



***Phragmotrichum chailletii* has a sibling species in North America**

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With 2 figures and 1 table

Abstract: The phylogenetic placement of *Phragmotrichum chailletii* in Melanommataceae (Pleosporales) is re-evaluated and its phylogeographic structure is assessed based on a large number of specimens from Europe and North America together with a four-gene (ITS, LSU, *RPB2*, *EF1- α*) dataset. Morphologically, all collections produced identical conidiomata and conidia on the same substrate, which is spruce cones on litter. Their fruiting season was also similar as they originated from early spring soon after snow melts at a similar range of elevation. However, all isolates collected in Canada and associated with *Picea* species native to North America, clustered together in a clade separate from collections made in Europe and occurring on host species native to central-eastern Europe. A sibling species, *Ph. thornhilliae*, is introduced to accommodate this group of isolates using molecular and phylogeographic evidence. One specimen belonging to the novel species was also collected in Switzerland. Possible scenarios to explain this anomaly are provided and the most likely explanation is an accidental, human mediated introduction.

Keywords: allopatry; anamorphic; cryptic speciation; phenotypic differences

Introduction

Phragmotrichum chailletii Kunze is a noteworthy anamorphic coelomycetous species with a conspicuous morphology. It produces distinct black stromatic conidiomata on dead cones of *Picea* species (rarely also on other conifers). These sporodochia-like fructifications may be individual or gregarious, forming large patches on the surface of the cone scales and having pale brown, catenate dictyoenidium formed inside and exposed through

the rupture of the upper and lateral walls of the fructifications. Nine species were historically described in *Phragmotrichum* Kunze until Sutton and Pirozynski (1965) revised and synonymised some of them based on study of authenticated material as well as reduced three monotypic genera *Taeniophora* Karst., *Alysisporium* Peyron. and *Seiridiella* Karst. to synonyms with *Phragmotrichum*. Sutton & Pirozynski (1965) and Sutton & Sandhu (1969) considered the type of conidiomata and the basipetal development and maturation of conidia in the chains important for generic delimitation. They also combined the phragmosporous *Trimmatostroma pini* W.B.Cooke into *Phragmotrichum* and accepted only four species: *Ph. chailletii*, *Ph. pini* (W.B. Cooke) B. Sutton & D.K. Sandhu, *Ph. rivoclarinum* (Peyronel) B. Sutton & Piroz and *Ph. quercinum* H. Hoffm. Two other taxa, *Ph. vassiljevae* Melnik and *Ph. andamanense* Bhat, W.B. Kendr. & Nag Raj, were added later and the genus currently comprises six species (Wijayawardene et al. 2016).

Due to its distinct morphology and common occurrence in temperate regions on old, empty seed cones of spruce from the previous year (still hanging or fallen off), *Ph. chailletii* has become a frequently collected and documented species. An online search in MyCoPortal (MyCoPortal 2023) shows a total of 228 records of the fungus associated with coniferous hosts in several countries of Europe, Canada and the USA. Hosts include mostly spruce (*Picea* spp.) and fir (*Abies* spp.) but less often the Douglas-fir [*Pseudotsuga menziesii* (Mirb.) Franco] or the European larch (*Larix decidua* Mill.) and very rarely the Scots pine (*Pinus sylvestris* L.). The fungus sometimes occurs on tree hosts outside their native range when planted in botanical gardens e.g. Lijiang spruce [*Picea likiangensis* (Franch.) E. Pritz.], a native of Bhutan and China (The Gymnosperm Database <https://www.conifers.org/index.php>). The IMI database (<http://www.herbimi.info/herbimi/home.htm>, accessed February 2023) contains 16 specimens from four European countries, Russia and Canada, all from native spruce species. Specimen IMI 24783 from the Philippines documents a rare occurrence in the tropics and most likely one associated with a planted and naturalized host tree (*P. abies*) outside its native range of temperate Europe. The virtual herbarium system JACQ (<https://www.jacq.org/#home>) also adds collections from Austria, Czech Republic and Germany. A search in Google Pictures also indicates > 1000 available photos of the fungus that document this species from further localities across Europe and also Canada.

