Phylogeny and ecology of the ubiquitous saprobe *Cladosporium sphaerospermum*, with descriptions of seven new species from hypersaline environments

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Abstract: Saprobic *Cladosporium* isolates morphologically similar to *C. sphaerospermum* are phylogenetically analysed on the basis of DNA sequences of the ribosomal RNA gene cluster, including the internal transcribed spacer regions ITS1 and ITS2, the 5.8S rDNA (ITS) and the small subunit (SSU) rDNA as well as β-tubulin and actin gene introns and exons. Most of the *C. sphaerospermum*-like species show halotolerance as a recurrent feature. *Cladosporium sphaerospermum*, which is characterised by almost globose conidia, is redefined on the basis of its ex-neotype culture. *Cladosporium dominicanum*, *C. psychrotolerans*, *C. velox*, *C. spinulosum* and *C. halotolerans*, all with globose conidia, are newly described on the basis of phylogenetic analyses and cryptic morphological and physiological characters. *Cladosporium halotolerans* was isolated from hypersaline water and bathrooms and detected once on dolphin skin. *Cladosporium dominicanum* and *C. velox* were isolated from plant material and hypersaline water. *Cladosporium psychrotolerans*, which grows well at 4 °C but not at 30 °C, and *C. spinulosum*, having conspicuously ornamented conidia with long digitate projections, are currently only known from hypersaline water. We also newly describe *C. salinae* from hypersaline water and *C. fusiforme* from hypersaline water and animal feed. Both species have ovoid to ellipsoidal conidia and are therefore reminiscent of *C. herbarum*. *Cladosporium langeronii* (= *Hormodendrum langeronii*) previously described as a pathogen on human skin, is halotolerant but has not yet been recorded from hypersaline environments.

Taxonomic novelties: *Cladosporium dominicanum* Zalar, de Hoog & Gunde-Cimerman, sp. nov., *C. fusiforme* Zalar, de Hoog & Gunde-Cimerman, sp. nov., *C. halotolerans* Zalar, de Hoog & Gunde-Cimerman, sp. nov., *C. psychrotolerans* Zalar, de Hoog & Gunde-Cimerman, sp. nov., *C. spinulosum* Zalar, de Hoog & Gunde-Cimerman, sp. nov., *C. velox* Zalar, de Hoog & Gunde-Cimerman, sp. nov.

Key words: Actin, β-tubulin, halotolerance, ITS rDNA, phylogeny, SSU rDNA, taxonomy.

INTRODUCTION

The halophilic and halotolerant mycobionta from hypersaline aqueous habitats worldwide frequently contain *Cladosporium* Link isolates (Gunde-Cimerman et al. 2000, Butinar et al. 2005). Initially, they were considered as airborne contaminants, but surprisingly, many of these *Cladosporium* isolates were identified as *C. sphaerospermum* Penz. because they formed globose conidia (data unpublished). *Cladosporium sphaerospermum*, known as one of the most common air-borne, cosmopolitan *Cladosporium* species, was frequently isolated from indoor and outdoor air (Park et al. 2004), dwellings (Aihara et al. 2001), and occasionally from humans (Badillet et al. 1982) and plants (Pereira et al. 2002). Strains morphologically identified as *C. sphaerospermum* were able to grow at a very low water activity (a_w 0.816), while other cladosporia clearly preferred a higher, less extreme water activity (Hocking et al. 1994). This pronounced osmotolerance suggests a predilection for osmotically stressed environments although *C. sphaerospermum* is reported from a wide range of habitats including osmotically non-stressed niches.

We therefore hypothesised that *C. sphaerospermum* represents a complex of species having either narrow or wide ecological amplitudes. The molecular diversity of strains identified as *C. sphaerospermum* has not yet been determined and isolates from humans have not yet been critically compared with those from environmental samples. Therefore, a taxonomic study was initiated with the aim to define phylogenetically and morphologically distinct entities and to describe their *in vitro* osmotolerance and their natural ecological preferences.

MATERIALS AND METHODS

Sampling

Samples of hypersaline water were collected from salterns located at different sites of the Mediterranean basin (Slovenia, Bosnia and Herzegovina, Spain), different coastal areas along the Atlantic Ocean (Monte Cristy, Dominican Republic; Swakopmund, Namibia), the Red Sea (Eilat, Israel), the Dead Sea (Ein Gedi, Israel), and the salt Lake Enriquillio (Dominican Republic). Samples from the Sečovlje salterns (Slovenia) were collected once per month in 1999. Samples from the Santa Pola salterns and Ebre delta river saltern (Spain) were taken twice (July and November) in 2000. A saltern in Namibia and one in the Dominican Republic were sampled twice (August and October) in 2002. Various salinities, ranging from 15 to 32 % NaCl were encountered in these ponds.

Isolation and maintenance of fungi

Strains were isolated from salterns using filtration of hypersaline water through membrane filters (pore diam 0.45 μm), followed by incubation of the membrane filters on different culture media with lowered water activity (Gunde-Cimerman et al. 2000). Only colonies of different morphology on one particular selective medium per sample were analysed further. Strains were carefully selected from different evaporation ponds, collected at different times, in order to avoid sampling of identical clones. Subcultures were maintained at the Culture Collection of Extremophilic Fungi (EXF, Biotechnical Faculty, Ljubljana, Slovenia), while a selection was deposited at the Centraalbureau voor Schimmelmicrocultures (CBS, Utrecht, The Netherlands) and the Culture Collection of the National Institute of Chemistry (MZKI, Ljubljana, Slovenia). Reference strains were obtained from CBS, and were selected either on the basis of the strain history, name, or on the basis of their ITS rDNA sequence. Strains were maintained on oatmeal agar (OA; diluted OA, Difco: 15 g of Difco 255210 OA medium, 12 g of agar, dissolved in 1 L of distilled water) with or without 5 % additional NaCl. They were preserved in liquid nitrogen or by lyophilisation. Strains studied are listed in Table 1.
Table 1. List of Cladosporium strains, with their current and original names, geography, GenBank accession numbers and references to earlier published sequences.

