

Paula Andrea Gómez-Zapata¹, Jorge Ronny Díaz-Valderrama², Samira Fatemi¹, Cristhian Orlando Ruiz-Castro¹ and M. Catherine Aime^{1*}

Abstract

Sphaerellopsis species are putative hyperparasites of rust fungi and may be promising biological control agents (BCA) of rust diseases. However, few detailed studies limit potential BCA development in *Sphaerellopsis*. Here, we explored the biogeography, host-specifcity, and species diversity of *Sphaerellopsis* and examined the early infection stage of one species, *S. macroconidialis,* to infer its trophic status. We randomly screened 5,621 rust specimens spanning 99 genera at the Arthur Fungarium for the presence of *Sphaerellopsis*. We identifed 199 rust specimens infected with *Sphaerellopsis* species on which we conducted morphological and multi-locus phylogenetic analyses. Five *Sphaerellopsis* species were recovered, infecting a total of 122 rust species in 18 genera from 34 countries. *Sphaerellopsis melampsorinearum* sp. nov. is described as a new species based on molecular phylogenetic data and morphological features of the sexual and asexual morphs. *Sphaerellopsis paraphysata* was the most commonly encountered species, found on 77 rust specimens, followed by *Sphaerellopsis macroconidialis* on 56 and *S. melampsorinearum* on 55 examined specimens. The type species, *Sphaerellopsis flum*, was found on 12 rust specimens and *Sphaerellopsis hakeae* on a single specimen. We also recovered and documented for the frst time, the sexual morph of *S. macroconidialis*, from a specimen collected in Brazil. Our data indicate that *Sphaerellopsis* species are not host spe‑ cifc and furthermore that most species are cosmopolitan in distribution. However, *S. paraphysata* is more abundant in the tropics, and *S. hakeae* may be restricted to Australia. Finally, we confrm the mycoparasitic strategy of *S. macroconidialis* through *in-vitro* interaction tests with the urediniospores of *Puccinia polysora*. Shortly after germination, hyphae of *S. macroconidialis* began growing along the germ tubes of *P. polysora* and coiling around them. After 12 days of co-cultivation, turgor loss was evident in the germ tubes of *P. polysora*, and appressorium-like structures had formed on urediniospores. The interaction studies indicate that *Sphaerellopsis* species may be more efective as a BCA during the initial stages of rust establishment.

*Correspondence: M. Catherine Aime maime@purdue.edu Full list of author information is available at the end of the article

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Introduction

Sphaerellopsis Cooke (Leptosphaeriaceae, Ascomycota) is the most commonly reported fungal genus associated with rust fungi (Pucciniales, Basidiomycota). *Sphaerellopsis* species have been reported on 369 rust species and 30 genera in more than 50 countries across the globe (Kranz and Brandenburger 1981). The fungus is usually described as solitary to gregarious spherical black pycnidia that develop on sori and, thus, presumably infect rust spores and prevent their dispersion (Eriksson [1966](#page-24-0)). These black pycnidia are typically found on uredinia, the spore stage most frequently associated with severe rust disease epidemics and long-distance dispersal across continents. However, pycnidia have also been found in association with other rust spore stages. Due to the intimate association of *Sphaerellopsis* with rust fungi, this fungal genus is tentatively considered a potential biological control agent (BCA) of rust fungi, many of which cause devastating disease epidemics and yield losses worldwide (Chen et al. [2002;](#page-24-1) Kolmer et al. [2009;](#page-25-1) Lidwell-Durnin and Lapthorn [2020](#page-25-2)). Nevertheless, characterization studies of *Sphaerellopsis* are scarce, which limits its use in applied biological control research.

In 1815, the type species *Sphaerellopsis flum* was initially described as *Sphaeria flum* by Bivona-Bernadi on rusts infecting *Convolvulus sepium* and *Populus nigra* in Sicily (Bivona-Bernardi [1815\)](#page-24-2). Fries transferred the species to *Phoma* as *Phoma flum* in 1823 (Fries [1823](#page-24-3)). Later, Castagne erected the genus *Darluca* and treated *Sphaeria flum* as a synonym of *Darluca vagans* (Castagne [1851\)](#page-24-4). However, in 1966 Eriksson considered the epithet "*vagans*" superfuous and prioritized "*flum*" over "*vagans*" (Eriksson [1966](#page-24-0)). In 1908, Spegazzini considered *Eudarluca caricis* the teleomorph of *Darluca flum* (Spegazzini [1908\)](#page-25-3). Later in 1951, Keener proved the connection between these two genera experimentally (Keener [1951](#page-25-4)). Yuan et al. [1998](#page-25-5) confrmed this connection by obtaining the asexual morph from the teleomorph in culture studies (Yuan et al. [1998\)](#page-25-5). Lastly, in 1977, Sutton transferred *Darluca flum* to the genus *Sphaerellopsis* as *S. flum* (Sutton [1977\)](#page-25-6). Species of *Sphaerellopsis* are commonly found in its asexual state, and the sexual morph is rarely observed. Although *Sphaerellopsis* and *Eudarluca* are now known to be congeneric, it is still uncertain which *Sphaerellopsis* species is conspecifc with *Eudarluca caricis*.

Although most scientifc publications posit *Sphaerellopsis* as a mycoparasite of rust fungi, its relationship with

these plant pathogens is still poorly understood. While there is some evidence of direct interaction between *S. flum* and several rust species, the nature of the interaction has not been consistently described and may vary among *S. flum* strains. For instance, some researchers argue that *S. flum* can colonize rust spores by penetrating nonspecialized hyphae and disrupting cytoplasm (Carling, D.E. Brown, M.F. Millikan, [1976;](#page-24-5) Płachecka [2005](#page-25-7); Sappin-Troufy [1896;](#page-25-8) Whelan et al. [1997\)](#page-25-9). However, other studies report no evident cytoplasmic disruptions of rust spores when *S. flum* is present (D'Oliveira, [1941](#page-24-6); Hulea [1939\)](#page-24-7). In vitro assays demonstrated hyphal growth and conidioma development of *S. flum* when cultured with intact or ruptured rust spores (Rambo and Bean [1970](#page-25-10)). However, changes in fungal growth rate do not necessarily demonstrate that *S. flum* can infect rust fungi. Similarly, lab and feld experiments have shown a signifcant reduction in rust infection when *S. flum* is present (Black [2012](#page-24-8); Gordon and Pfender [2012](#page-24-9); Yuan and Han [2000\)](#page-25-11), but these conclusions are contradicted by other studies (Yuan et al. [1999\)](#page-25-12). In recent years, through phylogenetic analyses, several isolates determined as *S. flum* have turned out to be incorrectly placed in the genus *Sphaerellopsis* (Trakunyingcharoen et al. [2014](#page-25-13)). Thus, new genera were created, and new species within *Sphaerellopsis* were introduced. Hence, the previous interaction tests of *S. flum* with rust fungi remain unanswered, as the *Sphaerellopsis* specimens used in those studies may represent diferent species, or even belong to other genera.

