



Phylogenetic and morphological circumscription of the *Orbilia aurantiorubra* group

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Abstract

The phylogeny of *Orbilia aurantiorugra* and related species is inferred from ITS sequence data. *Orbilia aurantiorubra* is redefined according to vital taxonomy. Integrated analyses of molecular and morphological data, and ecological (e.g. substrate) and geographical origin suggest the existence of three new species, which are described in this paper: *Orbilia xanthoguttulata* from Europe, *O. succulenticola* from the Canary Islands, and *O. jugulospora* from Ethiopia (Africa) and Taiwan (Southeast Asia).

Key words: Biodiversity, Europe, Canary Islands, Orbiliomycetes, taxonomy

Introduction

The genus *Orbilia* Fr. (*Orbiliaceae* Nannf.) was traditionally placed in the order *Helotiales* Nannf., and considered as a low diversity group (Spooner 1987). The advantages of using living cells (Baral 1992) for the taxonomic study of the *Orbiliaceae* have dramatically improved the knowledge of this family in the last two decades. Indeed, the family *Orbiliaceae* has undergone many changes since Baral & Marson (2001) introduced the genus *Hyalorbilia*, based on a small group of species previously included in *Orbilia*. Thus, in 2001 the *Orbiliaceae* comprised two genera and ~35 spp. (Kirk *et al.* 2001). In 2003 the family was segregated from the *Leotiomycetes* to constitute an order and class of its own, the *Orbiliales* and *Orbiliomycetes* (Eriksson *et al.* 2003). Further molecular studies found that this class formed an early diverging major clade within *Pezizomycotina* (Spatafora *et al.* 2006).

Thus far, *Orbilia* is represented by ca. 58 species worldwide, principally wood-saprobic fungi, particularly common in temperate regions (Kirk *et al.* 2008, Cannon & Kirk 2007). However, the forthcoming world monograph of Orbiliomycetes (Baral *et al.* in prep.) will recognize about 400 species within this genus, most of which are adapted to semihumid to arid, subtropical to tropical environments. Despite this considerable increase in species number, there is still a substantial lack of knowledge concerning host or habitat preferences and biogeography for many of the recognized species. Not surprisingly, this current lack of elementary data has impeded the assessment of many important aspects bearing on the evolutionary biology and systematic of this group.

Orbilia aurantiorubra Boud. is easily recognizable by its bright orange-red apothecia, and geniculate based helicoid spores containing narrowly tear-shaped spore bodies. It is briefly described by Boudier (1907) and appears in his *Icones mycologicae* (Boudier 1904–10). This species tolerates desiccation, and occurs throughout the year on different substrates in temperate, continental to Atlantic areas of Europe and West Africa (rarely in Mediterranean areas), between 0–1650 m (Baral *et al.* ined.). Specimens related to *O. aurantirubra* have ascospores variation between (7.5–)8–14.5(–16) × 1.1–1.8 µm and spore bodies between (1.8–)2.5–4.5(–5.5) × (0.5–)0.7–1.1(–1.3) µm. Some variation in spore dimensions correlated with host or geographical origins in *O. aurantiorubra* were noticed (Karasch *et al.* 2005, Priou 2005, Spooner 2001). Species considered as widespread fungi, usually showed a restricted distribution after taxonomical review (Stadler *et al.* 2004; Baral 1984). The correlation between ascospore size and host has been evidence for species differentiation (Petrini *et al.* 1987). Generally, morphological variation observed in species can

