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Tsugacorticium kenaicum (Hymenochaetales, Basidiomycota), a new corticioid genus and species from Alaska

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Abstract: The new corticioid genus and species, *Tsugacorticium kenaicum* from Alaska, is described. Primarily found on attached, dead, corticate branches of mountain hemlock in the Kenai Peninsula, *T. kenaicum* is characterized by small, soft, white to yellow basidiomata, thickened subhymenium, much branched dendrohyphidia, and small globose to subglobose basidiospores. Although morphologically similar to *Dendrothele* (Agaricales) and *Dendrocorticium* (Corticiales), phylogenetic analyses of the nuclear large subunit ribosomal RNA gene place this taxon in the *Rickenellaceae* clade in the Hymenochaetales. *Tsugacorticium kenaicum* is described, illustrated, and compared to morphologically similar and phylogenetically related taxa.

Key words: Hymenochaetales, dendrohyphidia, suburniform basidia, *Tsuga mertensiana*

Introduction: There are over 250 species of wood-inhabiting fungi reported from Alaska. The majority of the species are basidiomycetes, but ascomycetes and slime molds are represented also (Laursen et al. 2005). Volk et al. (1994) compiled a list of 254 wood-inhabiting basidiomycete species from Alaska obtained from studies of their own collections as well as from the literature. One of the species they included was misidentified as *Dendrothele incrustans* (Lemke) Lemke which represents a new genus and species, *Tsugacorticium kenaicum*. *Tsugacorticium* is compared with morphologically similar corticioid genera.

Materials and methods:

Morphological studies. —Thin, freehand sections from basidiomata were mounted in 2% aqueous potassium hydroxide and 1% aqueous phloxine or Melzer's reagent (Kirk et al. 2001) and examined under an Olympus BH2 compound microscope. Drawings were made with a camera lucida attachment. Photomicrographs of the hymenium were taken with an Olympus DP10 camera attachment, and photographs of the basidiomata were taken with an Olympus DP12 camera on an Olympus SZH Stereomicroscope. Cyanophily of basidiospore and hyphal walls were observed in 0.1% cotton blue in 60% lactic acid (Kotlaba and Pouzar 1964, Singer 1986). Q values were obtained from dividing average length by width of at least 30 basidiospores (Kirk et al. 2001). Color names are from Kornerup and Wanscher (1978) whereas capitalized name follow Ridgway (1912). Herbarium designations follow that of Thiers (2011, continuously updated).

Taxon selection and phylogenetic analyses. — Initial phylogenetic analysis placed *Tsugacorticium kenaicum* in the *Rickenellaceae* clade of the Hymenochaetales (Goranova 2003). Taxa included in the phylogenetic analyses were selected after reviewing Dentinger and McLaughlin (2006), Larsson et al. (2006), and Miettinen and Larsson (2011). Sequences of the nuclear large subunit ribosomal RNA (LSUrRNA)