Based on morphology and DNA sequence data, there are currently seven accepted *Sphaerellopsis* species. Five species are reported as mycoparasites of rust fungi: *Sphaerellopsis anomala*, *S. flum*, *S. hakeae*, *S. macroconidialis*, and *S. paraphysata* (Crous et al. [2016;](#page-24-10) Nag Raj [1993;](#page-25-14) Trakunyingcharoen et al. [2014](#page-25-13)); and two are considered saprobic: *S. artemisiae* and *S. isthmospora* (Doilom et al. [2021;](#page-24-11) Phookamsak et al. [2019](#page-25-15)). Although *S. hakeae* and *S. paraphysata* were reported to be associated with rust sori and plant tissue (Crous et al. [2016](#page-24-10), [2018\)](#page-24-12), it is unclear if the association with the host plant is parasitic or saprobic. Furthermore, it has not been proven that all *Sphaerellopsis* species associated with rust fungi are mycoparasites. Therefore, while significant improvements have been made to the taxonomy of *Sphaerellopsis* (Trakunyingcharoen et al. [2014\)](#page-25-13), the parasitic relationship between its members with rust fungi remain undetermined.

Among the fve *Sphaerellopsis* species known to associate with *Pucciniales*, *S. paraphysata* is the only one confrmed to have a mycoparasitic strategy. Secondary metabolites obtained from *S. paraphysata* disrupted the urediniospores cell wall of *Puccinia substriata*, leading to cellular component leakage (Ashmitha Sri et al. [2020\)](#page-24-13). Inoculation of the conidia of *S. paraphysata* on the uredinia of *P. substriata* reduced rust spore germination by up to 76% (Anandakumar et al. [2019\)](#page-24-14). In addition, the rust disease severity of the rust was 13% when *S. paraphysata* was present compared to the control of 86% (Anandakumar et al. [2019](#page-24-14)). However, because the species was also found in plant tissue (Crous et al. [2018](#page-24-12)), further studies are needed to discard a plant pathogenic strategy for *S. paraphysata* which would likely negate its application as a potential BCA for rust fungi.

In addition to interaction studies between members of *Sphaerellopsis* and rust fungi, other ecological studies are essential to characterize the genus and determine if any species could be suitable as a BCA of rusts. For example, knowledge of a natural enemy's host range and geographic distribution is crucial for environmental risk assessments to prevent releasing new diseases. Furthermore, host-specificity studies can help clarify whether/which *Sphaerellopsis* species are generalists or host-specifc on rust species or genera. Nevertheless, biogeography, species diversity, and the host-specifcity of *Sphaerellopsis* are unknown due to the few records of the currently accepted species. Most of these records are primarily from temperate regions (Ashmitha Sri et al. [2020](#page-24-13); Crous et al. [2016](#page-24-10); Trakunyingcharoen et al. [2014](#page-25-13)) with limited records from the tropics.

Because most *Sphaerellopsis* species are associated with rust fungi, we adopted a strategy of screening vouchered rust specimens for the presence of incidentally co-collected *Sphaerellopsis* species. The Arthur Fungarium (PUR), housed at Purdue University, is one of the world's largest collections of rust fungi. It holds approximately 160,000 specimens of 5,000 species collected across a broad geographic distribution and timeline, and it is one of the most diverse collections, with 132 rust genera in 14 families in the world (Purdue Herbaria [2022](#page-25-16)) with especially rich holdings (ca. 50%) of specimens from the Americas. Therefore, the present study had two aims: (1) to augment distribution and host data on the fungal genus *Sphaerellopsis* by screening PUR collections, with an emphasis on those originating from the Americas, and evaluating these for signals of host-specifcity, and (2) to elucidate the strategy of *S. macroconidialis* when interacting with rust fungi, using the urediniospores of the southern corn rust, caused by *Puccinia polysora*, as a model system.

Methods

Collected samples

We collected black fruiting bodies of *Sphaerellopsis* from preserved rust specimens in the Arthur Fungarium (PUR) supplemented with newly collected material in Peru in 2019 and Puerto Rico in 2018. Rust specimens at PUR are stored in folders sorted by rust species in host plant families and geographic regions. When collecting *Sphaerellopsis* samples at PUR, we randomly screened these rust specimens by selecting the top, middle, and bottom specimens from the Americas shelf in each rust species folder. When collecting *Sphaerellopsis* samples from other geographic regions, we randomly selected one rust specimen per folder. Although we screened rust specimens collected across the globe, the Americas was our preferred geographic region in an efort to close this information gap. We screened each rust-infected leaf of every rust specimen under a stereoscope Olympus Model SZ2-ILST (Tokyo, Japan) and screened for visible signs of *Sphaerellopsis*-type fruiting bodies developing on the sori. Only specimens fruiting exclusively on rust sori but not on surrounding host tissue were removed for further analyses, as the ability to also fruit on host plant tissues would indicate a non-rust-specific pathogen. Then, we removed one *Sphaerellopsis*-infected sorus with a sterile razor blade per rust specimen. A new blade was used per each specimen to prevent cross-contamination. Each infected sorus was placed in a microcentrifuge tube labeled with the PUR barcode of the rust specimen and a serial number.

When collecting *Sphaerellopsis* specimens in the feld, we first collected rust-infected plant leaves. Then, we looked for black fruiting bodies developing on sori under a stereoscope. If *Sphaerellopsis* was present, we isolated it by cutting a piece of the plant tissue containing both the sorus and *Sphaerellopsis* with a razor blade. Then, the plant tissue was sterilized with 1/10 dilution chlorine bleach for one minute and washed three times with sterile water. The piece of plant tissue was inoculated onto Petri dishes containing potato dextrose agar (PDA) and 50 mg/mL chloramphenicol. Petri dishes were shipped to the Aime Lab at Purdue University for further processing. Once the Petri dishes arrived at the Aime lab, we subcultured them until axenic cultures were achieved on PDA and 2% malt extract agar (MEA) with 50 mg/mL chloramphenicol. Isolates were stored long-term on PDA slants at 4 ° C and in 15% (v/v) glycerol at -80 ° C. Finally, we pressed, dried, and vouchered the collected rust specimens at PUR.

In total, we screened 5,621 *Pucciniales* collections for the presence of *Sphaerellopsis* (Supplementary Table 1). The following data were recorded for each *Pucciniales* specimen that was found to be co-infected with *Sphaerellopsis*: PUR accession number, rust species name, country of origin, year of collection, host plant family, genus, and species, and geolocation (Supplementary Table 2). Finally, we took macro- and microphotographs of some of the collected *Sphaerellopsis* samples with an Olympus SC30 camera and image software Olympus cellSens entry version 1.14 under a stereoscope Olympus Model SZ2-ILST and a compound microscope Olympus BH2-RFCA at PUR. Measurements of fungal structures were made using cellSens Standard 1.18 Imaging Software (Olympus).

Identifcation and species concept

The collected *Sphaerellopsis* samples were identified using an integrated species concept, based on morphological characters and phylogenetic analyses (Aime et al. [2021](#page-24-15)). Original descriptions of the currently accepted *Sphaerellopsis* species were used as references for morphological comparison (Cooke M.C., [1883](#page-24-16); Crous et al. [2016](#page-24-10); Doilom et al. [2021](#page-24-11); Nag Raj [1993](#page-25-14); Phookamsak et al. [2019;](#page-25-15) Trakunyingcharoen et al. [2014](#page-25-13)).