When Kunze & Schmidt (1823) introduced *Phragmotrichum*, with *Ph. chailletii* as the type species, they noted that the shape of conidia, which they named rhombic, had no analogy among other fungal species known to them. Though very common and frequently collected, *Ph. chailletii* has long been overlooked in phylogenetic studies until Crous et al. (2020) and most recently Wijesinghe et al. (2023) revealed its placement within Melanommataceae G. Winter, a family which also includes *Petrakia* Syd. & P. Syd. (Jaklitsch & Voglmayr 2017). In both studies, since the holotype of *Ph. chailletii* was destroyed during World War II, Crous et al. (2020) designated a specimen collected on cones of *P. abies* in Hindelbank, Switzerland, as the neotype, not far from the holotype locality, Neuchâtel. phylogenies based on rDNA showed that *Ph. chailletii* clustered together with species of *Mycopappus* Redhead & G.P. White, *Pseudodidymella* C.Z. Wei, Y. Harada & Katum., *Xenostigmina* Crous and *Petrakia*, all plant pathogens having my-

copappus-like propagules in their life cycles. These genera, once forming a separate family Pseudodidymellaceae A. Hashim. & Kaz. Tanaka ([Hashimoto et al. 2017](#)), were reduced to synonyms with *Petrakia* by [Beenken et al. \(2020\)](#), who preferred to keep its original wide generic concept ([Jaklitsch & Voglmayr 2017](#)).

Since [Beenken et al. \(2020\)](#) focused only on pathogenic species, they left room for refining the phylogenetic relationships between *Ph. chailletii*, a remarkable saprotrophic species, with members of *Petrakia* that also produce dictyococonidia. The aim of our study was thus to refine the phylogenetic placement of *Ph. chailletii* within the recently revised Melanommataceae and to address its phylogeographic structure and potential cryptic taxa in view of the widely documented distribution of the fungus and its multiple hosts. In order to achieve this aim, we focused on fresh collections of *Ph. chailletii* in Europe and also on recently isolated strains from North America.

Materials and Methods

Strains were isolated from mature conidiomata on spruce cones freshly collected on the litter. Conidia were picked by a sterile surgical needle and transferred into Petri dishes with Malt Extract Agar (MEA). Pure cultures were maintained on Malt Extract Agar and Potato Carrot Agar. Additional strains were obtained from the culture collection of Agriculture and Agri-Food Canada (AAFC). Slides for microscopy were mounted in tap water, 3% KOH and Melzer reagent. Microscopic structures were examined and documented with differential interference contrast (Olympus BX-51 with digital camera, Quick Photo software, Olympus, Japan). Representative specimens were deposited in PRC (Herbarium of the Charles University, Czech Republic) and living strains in the Culture Collection of Fungi (CCF, Faculty of Science, Charles University, Czech Republic).

DNA was extracted from 2-weeks old colonies using a Zymo Research Fungal/Bacterial Kit (Zymo Research, Orange, USA). Nuclear rDNA containing the ITS1-5.8S-ITS2 and 28S regions was amplified with primer set ITS1F/NL4 ([Gardes & Bruns 1993](#), [White et al. 1990](#)), and fragments of genes encoding translation elongation factor 1 α (EF1- α) and RNA polymerase II second largest subunit (RPB2) were amplified with primer sets 983F/2218R ([Rehner & Buckley 2005](#)) and RPB2-5F/fRPB2-7cR ([Liu et al. 1999](#)), respectively. The PCR products were viewed by means of electrophoresis on 1% (w/v) TAE agarose gel, stained with ethidium bromide. The PCR products were purified with the AMPure XP beads (Beckman Coulter, USA). Both strands of the PCR fragments were sequenced with the primers used for amplification in the Sequencing Laboratory of the Faculty of Science, Charles University, Czech Republic. All sequences were deposited in the GenBank (Table 1).