| Strain Nr.* | Source | Geography | GenBank accession Nr.* | actin | β-tubulin |
|------------|--------|-----------|------------------------|-------|----------|
| **Cladosporium bruhnei** | | | | |
| CBS 177.71 | Thuja tincture | The Netherlands, Amsterdam | DQ780399 / DQ780038 | EF101354 | EF101451 |
| CBS 812.71 | Polygonatum odoratum, leaf | Czech Republic, Lisen | DQ780401 / -- | -- | -- |
| **Cladosporium cladosporioides** | | | | |
| CBS 170.54 NT | Arundo, leaf | U.K., England, Kew | AY213640 / DQ780940 | EF101352 | EF101453 |
| EXF-321 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780408 / -- | -- | -- |
| EXF-780 | Hypersaline water | Bosnia and Herzegovina, Ston saltern | DQ780410 / -- | -- | -- |
| EXF-946 | Hypersaline water | Slovenia | DQ780412 / -- | -- | -- |
| **Cladosporium dominicanum** | | | | |
| CPC 11683 | Citrus fruit (orange) | Iran | DQ780391 / -- | EF101369 | EF101419 |
| EXF-696 | Hypersaline water | Dominican Republic, saltern | DQ780412 / -- | -- | -- |
| EXF-703 | Hypersaline water | Dominican Republic, salt lake Enriquillo | DQ780393 / -- | -- | -- |
| **Cladosporium fusiforme** | | | | |
| CBS 845.71 | Chicken food | Canada | DQ780394 / -- | EF101370 | EF101418 |
| EXF-397 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780395 / -- | -- | -- |
| EXF-449 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780396 / -- | EF101371 | EF101417 |
| **Cladosporium herbarum** | | | | |
| CBS 452.71 | Liver and intestine of diseased frog | U.S.A., New York, Geneva | AY361959 / DQ780939 | EF101372 | EF101446 |
| EXF-212 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780397 / -- | -- | -- |
| **Cladosporium halotolerans** | | | | |
| ATCC 6667.0, as Davidiella tassiana | CCA-treated Douglas-fir pole | U.S.A., New Jersey | AY361959 / DQ780939 | EF101372 | EF101446 |
| ATCC 26362 | Liver and intestine of diseased frog | U.S.A., New Jersey | AY361959 / DQ780939 | EF101373 | EF101446 |
| ATCC 64726 | Peanut cell suspension tissue culture | U.S.A., Georgia | AY361959 / DQ780939 | EF101374 | EF101446 |
| CBS 280.49 | Stem of Hypericum perforatum identified as Mycosphaerella hypenicola | Switzerland, Glarus, Mühlhern | DQ780399 / -- | EF101375 | EF101446 |
| CBS 191.54 | Laboratory air | Great Britain | -- / -- | -- | -- |
| CBS 573.78 | Aureobasidium cauliworum | Russia, Moscow region | -- / -- | -- | -- |
| CBS 626.82 | -- | Sweden, Stockholm | -- / -- | -- | -- |
| dh 12862; EXF-2533 | Culture contaminant | Brazil | DQ780371 / -- | EF101400 | EF101422 |
| dh 12991; EXF-2535 | Culture contaminant | Turkey | -- / -- | -- | -- |
| **Cladosporium halotolerans** | | | | |
| dh 12991; EXF-2535 | Brain | Turkey | DQ780372 / -- | EF101423 | EF101423 |
| dh 13911; EXF-2422 | Ice | Arctics | DQ780373 / -- | EF101401 | EF101430 |
| **Cladosporium herbarum** | | | | |
| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| EXF-1072   | Hypersaline water | Israel, Dead Sea | DQ780373 / – | – | – | EF101399 | EF101426 |
| EXF-2372   | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – | – | – | – |
| UAMH 7686  | Indoor air ex RCS strip, from Apis mellifera overwintering facility | U.S.A., Alta, Clyde Corner | AY625063 / – | – | – | – | – |
| –          | rDNA from bottlenose dolphin skin infected with Loboa loboi | U.S.A., Texas | AF035674 / – | – | – | – | – |
| –          | Microcolony, on rock | Turkey, Antalya | AJ971409 / – | – | – | – | – |
| –          | Microcolony, on rock | Turkey, Antalya | AJ971408 / – | – | – | – | – |
| –          | Tomato leaves | – | – | – | – | – | – |

**Cladosporium langeronii**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| CBS 189.54 NT | Mycosis | Brazil | DQ780379 / DQ780392 | – | – | EF101357 | EF101435 |
| CBS 701.84  | Picea abies, wood | Germany, Göttingen | DQ780382 / – | – | – | EF101360 | EF101438 |
| CBS 101880  | Moist aluminium school window frame | Belgium, Lichtervoorde | DQ780380 / – | – | – | EF101359 | EF101440 |
| dh 11736   | Biomat in a lake | Antarctica | DQ780381 / – | – | – | EF101363 | EF101436 |
| dh 12459   | Orig. face lesion | Brazil | DQ780378 / – | – | – | EF101358 | EF101439 |
| dh 13833   | Ice | Arctic | DQ780383 / – | – | – | EF101361 | EF101437 |
| –          | Nasal mucus | – | – | – | – | – | – |
| –          | Nasal mucus | – | – | – | – | – | – |
| –          | Mycorrhizal roots | – | – | – | – | – | – |

**Cladosporium oxysporum**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| ATCC 66689 | Creosote-treated southern pine pole | U.S.A., New York, Binghamton | AF303689 / DQ780395 | – | – | EF752192 | EF101454 |
| ATCC 76499 | Decayed leaf, Leptedea bicolor | – | – | – | – | AF393720 | – |
| CBS 125.80 | Cirsium vulgare, seedcoat | The Netherlands | AJ300332 / DQ780941 | – | – | EF101351 | EF101455 |
| EXF-697    | Hypersaline water | Dominican Republic, salt lake Enriquillo | DQ780392 / – | – | – | – | – |
| EXF-699    | Hypersaline water | Dominican Republic, saltern | DQ780394 / – | – | – | – | – |
| EXF-710    | Hypersaline water | Dominican Republic, saltern | DQ780393 / – | – | – | – | – |
| EXF-711    | Hypersaline water | Dominican Republic, saltern | DQ780391 / – | – | – | – | – |

**Cladosporium psychrotolerans**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| EXF-326    | Hypersaline water | Slovenia, Sečovlje saltern | DQ780387 / DQ780934 | – | – | EF101444 | – |
| EXF-332    | Hypersaline water | Slovenia, Sečovlje saltern | DQ780385 / DQ780933 | – | – | EF101364 | EF101441 |
| EXF-391 T, CBS 119412 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780386 / – | – | – | EF101365 | EF101442 |
| EXF-714    | Hypersaline water | Dominican Republic | DQ780384 / – | – | – | EF101366 | EF101443 |

**Cladosporium ramotenellum**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| EXF-454 T, CPC 12043 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780403 / – | – | – | – | – |

**Cladosporium salinae**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| EXF-322    | Hypersaline water | Slovenia, Sečovlje saltern | DQ780375 / – | – | – | EF101391 | EF101403 |
| EXF-335 T, CBS 119413 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780374 / DQ780931 | – | – | EF101390 | EF101405 |
| EXF-604    | Hypersaline water | Spain, Santa Pola | DQ780376 / – | – | – | EF101389 | EF101404 |

**Cladosporium sp.**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| CBS 300.96 | Soil along coral reef coast | Papua New Guinea, Madang, Jais Aben | DQ780352 / – | – | – | EF101385 | – |
| EXF-595    | Hypersaline water | Spain, Santa Pola saltern | DQ780402 / – | – | – | – | – |

