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Tassiloa, a new genus in the Teloschistaceae (lichenized ascomycetes)

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Kondratyuk, S. Y., Kärnefelt, I., Thell, A., Elix, J. A., Kim, J., Kondratiuk, A. S. & Hur, J.-S. 2015. *Tassiloa*, a new genus in the Teloschistaceae (lichenized ascomycetes). *Graphis Scripta* **27**(1–2): 22–26. Tartu. ISSN 0901-7593.

The new genus *Tassiloa*, proposed for the American *Caloplaca digitaurea*-group, is supported by phylogenetic analyses based on ITS and LSU nrDNA-sequences, and 12S SSU mtDNA-sequences. The genus is positioned in the *Catenarina*-clade in the subfamily Teloschistoideae of the family Teloschistaceae. The genus *Tassiloa* is described and compared with closely related genera. Two new combinations are proposed, *Tassiloa digitaurea* and *T. wetmorei*.

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Introduction

New species are continuously being discovered in the lichen family Teloschistaceae which now comprises more than 1000 species (e.g. Kondratyuk *et al*. 2013, Søchting *et al*. 2014). Molecular analyses have resulted in a completely revised taxonomy of the family, now divided in three subfamilies, Caloplacoidae, Teloschistoidae and Xanthorioidae, and includes more than 60 genera (Gaya *et al.* 2012, Arup *et al.* 2013, Kondratyuk *et al.* 2013, 2014a, b). The full taxonomy remains to be resolved since many of the more recently described genera will not be fully accepted until additional molecular evidence is available (Miadlikowska *et al.* 2014). *Caloplaca digitaurea* Søgaard, Søchting & Sancho is an example of a recently described species where molecular data were compared only with its closest relative, *C. wetmorei* Nimis, Poelt & Tretiach (Lumbsch *et al*. 2011). The isolated position of the strongly supported clade of these two species is proposed here as the new genus, *Tassiloa*.

Material and methods

The methods used for extraction, amplification and phylogenetic analyses are described in Kondratyuk *et al*. (2013, 2014a, b). Genomic DNA was obtained from fresh samples and herbarium specimens. Voucher specimens included in the phylogenetic analyses are indicated at each specimen in the phylogenetic tree (Fig. 1). The three regions targeted for this study are: 0.6 kb of the ITS1/ITS2 region using the primers ITS1 and ITS4 and the primer ITS1F, 0.8 kb of the 28S LSU using the primer LR5, and 0.8 kb of 12S SSU mtDNA using the primers mtSSU1-mtSSU3R and mtSSU2R.

Automated reaction clean up and visualization of the results were performed at the Lichen Bioresource Genome Sequencing and Analysis Core Facility of the Korean Lichen Research Institute, Sunchon National University, Republic of Korea. Sequence fragments were subjected to BLAST searches for the first verification of their identities; these were assembled and edited using Sequencher version 4.8 (Gene Codes Corporation, Ann Arbor, MI), and aligned manually.

The phylogenetic analyses of the manually aligned sequences were performed with PAUP version 4.0b10. Trees were calculated using the general heuristic search option, maximizing the number of saved trees to 1,000, whereas gaps were treated as missing characters. Bootstrap analyses with 1,000 replicates were performed using the same settings. Support values of 50 or above are marked in the consensus tree (Fig. 1).

The morphological results are based mainly on studies of the authors' material, collected during field trips in Europe, Asia, Australia and New Zealand. For anatomical studies, lichen sections were prepared manually or using a Kryomat, Leitz freezing microtome, then mounted in water or in lactophenol cotton blue and studied using a Zeiss Axioscope light microscope.

Both voucher specimens A34 and A35, i.e. the sequences with GeneBank numbers KP096222, KP096223, KP096224, KP096225 of *Tassiloa digitaurea* cited (Fig. 1), were taken from the same rich collections from Chile, Patagonia, 19.I.2013 *Oh S.-O., Hur J.-S. CL 130214* (KoLRI 017647).