DNA isolation and PCR amplifcation

The genomic DNA of each potential *Sphaerellopsis*, collected during the screening, was extracted using the EZNA HP Fungal DNA kit (Omega Bio-Tek, Norcross, Georgia), following the manufacturer's instructions and modifying only the incubation time in the third step. Instead of 30 min, we incubated the samples overnight to ensure complete lysis of cells in the suspension. We selected the following loci for amplifcation: the internal transcribed spacer (ITS) and the large subunit (LSU) of the ribosomal DNA repeat, the translation elongation factor 1-α (*tef1*) and the RNA polymerase II second largest subunit (*rpb2*). Because most of our *Sphaerellopsis* specimens were derived from fungarium collections and thus culturing was not possible, we designed specifc ITS and LSU primers for amplifcation of these loci (Table [1](#page-3-0)). For this, we downloaded all ITS and LSU sequences of verifed *Sphaerellopsis* species (Trakunyingcharoen et al. [2014](#page-25-13)) from GenBank. We also downloaded sequences of several rust species and of ubiquitous fungal species usually found in dead plant material. Multiple alignments were conducted using MUSCLE version 3.7 (Edgar [2004](#page-24-17)) in MEGA7 (Kumar et al. [2016\)](#page-25-17). Conserved regions were searched for both loci in *Sphaerellopsis* sequences, excluding rusts and other fungal sequences. We selected primers that amplify approximately 250 bp in length for ITS amplifcation and between 600 and 700 bp for LSU amplifcation. Finally, we performed a BLASTn database search using our selected primers as the query to confrm that the greatest matching hits were *Sphaerellopsis* sequences. Amplifcation for each locus was conducted with these new, and previously published (Table [1](#page-3-0)) primers in 25-µl PCR reactions on a Mastercycler ep gradient Thermal Cycler (Eppendorf model #5341, Hauppauge, New York) that consisted of 12.5 μ l of 2 \times MyTaq Mix (Bioline, Swedesboro, New Jersey), 1.25 µl of each 10 µM primer, and 10 µl of either 1/10 or 1/5 diluted DNA extract. Amplifcations of rDNA, *tef1* and *rpb2* loci were run under the following conditions: initial denaturation at 94 °C for 5 min (95 °C for *rpb2*/96°C for 2 min for *tef1*); followed by 40 cycles of denaturation (45 cycles for ITS) at 94 °C for 30 Sect. (95 °C for *rpb2*), annealing at 51.8 °C for 45 s for ITS/54°C for 45 s for LSU/56°C for 30 s for *tef1*/55°C for 45 s for *rpb2,* and elongation at 72 °C for 45 s (1 min for LSU and 30 s for *tef1*); and fnal extension at 72 °C for 7 min.

Electrophoresis and sequencing

We ran the PCR products in 1% agarose and stained them with GelRed (RGB4102, Phoenix Research Products) for 35 min at 110 V in a Bio-Rad electrophoresis tank to visualize PCR products. PCR products of samples that showed bands were sent to Genewiz (South Plainfeld, New Jersey) for purifcation and subsequent sequencing

Gene	Primer name	Orientation	Sequences (5' to 3')	Reference
ITS	FudITS2F		AACTTTCAACAACGGATCTCTTGGT	This study
	EudITS4R		ATGCTTAAGTTCAGCGGGTA	This study
	EuSP_ITS_R2	R	ATGTGCYRMGMTYCAGGC	This study
LSU	Spha 28sf1		GAGTGAAGCGGCAACAGCTC	This study
	Spha 28sr1		CGATTTGCACGTCAGAACCGC	This study
tef1	FF1-728 F		CATCGAGAAGTTCGAGAAGG	Carbone and Kohn 1999
	EF1-986R	R	TACTTGAAGGAACCCTTACC	Carbone and Kohn 1999
rpb ₂	RPB2-5F2		GGGGWGAYCAGAAGAAGGC	Sung et al. 2007
	fRPB2-7CR		CCCATRGCTTGYTTRCCCAT	Liu et al. 1999

Table 1 Primers for PCR amplification and sequencing used in this study

in both directions with the amplifcation primers (Table [1](#page-3-0)). Raw sequence reads were edited manually and assembled using Sequencher version 5.2.3 (Gene Codes Co., Ann Arbor, Michigan).

Sequence alignment and phylogenetic trees

The edited sequences were blasted against the NCBI GenBank nucleotide database [\(http://ncbi.nlm.nih.gov/](http://ncbi.nlm.nih.gov/blast/Blast.cgi) [blast/Blast.cgi](http://ncbi.nlm.nih.gov/blast/Blast.cgi)) to confrm placement in *Sphaerellopsis*. To construct datasets, we downloaded publicly available DNA sequences of *Sphaerellopsis* species as references for our phylogenetic analyses; *Alternaria consortialis* was chosen as the outgroup (Table [2](#page-4-0)). Sequences were aligned using MUSCLE version 3.7 (Edgar [2004](#page-24-17)) in MEGA7 (Kumar et al. 2016). Then, the aligned sequences were trimmed using trimAl version 1.2 (Capella-Gutiérrez et al. [2009\)](#page-24-19) with a minimum percentage of positions to conserve [0-100]: 50; and gap threshold, the fraction of positions without gaps in a column $[0-1]$: 0.6. We performed maximum likelihood (ML) inference using

Table 2 Reference sequences used in phylogenetic analyses

IQ-TREE (Minh et al. [2020\)](#page-25-20) under partitioned models (Chernomor et al. [2016](#page-24-20)) and selected the best nucleotide substitution model under Akaike's information criterion corrected for small sample size (AICc) using ModelFinder (Kalyaanamoorthy et al. [2017\)](#page-25-21). An ultrafast bootstrap analysis was implemented with 1,000 rep-licates (Hoang et al. [2018\)](#page-24-21). The "-bnni" option was used to reduce the risk of overestimating branch supports with UFBoot due to severe model violations. Finally, phylogenetic reconstructions with bootstrap values were visualized in FigTree version 1.4.3 ([http://tree.bio.ed.ac.uk/](http://tree.bio.ed.ac.uk/software/figtree/) [software/fgtree/](http://tree.bio.ed.ac.uk/software/figtree/)) and colored in Inkscape ([https://inksc](https://inkscape.org) [ape.org\)](https://inkscape.org).

Geographical distribution

The localities of Sphaerellopsis specimens with successfully amplifed gene regions were used to build a geographic map. We used the GPS coordinates of each of these specimens when present. Otherwise, we generated approximated coordinates according to the

locality description following a geocoding Python Script in the GitHub repository (Lynn [2017](#page-25-25)). We plotted the geographic data of each specimen on a map and colored each point by the clades formed in the multi-locus phylogenetic tree using the package Geopandas in Python (Jordahl [2014](#page-25-26)).

Interaction experiments between conidia of *Sphaerellopsis macroconidialis* **and urediniospores of** *Puccinia polysora*

Puccinia polysora was the host from which the strain SP28 of *S. macroconidialis*, used in this study, was collected. *Puccinia polysora* is an agriculturally important fungus that causes the destructive disease Southern rust of corn (Sun et al. [2021\)](#page-25-27).