**Cladosporium sphaerospermum**

| Strain Nr.  | Source | Geography | GenBank accession Nr.  | ITS rDNA | 18S rDNA | actin | β-tubulin |
|------------|--------|-----------|------------------------|----------|----------|-------|-----------|
| ATCC 12092 | Soil | Canada | AY361988 / – | – | – | – | – |
| ATCC 200384 | Compost biofilter | The Netherlands | AY361991 / – | – | – | – | – |
| CBS 109.14; ATCC 36950 | Carya illinoensis leaf scale | U.S.A. | DQ780350 / – | – | – | EF101384 | EF101410 |
| CBS 122.47; IFO 6377; IMI 49640; VKM F-772; ATCC 11292 | Decaying stem of Begonia sp., with Thielaviopsis basicola | The Netherlands, Aalsmeer | AJ244228 / – | – | – | – | – |
| CBS 188.54; ATCC 11290; IMI 049638 | de Vries (Engelhardt strain) | – | – | – | – | AY361990 & AY251077 / – | – |
| CBS 190.54; ATCC 11293; IFO 6380; – IMI 49641 | – | – | – | – | – | AY361992 / – | – |
| CBS 192.54; ATCC 11288; IMI 49636 | Nail of man | – | – | – | – | AY361999 / – | – |
| Strain Nr.* | Source | Geography | GenBank accession Nr.* |
|-------------|--------|-----------|------------------------|
| CBS 193.54 NT; ATCC 11289; IMI 46837 | Human nails | – | DQ780343 & AY361958 / DQ780925; EF101380 & EF101406 |
| CBS 122.63 | Plywood of Betula sp. | Finland, Helsinki | – / – | – / – |
| CBS 102045; EXF-2524; MZKI B-1006 | Hypersaline water | Spain, Barcelona, Salines de la Trinitat | DQ780351 / – | EF101378 & EF101411 |
| CBS 114065 | Outdoor air | Germany, Stuttgart | – / – | – / – |
| CPC 10944 | Gardening peat substrate | Russia, Kaliningrad | DQ780350 / – | – / – |
| EXF-131; MZKI B-1005 | Hypersaline water | Slovenia, Sečovlje saltern | AJ238670 / – | – / – |
| EXF-328 | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – / – |
| EXF-385 | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – / – |
| EXF-446 | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – / – |
| EXF-455 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780349 / – | EF101375 & EF101412 |
| EXF-458 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780345 / – | EF101374 & EF101409 |
| EXF-461 | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – / – |
| EXF-464 | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – / – |
| EXF-465 | Hypersaline water | Slovenia, Sečovlje saltern | – / – | – / – |
| EXF-598 | Hypersaline water | Spain, Santa Pola | – / – | EF101377 |
| EXF-644 | Hypersaline water | Spain, Santa Pola | – / – | – / – |
| EXF-645 | Hypersaline water | Spain, Santa Pola | – / – | – / – |
| EXF-649 | Hypersaline water | Spain, Santa Pola | – / – | – / – |
| EXF-715 | Hypersaline water | Dominican Republic, saltern | – / – | – / – |
| EXF-738 | Bathroom | Slovenia | DQ780348 / – | EF101383 & EF101414 |
| EXF-739 | Bathroom | Slovenia | DQ780344 / – | EF101381 & EF101407 |
| EXF-781; MZKI B-899 | Hypersaline water | Slovenia, Sečovlje | – / – | – / – |
| EXF-788 | Hypersaline water | Slovenia, Sečovlje | – / – | – / – |
| EXF-962 | Bathroom | Slovenia | DQ780347 / – | EF101382 & EF101413 |
| EXF-965 | Bathroom | Slovenia | – / – | – / – |
| EXF-1069 | Hypersaline water | Israel, Eilat saltern | – / – | EF101376 |
| EXF-1061 | Hypersaline water | Israel, Dead Sea | DQ780346 / – | EF101379 & EF101408 |
| EXF-1726 | Hypersaline water | Israel, Dead Sea | – / – | – / – |
| EXF-1732 | Hypersaline water | Israel, Eilat saltern | – / – | DQ780928 |
| – | Bryozoa sp. | – | AJ557744 / – | – / – |
| – | Nasal mucus | – | AF455481 / – | – / – |

**Cladosporium spinulosum**

| EXF-333 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780404 / – | – / – |
| EXF-334 T | Hypersaline water | Slovenia, Sečovlje saltern | DQ780406 / – | EF101355 & EF101450 |
| EXF-382 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780407 / DQ780936 | EF101356 & EF101449 |

**Cladosporium subinflatatum**

| EXF-343 T; CPC 12041 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780405 / – | EF101353 & EF101448 |

**Cladosporium tenuissimum**

| ATCC 38027 | Soil | New Caledonia | AF393724 / – | – / – |
| EXF-324 | Hypersaline water | Slovenia, Sečovlje saltern | – / DQ780926 | – / – |
| EXF-371 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780396 / – | – / – |
| EXF-452 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780397 / – | – / – |
| EXF-563 | Hypersaline water | Namibia, saltern | DQ780398 / – | – / – |

**Cladosporium velox**

| CBS 119417 T; CPC 11224 | Bamboo sp. | India, Charidij | DQ780361 / DQ780937 | EF101388 & EF101456 |
| EXF-466 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780359 / – | EF101386 & EF101387 |
| EXF-471 | Hypersaline water | Slovenia, Sečovlje saltern | DQ780360 / – | EF101387 & EF101387 |
Cultivation and microscopy
For growth rate determination and phenetic description of colonies, strains were point inoculated on potato-dextrose agar (PDA, Difco), OA and Blakeslee malt extract agar (MEA, Samson et al. 2002) and incubated at 25 °C for 14 d in darkness. Surface colours were rated using the colour charts of Komerup & Wanscher (1967). For studies of microscopic morphology, strains were grown on synthetic nutrient agar (SNA, Gams et al. 2007) in slide cultures. SNA blocks of approximately 1 × 1 cm were cut out aseptically, placed upon sterile microscope slides, and inoculated at the upper four edges by means of a conidial suspension (Pitt 1979). Inoculated agar blocks were covered with sterile cover slips and incubated in moist chambers for 7 d at 25 °C in darkness. The structure and branching pattern of conidiophores were observed at magnifications × 100, × 200 and × 400 in intact slide cultures under the microscope without removing the cover slips from the agar blocks. For higher magnifications (× 400, × 1 000) cover slips were carefully removed and mounted in lactic acid with aniline blue.

Morphological parameters
Morphological terms follow David (1997), Kirk et al. (2001) and Schubert et al. (2007 – this volume). Conidiophores in Cladosporium are usually ascending and sometimes poorly differentiated. Though the initiation point of conidiophore stipes could sometimes be determined only approximately, their lengths were in some cases useful for distinguishing morphologically similar species when observed in slide cultures. The branching patterns can be rotationally symmetric or unilateral. Characters of conidial scars were studied by light and scanning electron microscopy (SEM). Conidial chains show different branching patterns, determined by the numbers of conidia in unbranched parts, the nature of ramoconidia as well as their distribution in conidial chains. Measurements are given as (i) n1–n3 or (ii) (n1–n3)(n4–n5), with n1 = minimum value observed; n2 = maximum value observed; n3/n4 = first/third quartile. For conidia and ramoconidia also average values and standard deviations are listed. The values provided are based on at least 25 measurements for the conidiophores of each strain, and at least 50 measurements for conidia.

Ecophysiology
To determine the degree of halotolerance, strains were point-inoculated on MEA without and with additional NaCl at concentrations of 5, 10, 17 and 20 % NaCl (w/v) and incubated at 25 °C for 14 d. To determine cardinal temperature requirements for growth, plates were incubated at 4, 10, 25, 30 and 37 °C, and colony diameters measured after 14 d of incubation.