Results

Separate analyses

The ITS analysis included 74 specimens of 38 species and a total of 551 positions of which 346 were informative. The LSU analysis included 57 specimens representing 31 species and a total of 762 positions of which 150 were informative, whereas the 12S SSU mtDNA analysis included 71 specimens of 33 species and a total of 744 positions of which 218 were informative.

The new genus *Tassiloa*, described below, forms as a strongly supported clade in the separate analyses with maximum bootstrap support.

Combined analysis

The combined analysis of nuclear ITS, LSU and 12S SSU mtDNA data sets included 74 specimens of 38 species and a total of 2,057 positions of which 714 were informative.

The combined phylogenetic analysis strongly supports the proposal of a new genus (Fig. 1). *Tassiloa* appears as a sister group to the recently described genus *Catenarina* with which it forms a weakly supported clade in a neighboring joining analysis.

Taxonomy

Tassiloa S. Y. Kondr., Kärnefelt, A. Thell, Elix & J.-S. Hur, ***gen. nov.***
MycoBank no.: MB 810743

Thallus orange, crustose to microfruticose, areolate, smooth or thick, formed by terete isidia-like lobules. Lobules or isidia mostly distinct, vertically oriented. Apothecia zeorine or lecanorine, true exciple paraplectenchymatous. Chemistry: anthraquinones of the parietin chemosyndrome.

Type species: *Tassiloa digitaurea* (Søgaard, Søchting & Sancho) S. Y. Kondr., Kärnefelt, A. Thell, J. Kim, A. S. Kondratiuk & J.-S. Hur

Thallus vivid orange, crustose, areolate, smooth and isidiate to thick, formed by terete isidia-like lobules, often in microfruticose clusters. Lobules mostly well distinct, more or less vertically directed. Apothecia zeorine or lecanorine, disc deep orange, darker than thallus, true exciple paraplectenchymatous at the base; ascospores hyaline bipolar, with rather thin septa and thin spore end walls.

Chemistry. anthraquinones of the parietin chemosyndrome.

Ecology. The type species grows on rock, detritus and over other lichens on exposed outcrops in shrub vegetation and grassland in coastal areas, but not maritime, and another species is parasitic on various host lichens on non-calcareous rocks.

Etymology. The new genus is named after the German lichenologist Tassilo Feuerer (1949–), an important collector and discoverer of diverse lichens, colleague and friend.

Species diversity and distribution. The genus *Tassiloa* includes two species known from both American continents, *T. digitaurea* from southern Patagonia (Lumbsch *et al*. 2011), and *T. wetmorei,* known from the Sonoran Desert in southwestern North America (Nimis *et al*. 1994, Nash *et al*. 2001).

Notes. The genus *Tassiloa* differs from *Catenarina* in having a crustose to microfruticose, richly isidiate thallus, and presence of anthraquinones of the parietin chemosyndrome.

The morphology of *Tassiloa* resembles that of *Villophora* Søchting, Arup & Frödén, but the latter is more closely related to *Josefpoeltia* S. Y. Kondr. & Kärnefelt. Furthermore, the segregation of *Villophora* needs confirmation since its status was based on a single correctly identified specimen (Arup *et al*. 2013). The genus *Tassiloa* differs from foliose and fruticose genera of the *Teloschistes* clade, i.e. *Josefpoeltia*, *Teloschistes* Norm. and *Niorma* A. Massal., in having a crustose to microfruticose thallus and a paraplectenchymatous true exciple.

In the original description *Tassiloa digitaurea* was compared with *Caloplaca isidioclada* Zahlbr. (Lumbsch *et al*. 2011), but the latter taxon belongs to the subfamily Xanthorioideae (Kondratyuk *et al*. in prep.).

