A new species of Hypocrella, H. macrostroma, and its phylogenetic relationships to other species with large stromata

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Two specimens of a new species of Hypocrella with large stromata were collected in Bolivia and Costa Rica. The morphology of the new species, H. macrostroma nov., was compared with that of other species with large stromata, i.e. H. africana, H. gaertneriana, and H. schizostachyi. In addition, phylogenetic analyses of partial sequences from three genes, large subunit nuclear ribosomal DNA (LSU), translation elongation factor 1-α (EF1-α), and RNA polymerase II subunit 1 (RPB1), were conducted to determine the relationships of the new species to other species of Hypocrella/Aschersonia. Phylogenetic analyses show that H. macrostroma belongs to a strongly supported clade that includes H. africana, H. schizostachyi, and Aschersonia insperata, whereas other Hypocrella species belong to two sister clades. Hypocrella macrostroma is described and illustrated, and a lectotype is designated for H. gaertneriana.

INTRODUCTION

Species in the entomopathogenic genus Hypocrella (Clavicipitaceae, Hypocreales, Ascomycota) are frequently encountered in the tropics and less often in the subtropics. These fungi are found growing on scale insects (Coccidae, Homoptera) and whiteflies (Aleyrodidae, Homoptera) that parasitize living leaves, or rarely branches, of monocotyledonous and dicotyledonous plants. Hypocrella species have perithecia immersed in a brightly colored stroma and cylindrical asci that disarticulate at maturity. Anamorphs of Hypocrella are classified in the anamorph genus Aschersonia. The latter state is more commonly found in the field, and is sometimes associated with the teleomorph in the same stroma. Aschersonia is characterized by pycnidium-like conidiomata, phialides, sometimes paraphyses, and unicellular, fusiform, hyaline conidia that are brightly colored in mass and produced in copious slime.

Approximately 115 names in Hypocrella and 79 in Aschersonia have been validly published; however, only about 50 and 44 species, respectively, are currently accepted (Petch 1921, Dingley 1954, Mains 1959a, b, Hywel-Jones & Evans 1993). Only about 15 species have been linked to teleomorphs. Petch (1921) compiled the most complete taxonomic work on Hypocrella/Aschersonia to date; he accepted 42 species. Fungal biodiversity surveys in poorly explored geographical regions, detailed morphological examinations, and DNA sequence analyses will probably reveal many undescribed species.

Two specimens of an unidentified species of Hypocrella with large stromata (3–22 mm diam) were collected in Costa Rica and Bolivia on stems of living dicot vines. Generally, the stromata of Hypocrella/Aschersonia are 2–5 mm diam, however, H. africana, H. gaertneriana, H. schizostachyi (Hywel-Jones & Samuels 1998), and the unidentified Hypocrella have markedly larger stromata that measure ca 5–30 mm in diameter. These species are probably on scale insects attached to branches of living dicotyledonous plants (H. africana and the unidentified Hypocrella) or bamboo culms (H. gaertneriana and H. schizostachyi), whereas the majority of the Hypocrella/Aschersonia species occur on scale insects or whiteflies on living leaves. The unidentified species resembles H. gaertneriana in the shape and size of the stroma; however, the colour of the stroma and that the unidentified species is on an insect on living dicotyledonous vines suggested that it might be a new species.

H. gaertneriana was described and illustrated by Möller (1901) based on a specimen from Brazil. Specimens were deposited in the Berlin Botanical...
Garden and Museum herbarium (B), but, unfortunately, a large part of the herbarium’s collection, including Møller’s, was destroyed in 1943 (http://www.bgbm.fu-berlin.de/bgbm/research/colls/herb/). 

H. gaertneriana was re-described and illustrated based on collections from Venezuela and French Guiana (Hywel-Jones & Samuels 1998); however, the authors did not designate a neotype. In the present paper, H. gaertneriana is lectotypified with the original illustration in Møller (1901).