DNA extraction, sequencing and analysis
For DNA isolation strains were grown on MEA for 7 d. DNA was extracted according to Gerrits van den Ende & de Hoog (1999) by mechanical lysis of approx. 1 cm3 of mycelium. A fragment of the rDNA including the Internal Transcribed Spacer region 1, 5.8S rDNA and the ITS 2 (ITS) was amplified using the primers V9G (de Hoog & Gerrits van den Ende 1998) and LS266 (Masclaux et al. 1995). Sequence reactions were done using primers ITS1 and ITS4 (White et al. 1990). For amplification and sequencing of the partial actin gene, primers ACT-512F and ACT-783R were applied according to Carbone & Kohn (1999). For amplification and sequencing of the β-tubulin gene primers T1 and T22 were used according to O’Donnell & Cigelnik (1997). A BigDye terminator cycle sequencing kit (Applied Biosystems, Foster City, CA, U.S.A.) was used in sequence reactions. Sequences were obtained with an ABI Prism 3700 DNA Analyzer (Applied Biosystems). They were assembled and edited using SeqMan v. 3.61 (DNASTar, Inc., Madison, U.S.A.). Sequences downloaded from GenBank are indicated in the trees by their GenBank accession numbers; newly generated sequences are indicated by strain numbers (see also Table 1). Sequences were automatically aligned using ClustalX v. 1.81 (Jeanmougin et al. 1998). The alignments were adjusted manually using MEGA3 (Kumar et al. 2004). Phylogenetic relationships of the taxa were estimated from aligned sequences by the maximum parsimony criterion as implemented in PAUP v. 4.0b10 (Swofford 2003). Data sets of the SSU rDNA, ITS rDNA and the β-tubulin and actin genes are analysed separately. Species of Cladosporium s. str. were compared with various taxa of the Mycosphaerellaceae using SSU rDNA sequences and Fusarium effusum G. Winter (Venturicaceae) as outgroup. The other data sets focus on Cladosporium s. str., using Cladosporium salinae Zalar, de Hoog & Gunde-Cimerman as an outgroup, because this species was most deviant within Cladosporium in the SSU rDNA analysis (see below). Heuristic searches were performed on all characters, which were unordered and equally weighted. Gaps were treated as missing characters. Starting tree(s) were obtained via stepwise, random, 100 times repeated sequence addition. Other parameters included a “MaxTrees” setting to 9 000, the tree-bisection-reconnection as branch-swapping algorithm, and the “MulTrees” option set to active. Branch robustness was tested in the parsimony analysis by 10 000 search replications, each on bootstrapped data sets using a fast step-wise addition bootstrap analysis. Bootstrap values larger than 60 are noted near their respective branches. Newly generated sequences were deposited in GenBank (www.ncbi.nlm.nih.gov); their accession numbers are listed in Table 1. Alignments and trees were deposited in TreeBASE (www.treebase.org).

Table 1. (Page 158–160).

a Abbreviations used: ATCC = American Type Culture Collection, Virginia, U.S.A.; CBS = Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands; CPC = Culture Collection of Pedro Crous, housed at CBS, Utrecht, The Netherlands; dH = de Hoog Culture Collection, housed at CBS, Utrecht, The Netherlands; EXF = Culture Collection of Extremophilic Fungi, Ljubljana, Slovenia; IFO = Institute for Fermentation, Culture Collection of Microorganisms, Osaka, Japan; IMI = The International Mycological Institute, Egham, Surrey, U.K.; MZKI = Microbiological Culture Collection of the National Institute of Chemistry, Ljubljana, Slovenia; UAMH = University of Alberta Microfungus Collection, Alberta, Canada; VKM = All-Russian Collection of Microorganisms, Russian Academy of Sciences, Institute of Biochemistry and Physiology of Microorganisms, Pushchino, Russia; NT = ex-neotype strain; T = ex-type strain.

b Reference: de Hoog et al. 1999; Park et al. 2004; Braun et al. 2003; Buzina et al. 2003; Meklin et al. 2004; Haubold et al. 1998; Sert & Sterflinger, unpubl.; Curtis et al. 1994; Menkis et al. 2005; Managbanag et al. unpubl.; Crous et al. 2004; Wirth et al. 2002. All others are newly reported here.
Table 2. Statistical parameters describing phylogenetic analyses performed on sequence alignments of four different loci.

| Parameter                                | SSU rDNA | ITS rDNA¹ | β-tubulin¹ | Actin¹ |
|------------------------------------------|----------|-----------|------------|--------|
| Number of alignment positions            | 1031     | 498       | 654        | 210    |
| Number of parsimony informative characters (PIC) | 50       | 68        | 220        | 103    |
| Length of tree / number of steps         | 103      | 102       | 714        | 338    |
| Consistency Index (CI)                   | 0.631    | 0.804     | 0.538      | 0.586  |
| Retention Index (RI)                     | 0.895    | 0.975     | 0.883      | 0.885  |
| Rescaled Consistency Index (RC)          | 0.565    | 0.784     | 0.475      | 0.518  |
| Homoplasy index (HI)                     | 0.369    | 0.196     | 0.462      | 0.414  |
| Number of equally parsimonious trees retained | 30     | 600       | 90         | 32     |

¹Including the internal transcribed spacer region 1 and 2 and the 5.8S rDNA.
²Including partial sequences of 4 exons and complete sequences of 3 introns.
³Including partial sequences of 3 exons and 2 introns.
RESULTS

Descriptive statistical parameters of phylogenetic analyses and calculated tree scores for each analysed sequence locus are summarised in Table 2. Mainly reference material such as ex-type or ex-neotype strains was analysed on the level of SSU rDNA sequences. Downloaded and newly generated SSU rDNA sequences of members of *Cladosporium* s. str. were compared with related taxa of the *Mycosphaerellaceae*, *Dothioraceae* and *Dothideaceae*. The somewhat more distantly related *Fusicladium effusum* (Venturiaeaceae) (Braun et al. 2003: Fig. 2) was selected as outgroup. *Anungitopsis amoena* R.F. Castañeda & Dugan (now placed in *Fusicladium* Bonord., see Crous et al. 2007b), also a member of the *Venturiaeaceae*, was included in the analyses. All taxa included in the SSU rDNA analysis belong to the *Dothideomycetes* (Schoch et al. 2006), within which the ingroup is represented by the orders *Capnodiales* (*Davidiellaceae*, *Mycosphaerellaceae*, *Teratosphaeriaceae*) and *Dothideales* (*Dothioraceae*, *Dothideaceae*) (see also Schoch et al. 2006). The genus *Cladosporium*, of which some species are linked to *Davidiella* Crous & U. Braun teleomorphs (Braun et al. 2003), forms a statistically strongly supported monophyletic group (*Davidiellaceae*). It also accommodates species newly described in this paper, namely, *C. halotolerans* Zalar, de Hoog & Gunde-Cimerman, *C. fusiforme* Zalar, de Hoog & Gunde-Cimerman, *C. dominicanum* Zalar, de Hoog & Gunde-Cimerman, *C. salinae*, *C. psychrotolerans* Zalar, de Hoog & Gunde-Cimerman, *C. velox* Zalar, de Hoog & Gunde-Cimerman and *C. spinulosum* Zalar, de Hoog & Gunde-Cimerman (Fig. 1). A sister group relationship of *Cladosporium* s. str. with a clade of taxa characterised, among others, by *Mycosphaerella* Johanson teleomorphs, containing various anamorphic genera such as *Septoria* Sacc.,...
Ramularia Unger, Cercospora Fresen., Pseudocercospora Speg., "Trimmatostroma" Corda (now Catenulostroma Crous & U. Braun) (see Crous et al. 2004, 2007a – this volume) and the somewhat cladosporium-like genus Devriesia Seifert & N.L. Nick. (Seifert et al. 2004), was statistically only moderately supported (Fig. 1), whereas in an analogous analysis by Braun et al. (2003: Fig. 2) it was highly supported. These data also support the conclusion by Braun et al. (2003) and Crous et al. (2006) that Cladosporium is not a member of the distantly related Herpotrichiellaceae (Chaetothyriomycetes), which is also rich in cladosporium-like taxa (Crous et al. 2006). None of the fungi isolated from hypersaline environments belonged to the Herpotrichiellaceae. The SSU rDNA sequences do not resolve a phylogenetic structure within Cladosporium s. str. Only a moderately supported clade comprising C. halotolerans, C. dominicanum, C. velox, C. sphaerospermum and C. fusiforme is somewhat distinguished from a statistically unsupported clade with C. herbarum (Pers. : Fr.) Link, C. cladosporioides (Fresen.) G.A. de Vries, C. oxysporum Berk. & Broome, C. spinulosum, and C. psychrotolerans, etc. Because C. salinae appeared most distinct within the genus Cladosporium in analyses of the SSU rDNA (Fig. 1), it was used as outgroup in analyses of the ITS rDNA and the β-tubulin and actin genes.