New combinations

Tassiloa digitaurea (Søgaard, Søchting & Sancho) S. Y. Kondr., Kärnefelt, A. Thell, Elix, J. Kim, A. S. Kondratiuk & J.-S. Hur, *comb. nova* [MycoBank no: MB 810744]. – Basionym: *Caloplaca digitaurea* Søgaard, Søchting & Sancho, in Lumbsch *et al*., *Phytotaxa* **18**: 31 (2011).

Tassiloa wetmorei (Nimis, Poelt & Tretiach) S. Y. Kondr., Kärnefelt, A. Thell, Elix, J. Kim, A. S. Kondratiuk & J.-S. Hur, *comb. nova* [MycoBank no: MB 810745]. – Basionym: *Caloplaca wetmorei* Nimis, Poelt & Tretiach, *Bryologist* **97**: 183 (1994).

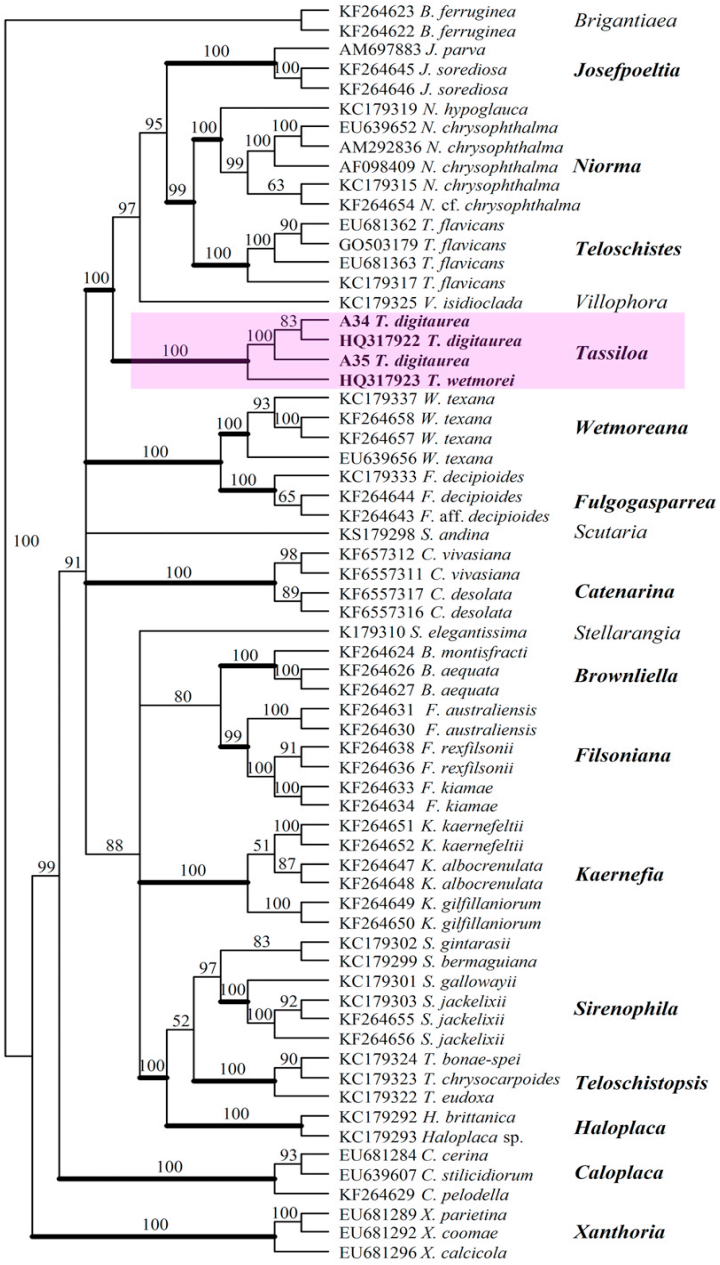

Figure. 1. Phylogenetic tree of teloschistoid lichens based on a combined data set of nuclear ITS and 28S LSU-sequences and 12S SSU mtDNA-sequences.

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