Other genera in the Clavicipitaceae, such as Ascomyces, Dussiella, and Hyperdermium, also parasitize scale insects and have relatively large stromata. In all these genera, the stromatal mass greatly exceeds that of the scale insect host. Sullivan et al. (2000) suggested that the large size of the stromata results from a kind of secondary plant parasitism: once the fungus has consumed the scale insect body, the fungus may continue to access plant nutrients through the insect’s stilet. Other authors have suggested that the mechanism of nutrient acquisition in species of Hypocrella with large stromata is through the living scale insect that forms a bridge between the fungus and the plant (Hywel-Jones & Samuels 1998). A similar mechanism has been observed in Septobasidium (Couch 1938). More detailed research is needed to elucidate this phenomenon.

The main objectives of the present paper are: (1) to describe a new species of Hypocrella with large stromata; and (2) to show its phylogenetic relationships to other species of Hypocrella/Aschersonia, by using partial DNA sequences of three genes, i.e., large subunit nuclear ribosomal DNA (LSU), translation elongation factor 1-α (EF1-α), and RNA polymerase II subunit 1 (RPB1). We also discuss whether Hypocrella species with large stromata should be classified in a separate genus.

**MATERIALS AND METHODS**

**Morphological examination**

Dried reference specimens were obtained from US National Fungus Collection (BPI; H. africana holotype BPI 635731, and H. schizostachyi isotype BPI 635854) and the William and Lynda Steere Herbarium (NY; H. gaertneriana GJS 1776). Other specimens (Hypocrella sp. J.B. 115 = CUP 67509 and P.C. 605 = CUP 67508, and H. africana P.C. 736 = CUP 67510) were collected during recent expeditions to Ghana, Costa Rica and Bolivia; these specimens are deposited at the Cornell University Plant Pathology Herbarium (CUP). Stromata of J.B. 115 and P.C. 605 were rehydrated briefly in distilled water with a trace of Tween® 80 (J. T. Baker Chemical, Phillipsburg, NJ). Then, rehydrated stromata were supported by Tissue-Tek O.C.T. Compound 4583 (Miles, Elkhart, IN) and sectioned at a thickness of ca 15 μm with a freezing microtome. The characteristics of the stroma tissue, perithecia, asci and ascospores were characterized by light microscopy. Colour terminology is from Kornerup & Wanscher (1978).

The only culture available for the unidentified species of Hypocrella was obtained from J.B. 115 (ARSEF 7748) by isolating asci containing ascospores and placing them on Difco potato dextrose agar (PDA) with antibiotics. Morphological observations of the colonies and anamorph were based on cultures grown on PDA for four weeks in an incubator at 25 °C with alternating 12 h fluorescent light and 12 h darkness.

Measurements of continuous characters such as spore length were made using the beta 4.0.2 version of Scion Image software (Scion, Frederick, MD). Confidence intervals (α = 0.05), minimum and maximum values for 10–30 anamorph and teleomorph measurements (except where indicated) were calculated using Systat 8.0 (SPSS, Chicago, IL).

**DNA extraction, PCR, and sequencing**

Cultures of Hypocrella sp. J.B. 115 and other Hypocrella/Aschersonia species in the phylogenetic analyses (Table 1) were grown on potato-dextrose broth in a 6-cm-diam Petri plate for about one week. The mycelial mat was harvested in a laminar flow hood and then dried using clean, absorbent paper towels. DNA was extracted with Ultra Clean™ Plant DNA Isolation Kit (MO BIO Laboratories, Solana Beach, CA). To extract DNA from the herbarium specimen of Hypocrella sp. P.C. 605, the surface of the stroma was first cleaned briefly with sterilized distilled water, then rehydrated by placing the stroma in a small Petri plate with sterilized distilled water and letting it stand for a few minutes until the stroma became softer. Subsequently, a very thin layer of the surface of the stroma was shaved off using a scalpel and then discarded. Pieces of the clean inner stroma, including centri, were cut out and then placed in a 1.5-mL Eppendorf tube for immediate DNA extraction with Ultra Clean™ Plant DNA Isolation Kit.