Collection and identifcation of urediniospores of *Puccinia polysora from* **maize crops**

In the summer of 2021, maize leaves infected with *P. polysora* were harvested from feld-grown maize plants at the Southwest Purdue Agricultural Center, Indiana, USA, and brought to the Aime Lab. Urediniospores were collected using a mini cyclone spore collector (Tallgrass Solutions, INC; Manhattan, KS) and stored in gelatin capsules at -80 °C until further use. To confrm the identifcation of the rust, we amplifed the LSU region using the primers of Aime [\(2006\)](#page-24-22) and the methodologies of Aime et al. ([2018\)](#page-24-23) and Aime and McTaggart [\(2020](#page-24-24)). We amplifed the LSU as it has been shown to be the most informative gene for rust species identifcation (Aime et al. [2017\)](#page-24-25). The resulting DNA fragment was blasted against the NCBI and the Rust HUBB (Kaishain et al. [2024](#page-25-28)) databases to confrm identity.

Cultivation of corn plants in the greenhouse and installation of humidity chamber for inoculations

Healthy corn plants (P0574AM™) were cultivated in the greenhouse facility at Lily Hall of Life Sciences, Purdue University. We planted seven 3-gallon pots with two corn seeds per pot. Following germination, we removed the weaker seedling leaving one plant per pot. Plants were maintained at a temperature range between 24 and 30 °C and watered and fertilized as needed. Next, we installed a humidity chamber for rust inoculation in the same room where plants were growing. This chamber consisted of a simple cubic structure (30 cm^3) made of PVC pipes and covered with a white four mil plastic sheeting. A door was installed on the chamber for easy access and manipulation of the corn plants once these were inside. A PVC pipe (2 cm diam. and 20 cm length) was also inserted in one side of the chamber to connect a 2.2 L humidifer $(AquaOasis[™])$ placed outside the chamber. Finally, we placed a hygrometer inside the chamber to track temperature and humidity.

Rehydration of urediniospores of *P. polysora* **for inoculation**

Before inoculating healthy corn plants with *P. polysora*, we took the urediniospores stored at -80 \degree C in gel capsules and rehydrated them in two steps. First, the spores contained in gel capsules were thawed at 4 °C for 16 h. Then, the urediniospores contained in gel capsules were placed inside a humidified chamber. This chamber consisted of a sterile plastic container with a 23.5% KOH beaker as a source of water vapor. This concentration of KOH gives approx. 80% of relative humidity inside the container while avoiding water condensation (Rowell [1984](#page-25-29)). Then, we sealed the chamber with a lid and let the urediniospores rehydrate for 12 h at room temperature. Once urediniospores were rehydrated, we added them into a sterile glass vial containing 0.1% tween 20. We gently mixed the spores with the solution to resuspend them and ensure no clumps were formed.

Inoculation of corn plants with urediniospores of *P. polysora* **in the greenhouse**

We used a spore inoculator (Tallgrass Solutions, Manhattan, Kansas) attached to an air compressor (California Air Tools CAT-1P060S) operating in the 2–5 psi range to inoculate healthy corn plants with urediniospores immersed in 0.1% tween 20. Each healthy corn leaf was sprayed with the spore solution at 2 cm from the leaf. Once each plant was covered entirely with the spore solution, we placed them in the humidity chamber and did not close the chamber completely to ensure air circulation. Inoculations were done in the late afternoon when temperatures were lower, which helped moisture stay longer on the leaf surface and facilitated spore germination for successful infection (Borlaug Global Rust [2017](#page-24-26)). During the infection period, temperatures were held at between 23 and 30 °C and the humidifier was continuously flled with sterile distilled water to keep relative humidity between 50 and 80%. We used 16 daylight hours and eight night hours. Under optimal conditions, we observed rust symptoms on corn leaves between 7 and 15 days after inoculation.

Harvesting of fresh conidia of *S. macroconidialis* **and urediniospores of** *P. polysora* **for the in‑vitro interaction test**

Conidia of *S. macroconidialis* SP28 from a two-week-old PDA culture were harvested for the interaction test. We added 1 mL of sterile water to the medium, then slightly agitated the petri dish to let the water mix with the conidia for about a minute. Once the water turned milky from presence of suspended conidia, we collected the conidia solution with a micropipette and transferred it to a 2mL tube. Fresh urediniospores of *P. polysora* infecting corn plants in the greenhouse were also harvested

for the interaction test. We collected urediniospores from open and pulverulent sori to ensure the urediniospores were mature and ready to germinate. We gently tapped the rust-infected leaf against a 2mL tube containing 0.1% tween 20 to allow the spores to fall into it. Once the tween 20 solution turned light brown, we closed the lid. The concentration of conidia and urediniospores was measured with a hemocytometer to reach a dilution of 10^4 spores per mL. The viability of the conidia and urediniospores was checked with Trypan Blue. We used≥80% viable spores as the threshold for the interaction test.

In‑vitro interaction between spores of *S. macroconidialis* **and** *P. polysora*

We poured 1 mL of 1% water agar with 50 mg/mL Chloramphenicol into small Petri dishes (50 mm diam.) to set up the interaction test. Then, we added 40 uL of the urediniospore suspension to fve Petri dishes. To locate the urediniospores during the interaction test, we drew two points on each side of the bottom of each petri dish with a marker. Each Petri dish was sealed with paraflm and incubated in the dark at 25°C overnight to facilitate urediniospore germination. We observed each petri dish under a compound microscope Olympus BH2-RFCA using a 20X objective the day following inoculation. Petri dishes in which>70% of the urediniospores germinated were kept for the next step. A minimum of three Petri dishes with > 70% urediniospore germination were used as replicates for the interaction test. Then, we added the conidia of *Sphaerellopsis*, suspended in water, to the same Petri dishes containing germinated urediniospores at a 1 mm distance from the urediniospores. Petri dishes were sealed again with paraflm and incubated for 24 h at room temperature. After 24 h of co-inoculation, we conducted daily screenings of the plates over the next 12 days. Interactions were observed under a microscope using the 20X objective without opening the lid to avoid contamination. Lids were only removed on the last day of observation to use a 40x objective and to take fnal pictures. Two negative controls were also used in this interaction test. The first one consisted of three Petri dishes containing urediniospores only. The second consisted of three Petri dishes containing only conidia of *S. macroconidialis*. The experiment was repeated three times.

Results

Sphaerellopsis **recovery from PUR collections**

We randomly screened 5,621 rust specimens in 99 rust genera, representing 5% of the total collections at PUR and 58% of the accepted rust genera (Berndt & Aime, [n.d.](#page-24-27) unpublished), for the presence of *Sphaerellopsis* species that were incidentally co-collected with rust specimens (Supplementary Table 1). Of these 5,621 specimens, we collected 523 black fruiting bodies resembling the fungal genus *Sphaerellopsis* (Supplementary Table 2). Of these 523 collections, 199 were confrmed as *Sphaerellopsis* members through phylogenetic analyses and morphology (Table [3\)](#page-7-0). Five *Sphaerellopsis* species were recovered, infecting 122 rust species in 18 genera from 34 countries.

We successfully amplifed 195 DNA sequences of *Sphaerellopsis* from ITS rDNA, 58 sequences from LSU rDNA, 48 from *tef1*, and eight from *rpb2*. Although we amplifed the four loci for some *Sphaerellopsis* specimens, degradation of DNA in older specimens limited the ability to obtain complete locus datasets for many specimens. Nevertheless, we successfully amplifed the ITS region of 163 specimens collected between 1883 and 1998. The oldest Sphaerellopsis specimen whose ITS region was successfully amplifed was collected in 1883 on *Melampsora medusae* from the United States (voucher number: PUR2041, GenBank accession number: OQ418220). Lastly, we isolated a strain of *S. macroconidialis* (SP28) from freshly collected material, which was the basis of the interaction experiments between the conidia of *S. macroconidialis* and germinated urediniospores of *Puccinia polysora*, the host from which it was collected.