were obtained from Genbank. Current names used in the phylogenetic tree shown in Figure 1 are in boldface type, followed by the name from Genbank, if different, and Genbank accession number. Tentative generic names are enclosed by single quotation marks. The taxa chosen for the phylogenetic analysis were ***Alloclavaria purpurea*** B. Dentinger & D.J. McLaughlin DQ284900; ***Blasiphalia pseudogrisella*** (A. H. Sm.) Redhead/*Rickenella pseudogrisella* U66437; ***Contumyces rosellus*** (M.M. Moser) Redhead, Moncalvo, Vilgalys & Lutzoni/*Omphalina rosella* U66452; ***Ginnsia viticola*** (Schwein.) Sheng H. Wu & Hallenb./*Phanerochaete viticola* GQ470670, GQ470671, GB845003; ***Globulicium hiemale*** (Laurila) Hjortstam DQ873595; **'*Hyphoderma*' capitatum** J. Erikss. & Å. Strid DQ677491; **'*Hyphoderma*' orphanellum** (Bourdot & Galzin) Donk DQ677500; ***Muscinupta laevis*** (Fr.) Redhead/*Cyphellostereum laeve* EU118621, AY745705; ***Peniophorella praetermissa*** (P. Karst.) K.H. Larss./*Hyphoderma praetermissum* DQ873597; ***Peniophorella tsugae*** (Burt) K.H. Larss./*Hyphoderma tsugae* DQ677505; **'*Phlebia*' georgica** Parmasto DQ873645; ***Resinicium bicolor*** (Alb. & Schwein.) Parmasto AY586709; **'*Resinicium*' chirichahuaense** Gilb. & Budington/*Phlebia chirichahuaensis* DQ863692; ***Resinicium friabile*** Hjortstam & Melo DQ863690; **'*Resinicium*' furfuraceum** (Bres.) Parmasto DQ873648; **'*Resinicium*' furfurellum** (Bres.) Nakasone/*Skvortzovia furfurella* DQ873649; **'*Resinicium*' meridionale** (Burds. & Nakasone) Nakasone AY293197; **'*Resinicium*' pinicola** (J. Erikss.) J. Erikss. & Hjortstam/*Mycoacia pinicola* DQ873637; ***Resinicium saccharicola*** (Burt) Nakasone DQ863691; ***Rickenella fibula*** (Bull.) Raithehl. AY700195; ***Rickenella mellea*** (Singer & Cléménçon) Lamoure U66438; ***Sidera lunata*** (Romell ex Bourdot & Galzin) K.H. Larss./*Athelopsis lunata* DQ873593; ***Sphagnomphalia brevibasidiata*** (Singer)

Redhead, Moncalvo, Vilgalys & Lutzoni/*Omphalina brevibasidiata* U66441; ***Tsugacorticium kenaicum*** Nakasone & Burds. JN368224, JN368221 holotype. ***Antrodia albida*** (Fr.) Donk AY515348 and ***Ganoderma adspersum*** (Schulzer) Donk AM269829 were selected as the outgroup taxa.

Thirty LSUrRNA sequences were aligned using ClustalW in MEGA version 5 (Tamura et al. 2011) then manually adjusted. Phylogenetic analysis used the maximum likelihood (ML) method, based on the Tamura-Nei model (Tamura and Nei 1993) using the close neighbor interchange (CNI) algorithm (Nei and Kumar 2000), was conducted in MEGA5. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method (Gascuel 1997) with Markov cluster (MCL) distance matrix was used. Uniform evolutionary rate among sites was assumed. All positions containing gaps and missing data were eliminated from the analysis. Five hundred ML bootstrap replicates were conducted with the parameters unchanged. Maximum parsimony (MP) analyses were also conducted using CNI algorithm in which the initial trees were obtained with random addition of sequences (10 replicates).

Results:

Phylogenetic analyses. —Sequences of the 5'-end of the LSUrRNA gene were fairly easily aligned although a number of gaps were required. The full alignment was 947 base pairs in length with 264 variable and 163 parsimony informative positions. In the ML and MP analyses, all positions containing gaps and missing data were eliminated which resulted in a total of 537 positions in the final dataset. In both analyses, *T. kenaicum* did not show a strong phylogenetic relationship to any represented taxon. The ML tree with the highest log likelihood (-3335.2059) is shown in Figure 1. In this tree *T. kenaicum* and

Ginnsia viticola are paired in a weakly supported clade. In the MP analysis, 8 most parsimonious trees were recovered with a consistency index of 45.70%, retention index of 55.68%, and composite index of 25.44%. In the strict consensus MP tree, *T. kenaicum* did not cluster with any taxa; filled in circles on branches in Figure 1 indicate groups that were present in the strict consensus. The MP bootstrap consensus tree showed *T. kenaicum* in a weakly supported clade (27% frequency) with *G. viticola*.

Tsugacorticium Nakasone & Burds., *gen. nov.*

MycoBank No. MB561955

Basidioma effusum, adnatum, molle, laeve, margine distincto abrupto. Systema hypharum monomiticum, hyphae generativae fibulatae. Subhymenium constatum ex hyphis et dendrohyphidiis. Dendrohyphidia filamentosa vel ramosa, laevia. Cystidia adsunt. Basidia suburniformis elongata, pedunculo distincto, 4-sterigmatibus. Basidiosporae globosae vel subglobosae, tenuitunicatae, hyalinae, laeves, acyanophilae, inamyloideae.