Three partial gene regions were amplified, i.e., large subunit nuclear ribosomal DNA (LSU), translation elongation factor 1-α (EF1-α), and RNA polymerase II subunit (RPB1). The primers used were LSU: LRORf (5'-GTACCCGCTGAACCTAAGC-3') and LRSr (5'-ATCTCTGAGGAAACTCTC-3') (Vilgalys & Hester 1990); EF1-α: 983f (5'-GCYCYGGHCAYGCTG-AYTYYAT-3') (Carbone & Kohl 1999) and 2218r (5'-ATGACACCRACRCGRGTYTGYT-3') (Rehner 2001); RPB1: cRPB1Af (5'-CAYCCWGYYTTA-TCAAGAA-3') and RPB1Cr (5'-CCNGCDATNCTC RRTTCCCATRITA-3') (Castlebury et al. 2004). PCR protocols for LSU and EF1-α are described in Sung et al. (2001) and Chaverri & Samuels (2003), respectively. PCR for RPB1 was conducted as follows: (1) 5 min at 95 °C, (2) 40 cycles of denaturation at 95 °C for 1 min, annealing at 50 °C for 2 min, and extension at 72 °C for 2 min, and (3) 72 °C for 10 min. The resulting
PCR products were purified with the QIAquick™ PCR Purification Kit (Qiagen, Valencia, CA). Sequencing of forward and reverse strands was performed at the DNA Sequencing Facility (Center for Agricultural Biotechnology, University of Maryland, College Park, MD). Sequences were assembled and edited with Sequencher 4.2 (Gene Codes, Madison, WI). Sequences have been deposited in GenBank (Table 1) and the alignment in TreeBASE (study accession number S1279, http://treebase.bio.buffalo.edu/treebase/).

Phylogenetic analysis

The sequences produced were aligned using Clustal X 1.81 (Thompson et al. 1997), and then the alignment was refined by hand. Maximum Parsimony (MP) and Bayesian Inference (BI) were carried out with all sequences. The MP analysis was done in PAUP* version b10 (Swofford 1999) using a heuristic search, with a starting tree obtained via 1000 random stepwise addition sequences, tree-bisection-reconnection as the branch-swapping algorithm, and MULTREES off. Bootstrap values from 1000 replicates were calculated using a ‘fast’ stepwise addition search. MrBayes 3.0 b4 (Huelsenbeck 2000, Huelsenbeck et al. 2001) was used to reconstruct phylogenetic trees using the Bayesian approach (Rannala & Yang 1996, Mau, Newton & Larget 1999). The Bayesian analysis used a different model of evolution for each of the three partitions (LSU, EF1-α, RPB1). The models of DNA substitution were estimated using Modeltest 3.6 (Posada & Crandall 1998). Four chains and 5 M Markov Chain Monte Carlo generations were run and the current tree was saved to a file every 100 generations. After confirming that stability had been reached both in terms of likelihood scores and parameter estimation, the first 5000 trees were discarded as ‘burn-in’. The remaining ‘post-burn-in’ trees were pooled and a 50% majority-rule consensus tree was obtained with MrBayes.

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To determine whether the sequences from the three genes should be combined in a single analysis, topological incongruence was examined using a reciprocal 70% bootstrap (BP) or a 95% posterior probability (PP) threshold (Mason-Gamer & Kellogg 2001, Rambaut et al. 2003).
1996, Reeb, Lutzoni & Roux 2004). Bootstrap values were generated using neighbour-joining (NJ) with 1000 replicates and a maximum likelihood distance. Posterior probabilities were calculated using Bayesian analysis in MrBayes. A conflict was assumed to be significant if two different relationships for the same taxa – one being monophyletic and the other non-monophyletic, both with BP \( \geq 70\% \) and PP \( \geq 95\% \) – were observed on each of the LSU, EF1-\( \alpha \), and RPB1 majority-rule consensus trees. The three partitions could be combined if no significant conflicts were detected.