Nucleotide alignment dataset and phylogenetic inferences

Our multi-locus phylogenetic analysis consisted of a four-locus-concatenated dataset of 1996 characters, of which 352 were parsimony-informative. The percentage of parsimony-informative characters per gene region was 3.4% for ITS, 1.3% for LSU, 7.1% for *tef1*, and 5.8% for *rpb2*. We analyzed 219 individuals, of which 16 were sequences from previously identifed *Sphaerellopsis* taxa, and *Alternaria consortialis* served as an outgroup taxon (Table 3). The following models were selected by ModelFinder (AICc): JC for ITS, GTR+F+R2 for LSU, TIM+F+G4 for *tef1*, and TIM2e+I for *rpb2*. Our maximum likelihood analysis revealed eight supported clades (Fig. [1](#page-16-0), supplementary Figure S1), all of which have bootstrap support≥70%.

Species Diversity of *Sphaerellopsis* **associated with rust fungi**

Five species of *Sphaerellopsis* were recovered from our sampling: four of the seven previously accepted species, and one undescribed species (Fig. [1](#page-16-0)). *Sphaerellopsis paraphysata* was the most common species within our screened collections, found on 77 rust specimens, followed by *S. macroconidialis* on 56 and *S. flum* on 12. *Sphaerellopsis hakeae* was found in one rust specimen, and *S. artemisiae* and *S. isthmospora* were not found in this study. One species, *Sphaerellopsis anomala* is not

Table 3 *Sphaerellopsis* members associated with rust fungi from PUR and identifed through molecular and morphological analyses. Reference sequences in bold; NA: data not available

represented in our analyses, due to lack of sequence data. Two other well-supported clades were found in the phylogeny that do not represent previously published *Sphaerellopsis* species. One of these consisted of a single specimen found on sori of *Puccinia montanensis* from the United States collected in 1896 (voucher number: PUR23925). We amplifed the ITS region of this specimen and took macro photographs. However, due to the scarce and dry material, the specimen's morphology and amplifcation of other gene regions were impossible. Thus, it is uncertain whether this represents an undescribed species. The other clade comprised 55 specimens from *Pucciniales* collected between 1883 and 2016, including a specimen that contained both the asexual and sexual morphs. This new species is described as *Sphaerellopsis melampsorinearum* sp. nov. below.

Taxonomy

Sphaerellopsis melampsorinearum **Gomez-Zap. & Aime, sp. nov.**

Figure [2.](#page-18-0)

Mycobank No: MB847464.

Etymology: Named after the large number of rust hosts that belong to the suborder *Melampsorineae*.

Diagnosis: Similar to *S. flum* but difers in conidiomata size (up to 107 μm diam.), and conidia length [(9.1– $(10.3-14.3(-16.6) \,\mu m).$

Type: Holotype: United States, Indiana, Tippecanoe County, West Lafayette, on urediniospores of *Melampsora medusae* infecting *Populus deltoides*, 19 September 2015, M. Catherine Aime, s.n. (PUL F29362 (ex-PURN15307); GenBank accessions ITS–OQ418354, LSU–OQ418183, *tef1–O*Q743726, *rpb2–O*Q587607).

Description: Asexual morph–conidiomata associated with rust sori, pycnidial, erumpent, aggregated, globose, 48–107 μm, with central ostiole, outer layers dark brown

cells textura angularis, 3.8–6.92 μm diam. Paraphyses not observed. Conidiophores reduced to conidiogenous cells. Conidiogenous cells line the inner cavity and are smooth, hyaline, globose to ampulliform. Conidia fusoid, hyaline, smooth, guttulate, 1-septate, slightly constricted at the septum, apex subobtuse, tapering to truncate hilum, $(9.1–)10.3–14.3(-16.6) \times (3–5) \mu m$. Sexual morph–ascomata associated with rust sori, 76–162 μm diam., solitary or gregarious; loci immersed, brown in outer zone consisting of two to three rows of dark cells, hyaline in inner part, subglobose to ampulliform, with protruding papillate neck and ostiole. Pseudoparaphyses are fliform, septate, hyaline. Asci numerous, 8-spored, bitunicate, cylindrical-clavate, short stipitate, 59.6–101.3×8.5– 10.4 μm. Ascospores irregularly biseriate, fusiform, hyaline to pale yellow, $15.2-21.3\times3.8-6.0$, 1-septate, slightly constricted at the septum, surrounded by a mucous sheath not easily perceived.

Substrate/Host: on rust sori of several rust species, principally species of the genus *Melampsora*, but also known to infect *Coleosporium* spp., *Puccinia* spp., *Uromyces* spp., and *Gerwasia holwayi.*

Distribution: Argentina, Bolivia, Brazil, Colombia, Ecuador, Germany, Japan, Peru, Trinidad, the continental United States of America, Venezuela.

Additional materials examined: Brazil, São Paulo, on urediniospores of *Puccinia vernoniae*-*mollis* infecting leaves of *Vernonia* sp., 17 February 1989, Anibal de Carvalho 89−7, containing teleomorph, (PUL F29361 (ex-PURN9763); GenBank accessions: ITS–OQ418405; LSU– OQ418210). **Colombia**, Antioquia, on urediniospores of *Melampsora larici*-*populina* infecting *Populus nigra*, 20 March 1989, V.M Pardo-Cardona s.n.

Fig. 1 The top-scoring ML phylogenetic tree of the genus *Sphaerellopsis* reconstructed from the four-locus-concatenated dataset (ITS, LSU, *tef1*, and *rpb2*). The ML bootstrap value is presented above each branch. Colors delimit clades, each labeled with the corresponding *Sphaerellopsis* species. Taxa labels are written on the tree as"PUR voucher," "the host rust where *Sphaerellopsis* was found," and"the origin/locality of each specimen." Reference sequences and outgroup taxa are written in bold. The tree was rooted to *Alternaria consortialis* CBS 104.31. Refer to supplementary fgure S1. to see the fully resolved phylogram showing branch lengths and support values

Fig. 1 continued

Fig. 2 *Sphaerellopsis melampsorinearum* sp. nov. (PUL F29362, PUL 29,360, PUL F29361). **A**, **B** Conidiomata developed on sori. **C**, **D** Ascomata developed on sori. **E** Outer layers of conidioma, textura angularis. **F**, **G** Conidia. H Vertical section through ascomata. **I** Conidiogenous cells. **J**, **K** Asci and pseudoparaphyses. **K**, **L** Ascospores. Bars: a–d=100 μm, e–g=10 μm, h=20 μm, i–l=10 μm

(PUL F29359 (ex-PURN4015); GenBank accessions: ITS–OQ418383; LSU–OQ418199). **Peru**, Ucayali, on urediniospores of *Uromyces yurimaguasensis*, 22 October 2016, M. Catherine Aime MCA6471. (PUL F29363 (ex-PURN16392); GenBank accessions: ITS–OQ418361; LSU–OQ418189). **United States of America**, Illinois, on urediniospores of *Melampsora* sp. infecting *Populus* sp., 22 September 2012, M. Catherine Aime MCA5030 (PUL 29,360 (ex-PURN6730); GenBank accessions: ITS– OQ418402, LSU–OQ418209, *tef1–O*Q743742); Georgia, on urediniospores of *Coleosporium helianthi* infecting *Silphium compositum*, 24 August 1977, Yoshitaka Ono, John McCain & Joe F. Hennen 10,185 (PUL F29357 (ex-PUR88233); GenBank accession: ITS–OQ418265).