Type species: *Tsugacorticium kenaicum* Nakasone & Burds.

Basidioma effuse, adnate, soft, smooth, with distinct, abrupt margin. Hyphal system monomitric with clamped generative hyphae. Subhymenium thickening, composed of hyphae and dendrohyphidia. Dendrohyphidia filamentous to frequently branched, smooth. Cystidia present. Basidia suburniform, elongate, with a distinct stalk, 4-sterigmate. Basidiospores globose to subglobose with thin walls, hyaline, smooth, acyanophilous, inamyloid.

The most striking features of *Tsugacorticium* are the soft textured basidioma, elongate, stalked suburniform basidia bearing subglobose to globose basidiospores, and large, smooth, branched dendrohyphidia. Also striking is the

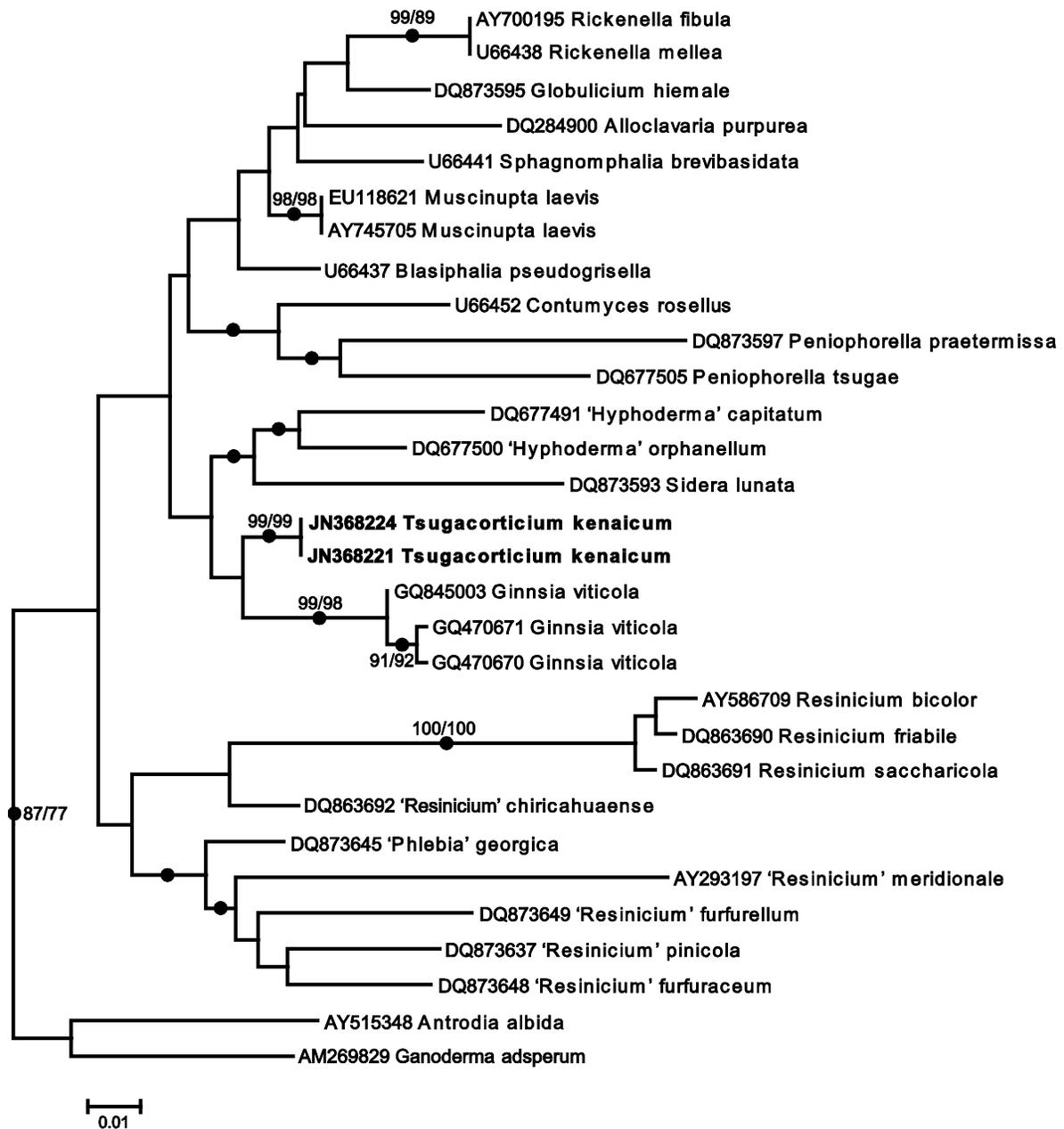


Fig. 1. Phylogenetic placement of *Tsugacorticium kenaicum* in the *Rickenellaceae* clade based on maximum likelihood (ML) and maximum parsimony (MP) analyses of the LSU rRNA gene sequences. This is the optimal tree, drawn to scale, obtained with ML with branch lengths measured in the number of substitutions per site. Filled circles on the branches indicate groups that are also present in the strict consensus of eight equally most parsimonious trees. Numbers along branches before the slash marks are frequencies from 500 ML bootstrap analyses and after the slash marks from 10000 MP bootstrap analyses. Bootstrap frequencies below 70% are not shown.

Table 1. Comparison of *Tsugacorticium* and morphologically similar genera.

Genus Order	<i>Tsugacorticium</i> Hymenochaetales	<i>Dendrothele</i> Agaricales	<i>Dendrocorticium</i> Corticales	<i>Corticium</i> Corticales	<i>Dentocorticium</i> Corticiaceae s.l.	<i>Leptocorticium</i> Corticiaceae s.l.