**RESULTS**

**Morphology**

The new species of *Hypocrella*, *H. macrostroma*, is distinguished from the other species with large stromata by its substrate, stroma colour, and part-ascospore size (Table 2). It was found on an insect (probably a scale insect based on the type of host of related species) on living dicotyledonous vines, whereas *H. gaertneriana* and *H. schizostachyi* were found on bamboo culms. *H. africana* type material (BPI 635731) was found on scale insects on living dicot twigs, as was the additional specimen examined in this study (P.C. 736). The part-ascospores of *H. macrostroma* are significantly larger than the other species. The stroma of *H. gaertneriana* releases reddish pigment when 3% KOH is added, whereas the other species do not react to KOH. *Hypocrella gaertneriana* and *H. macrostroma* have the largest stroma; *H. africana* and *H. schizostachyi* have smaller stromata (Table 2). The specimen of *H. africana* (P.C. 736) has smaller stromata (ca 5–6 mm diam) than those of the type specimen (8–17 mm) of the proposed new species. All other morphological characteristics, including the substrate, otherwise fit the concept of *H. africana*, which has so far been known only from Africa.

Anamorphs of *Hypocrella* species with large stromata are known only for *H. schizostachyi* and *H. macrostroma*. The anamorph of *H. macrostroma* is a true *Aschersonia* with pycnidia-like conidiomata that produce fusiform conidia from slender phialides. *Hypocrella schizostachyi*, on the other hand, produces a pycnidial anamorph that is not typical of *Aschersonia* (Hywel-Jones & Samuels 1998) in that its conidia are allantoid. The conidiogenous cells, especially the polyphialides of the pycnidial ‘B’ anamorph, and the shapes of the ‘B’-type conidia are more reminiscent of *Hirsutella* than of the typical *Aschersonia* type.

**Phylogenetic analyses**

Sequencing of three genes resulted in an aligned dataset of 2594 characters, including gaps (insertions and/or deletions): 905 for LSU, 934 for EF1-\( \alpha \), and 755 for RPB1 (Table 3). RPB1 had the majority of the polymorphisms and phylogenetically informative characters (38%), followed by EF1-\( \alpha \) with 27% and LSU with 14%. The models of nucleotide substitution suggested by Modeltest 3.6 for each locus were General Time Reversible (GTR + G + I, nst = 6) with
gamma distributions and invariable sites. The parameters selected for the LSU model were: base frequencies = 0.2283, 0.2716, 0.3201; rates (Rmat) = 0.4772, 2.7390, 0.5495, 0.7659, 6.3667; gamma shape = 0.4985; proportion invariable sites (pinvar) = 0.6212.

The parameters for the EF1-α model were: base frequencies = 0.1952, 0.3442, 0.2443; rates (Rmat) = 0.6044, 1.0873, 0.7875, 0.5494, 4.6887; gamma shape = 1.1425; proportion invariable sites (pinvar) = 0.551.

The parameters for the RPB1 model were: base frequencies = 0.2335, 0.2826, 0.2611; rates (Rmat) = 1.8006, 3.6967, 0.8486, 0.9245, 6.9621; gamma shape = 0.8631; proportion invariable sites (pinvar) = 0.3752. These models were then used to analyze incongruence among loci. The reciprocal 70% bootstrap and 95% posterior probability thresholds for individual loci show that the topologies of the three genes are congruent and therefore the partitions were combined.

The combined MP and BI analyses of selected species of *Hypocrella/Aschersonia* reveal three major clades that are supported by high BP and PP and correlated with morphological characters: the ‘Effuse’ group (BP 70%, PP 100%), the ‘Pulvinate’ group (BP 86%, PP 100%), and the ‘Globose’ group (BP 70%, PP 100%) (Fig. 1). All the species in the Effuse group, except *A. basicystis* (teleomorph *H. phyllogena*), have flattened to effuse anamorphic stromata that are formed mainly of loose hyphal tissue and a relatively extensive hypothallus. *Aschersonia basicystis* in its first stages of development has a stroma composed of loose hyphal tissue that is flattened, and has a wide hypothallus. The hypothallus persists, and the stroma
Hypocrella macrostroma Chaverri & K. T. Hodge, sp. nov.

Anamorph: A. turbinata (Fig. 1).