Our dataset was built based on that assembled by [Beenken et al. \(2020\)](#) (Electronic Supplementary Materials 1). Alignment was performed using the MAFFT algorithm implemented in Geneious 6.1.5 software and manually edited in the same software (Electronic Supplementary Materials 2). Phylogenetic analyses were performed by Bayesian in-

Table 1. Living cultures included in this study, DNA regions sequenced and their GenBank accession numbers.

Species name	Voucher specimen or living strain	Country of origin	Host	ITS + LSU rDNA	RPB2	EF-1-α
<i>Phragmotrichum chailletii</i>	CCF 5759	Czech Republic	<i>Picea abies</i>	OQ919283	OQ884629	OQ884635
	CCF 6071	Czech Republic	<i>Picea abies</i>	OQ919286		
	PRC 9003	Czech Republic	<i>Picea abies</i>	OQ919285	OQ884625	OQ884637
	PRC 9004	Czech Republic	<i>Picea abies</i>	OQ919284	OQ884630	OQ884636
	PRC 8998	Czech Republic	<i>Picea abies</i>	OQ919288		
	PRC 9000	Czech Republic	<i>Picea abies</i>	OQ919287	OQ884633	
	PRC 9002	Czech Republic	<i>Picea abies</i>	OQ919289		
	PRC 7900	Switzerland	<i>Picea abies</i>	OQ919290	OQ884631	OQ884638
	PRC 9006	Germany	<i>Picea abies</i>	OQ919282	OQ884628	OQ884634
NK463		Switzerland	<i>Picea abies</i>	OQ919291		
PRC 5138		Switzerland	<i>Picea abies</i>	OQ919292		
PRC 7897		Germany	<i>Picea abies</i>	OQ919292		
PRC 7899		Switzerland	<i>Picea omorika</i>	OQ919294	OQ884640	
NK471		Switzerland	<i>Picea abies</i>	OQ919295	OQ884632	OQ884641
AAFC CHEM_J_2959		Canada	<i>Picea pungens</i>	OQ919298	OQ884624	
<i>Phragmotrichum thornhilliae</i>						
AAFC CHEM_J_2961		Canada	<i>Picea pungens</i>	OQ919299		
PRC 9001		Canada	<i>Picea glauca</i>	OQ919297	OQ884626	OQ884642
AAFC KAS6383		Canada	<i>Picea</i> sp.	OQ919300	OQ884623	
PRC 7898		Switzerland	<i>Picea abies</i>	OQ919296	OQ884627	OQ884643

ferent-cc using MrBayes version 3.2 (Ronquist et al. 2012) and by Maximum likelihood analysis using the RAxML Web Server version 7.7.1 (Stamatakis et al. 2008) accessed through the CIPRES Science Gateway (Miller et al. 2010). For the Bayesian analysis, the best-fit models were determined using PartitionFinder 2 (Lanfear et al. 2016). Two independent runs of 9,000,000 generations were ran with sampling every 1000th generation and the first 25% of samples discarded as burn-in. Posterior probabilities (PP) were used as Bayesian branch support for consensus trees. The average standard deviation of split frequencies estimating convergence reached the level of 0.004 at the end of the analysis.

Results

Combination of two rDNA markers and two coding single copy genes revealed that our collections identified as *Phragmotrichum chailletii* formed a well-supported clade sister to three members of the genus *Seifertia* (Fig. 1). Within *Ph. chailletii*, two fully supported subclades were well differentiated. One of them included European collections that had identical ITS and LSU rDNA with those originating from strain CBS144994 (MN313812 and MN317293, respectively), the neotype of *Ph. chailletii* designated by Crous et al. (2020). The other clade includes all collections from North America together with one specimen from Switzerland (PRC 7898). In this case they differed in five and six bp of their ITS and LSU sequences, respectively, compared to sequences obtained from the neotype. One transversion (A/G) was present also in a 13 bp long intron in the ITS rDNA that was distinct for all *Phragmotrichum* sequences.