Character						
Basidioma texture	soft	soft to ceraceous	firm, subceraceous to ceraceous	soft, tomentose	soft to firm	soft, fragile
Subhymenium	much thickened	slightly thickened	slightly thickened	much thickened	slightly thickened	slightly thickened
Basidia	suburniform stalked	suburniform ± stalked	cylindrical to tubular with basal swelling	cylindrical with thick-walled probasidia	clavate to cylindrical	cylindrical, subclavate, or suburniform
Basidiospore walls	thin ± cyanophilous	slightly thick cyanophilous	thin acyanophilous	thin acyanophilous	thin acyanophilous	thin to slightly thick acyanophilous
Cystidia	present	present	none	none	none	present
Dendrohyphidia	smooth	encrusted	encrusted	encrusted	encrusted	encrusted
Substrate	bark of dead, attached and fallen branches of gymnosperms	bark of living angiosperms and gymnosperms	bark and wood of dead angiosperms	bark and wood of dead, attached angiosperm branches	bark and wood of dead angiosperms	fern petioles, woody monocot stems, rarely wood of dead angiosperms

thickened subhymenium that constitutes most of the context and is composed primarily of collapsed, deteriorated hymenial elements. At first glance, it appears that *Tsugacorticium* is morphologically similar to *Dendrothele* Höhn. & Litsch. (Agaricales), *Dendrocorticium* M.J. Larsen & Gilb. (Corticiales), *Corticium* Pers. (Corticales), *Dentocorticium* (Parmasto) M.J. Larsen & Gilb. (Corticaceae s.l.), and *Leptocorticium* Hjortstam & Ryvarden (Corticaceae s.l.). Closer examination, however, reveals a number of small, but significant differences among these genera; see Table 1 for a summary.

