurate identification (White et al., 1990; Bardin et al., 1999). The absence of amplification in some samples may be related to low fungal biomass or uneven pathogen distribution on leaf tissues.

Phylogenetic analysis of ITS sequences demonstrated that Mongolian isolates clustered within the *Podosphaera xanthii* clade together with reference sequences from different geographic origins, confirming species identity. Minor genetic variation among

isolates was observed, which is consistent with previous reports of intraspecific diversity within *P. xanthii* populations and may reflect local adaptation to environmental conditions or host genotypes. The predominance of *P. xanthii* observed in this study agrees with reports from other cucurbit-growing regions, where this species commonly dominates under protected cultivation systems and has been reported to infect a wide range of host plants (Cheng et al., 2006; Hsieh, 1983; Kuo et al., 1991).

In summary, this study provides the first integrated morphological, molecular, and phylogenetic identification of cucumber powdery mildew pathogens in Mongolia and confirms *Podosphaera xanthii* as the primary causal agent under greenhouse conditions. These findings provide an important foundation for future studies on disease epidemiology, fungicide resistance, and the development of targeted and sustainable disease management strategies for greenhouse cucumber production in Mongolia.

5 CONCLUSIONS

This study provides the first integrated morphological, molecular, and phylogenetic identification of the pathogen causing cucumber powdery mildew in Mongolia. Morphological characteristics, including ovoid to ellipsoid–ovoid conidia with fibrosin bodies, together with PCR amplification and ITS-based phylogenetic analysis, confirmed *Podosphaera xanthii* as the causal agent under greenhouse conditions. The consistent detection of *P. xanthii* across multiple regions indicates that this pathogen is well adapted to protected cucumber production systems in Mongolia. These findings clarify the etiology of cucumber powdery mildew and provide a scientific basis for the development of effective and targeted disease management strategies.

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Author Contributions

All the authors contributed equally to this work.

Data availability

All datasets relevant to this study's findings are fully available within the article.

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