Taxonomy

Phragmotrichum thornhilliae Koukol & G. Delgado, sp. nov.

(Fig. 2)

Mycobank Accession Number: MB 848350

Diagnosis: Similar to *Phragmotrichum chailletii* in conidial size and morphology, but differing in DNA sequence data; in ITS1 rDNA substitutions at bases: 56 (C/T), 79 (C/T) and 104 (G/A), in ITS2 rDNA at bases: 22 (C/T) and 46 (T/C); in LSU rDNA at bases: 50 (G/A), 69 (C/T), 443 (C/T), 485 (T/C), 504 (T/C) and 521 (G/A), and in host association; occurring mainly on *Picea pungens* and *Picea glauca*.

Description: Conidiomata solitary or gregarious, sometimes confluent, globose, elongated or somewhat irregular in shape, black, subepidermal and erumpent, the conidial mass is exposed after the cracking and rupture of the upper and lateral, dark brown to blackish brown, glistening walls. *Conidiogenous* cells holothallic, terminal, producing basipetal chains of conidia. *Conidia* broadly fusiform to broadly ellipsoidal, straight or flexuous, muriform, smooth, yellowish-brown to brown, 30–50 × 12–19.5 µm, bearing 3–4 short median and lateral appendages, 3–4 µm long, catenate, formed in unbranched



chains of up to six conidia, with pale basal conical cell, up to 13 µm long and 3.5–4 µm wide.

Colonies on MEA after 7 days moderately fast-growing reaching (20) 24–28 mm diam., cottony, circular, white, slightly depressed around the centre, margin entire, reverse off-white.

Type: Canada, Ontario, Peterborough Co., Havelock, 1903 Line Belmont, 44°27'25.900" N, 77°47'52.000" W, 198 m a.s.l., on cone scales of *Picea glauca*, June 16th 2017, leg. J. Thornhill, (PRC 9001 – **holotype**)

Ex-type living strain CCF 7005. GenBank OQ919297 (ITS + LSU rDNA), OQ884626 (RPB2), OQ884642 (EF1- α)

Other specimens examined: Same as holotype, Mar 14th 2016, leg. J. Thornhill (BPI 925131); Ontario, Ottawa, Dominion Arboretum, 45°23'31.641" N, 75°42'22.013" W, 82 m a.s.l., on a cone of *Picea pungens*, 26 Apr 2015, leg. J. Mack (AAFC CHEM_JM_2959); ibid., Carleton University, 45°23'0.215" N, 75°41'57.804" W, 80 a.s.l., on a cone of *P. pungens*, 26 Apr 2015, leg. J. Mack (AAFC CHEM_JM_2961); Quebec, Montreal, on a cone of *Picea* sp., Apr 2015, leg. unknown. (AAFC KAS 6383). Switzerland, Ticino, Leventina, Airolo, 46°31'37.992" N, 8°35'56.40" E, 1160 m a.s.l., on a cone of *P. abies* on litter, 10 May 2019, leg. L. Beenken (PRC 7898).

Etymology: Referring to Jan Thornhill, amateur mycologist, who documented this species on her blog and eagerly shared her specimens for research.

Known distribution: This fungus is known from Canada and Switzerland.

Remarks: Morphologically, the newly described species *Ph. thornhilliae* cannot be distinguished from *Ph. chailletii*. It produces identical conidiomata and conidia on the same substrate which is spruce cones on litter. The fruiting season is also similar for both species: collections of *Ph. thornhilliae* and *Ph. chailletii* originate from (early) spring soon after snow melts and come from similar range of elevation (80–1160 and 446–1156 m a.s.l., respectively). However, the spruce host species and geographical region differ between them. The native range of *Ph. thornhilliae* hosts, *Picea glauca* and *P. pungens*, is Canada and the northern or western montane areas of the United States. In contrast, *P. abies* and *P. omorika* the hosts of *Ph. chailletii*, are native of central-eastern Europe (The Gymnosperm Database 2023).