References

- Akaike, H. (1974) A new look at the statistical model identification. *IEEE Transactions on Automatic Control* 19: 716–723.
- Baral, H.O. (1984) Taxonomische und ökologische Studien über *Sarcoscypha coccinea* agg., Zinnoberrote Kelchbecherlinge. (Kurzfassung). *Zeitschrift für Mykologie* 50: 117–145.
- Baral, H.O. (1992) Vital versus herbarium taxonomy: morphological differences between living and dead cells of *Ascomycetes*, and their taxonomic implications. *Mycotaxon* 44: 333–390.
- Baral, H.O. & Marson, G. (2000) Monographic revision of *Gelatinopsis* and *Calloriopsis* (*Calloriopsidaceae, Leotiales*). In: *Micologia 2000*: 23–46. Associazione Micologica Bresadola, Trento.
- Baral, H.O. & Marson, G. (2001) Monographic revisión of *Gelatinopsis* and *Calloriopsis* (*Calloriopsidaceae, Leotiales*). In: *Mycologia 2000*. Associazione Micologica Bresadola, Trento, 23–46.
- Boudier, É. (1904–1910) *Icones mycologicae*. 4 vols. Paul Klincksieck, Paris (reprint 1981–82, Lausanne).
- Boudier, É. (1907) *Histoire et Classification des Discomycètes d'Europe*. Librairie des Sciences Naturelles, Paris, 221 pp.
- Cannon, P.F. & Kirk, P.M. (2007) *Fungal families of the world*. CABI, United Kingdom, 456 pp.
- Castresana, J. (2000) Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular and Evolution* 17: 540–552.
<http://dx.doi.org/10.1093/oxfordjournals.molbev.a026334>
- Clopton, R.E. (2004) Standard nomenclature and metrics of plane shapes for use in gregarine taxonomy. *Comparative Parasitology* 71: 130–140.
<http://dx.doi.org/10.1654/4151>
- Goloboff, P.A., Farris, J.S. & Nixon, K.C. (2008) TNT, a free program for phylogenetic analysis. *Cladistics* 24: 774–786.
<http://dx.doi.org/10.1111/j.1096-0031.2008.00217.x>
- Eriksson, E., Baral, H.O., Currah, R.S., Hansen, K., Kurtzman, C.P., Rambold, G. & Lassøe, T. (2003) Outline of Ascomycota 2003. *Myconet* 7: 1–89.
- Huelsenbeck, J.P. & Ronquist, F. (2001) MRBAYES, Bayesian inference of phylogenetic trees. *Bioinformatics* 17: 754–755.
<http://dx.doi.org/10.1093/bioinformatics/17.8.754>
- Hustad, V.P., Miller, A.N., Dentinger, B.T.M. & Cannon, P.F. (2013) Generic circumscriptions in *Geoglossomycetes*. *Persoonia* 31: 101–111.
<http://dx.doi.org/10.3767/003158513x671235>
- Hyde, K.D., Gareth Jones, E.B., Liu, J.K., Ariyawansa, H., Boehm, E., Boonmee, S., Braun, U., Chomnunti, P., Crous, P.W., Dai, D.Q., Diederich, P., Dissanayake, A., Doilom, M., Doveri, F., Hongsanan, S., Jayawardena, R., Lawrey, J.D., Li, Y.M., Liu, Y.X., Lücking, R., Monkai, J., Muggia, L., Nelsen, M.P., Pang, K.L., Phookamsak, R., Senanayake, I.C., Shearer, C.A., Suetrong, S., Tanaka, K., Thambugala, K.M., Wijayawardene, N.N., Wikee, S., Wu, H.X., Zhang, Y., Aguirre-Hudson, B., Alias, S.A., Aptroot, A., Bahkali, A.H., Bezerra, J.L., Bhat, D.J., Camporesi, E., Chukeatirote, E., Gueidan, C., Hawksworth, D.L., Hirayama, K., Hoog, S.D., Kang, J.C., Knudsen, K., Li, W.J., Li, X.H., Liu, Z.Y., Mapook, A., McKenzie, E.H.C., Miller, A.N., Mortimer, P.E., Phillips, A.J.L., Raja, H.A., Scheuer, C., Schumm, F., Taylor, J.E., Tian, Q., Tibpromma, S., Wanasinghe, D.N., Wang, Y., Xu, J.C., Yacharoen, S., Yan, J.Y., Zhang, M (2013) Families of Dothideomycetes. *Fungal diversity* 63: 1–313.
- Karasch, P., Dämon, W., Jaklitsch, W. & Baral, H.O. (2005) Beiträge zur Pilzflora der Kanaren-Inseln La Palma 2. Weitere bemerkenswerte Pilzfunde auf *Chamaecytisus proliferus*. *Österreichische Zeitschrift für Pilzkunde* 14: 275–289.
- Katoh, K., Misawa, K., Kuma, K., Miyata, T. (2002) MAFFT, a novel method for rapid multiple sequence alignment base don fast Fourier transform. *Nucleic Acids Research* 30: 3059–3066.
- Katoh, K. & Toh, H. (2008) Improved accuracy of multiple ncRNA alignment by incorporating structural information into a MAFFT-based framework. *BMC Bioinformatics* 9 (Paper 212).
<http://dx.doi.org/10.1186/1471-2105-9-212>
- Kirk, P.M., Cannon, P.F., David, J.C. & Stalpers, J.A. (2001) *Dictionary of the Fungi. 9th Edition*. CAB international, United Kingdom, 655 pp.
- Kirk, P.M., Cannon, P.F., Minter, D.W. & Stalper, J.A. (2008) *Ainsworth and Bisby's Dictionary of the Fungi. 10th ed.* CAB international, United Kingdom, 771 pp.
- McCune, B. & Grace J.B. (2002) Analysis of ecological communities. MjM Software, Gleneden Beach. Oregon.
- Petrini, L.E., Petrini, O. & Sieber, T.N. (1987) Host specificity of *Hypoxyylon fuscum*: A statistical approach to the problema. *Sydowia* 40: 227–234.
- Posada, D. (2008) jModelTest: phylogenetic model averaging. *Molecular Biology and Evolution* 25: 1253–1256.
<http://dx.doi.org/10.1093/molbev/msn083>