Analyses of the more variable ITS rDNA and partial β-tubulin and actin gene introns and exons supported the species clades of C. halotolerans, C. dominicanum, C. sphaerospermum, C. fusiforme and C. velox (Figs 2–4), of which C. velox was distinguished in the β-tubulin tree by a particular long terminal branch of the only sequenced strain (Fig. 3). Cladosporium salinae also clustered as a well-supported species clade in preliminary analyses using various Mycosphaerella species as outgroup (not shown). All strains of C. langeronii (Fonseca, Leão & Nogueira) Vuill. are particularly well distinguishable from other Cladosporium species by strikingly slow-
Cladosporium sphaerospermum SpecieS coMplex

Growing colonies at all tested temperatures and relatively large, oblong conidia. However, phylogenetic analyses of the β-tubulin and actin gene indicate that C. langeronii presents two cryptic species (Figs 3–4). The species clade of C. psychrotolerans is moderately supported in analyses of the actin gene but highly by means of the β-tubulin gene. It is evident from all three analyses (Figs 2–4) that C. langeronii and C. psychrotolerans are closely related species. The species node of Cladosporium spinulosum, which is morphologically clearly distinguished from all other species by its conspicuous ornamentation consisting of digitate projections (Fig. 5), is supported by β-tubulin (Fig. 3) and actin (Fig. 4) sequence data but not by those of the ITS rDNA (Fig. 2). Analyses of all loci, however, indicate that it is a member of the C. herbarum complex.

The analyses of sequences of the ITS and the β-tubulin and actin gene introns and exons (Figs 2–4) do not allow the full elucidation of phylogenetic relationships among these Cladosporium species. Statistical support of the interior tree branches resulting from analyses of the β-tubulin and actin genes is low (bootstrap values mostly < 50 %). While the sister group relationship of C. sphaerospermum and C. fusiforme is highly supported in the analysis based on the β-tubulin gene, analysis of the ITS rDNA indicate that these two species are unrelated, and that C. sphaerospermum is closely related to C. dominicanum. It is clear from the data that the species morphologically resembling C. sphaerospermum are not phylogenetically closely related and that the data we present here do not allow their classification in natural subgroups of the genus Cladosporium. Only C. spinulosum was placed in all analyses among species of the C. herbarum complex.

Fig. 4. One of 32 equally most parsimonious and equally looking phylogenetic trees based on a heuristic tree search using aligned exons and introns of the partial actin gene. The tree was randomly selected. Support based on 10 000 replicates of a fast step-wise addition bootstrap analysis is indicated near the branches. Trees were rooted with the strains of Cladosporium salinae. Most monophyletic species clades received high, but deeper branches weak or no, bootstrap support (CI = 0.586, RI = 0.885, PIC = 103).
and all analyses supported close relatedness of *C. langeronii* and *C. psychrotolerans*.

The majority of species described here have slightly ornamented conidia ranging from minutely verruculose (*C. fusiforme*, *C. langeronii*, *C. psychrotolerans*, *C. sphaerospermum*, *C. velox*) to verrucose (*C. halotolerans*) (Fig. 5). The verrucose conidia of *C. halotolerans* can be recognised also under the light microscope and used as a distinguishing character. Almost smooth to minutely verruculose conidia are encountered in *C. dominicanum* and *C. salinae* (Fig. 5). *Cladosporium spinulosum*, a member of the *C. herbarum* species complex, has conidia with a digitate ornamentation that can appear spinulose under the light microscope; however, when using the SEM it became clear that its projections have parallel sides and a blunt end (Fig. 5).

**DISCUSSION**

The genus *Cladosporium* was established by Link (1816) who originally included four species, of which *C. herbarum* is the type species of the genus (Clements & Shear 1931). In 1950, von Arx reported a teleomorph connection for this species with *Mycosphaerella tassiana* (De Not.) Johanson. Based on SSU rDNA data the majority of *Mycosphaerella* species, including the type species of the genus, *M. punctiformis* (Pers.) Starbäck, clustered within the *Mycosphaerellaceae*, a family separated from *M. tassiana* (Braun et al. 2003). Therefore, *Mycosphaerella tassiana* was reclassified as *Davidiella tassiana* (De Not.) Crous & U. Braun, the type of the new genus *Davidiella*. All anamorphs with a cladosporium- and heterosporium-like appearance and with a supposed *Dothideomycetes* relationship were maintained under the anamorph name *Cladosporium*, morphologically characterised by scars with a protuberant hilum consisting of a central dome surrounded by a raised rim (David 1997).

The concept of distinguishing ramoconidia from secondary ramoconidia has been adopted from Schubert et al. (2007). In the species described here, ramoconidia have been observed often in *C. sphaerospermum*, sometimes in *C. psychrotolerans*, *C. langeronii* and *C. spinulosum*, and only sporadically in all other species. Therefore, ramoconidia can be seen as important for distinguishing species although sometimes, they can be observed only with difficulty. When using ramoconidia as a diagnostic criterion, colonies only from SNA and not older than 7 d should be taken into account.