Notes. The conidiomata and length of conidia of *S. melampsorinearum* are smaller than for any other described *Sphaerellopsis* species. However, the width of the conidia of *S. melampsorinearum* is similar to *S. anomala*, *S. flum*, and *S. macroconidialis*. *Sphaerellopsis melampsorinearum* is distributed worldwide and infects a range of rust species in the *Pucciniaceae*, *Phragmidiaceae*, *Melampsoraceae*, and *Coleosporiaceae*. However, 41 out of 55 hosts rust hosts of *S. melampsorinearum* belong to suborder *Melampsorineae*.

The sexual morph of *S. macroconidialis*

Sphaerellopsis macroconidialis is known from the asexual morph, and no sexual morph has been described. However, in this study, we recovered one specimen containing the sexual morph of *S. macroconidialis* (Fig. [3\)](#page-19-0). This specimen was found in Brazil, Rio de Janeiro, associated with telia of *Puccinia wedeliicola* infecting the host plant *Wedelia trichostephia*, collected on 7 May 1922, by E.W.D Holway, #1822, (PUL F29358 (ex-PURF8347)) (Fig. [3](#page-19-0)). The ITS sequence obtained from this specimen shared 100% identity (239/239 no gaps) with *S. macroconidialis* CBS 233.51 (GenBank Accession No. MH856836.1). Morphology of the sexual morph is as follows: ascomata developing on rust sori, up to 123 μm diam., brown in outer zone, cells textura parenchymatic, hyaline in inner part, erumpent, gregarious; loci subglobose to ampulliform. Pseudoparaphyses are fliform, septate, hyaline. Asci are numerous, 8-spored, bitunicate, cylindrical-clavate, short stipitate, 68.2–106.7×7.3–11.1 μm. Ascospores are irregularly biseriate, fusiform, hyaline to pale yellow, $17.2-23\times4.8-6.0$, 1-septate, slightly constricted at the septum, surrounded by a hyaline mucous sheath not easily perceived.

Fig. 3 Teleomorph of *S. macroconidialis* (PUL F29358). **A** Ascomata. **B** Vertical section through ascomata. **C** Ascospore. **D** Asci and pseudoparaphyses. **E** Asci and ascospores. Bars: a=200 μm, b, c=20 μm, d, e=10 μm

In‑vitro interaction test between *S. macroconidialis* **and** *P. polysora*

The interaction test of this study confirms the mycoparasitic strategy of *S. macroconidialis* on rust fungi. Five days after the co-cultivation, we observed hyphae of *S. macroconidialis* growing along the germ tubes of *P. polysora* and coiling around them (Fig.[4](#page-20-0)). The germ tubes of *P. polysora* measured 6.5 μm in diam., while those of *S. macroconidialis* measured 1.8 μm in diam., making them easy to distinguish. During the frst day after cocultivation, we observed the frst contact between germinated conidia of *S. macroconidialis* and germ tubes of urediniospores of *P. polysora*. Then, during the next four days, hyphae of *S. macroconidialis* started to grow over the urediniospores and their germ tubes, but without clear evidence of antagonism. However, on the ffth day of co-cultivation, *S. macroconidialis* began coiling around rust germ hyphae. Coils tightly encircled the germ tubes. However, the cell wall of the germ tubes was not disrupted. Such coils were not seen on *S. macroconidialis* hyphae inoculated alone. During the next six days, we did not notice any new sign of mycoparasitic mechanism against *P. polysora*. Nonetheless, on day 12, we noticed the formation of an appressorium attached to a urediniospore and turgor loss of a few germ tubes already coiled by *S. macroconidialis*. Loss of turgor was not seen on germinated urediniospores inoculated alone. After 12 days of observations, *S.* *macroconidialis* hyphae grew abundantly, and no other antagonistic events could be observed.

Discussion

Characterization studies of fungi with potential as BCAs are essential to the development of applied microbial biocontrol of plant diseases. Although the fungal genus *Sphaerellopsis* is commonly considered a rust mycoparasite due to its association with several rust species, studies of this genus are scarce, and its biocontrol potential is unknown. To evaluate *Sphaerellopsis* as a candidate BCA, we screened thousands of rust collections for the presence of *Sphaerellopsis* (Supp. Table 1). We generated sequence data for nearly 200 *Sphaerellopsis* specimens found on rust fungi collections at four loci, including the ITS, which has previously been shown as a good barcoding region for *Sphaerellopsis* species (Trakunyingcharoen et al. [2014](#page-25-13)) and three other loci—LSU, *rpb2*, and *tef1* for phylogenetic resolution (Fig. [1\)](#page-16-0). We then use these data to characterize various aspects of *Sphaerellopsis* biology including species diversity, geographic distribution, and host specifcity. Finally, we examined the interactions between *S. macroconidialis* and *Puccinia polysora* to infer initial infection strategies. These results can help determine the suitability of the application based on the BCA's location and mode of action.

Sphaerellopsis **species frequencies**

Sphaerellopsis macroconidialis and *S. paraphysata* were the most common species associated with rust fungi in this study. *S. macroconidialis* was found on species in ten rust genera, and *S. paraphysata* on 12 rust genera (Fig. [1](#page-16-0)). Contrary to expectations, the type species, *S. flum*, previously reported from 30 rust genera and 369 rust species (Kranz and Brandenburger [1981\)](#page-25-0), was not frequently collected. We found *S. flum* associated with only three rust genera: *Melampsora*, *Puccinia*, and *Tranzschelia.* As prior studies have shown, other species of *Sphaerellopsis* were frequently misidentifed as *S. flum* in the past (Trakunyingcharoen et al. [2014\)](#page-25-13), which could explain the discrepancy.

Host‑specifcity of *Pucciniales***‑infecting** *Sphaerellopsis* **species**

Prior studies have found host-specifcity in species of *Sphaerellopsis* (Liesebach and Zaspel [2004](#page-25-23)), Nischwitz et al. [2005\)](#page-25-24), Kajamuhan et al. [2015](#page-25-30)). In contrast, our study does not show any signature of host-specifcity for the *Sphaerellopsis* species analyzed (Fig. [1](#page-16-0)). For example, *S. macroconidialis* was found to be associated with species from several genera across the rust tree of life (Aime and McTaggart [2020\)](#page-24-24) including *Chaconia*, *Phakopsora*,

Fig. 4 Light micrographs of *Sphaerellopsis macroconidialis* interacting with germinated urediniospores of *Puccinia polysora in-vitro*. A─B Day one after co-cultivation. A Red arrows point to the urediniospore and its germ tube, and the green arrow points to S. macroconidialis*S. macroconidialis* hypha. B Black arrows point to the frst contact. C Negative control, hyphae of *S*. *macroconidialis* alone on day 12. D─E Day fve after co-cultivation. Hyphae of *S. macroconidialis* form coils and tightly encircle germ tubes of *P. polysora*. Black arrows point to dense coils. F Negative control, urediniospores, and germ tubes alone on day 12. G- J Day 12 after co-cultivation. G Dense coils around a germ tube of *P. polysora*. H An appressorium (arrow) attached to the urediniospore. I and J Loss of turgor of germ tube of *P. polysora*. Scale bars: A-B, D-J=20 μm, C=50 μm

Phragmidium, *Puccinia*, *Ravenelia*, and *Uropyxis*, among others (Fig. [1\)](#page-16-0). Similarly, *S. paraphysata* was associated with species from multiple rust genera including *Crossopsora*, *Kweilingia*, *Melampsora*, *Mikronegeria*, *Phakopsora*, *Puccinia*, *Sorataea*, and *Uromyces*, among others. *Sphaerellopsis flum* was recovered infecting hosts from three suborders of *Pucciniales*; and *S. melampsorinearum* was found on four families of *Pucciniales*, with the majority of hosts within the subphylum *Melampsorineae*.