Fig. 1. Phylogenetic hypothesis showing the placement of *Phragmotrichum chailletii* and *Ph. thornhilliae* based on combined analysis of ITS+LSU rDNA, RPB2 and EF1- α sequences. Numbers above branches represent ML bootstrap support values (BS>95), thickened lines at branches indicate PP>0.95. Countries of origin are represented by codes, specimens in bold represent neotype and holotype of *Ph. chailletii* and *Ph. thornhilliae*, respectively.

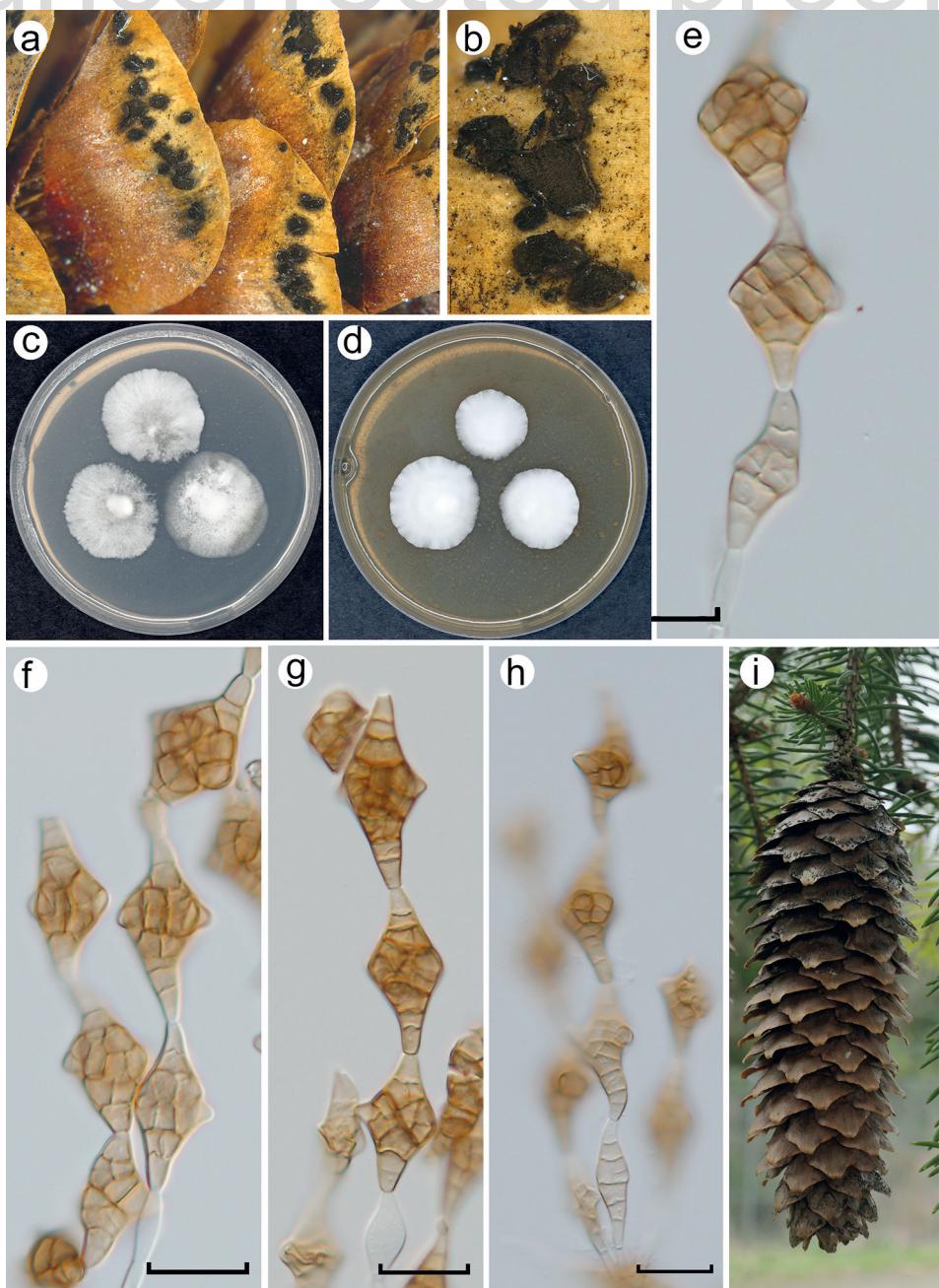


Fig. 2. *Phragmotrichum thornhilliae* (PRC 9001, holotype, a-h) and *Ph. chailletii* (PRC 5138, i). a-b) detail of conidiomata on the cone scales, c) colony on PCA and d) on MEA after 7 days, e-h) conidial chains including conidiogenous cell and immature conidia, i) dead cone with *Ph. chailletii* still on the tree with numerous conidiomata, Scale bars = 20 μm .

Phragmotrichum chailletii Kunze, in Kunze & Schmidt, Mykologische Hefte (Leipzig) 2: 84, 1823.

Specimens examined: Austria, Kleinwalsertal, Waldstück hinter dem Marburger-Haus (Wäldelestrasse) ca. 1156 m a.s.l., on a cone of *P. abies* on the litter, 29 Sep 2013, leg. H. Lotz-Winter, HLW 12 A-290913 (PRC 9005).