*Cladosporium sphaerospermum* was described by Penzig (1882) from decaying *Citrus* leaves and branches in Italy. He described *C. sphaerospermum* as a species with (i) branched, septate and dark conidiophores having a length of 150–300 µm and a width of the main conidiophore stipe of 3.5–4 µm, (ii) spherical to ellipsoidal, acrogenously formed conidia of 3.4–4 µm diam, and (iii) ramoconidia of 6–14 × 3.5–4 µm. Penzig’s original material is not known to be preserved. Later, a culture derived from CBS 193.54, originating from a human nail, was accepted as typical of *C. sphaerospermum*. However, de Vries (1952), incorrectly cited it as “lectotype”, and thus the same specimen is designated as neotype in this study (see below), with the derived culture (CBS 193.54)
used as ex-neotype strain. Numerous strains with identical or very similar ITS rDNA sequences as CBS 193.54 were isolated from hypersaline water or organic substrata including plants or walls of bathrooms. It is not clear yet whether surfaces in bathrooms and of plants, colonised by *C. sphaerospermum*, can have a similar low water activity as sallters. In our experiments, the strains of this species, however, grew under *in vitro* conditions at a water activity of up to 0.860, while Hocking *et al.* (1994) and Alhara *et al.* (2002) reported that it can grow even at 0.815. Therefore, we consider *C. sphaerospermum* as halo- or osmotolerant. Hardly any reports are available unambiguously proving that *C. sphaerospermum* is a human pathogen. It is therefore possible that CBS 193.54 was not involved in any disease process but rather occurred as a contaminant on dry nail material. *Cladosporium sphaerospermum* is a phylogenetically well-delineated species (Figs 2–4).

Strains of *C. halotolerans* were isolated sporadically from substrata such as peanut cell suspension, tissue culture, bathroom walls and as culture contaminants. This surprising heterogeneity of substrata suggests that *C. halotolerans* is distributed by air and that it can colonise whatever substrata available, although it may have its natural niche elsewhere. We have recurrently isolated it from hypersaline water of salters and other saline environments and it was also detected with molecular methods (but not isolated) from skin of a salt water dolphin. There are only few reports of this species from plants (Table 1). It is therefore possible that *C. halotolerans* is a species closely linked to salty or hypersaline environments although additional sampling is necessary to prove that. *Cladosporium halotolerans* is morphologically recognisable by relatively oblong to spherical, coarsely rough-walled conidia. The ITS rDNA sequence of a fungus in the skin of a bottlenose dolphin, suffering from lobomycosis, is identical to the sequences of *C. halotolerans*. This sequence was deposited as *Lacazia loboii* Taborda, V.A. Taborda & McGinnis (GenBank AF035674) by Haubold *et al.* (1998), who apparently concluded wrongly that a fungus with a *cladosporium*-like ITS rDNA sequence similar to that of *C. halotolerans* can be the agent of lobomycosis. Later, Herr *et al.* (2001) showed that *Lacazia loboii* phylogenetically belongs to the Onygenales on the basis of amplified SSU rDNA and chitin synthase-2 gene sequences generated from tissue lesions. By this, they confirmed an earlier supposition by Lacaz (1996) who reclassified the organism as *Paracoccidioides loboii* O.M. Fonseca & Silva Lacaz (*Onygenales*). It is therefore possible that *C. halotolerans* was not the main etiological agent for the lobomycosis and it was colonising the affected dolphin skin secondarily while inhabiting other seawater habitats.

*Cladosporium langeronii* and *C. psychrotolerans* are closely related but *C. langeronii* is particularly well distinguishable from all other *Cladosporium* species by its slow growing colonies (1–7 mm diam / 14 d) and relatively large conidia (4–5.5 × 3–4 μm). *Cladosporium psychrotolerans* has smaller conidia (3–4 × 2.5–3 μm) but a similar length : width ratio and faster expanding colonies (8–18 mm diam / 14 d). *Cladosporium langeronii* is most likely a complex of at least two species. Strains isolated from the Arctic and the Antarctic may need to be distinguished from *C. langeronii* *s. str.* on species level. This inference is particularly supported by analyses of the β-tubulin and actin genes (Figs 3–4). *Cladosporium langeronii* *s. str.* represented by an authentic strain of *Hormodendrum langeronii* Fonseca, Leão & Nogueira, CBS 189.54 (Trejos 1954), has been isolated from a variety of substrata but is tolerating only up to 10 % NaCl. It was originally described by da Fonseca *et al.* (1927a, b) and subsequently reclassified as *Cladosporium langeronii* by Vuillemin (1931). The authentic strain derived from an ulcerating nodular lesion on the arm of a human patient. Because other strains of this species are ubiquitous saprobes originating from various substrata, we suspect that *C. langeronii* is not an important human pathogen. *Cladosporium psychrotolerans* has been isolated from hypersaline environments only, and tolerates up to 20 % NaCl in culture media.

In general, the human- or animal-pathogenic role of the *Cladosporium* *sphaerospermum*-like species described here seems to be limited. It is possible that pathogenic species of *Cladophialophora* have been misidentified as *C. sphaerospermum* or as other species of *Cladosporium* (de Hoog *et al.* 2000). Alternatively, true *Cladosporium* species isolated as clinical strains could have been secondary colonisers since they are able to dwell on surfaces poor in nutrients, possibly in an inconspicuous dormant phase and may then be practically invisible. More likely, they could be air-borne contaminations of lesions, affected nails etc. (Summerbell *et al.* 2005) or are perhaps disseminated by insufficiently sterilised medical devices, as melanised fungi can be quite resistant to disinfectants (Phillips *et al.* 1992). They can easily be isolated and rapidly become preponderant at isolation and thus difficult to exclude as etiologic agents of a disease. For example, in 2002, a case report on an intrabronchial lesion by *C. sphaerospermum* in a healthy, non-asthmatic woman was described (Yano *et al.* 2002), but we judge the identification of the causal agent to remain uncertain, as it was based on morphology alone and no culture is available. The present authors have the opinion that all clinical cases ascribed to *Cladosporium* species need careful re-examination.

**General characteristics and description of *Cladosporium sphaerospermum*-like species**

The present paper focuses on *Cladosporium* strains isolated from hypersaline environments. Comparison of data from deliberate sampling and analysis of reference strains from culture collections inevitably leads to statistical bias, and therefore a balanced interpretation of ecological preferences of the species presented is impossible. Nevertheless, some species appeared to be consistent in their choice of habitat, and for this reason we summarise isolation data for all species described. Strains belonging to a single molecular clade proved to have similar cultural characteristics and microscopic morphology. Although within most of the species there was some molecular variation noted (particularly when intron-rich genes were analysed), some consistent phenetic trends could be observed.

Conidiophores of all *C. sphaerospermum*-like species lack nodule inflations (McKemy & Morgan-Jones 1991). They are usually ascending and can sometimes be poorly differentiated from their supporting hyphae. Though the initiation point of conidiophore stipes could sometimes be determined only approximately, their lengths were in some cases useful for distinguishing *Cladosporium* species of *Cladophialophora* species closely linked to salty or hypersaline habitats. Generally, the branched part of a conidiophore forms a complex tree-like structure. The number and orientation of early formed secondary ramoconidia, however, determines whether it is rotationally symmetric or unilateral.

The variability in ITS rDNA sequences observed in all *C. sphaerospermum*-like species (about 10 %) spans the variation observed in all members of the genus *Cladosporium* sequenced to date. Thus, the *C. sphaerospermum*-like species described here may not present a single monophyletic group but may belong to various species complexes within *Cladosporium*. Verifying existing literature with sequence data of these species (Wirsel *et al.* 2002, Park *et al.* 2004), we noticed that names of the common saprobes seem to be distributed nearly at random over phylogenetic trees.
For most commonly used names, no type material is available for sequencing. Also verification of published reports is difficult without available voucher strains.