- Priou, J.P. (2005) Sur quelques *Orbiliaceae* récoltées en situation aérienne. *Bulletin Mensuel de la Société Linnéenne de Lyon* 74: 53–63.
- Quijada, L., Baral, H.O. & Beltrán-Tejera, E. (2012) New species of *Orbilia* (*Orbiliales*) from arid ecosystems of the Canary Islands (Spain). *Nova Hedwigia* 96: 237–248.
<http://dx.doi.org/10.1127/0029-5035/2012/0073>
- Quijada, L., Baral, H.O., Jaén-Molina, R., Weiss, M., Caujapé-Castells, J & Beltrán-Tejera, E. (2013) D-DNASE-91 <<http://www.demiurge-project.org/matrix/digests/D-DNASE-91>>
- Spatafora, J.W., Sung, G.H., Johnson, D., Hesse, C., O'Rourke, B., Serdani, M., Spotts, R., Lutzoni, F., Hofstetter, V., Miadlikowska, J., Reeb, V., Gueidan, C., Fraker, E., Lumbsch, T., Lücking, R., Schmitt, I., Hosaka, K., Aptroot, A., Roux, C., Miller, A.N., Geiser, D.M., Hafellner, J., Hestmark, G., Arnold, A.E., Büdel, B., Rauhut, A., Hewitt, D., Untereiner, W.A., Cole, M.S., Scheidegger, C., Schultz, M., Sipman, H., Schoch, C.L. (2006) A five-gene phylogeny of *Pezizomycotina*. *Mycologia* 98: 1018–1028.
- Spooner, B.M. (1987) *Helotiales of Australasia: Geoglossaceae, Orbiliaceae, Sclerotiniaceae, Hyaloscyphaceae*. J. Cramer, Great Britain, 711 pp.
- Spooner, B.M. (2001) New British records. *Mycologist* 15: 135.
- Stamatakis, A. (2006) RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 22: 2688–2690.
<http://dx.doi.org/10.1093/bioinformatics/btl446>
- Stamatakis, A., Hoover, P., Rougemont, J. (2008) A rapid bootstrap algorithm for the RAxML web servers. *Systematic Biology* 57: 758–771.
<http://dx.doi.org/10.1080/10635150802429642>
- Standler, M., Wollweber, H., Jäger, W., Briegert, M., Venturella, G., Castro, J.M., Tichy, H.-V. (2004) Cryptic species related to *Daldinia concentrica* and *Daldinia eschscholzii*, with notes on *Daldinia bakeri*. *Mycological Research* 108: 257–273.
<http://dx.doi.org/10.1017/s0953756204009335>
- Talavera, G. & Castresana, J. (2007) Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. *Systematic Biology* 56(4): 564–577.
<http://dx.doi.org/10.1080/10635150701472164>
- Tellería, M.T., Dueñas, M., Melo, I., Beltrán-Tejera, E., Rodríguez-Armas, J.L., Salcedo, I. & Martín, M.P. (2012) *Gloeocystidiellum kenyense* Hjorstam in Azores and Madeira. *Mycotaxon* 119: 337–343.
<http://dx.doi.org/10.5248/119.337>
- Ter Braak, C.J.F. & Šmilauer, P. (2002) *Reference Manual and CanoDraw for Windows User's Guide: software for canonical community ordination (Version 4.5)*. Microcomputer Power, Ithaca, New York, 500 pp.
- White, T.J., Bruns, T., Lee, S. & Taylor, J. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis, M.A., Gelfand, D.H., Sninsky, J.J. & White, T.J. (Eds) *PCR Protocols: A Guide to Methods and Applications*, Academic Press Inc., San Diego, pp. 315–322.
- Yu, Z., Quiao, M., Zhang, Y., Baral, H.O. & Zhang, K. (2007) *Orbilia vermiformis* sp. nov. and its anamorph. *Mycotaxon* 99: 271–278.
- Zhao-Quing, Z. & Zuang, W.-Y. (2013) Four new taxa of *Ilyonectria* and *Thelonectria* (*Nectriaceae*) revealed by morphology and combined ITS and β-tubulin sequence data. *Phytotaxa* 85: 15–25.
<http://dx.doi.org/10.11646/phytotaxa.85.1.3>