Czech Republic. Northern Bohemia. Bohemian Switzerland NP, Křídelní stěna, 50°53'1.091" N, 14°18'3.788" E, 466 m a.s.l., on a cone of *P. abies* on the litter, Feb 26th 2018, leg. Z. Palice & P. Uhlík (living culture CCF 6071); Western Bohemia, Abertamy, Hřebečná, forest margin, 150 m east from the village, 50°22'48.909" N 12°49'49.241" E, 884 m a.s.l., on a cone of *P. abies* on the litter, 29 Apr 2017, leg. O. Koukol, OK309 (PRC 3989, living culture CCF5759); Northern Bohemia, Jizerské hory Mts., NW slope of Oldřichovský Špičák Mt. (green tourist path), 15°4.22532' N 50°51.95548' E, 580 m a.s.l., on a cone of *P. abies* on the litter, 08 Apr 2018, leg. O. Kubátová, OK321 (PRC 9004); Northern Bohemia, Jizerské hory Mts., valley Bílý Štolpich (under Bílá kuchyně cross-road), 15°9.31758' N 50°51.03573' E, 770 m a.s.l., on a cone of *P. abies* on the litter, 08 Apr 2018, leg. A. Kubátová, OK322 (PRC 9003); Northern Bohemia, Krkonoše Mts., between Medvedi koleno road curve and Patejdlova bouda cottage, 50°45'4.900" N 15°35'45.600" E, 894 m a.s.l., on a cone of *P. abies* on the litter, 09 Apr 2018, leg. M. Vinkler, OK323, (PRC 9000). ibid. OK324 (PRC 8998, CCF6072), ibid. OK325 (PRC 8999); Western Bohemia, Krušné hory Mts., Jáchymov, SW slope of Klínovec Mt., next to the lower station of ski-lift, 50°23'8.767" N 12°56'30.608" E, 755 m a.s.l., on a cone of *P. abies* on the litter, 17 March 2019, leg. O. Koukol, OK348 (PRC 9002).