*Cladosporium cladosporioides* was incorrectly lectotypified based on CBS 170.54 (de Vries 1952), which Bisby considered a standard culture of *C. herbarum*. The *Cladosporium cladosporioides* species complex requires revision, and will form the basis of a future study. *Cladosporium herbarum* is maintained as a dried specimen in the Leiden herbarium; Prasi & de Hoog (1988) selected CBS 177.71 as a representing living strain. Strains, earlier accepted as living representatives of *C. herbarum*, CBS 177.71 and CBS 812.71 (Prasi & de Hoog 1988, Wirsel et al. 2002) and ATCC 66670 (Braun et al. 2003, as Davidiella tassiana) have been re-identified as *C. brunnei* Linder by Schubert et al. (2007 – this volume). Ho et al. (1999) used strain ATCC 38027 as a representative of *C. tenuissimum* Cooke and this strain has identical ITS sequences as the non-deposited *C. tenuissimum* material used by Morica et al. (1999). We tentatively accept this concept although we could not include ATCC 38027 in our analyses. The ITS sequence of strain CBS 125.80, identified by Wirsel et al. (2002) as *C. oxysporum*, is identical to the sequence of ATCC 38027. Strain ATCC 76499, published by Ho et al. (1999) as *C. oxysporum*, appears to be identical to a number of currently unidentified *Cladosporium* strains from Slovenian salters that compose a cluster separate from all remaining species. Strains of this cluster, represented in Fig. 2 by strain ATCC 76499, morphologically resemble *C. oxysporum*.

Strain CBS 300.96 has not been identified to species level in the present study. It clusters outside the species clade of *C. sphaerospermum*, with the latter being its nearest relative. CBS 300.96 differs from *C. sphaerospermum* by having smaller structures: conidiophore stipes [(5–)20–80 × (2–)2.5–3(–4) μm], 0–1 septate ramoconidia [(13–)19–27(–32) × 2–2.5 μm], conidia [(2.5–)3–3.5(–4) × (2–)2–2.5(–3) μm] and secondary ramoconidia [(5–)9–18–30 × (2–)2.5(–3) μm]. However, based on a single isolate, we currently refrain from describing it as a new species.

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### Key to species treated in this study

Macro-morphological characters used in the key are from colonies grown on PDA and MEA 14 d at 25 °C, if not stated otherwise; microscopical characters are from SNA slide cultures grown for 7 d at 25 °C.

1. Conidial ornamentation conspicuously echinulate / digitate because of up to 1.3 μm long projections that have more or less parallel sides .......................................................... *C. spinulosum* ................................. 2

2. Conidiophores micronematous, poorly differentiated, once or several times geniculate-sinuous, short, up to 60 μm long; terminal conidia obovoid .................................................................................. *C. salinae* ................................. 3

3. Secondary ramoconidia 0–3(–4)-septate; septa of conidiophores and conidia darkened and thickened .......................................................... *C. sphaerospermum* ................................. 4

4. Conidiophores (5–)10–50(–300) × (2–)2.5–3(–5.5) μm; terminal conidia (2–)3–4(–6) × (2–)2.5–3(–5) μm; secondary ramoconidia (5–)7–12(–37.5) × (2–)2.5–3(–6.5) μm; ramoconidia sporadically formed ........................................................................ *C. halotolerans* ................................. 5

5. Terminal conidium usually fusiform .................................................................................. *C. fusiforme* ................................. 6

6. Conidia and secondary ramoconidia irregularly verruculose to sometimes loosely verrucose; radial growth on PDA at 25 °C after 14 d typically less than 5 mm .......................................................... *C. langeronii* ................................. 7

7. Conidiophores (3–)3.5–4(–7.5) μm wide, thick-walled; conidiogenous loci and conidial hila 0.5–2 μm diam; ramoconidia sometimes formed with a broadly truncate, up to 2 μm wide non-cladosporioid base; no growth observed after 14 d at 30 °C on MEA .................................................................................. *C. psychrotolerans* ................................. 8

8. Secondary ramoconidia (4–)6.5–13(–24.5) μm long; no visible colony growth after 14 d at 10 °C on MEA .................................................................................. *C. dominicanum* ................................. 9

9. Secondary ramoconidia mostly longer, (3.5–)5.5–19(–42) μm; radial growth of colonies after 14 d at 10 °C on MEA more than 5 mm .................................................................................. *C. velox* .................................
Description of Cladosporium species

Cladosporium dominicanum Zalar, de Hoog & Gunde-Cimerman, sp. nov. MycoBank MB510955. Fig. 6.

Etymology: Refers to the the Dominican Republic, where most strains were encountered.

Conidiophora lateralia vel terminalia ex hyphis rectis orundis; stipes longitudine variabilis, (5–)10–100(–200) × (1.5–)2.5–5.3 μm, olivaceo-brunneus, levis vel lenticulcrum, tenutunicatus, plerumque uncinularis, simile vel ramosum. Conidiorum catenatorum undique divergentes, ad 8 conidia in parte continua continentes. Cellulae conidiogenae indistinctae. Conidia levia vel lenticulcrum, dilute brunnea, uninciliaris, plerumque breviter ovoidea, utrinque angustata, (2.5–)3–3.5(–5.5) × (2–)2.5–2.5(–5.5) μm, long.: lat. I. 1.4–1.6; ramoconidia secundaria cylindrica vel quasi globosa, 0–1-septata, (4.5–)6.5–13(–24.5) × (2–)2.5–3(–4.5) μm, ad 4 cicatrices terminales ferentia; cicatrices inspissatae, protuberantes, 0.5–1.2 μm diam. Hyphae vagina polysaccharidicae carentes.

Mycelium without extracellular polysaccharide-like material.

Conidiophores arising laterally and terminally on erect hyphae, micromonematous and semimicromonematous, stipes of variable length, (5–)10–100(–200) × (1.5–)2.5–5.3 μm, olivaceo-brown, smooth to minutely verruculose, thin-walled, almost non-septate, unbranched or branched. Conidial chains branching in all directions, up to eight conidia in the unbranched parts. Conidigenous cells undifferentiated. Ramoconidia rarely formed. Conidia smooth to minutely verruculose, subhyaline to light brown, non-septate, usually short-ovoid, narrower at both ends, length : width ratio = 1.4–1.6; (2.5–)3–3.5(–5.5) × (2–)2.5–2.5(–5.5) μm [av. (± SD) 1.4 ± 0.6] (2.5–)2.5–3(–2.5) μm; (av. ± SD) 3.4 ± 0.2; secondary ramoconidia cylindrica to almost spherical, 0–1-septate, (4.5–)6.5–13(–24.5) × (2–)2.5–3(–4.5) μm [av. (± SD) 10.3 ± 5.2] 2.7 ± 0.6], with up to four distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.5–1.2 μm diam.

Cultural characteristics: Colonies on PDA reaching 18–36 mm diam, olive-yellow (2D6), hairy granular, flat or slightly furrowed, with flat margin. Droplets of light reseda-green (2E6) exudate sometimes present. Reverse dark green to black. Colonies on OA reaching 19–33 mm diam, olive (2DF5), loosely powdery with raised central part due to fasciculate bundles of conidiophores. Reverse dark green. Colonies on MEA reaching 30–32 mm diam, reseda green (2C6), velutinous, furrowed, with undulate margin. Reverse dark green-brown. Colonies on MEA + 5 % NaCl reaching 37–41 mm diam, reseda-green (2C6), radially furrowed, velvety, sporulating in the central part or all over the colony, margin white and regular. Reverse brownish green.