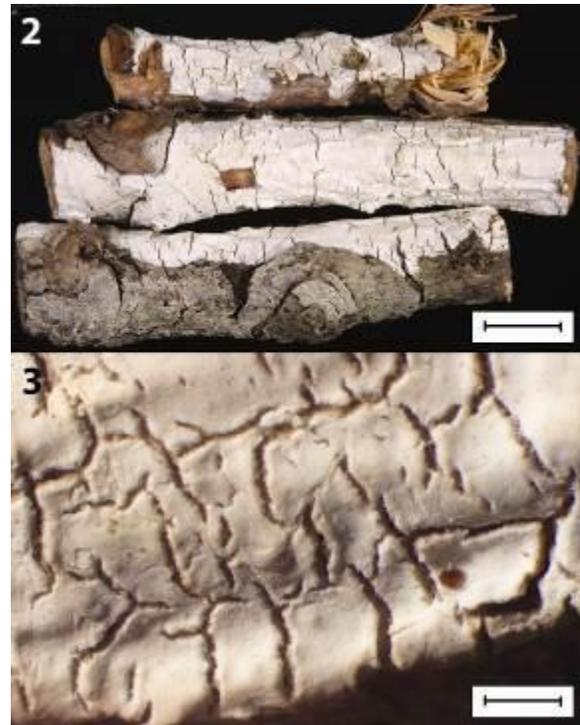
Tsugacorticium kenaicum Nakasone & Burds., *sp. nov.* Figs. 2-6

MycoBank No. MB561956

Basidioma effusum adnatum molle laeve, margine distincto abrupto. Systema hypharum monomiticum, hyphae generativae fibulatae. Subhymenium spissescens, constatum ex hyphis et dendrohyphidiis. Dendrohyphidia filamentosa vel ramosa, abundantia vel rara, 30–50 × 2–5 μm, fibulata at basim, laevia. Cystidia subfusiformia vel cylindrica, 15–33 × 4.5–6 μm, fibulata at basim. Basidia suburniformis elongata, pedunculo distincto, 32–50 × 6–8 μm, fibulata at basim, 4-sterigmatibus. Basidiosporae globosae vel subglobosae interdum compressae, 5–7 × 4.5–6.5 μm, Q = 1.1, tenuitunicatae, hyalinae, laeves, acyanophilae, inamyloideae.

Holotype — United States. Alaska, Kenai Peninsula, Golden Fin Trail 60°15.4'N 149°21.4'W, on bark of fallen *Tsuga heterophylla* Sarg., 28 July 1998, H. H. Burdsall, Jr., HHB17333 (BPI; isotype CFMR).

Etymology. Named after the Kenai Peninsula of Alaska.