Germany, Bavaria, München, Allacher Forst, 48°12'18.576" N 11°28'19.164" E, 500 m a.s.l., on a cone of *P. abies* on the litter, 22 Apr 2019, leg. L. Beenken, OK364 (PRC 7897); Baden-Württemberg, Bernsteinweg, Black Forest Nationalpark, 48°40'27.264" N, 8°14'7.332" E, 750 m a.s.l., on a cone of *P. abies* on the litter, 08 Apr 2019, leg. F. Popa, FP; 422, (PRC 9006); Baden-Württemberg, hintere Bergwaldhütte, Black Forest National Park, 48°39'34.232" N, 8°14'34.411" E, 750 m a.s.l., on a cone of *P. abies* on the litter, 08 Apr 2019, leg. F. Popa, FP424, (PRC 9008); Hessen, Wiesbaden Naurod, Trockenbornweg nahe Kellerskopf (Taunus), ca. 446 m. a.s.l., on a cone of *P. abies* on the litter, 22 Jan 2014, leg. H. Lotz-Winter, HLW 3862, (PRC 9007).

Slovakia, Telgárt, Čeršla, above the playground, 48°50'41.968" N, 20°12'39.567" E, 1000 m a.s.l. on a cone of *P. abies* on the litter, 1 May 2018, leg. I. Černajová (without voucher).

Switzerland, Jura, Saignelégier, Patura de-Les Royes, 47°15'7.776" N 7°1'18.588" E, 967 m a.s.l., on a cone of *P. abies* on the litter, 06 Apr 2019, leg. E. Stöckli, OK365 (PRC 7900); Zurich, Winterthur, Frohbergpark, 47°29'46.320" N 8°43'21.000" E, 455" m a.s.l., on a cone of *P. abies* on the litter and still on the tree, 19 Apr 2019, leg. L. Beenken, OK363 (PRC 5138); Birmensdorf, 47°21'46.728" N, 8°27'17.928" E, 545 m a.s.l., 18 Apr 2019, leg. L. Beenken (living culture NK463); Ticino, Leventina, Airolo, 46°31'40.440" N 8°35'56.256" E, 1160 m a.s.l., on a cone of *P. omorika* on the litter, 10 May 2019, leg. L. Beenken, OK359 (PRC 7899); Grisons, San Bernardino, Pian San Giacomo,

46°25'17.220" N, 9°13'40.332" E, 1210 m a.s.l., on a cone of *P. abies* on the litter, 10 May 2019, leg. L. Beenken (culture NK471).

Discussion

Cryptic speciation and geographical distribution

Cryptic species are generally understood as species that are morphologically very similar, even indistinguishable, but may be differentiated only based on molecular data (Queloz et al. 2011). Identical morphology, however, can be retained after allopatric divergence and limited gene flow among populations eventually gives rise to two sibling species with different life histories and thus distinct phenotypic differences. Differentiation of morphologically identical species may be assisted with different hosts in the case of pathogens or other types of symbionts (Sochorová et al. 2019). Even for saprotrophs, one should be cautious with the application of a name based solely on morphological characteristics when further phenotypic data exist. Martinović et al. (2016) revealed several distinct lineages within *Desmazierella acicola* Lib. that did not differ in the morphology of the anamorph but differed in their pine host species and geographical regions.