Specimens of Hypocrella macrostroma and compact stromata that are generally larger than those in the other clades. Within the Globose group, clade ‘A’ is ‘sister’ to clade B. This group includes the only known species of Hypocrella/Aschersonia that change color (reddish or brownish) when mounted in 3% KOH (H. discoidea, the type of the genus, H. gaertneriana, A. napoleonae, and A. viridans).

The Globose group consists of species that have globose to subglobose, compact and hard stromata that are generally larger than those in the other clades. Within the Globose group, clade ‘A’, supported by BP 74% and PP 100%, includes species with large stromata that are generally tuberculate and with deep creases giving the appearance of a compound stroma (i.e. A. insperata, H. africana, H. macrostroma, and H. schizostachyi), plus Hypocrella sp. P.C. 603, which has globose, non-tuberculate, hard and compact stromata that are ca 3–4 mm diam. Two specimens of H. macrostroma form a monophyletic group supported by 100% BP and 100% PP. Within the Globose group, clade A is ‘sister’ to clade B. The latter contains the similar species A. cubensis and A. turbinata (Fig. 1).

**TAXONOMY**

**Hypocrella macrostroma** Chaverri & K. T. Hodge, sp. nov. (Figs 2–18)

Anamorph: Aschersonia sp.

Stromata globose ad subglobose, flava, tuberculata, 3–22 cm diam. Ascosporae multicellulares, ad septum disarticulatae, incolora, partis fusiformi ad subcylindrici, (8.7–)10.5–11.5(–18.0) × (2.2–)2.5–2.7(–3.0) μm. Anamorphosis: Aschersonia sp. Holotypus CUP 67508 (=P.C. 605).

**Typus**: Bolivia: La Paz Department: Province Franz Tamayo, San José de Uchipiamonas, Madidi National Park, trail to the top of the mountain, along Eslabón River starting at ‘Senda RAP’ camp, elev. 400–600 m, ca 14° 27’ 80.2” S, 67° 56.927” W, on insects on living vine of dicotyledonous plant, 12 June 2004, D. De La Quintana, M. Sogonon, A. Alvarez, P. Chaverri P.C. 605 (CUP 67508 – holotypus).

Stromata large, 3–22 mm diam, yellow, somewhat globose, cerebriform, surface smooth, somewhat glossy, ostiolar openings visible, flush with surface, brownish yellow, stromatic tissue not changing colour in KOH, stromata formed of closely aggregated tubercles, tubercles 1–4 mm diam, stroma outer tissue of textura angularis composed of thin-walled cells, stroma internal tissue pale yellow, hard and coriaceous, tissue of textura epidermoidea composed of thick-walled cells. Perithecia completely immersed in stroma, obpyriform, (377–)389–441(–451) × (137–)138–149(–152) μm. Ascii cylindrical, (140–)146–189(–197) × (5.2–)5.5–6.5(–7) μm, capitate, cap depth 3–4 μm, 8-spored. Ascospores hyaline, smooth, filiform, multiseptate, disarticulating at septa, part-ascospores fusiform to subcylindric, (8.5–)10.5–11.5(–18) × (2–)2.5(–3) μm (n = 51).

The following anamorph description is based on J.B. 115 (ARSEF 7748); the ascospores of P.C. 605 did not germinate. The specimen J.B. 115 included conidiomata in the same stroma as the teleomorph. Conidiomata from original substrate, with pycnidium-like depressions in the stroma, lacking well-defined walls, irregular in shape. Conidia fusiform, hyaline, smooth, unicellular, (10.5–)11.5–13(–14.5) × (2–)2.5(–3) μm; phialides not observed, probably degraded. Colony on PDA at 25° after ca 4 wk 12–14 mm diam, floccose or fluffy, light yellow, forming irregular pycnidia-like concave depressions or cavities in colony and lacking a differentiated wall; conidial masses oozing from conidiomata in pale yellow, slimy cirri. Conidiodophores on PDA short, almost indiscernible, mononematous, aggregated into compact hymenium-lined cavities. Phialides on PDA slender, tapering towards tip, somewhat irregular not straight, (23.5–)25–27(–27.5) × (2.5–)3(–3.5) μm; paraphyses not observed. Conidia on PDA fusiform, hyaline, (13.5–)15.5–17(–19) × (2–)2.5(–3) μm.