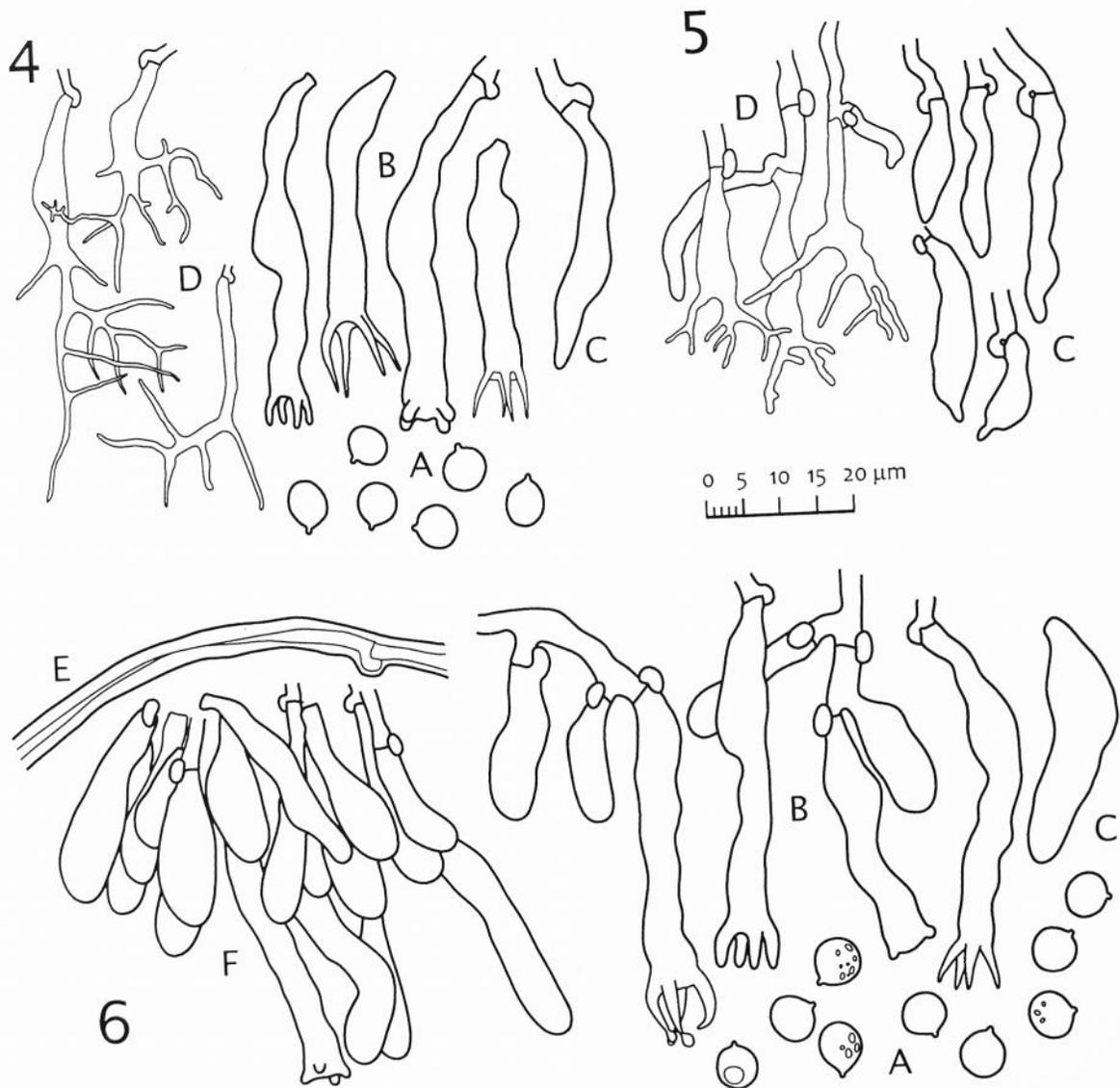
Figs. 2-3. Basidiomata of *Tsugacorticium kenaicum*, holotype, HHB17333. **Fig. 2.** Basidiomata on corticate branches. Scale bar = 10 mm. **Fig. 3.** Close-up of rimose hymenial surface. Scale bar = 1 mm.

Basidioma resupinate, broadly effused, thin to moderately thick, 125–450 μm thick, soft.

Hymenial surface smooth, occasionally finely farinaceous or felty, white, yellowish white (4A2), pale yellow (4A3), greyish yellow (4B3), greyish orange (5B3), Cartridge Buff, or Ivory Yellow, sparsely to extensively rimose. **Margin** distinct, adnate, abrupt, rapidly thinning out, white.

Hyphal system monomitic with clamped generative hyphae. **Subiculum** a narrow, indistinct hyphal layer closely appressed to substrate, observed only at margins.

Subhymenium thickening, up to 400 μm thick, a dense to moderately dense tissue of partially agglutinated hyphae, embedded dendrohyphidia, and hyaline crystal clusters, in over-mature specimens hymenial elements collapsed, deteriorated to form a more open, lacunose trama; subhymenial hyphae 2.2–4(–4.5) μm diam, clamped, frequently branched, walls



Figs. 4-6. Line drawings of microscopic characters of *Tsugacorticium kenaicum*. Fig. 4. From holotype HHB 17333. Fig. 5. From HHB 17261. Fig. 6. From HHB 17262. A, basidiospores; B, basidia; C, cystidia; D, dendrohyphidia; E, subicular hypha; F, section through hymenium.

hyaline, thin to 1.5 μm thick, smooth.