Huge geographical barriers typically allow such divergence and one should always be suspicious when European names are applied to morphologically identical collections in North America (Nguyen et al. 2013). Numerous examples of intercontinental divergence were already reported for presumed cosmopolitan, pantropical or pantropical species of agarics and polypores (Hughes & Petersen 2015, Oliveira et al. 2022). In these fungal groups, supporting evidence for the interpretation of inter- and intraspecific variability was derived also from mating tests and dikaryotization, which is however not possible in asexual ascomycetes. Also, *Phragmotrichum chailletii* was considered to be a widespread and conspicuous species that may be easily identified based on the substrate (spruce cones in the litter) and distinctly catenate dictyocnidia. However, application of this name to collections from North America on cones of local spruce species was obviously erroneous. Distant region and different host species agree with the observed genetic distances and imply that the two morphologically indistinguishable groups actually represent two different species. Rather surprisingly, we recorded *Ph. thornhilliae* also in Europe and one of our collections on a cone of *P. abies* from Airolo (Switzerland) turned out to belong to this newly described species. Two potential scenarios may explain this anomaly: 1) the two species developed in Europe sympatrically and only one of them was introduced to North America, where it established association with local spruce species; or 2) the two species developed allopatrically in North America and Europe in association with local species and the single record of *Ph. thornhilliae* in Europe is an accidental, most probably human mediated introduction. With the intensity of global traffic and widespread occurrence of natural spruce forests and artificial plantations, the second scenario seems to be more likely. A similar pattern was recorded by Hughes & Petersen (2015), who

analysed multiple collections of *Gymnopus confluens* (Pers.) Antonín, Halling & Noordel. from Europe and Northern America. Analysis of both ITS and LSU rDNA indicated two distinct clades reflecting the transatlantic disjunction with an exception in one specimen from California, USA, clustering within the European clade. [Hughes & Petersen \(2015\)](#) also concluded that this discrepancy was caused by human mediated transfer.

Search performed with ITS1 rDNA in the Global Fungi database ([Větrovský et al. 2020](#)) confirmed the presence of *Ph. chailletii* in Europe (six records from soils in Estonia), but did not retrieve any match with sequence of *Ph. thornhilliae*.

Ecology

Both *Ph. chailletii* and *Ph. thornhilliae* are mostly reported from spruce cones on the litter in early spring, but their conidiomata are present already on cones still hanging from the twigs (Fig. 2i). The infection pathway of young cones is thus most probably mediated via dictyococonidia that are dispersed by wind to young developing cones. Potential decomposing activity of both species on fallen cones during the rest of the season is unknown.

Phylogenetic relationships

When [Crous et al. \(2020\)](#) provided the phylogenetic placement of *Ph. chailletii* based on LSU rDNA, the neotype they selected clustered within Melanommataceae in a poorly supported clade consisting of several genera that were later synonymized by [Beenken et al. \(2020\)](#) in *Petrakia*. Our study thus provided the first placement of *Ph. chailletii* and *Ph. thornhilliae* based on a robust four-gene regions dataset. In our phylogeny, although the genus *Phragmotrichum* is placed close to *Petrakia*, the similarity of its conidia to those of *Petrakia echinata* is rather a consequence of a convergent adaptation than a sign of their relationship. The differences in conidiogenesis support that conidial morphology is not a synapomorphic characteristic of the two genera. Conidia of *Phragmotrichum* are born from holothallic conidiogenous cells, whereas those of *Petrakia* are produced from annellidic conidiogenous cells ([Li et al. 2016](#)). Additionally, the sister genus of *Phragmotrichum*, *Seifertia*, has different, unicellular conidia that are formed on synnemata ([Beenken et al. 2020](#)). The genera are also differentiated ecologically. *Seifertia* species are parasitic or saprophytic on *Rhododendron* species, whereas *Petrakia* species are leaf pathogens of broadleaf trees ([Beenken et al. 2020](#)).

After the very recent description of a new pathogen *Microstrobilinia castrans* [Beenken & Andr. Gross \(Beenken et al. 2023\)](#), *Ph. thornhilliae* is another species described from spruces documenting that novel taxa can be found also on intensively studied hosts and substrates.

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Elektronischer Supplement

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Table of contents – Electronic Supplementary Material (ESM)

Supplementary Materials 1: Species and sequences of ITS and LSU rDNA, RPB2 and EF1- α with their accession numbers that were obtained from GenBank and used to build the dataset.

Supplementary Materials 2: Alignment of dataset consisting of ITS and LSU rDNA, RPB2 and EF1- α sequences.