Diferences between our and previous work are likely due to limited sampling in prior studies, which only examined *Sphaerellopsis* species associated with *Puccinia* species on grass hosts and *Melampsora* species on poplars. The dataset of Liesebach and Zaspel ([2004](#page-25-23)) and Nischwitz et al. ([2005](#page-25-24)) did not exceed 20 isolates, and the sampling of Kajamuhan et al. [\(2015\)](#page-25-30) comprised 82 isolates collected from *Puccinia* species. In contrast, our dataset covered 19 rust genera and 216 specimens. Although *S. paraphysata* and *S. macroconidialis* are predominantly associated with *Puccinia* specimens and *S. melampsorinearum* with *Melampsora* specimens, both are also associated with rust species from other genera. Likewise, our data do not show preference of *Sphaerellopsis* species for rusts at even the family rank. For example, *S. paraphysata* included rust hosts in the families *Melampsoraceae*, *Phakopsoraceae*, and *Pucciniaceae*, which span three diferent rust subphyla.

Interestingly, we found *Sphaerellopsis* species infecting rusts on many economically important hosts such as maize, wheat, and poplars. However, we did not fnd any *Sphaerellopsis* infecting *Hemileia vastatrix*, the causal agent of cofee leaf rust, despite examination of 42 specimens of this rust collected from throughout its range. Nor does *Hemileia vastatrix* appear on prior lists of *Sphaerellopsis* rust hosts (Kranz and Brandenburger [1981](#page-25-0)). Keener ([1934\)](#page-25-31) suggested that a possible limiting factor of *Sphaerellopsis* infection could be the type of sorus produced. *Hemileia* species, for example, form suprastomatal sori that protrude through the stoma like a "bouquet" (McCain [1983\)](#page-25-32) and do not tear the epidermis of the host plant. In addition to *Hemileia*, we also screened other rust specimens of the family *Zaghouaniaceae* that form suprastomatal sori; all were also free of *Sphaerellopsis* (Supplementary Table 1). Only one specimen of *Mikronegeria fagi* was found with associated black fruiting bodies resembling *Sphaerellopsis*. However, due to the scarcity and age of this particular specimen, we were unable to confrm it as a species of *Sphaerellop*sis. Thus, it remains inconclusive, but likely, that *Sphaerellopsis* species are restricted to infecting hosts that do not form suprastomatal sori.

Fig. 5 Origin/localities of the confrmed *Sphaerellopsis* specimens associated with rust fungi. The numerator above the bar indicates the number of *Sphaerellopsis* specimens collected per country; the denominator indicates the total rust specimens screened at PUR for the presence of *Sphaerellopsis* per country. Countries are colored by geographic regions

Geographic distribution

This study included *Sphaerellopsis* specimens associated with *Pucciniales* collected in 34 countries across the globe. Eight specimens were from Africa, 11 from Asia, three from Europe, 55 from North America, 115 from the Neotropics, and fve from Oceania (Fig. [5](#page-21-0); Table [3\)](#page-7-0). Our results suggest that *S. macroconidialis, S. paraphysata, S. flum*, and *S. melampsorinearum* have a cosmopolitan distribution and are adapted to diferent environmental conditions in both temperate and tropical regions (Fig. [6](#page-22-0)). However, *S. paraphysata* appears to be more abundant in the tropics. *Sphaerellopsis hakeae* may be an exception to this pattern, as both specimens of this species analyzed were from Australia, from where it was also described (Crous et al. [2016](#page-24-10)). The small sample size in our study limits any conclusive inferences, but it is worth noting that this species was not recovered even among the other Oceania specimens examined. Similarly, our study did not recover any additional specimens of *S. artemisiae* or *S. isthmospora*, both currently only known from China (Doilom et al. [2021;](#page-24-11) Phookamsak et al. [2019](#page-25-15)).

The dispersal biology of *Sphaerellopsis* species is not well studied. Kuhlman et al. ([1978](#page-25-33)) hypothesized that conidia of *Sphaerellopsis* did not disperse over long distances but rather spread locally via water splashing to nearby hosts. Our results would suggest that *Sphaerellopsis* could also be capable of long-distance dispersal. Rust spores can be dispersed through wind currents and may cross continents, and it is possible that the much smaller conidia of *Sphaerellopsis* species may be passively dispersed along with their much larger host spores. However, further studies in the dispersion mode of *Sphaerellopsis* are necessary to support this hypothesis.

Sexual morphs of *Sphaerellopsis*

Eudarluca has been considered the sexual morph of *Sphaerellopsis*. Because these are congeneric (Keener [1951](#page-25-4); Yuan et al. [1998](#page-25-5)), *Sphaerellopsis*, the older name, has priority for these fungi. The genus *Eudarluca* was erected in 1908 by Spegazzini to place "a new pyrenomycete" associated with the uredosori of an unknown rust, infecting *Canna* sp. in the Botanical Garden in São Paulo, Brazil (Spegazzini [1908](#page-25-3)). Spegazzini subsequently named *Eudarluca australis* as the type species of the genus. However, later in 1966, Eriksson combined several species with *E. australis* into *E. caricis* based on an overview of the taxonomy, nomenclature, and ecology of *E. caricis* (Eriksson 1966). The specific epithet "caricis" was kept based on the basionym *Sphaeria caricis* described by Fries in 1823 (Fries [1823\)](#page-24-3). The original specimen of *Sphaeria caricis* was collected from uredinia of a rust species on *Carex* spp. Since *Sphaerellopsis flum* was misapplied in the past as the most common species associated with rust fungi, it was thought to be congeneric with *E. caricis*

Fig. 6 Geographical distribution of *Sphaerellopsis* specimens examined in this study. Each circle represents one specimen, and each color represents one *Sphaerellopsis* species

(Yuan et al. [1998](#page-25-5)), a position that was not supported by the detailed analyses of Trakunyingcharoen et al. [\(2014](#page-25-13)). While we were able to identify the sexual morph of *S. macroconidialis* on telia of *Puccinia wedeliicola* infecting the host plant *Wedelia trichostephia*, and the sexual morph of *S. melampsorinearum* on uredinia of *Puccinia vernoniae-mollis* on the leaves of *Vernonia* sp., we were unsuccessful in locating a sexual morph of a *Sphaerellopsis* specimen that would be consistent with *E. caricis*, and thus the asexual morph and correct name for this species remains unknown.