**Habitat**: Probably on scale insects on living dicotyledonous vines.

**Distribution**: Bolivia and Costa Rica.

**Paratype**: Costa Rica: Heredia: Sarapiquí, La Selva Biological Station, Oriental Trail at 350 m from the beginning, stromata found on ground, substrate unknown, 26 June 2002, J. F. Bischoff (J.B. 115 = CUP 67509, culture ARSEF 7748).


**Illustrations**: Møller (1901 taf. III fig. 51, taf. IV fig. 62), and Hywel-Jones & Samuels (1998: figs 8–14).

**Notes**: Specimens of H. gaertneriana deposited in (B) were destroyed in a fire in 1943; for that reason we have designated the original illustration as a lecto-type above. Because the specimen of H. gaertneriana is deposited in NY does not have a living culture, we prefer not to designate it as an epitype. However, we consider it a specimen that fits Møller’s description.

**Additional specimen**: Venezuela: Río Negro Department: Cerro de la Neblina, along Rio Mawarinuma, just outside Cañón Grande, near Nebílina Base Camp, ca 140 m elev., 00° 50’ N, 66° 10’ W, on bamboo culms, April-May 1984, G. J. Samuels 1776 (NY).

**DISCUSSION**

Species of Hypocrella/Aschersonia with large stromata are uncommon. Hywel-Jones & Samuels (1998) considered these species to be very distinct but did not propose a new genus for them because they lacked sufficient information about their life-cycles. Our
morphological and molecular evidence suggests that species with large stromata are derived from within *Hypocrella*. The anamorph of *H. macrostroma* is clearly an *Aschersonia*; whereas *H. schizostachyi* has an anamorph that deviates somewhat from the typical *Aschersonia* (type species *A. taitensis*). Phylogenetic analyses of three loci show that the species with large stromata used in this study have a single evolutionary origin and form a monophyletic group that includes two other species with smaller stromata, *A. insperata* and *Hypocrella* sp. P.C. 603. Unfortunately, we cannot unequivocally conclude that *H. gaertneriana* is part of this group because we lack fresh material that can be used for DNA sequencing. However, the morphology of the stroma and the ascospores suggest that *H. gaertneriana* does belong in *Hypocrella*.

Three major groups, referred to as ‘Effuse’, ‘Globose’ and ‘Pulvinate’, are revealed in the phylogenetic
analyses of DNA sequences. Phylogenetically informative morphological characters correlate with each of the groups as defined by DNA sequence data. In general, species in the Effuse group have flat, effuse stromata of loose hyphal tissue, broad hypothalli, and whitish colouration, except in the *A. basicystis* species complex where it is pale yellow to orange. The Globose group includes species that have globose stromata that are generally darker in colour (yellow to brownish), large, compact tissue, hard or coriaceous, moderately to strongly tuberculate, and without hypothalli. The Pulvinate group contains species that have pulvinate or cushion-like stromata, somewhat compact and flattened, yellowish or green, with or without hypothalli, sometimes changing color in KOH.

‘The genus for genus concept’ symposium at the XVI International Botanical Congress (Saint Louis, MO) in 1999 discussed theoretical concepts and data with the fundamental idea that fungal taxonomy should move towards a 1:1 correlation of teleomorph and anamorph generic concepts and nomenclatural unity. Because of the morphological synapomorphies that characterize the genus *Hypocreella*/*Aschersonia* and to follow the ‘genus for genus’ concept (Seifert et al. 2000), we do not propose a formal generic or subgeneric revision of the taxonomy to distinguish the Effuse, Globose, and Pulvinate groups. Even though there are apparently distinct phenotypic characteristics that distinguish each of the three major groups, all have the typical characteristics of the genus *Hypocreella: Aschersonia s. str.* anamorphs, perithecia embedded in a well-developed stroma, filiform multiseptate ascospores that disarticulate at each septum, and parasitism of scale insects and whiteflies. Sampling of more species is needed to further investigate whether these clades should be considered taxa of subgeneric or generic rank.

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REFERENCES


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