Hymenium composed of dendrohyphidia, cystidia, and basidia. **Dendrohyphidia** abundant in young specimens to scarce in mature specimens, filamentous, unbranched to elaborately branched, 30–50 \times 2–5 μm , clamped

at base, walls hyaline, thin, smooth. **Cystidia** subfusiform, rarely cylindrical and strangled, 15–33 \times 4.5–6 μm , clamped at base, walls hyaline, thin, smooth. **Basidia** suburniform to cylindrical with basal swelling and median constriction, stalked, protruding in maturity,

(32–)35–45(–50) × 6–8 μm, clamped at base, walls hyaline, thin, occasionally slightly thickening near base, smooth, 4-sterigmate, sterigmata up to 15 × 2 μm. **Basidiospores** globose to subglobose, sometimes compressed, 5–6.5(–7) × (4.5–)5–6(–6.5) μm, average of three specimens 5.7–6.2 × 5.1–5.7 μm, Q = 1.1, usually filled with resinous materials, walls hyaline, thin, smooth, acyanophilous or occasionally weakly cyanophilous, not reacting in Melzer's reagent.

Habitat and distribution. Frequently on bark of dead branches attached to living *Tsuga mertensiana* Sarg., also on bark of fallen branches of *T. mertensiana*, *T. heterophylla*, and *Picea sitchensis* (Bong.) Carrière; known only from southeast Alaska.

Additional specimens examined, all at CFMR. UNITED STATES. Alaska, Girdwood, Virgin Creek, on *P. sitchensis*, 9 July 1990, H.H. Burdsall, Jr., HHB 13209. Kenai Peninsula, turnout at base of hill at south end of Turnagain Arm, across from Portage, on dead branch of living *T. mertensiana*, 5 July 1990, HHB 13122, HHB 13127, HHB 13129, HHB 13130, HHB 13136, HHB 13163; 29 July 1998, HHB 17347, HHB 17348. North of Summit Pass area, on down twigs of *T. mertensiana*, 27 July 1998, HHB 17262; on dead branches of living *T. mertensiana*, 27 July 1998, HHB 17261. 10 miles north of Seward, on *Tsuga* sapling, 27 July 1998, HHB 17315. Seward Highway at 12 mile post, on dead branches of living *T. mertensiana*, 15 September 1988, HHB 12482. Chugach National Forest, south end of Johnson Pass Trail, on dead branches of living *T. mertensiana*, 18 July 1990, HHB 13368, HHB 13370.

The most remarkable features of *Tsugacorticium kenaicum* are the soft textured basidioma, thick subhymenium, highly branched and smooth dendrohyphidia, elongate suburniform basidia, and small, globose to subglobose basidiospores. Its preference for attached, but dead, corticate

branches of living *Tsuga* and *Picea* trees in south-central Alaska is noteworthy also. The hymenial surface of fertile specimens is dense, even, and smooth. Microscopically, dendrohyphidia are scattered throughout a dense palisade of developing basidia, protruding mature basidia, and cystidia. In contrast, over-mature specimens have an irregular felty surface; dendrohyphidia are abundant but a distinct hymenial palisade is lacking although immature basidia embedded in the subhymenium may be present in some collections.

Previously, *T. kenaicum* was reported from Alaska as *D. incrustans* (Volk et al. 1994), however, the latter species has larger globose to broadly ellipsoid basidiospores (9–12 × 8–10 μm), encrusted dendrohyphidia, and lacks cystidia.

Discussion:

Molecular sequence analyses establish *Tsugacorticium* as a member of the *Rickenellaceae* in the Hymenochaetales, which includes an assemblage of morphologically diverse taxa (Larsson et al. 2006). *Tsugacorticium* does not appear to share any morphological traits with other species in the *Rickenellaceae*. In fact, its suburniform basidia are unique in the *Rickenellaceae*. In phylogenetic analyses, *Tsugacorticium* and *Ginnsia viticola*, more familiarly known as *Phanerochaete viticola* (Schwein.) Parmasto, are sometimes paired in a weakly supported clade. Despite their phylogenetic relatedness, *Ginnsia* and *Tsugacorticium* lack any obvious morphological similarities. Rather, *Tsugacorticium* appears to share more basidioma and microscopic features with *Dendrothele* (Agaricales), and to a lesser extent, *Dendrocorticium* (Corticiales), *Corticium* (Corticiales), *Dentocorticium* (Corticaceae s.l.) and *Leptocorticium* (Corticaceae s.l.), although these genera are in distantly related orders. Molecular phylogenetics continues to demonstrate its importance and singular value in advancing the systematics of corticioid fungi.

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