The two sexual specimens of *Sphaerellopsis* described in this study (Figs. [2](#page-18-0) and [3\)](#page-19-0) were collected in the Neotropics. Eriksson ([1966](#page-24-0)), Ramakrishnan and Narasim-halu ([1941\)](#page-25-34), and Sebesta [\(1963\)](#page-25-35) found that high humidity, such as is found in the tropics, favored production of the sexual morph in *Sphaerellopsis*. Similarly, when Västerbotten found the teleomorphic state of *Sphaerellopsis* in the Summer of 1962 in northern Sweden, the locality was a hollow in a compost heap, a few meters from a rivulet giving microclimate conditions "similar to the tropics" (Eriksson [1966](#page-24-0)). The host plant may also play a role in development of the sexual morph of *Sphaerellopsis*. For example, Eriksson ([1966](#page-24-0)) noted that the sexual morph was most commonly found on plants in Poaceae and Cyperaceae due to their continuous growth and ability to form high-humidity microclimates. Although this hypothesis has not yet been experimentally tested, our fndings are consistent with a high humidity requirement for sexual morph development.

Sphaerellopsis **infection strategies and antagonism between** *S. macroconidialis* **and** *P. polysora*

The two earliest diverging species in our analyses, *S. artemisiae* and *S. isthmospora*, were not recovered on any rust samples in our study and are likely not associated with *Pucciniales* (Fig. [1\)](#page-16-0). It has been posited that several trophic strategies ranging from mycoparasitism to saprotrophism to plant pathogen may have evolved within *Sphaerellopsis* (e.g., Hulea [1939;](#page-24-7) Eriksson [1966](#page-24-0)). Nicolas and Villanueva [\(1965\)](#page-25-36) posited that the anamorph of *Sphaerellopsis* species might be able to utilize a large number of carbon compounds; Eriksson ([1966](#page-24-0)) hypothesized that *Sphaerellopsis* species might feed on plant tissue but that other factors, such as specifc compounds secreted from the rust, might be required for *Sphaerellopsis* to develop its fruiting bodies. Our data would support a hypothesis of an original plant-associated trophic strategy for members of this genus, that later transitioned to a mycoparasitic strategy on plant pathogenic rusts.

This study confirms *S. macroconidialis* as a mycoparasite of rust fungi. Coiling and appressorium formation by *S. macroconidialis* and turgor loss of germ tubes of *P. polysora* are evident signs of antagonistic relationships between these two fungi (Fig. [4](#page-20-0)). Appressorium formation and coiling are the most common mechanisms of mycoparasites to attack their host pathogens.

For example, *Trichoderma harzianum* and *Trichoderma atroviride* show the same mechanism, coiling around its host, *Rhizoctonia solani*, and forming appressoria as an early event before hyphal damage (Benhamou and Chet [1993](#page-24-28); Benítez et al. [2004;](#page-24-29) Chet et al. [1981;](#page-24-30) Rocha-Ramírez et al. [2002\)](#page-25-37). Similarly, *Simplicillium lanosoniveum* and *Cladosporium tenuissimum* form appressoria and helixshaped hyphae around urediniospores of the soybean rust *Phakopsora pachyrhizi* (Ward et al. [2011](#page-25-38)), and aeciospores of the two-needle pine stem rusts *Cronartium faccidum*, and *Peridermium pini* (Moricca et al. [2001](#page-25-39)), respectively. *Sphaerellopsis paraphysata* has also been found coiling around urediniospores of *Puccinia substriata*, but appressorium formation was not seen in this study (Anandakumar et al. [2019\)](#page-24-14).

The formation of helix-shaped hyphae of mycoparasites around the structures of their fungal hosts is a phenomenon usually dependent on lectin recognition. Fungal lectins are carbohydrate-binding proteins located on the fungal surface, which play a role in the recognition and defense of other organisms (Lebreton et al. [2021\)](#page-25-40). Once the mycoparasite recognizes the lectins of the fungal host upon frst physical contact, the mycoparasite hyphae start coiling around the fungal host for colonization and further infection (Omann and Zeilinger [2010\)](#page-25-41). Thus, since *S. macroconidialis* was observed coiling around germ tubes of *P. polysora* on day fve after co-cultivation, genes coding for lectins-binding proteins might be upregulated during the frst four days. Many lectins have been identifed in flamentous fungi and yeasts (Lebreton et al. [2021\)](#page-25-40), but information on these proteins in rust fungi is scarce.

Although we observed appressorium formation by *S. macroconidialis* in the interaction test, these were rare. We only observed one appressorium-like structure attached to a urediniospore on day 12 of co-cultivation (Fig. 4 H). This appressorium was not formed over the germ pore of the urediniospore, and the spore showed no signs of turgor loss. Because we stopped our observations on day 12 due to the overgrowth of *S. macroconidialis* hyphae, it is impossible to know if the appressorium had any mycoparasitic efect on the rust spore. Appressorium formation was also not observed on *Sphaerellopsis paraphysata* infecting urediniospores of *P. substriata* previously (Anandakumar et al. [2019\)](#page-24-14). Given the late appearance of appressoria, *Sphaerellopsis* likely do not utilize these as the primary mode for penetrating rust fungi. In contrast, *Sphaerellopsis* species are likely to secrete lytic enzymes (e.g., chitinases, glucanases, and proteases) to infect host rusts once their hyphae coiled around rust structures. We noticed this efect on day 12, where some germ tubes of *P. polysora* lost turgor (Fig. [4](#page-20-0) I, J). Although we did not conduct studies to detect

enzymatic secretion, our experimental design may be helpful for future secretome analyses.

Conclusion

In this study we attempted to fill some of the knowledge gaps surrounding *Sphaerellopsis*, with emphasis on obtaining data that would help to evaluate species as potential biological control agents for diseases caused by rust fungi. We demonstrate that *Sphaerellopsis* species are widespread and often incidentally co-collected with their rust hosts. Therefore, herbarium specimens may provide a rich source of data about these fungi. Also, *Sphaerellopsis* species do not appear to be specific to their rust hosts, in general, although there is a signal that some species may be climatically adapted. One new species recovered from herbarium specimens was described, *S. melampsorinearum,* and the sexual morph of *S. macroconidialis* was characterized. Finally, we confirmed that mycoparasitic strategy of *S. macroconidialis* on *P. polysora*.

Abbreviations

Supplementary Information

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Adherence to national and international regulations

All necessary permits were obtained for the feld trips to Peru and Puerto Rico.

Authors' contributions

PAGZ conceived the study, performed wet lab and greenhouse procedures, data collection, data analyses, drafted and edited the manuscript; JRDV performed data collection, data analyses, and helped edit the manuscript; SM and CORC performed wet lab and greenhouse procedures, and helped edit the manuscript; MCA conceived the study, performed data analysis, edited, and wrote portions of the manuscript. All authors read and approved the fnal manuscript.

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Availability of data and materials

All data generated or analyzed during this study are included in this published article [and its supplementary information fles].

Declarations

Ethics approval and consent to participate Not applicable

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹ Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN, USA. ² Grupo de Investigación en Fitopatología y Micología, Instituto de Investigación para el Desarrollo Sustentable de Ceja de Selva, Universidad Nacional Toribio Rodríguez de Amazonas, Chachapoyas, Amazonas, Peru.

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