Maximum tolerated salt concentration: 75 % of tested strains develop colonies at 20 % NaCl after 7 d, while after 14 d all strains grow and sporulate.

Cardinal temperatures: No growth at 4 and 10 °C, optimum 25 °C (30–32 mm diam), maximum 30 °C (2–15 mm diam), no growth at 37 °C.

Specimen examined: Dominican Republic, from hypersaline water of salt lake Enriquillo, coll. Nina Gunde-Cimerman, Jan. 2001, isol. P. Zalar 25 Feb. 2001, CBS H-19733, holotype, culture ex-type EXF-732 = CBS 119415.

Habitats and distribution: Fruit surfaces; hypersaline waters in (sub)tropical climates.

Differential parameters: No growth at 10 °C, ovoid conidia, large amounts of sterile mycelium.

Strains examined: CPC 11683, EXF-696, EXF-718, EXF-720, EXF-727, EXF-732 (= CBS 119415; ex-type strain).

Note: Cultures of C. dominicanum sporulate less abundantly than C. sphaerospermum and C. halotolerans and tend to lose their ability to sporulate with subculturing.

Cladosporium fusiforme Zalar, de Hoog & Gunde-Cimerman, sp. nov. MycoBank MB510997. Fig. 7.

Etymology: Refers to its usually fusiform conidia.

Conidiophora erecta, lateralia vel terminalia ex hyphis rectis orundis; stipes of variable length, (10–)25–50(–100) × (2–)2.5–3.5(–4) μm, olivaceo-brown, smooth and thick-walled, regularly-septate (cell length 9–23 μm), mostly unbranched. Conidial chains branching in all directions, up to 5 conidia in the unbranched parts. Conidigenous cells undifferentiated. Ramoconidia rarely formed. Conidia minutely verruculose, light brown, aseptate, usually fusiform and narrower at both ends, length : width ratio = 1.8–2.0; (2.5–)3.5–5.6(–5.5) × (2–)2.5–2.5(–3) μm [av. (± SD) 4.4 ± 0.8] 2.2 ± 0.2; secondary ramoconidia cylindrical, 0–1-septate, (5–)6(–)11(–22) × (2.5–)3.5–3.5(–3) μm [av. (± SD) 9.0 ± 4.7] 2.6 ± 0.3], with up to 4 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.7–1.0 μm diam.

Cultural characteristics: Colonies on PDA reaching 20–26 mm diam, dull green (3E3), granular due to profuse sporulation, flat, with flat margin. Sterile mycelium absent. Reverse blackish green. Colonies on OA reaching 24–28 mm diam, olive (3F3), granular in concentric circles, consisting of two kinds of conidiophores (low and high), flat, with flat margin. Reverse black. Colonies on MEA reaching 23–28 mm diam, olive (3E5), deeply furrowed, velvety (sporulating all over) with undulate, white margin. Reverse brownish green. Colonies on MEA + 5 % NaCl reaching 28–43 mm diam, olive (3E6), granular due to profuse sporulation, slightly furrowed with flat, olive-grey (3F2) margin. Reverse dark green.

Maximum tolerated salt concentration: Only one of three strains tested (CBS 452.71) developed colonies at 17 % NaCl after 14 d, the other two strains grew until 10 % NaCl.

Cardinal temperatures: For one of three strains (CBS 452.71) the minimum temperature of growth was 4 °C (6 mm diam), for the other two 10 °C (8–9 mm diam); optimum 25 °C (23–28 mm diam), maximum 30 °C (only strain CBS 452.71 grew 5 mm diam), no growth at 37 °C.

Specimen examined: Slovenia, from hypersaline water of Sečovlje saltmarshes, coll. and isol. L. Butinar, Dec. 1999, CBS H-19732, holotype, culture ex-type EXF-449 = CBS 119414.

Habitats and distribution: Osmotic environments worldwide.

Differential parameters: Oblong conidia, relatively low degree of halotolerance.

Strains examined: CBS 452.71, EXF-397, EXF-449 (= CBS 119414; ex-type strain).
Fig. 6. Cladosporium dominicanum. Macro- and micromorphological characters. A–D. Colony surface grown on PDA (A), OA (B), MEA (C) and MEA plus 5 % NaCl (D) of strains incubated for 14 d at 25 °C in darkness. E–F. Habit of conidiophores. G. Conidiophore. H–I. Secondary ramoconidia and conidia. E–I. All from 7-d-old SNA slide cultures. A, D, F–H, from EXF-2519; B, C, E from EXF-727; I, EXF-732 (ex-type strain). Scale bars A–D = 10 mm, E = 100 µm, F = 30 µm, G–I = 10 µm.
Fig. 7. Cladosporium fusiforme. Macro- and micromorphological characters. A–D. Colony surface grown on PDA (A), OA (B), MEA (C) and MEA plus 5 % NaCl (D) of strains incubated for 14 d at 25 °C in darkness. E–G. Habit of conidiophores, H–I. Ramoconidia and conidia. E–I. All from 7-d-old SNA slide cultures. A–H, from EXF-449 (ex-type strain); I, from CBS 452.71. Scale bars A–D = 10 mm, E = 100 μm, F–G = 30 μm, H–I = 10 μm.
Cladosporium halotolerans Zalar, de Hoog & Gunde-Cimerman sp. nov. MycoBank MB492439. Fig. 8.

Etymology: Refers to its halotolerant habit.

Conidiophora erecta, lateralia vel terminalia ex hyphis rectis oriunda; stipes longitudine variabilis, (5–)10–50(–300) × (2–)2.5–3(–5.5) μm, pallide olivace brunneus, levis vel leniter verruculosus, tenutunicatus, 0–3-septatus, interdum pluriseptatus, simplex, denticulatus. Conidiornae catenae undique divergentes, terminales ad 9 conidia continent. Ex corticis conidiigenae indistinctae. Conidia verrucosa, brunnea vel fusca, unicellularia, plerumque subglobosa vel globosa, raro breviter ovoidea, utrinque angustata, (2–)3–4(–6) × (2–)2.5–3(–5) μm, long. : lat. 1.2–1.5; ramoconidia secundaria cylindrica vel quasi globosa, 0(–1)-septata, (5–)7–12(–37.5) × (2–)2.5–3(–6.5) μm, ad 4 cicatrices terminales ferentia; cicatrices inspissatae, conspicuae, protuberantes, 0.7–1.0(–1.5) μm diam. Hyphae vagina polysaccharidica carentes.
Mycelium partly submerged, partly superficial; hyphae without extracellular polysaccharide-like material. Conidiophores erect, arising laterally and terminally from straight hyphae, stipes of variable length, (5–)10–50(–300) μm × (2–)2.5–3(–5.5) μm, pale olivaceous-brown, smooth to minutely verrucose, thin-walled, 0–3-septate, unbranched, with pronounced denticles. Conidial chains branching in all directions, terminal chains with up to 9 conidia. Conidiogenous cells undifferentiated. Ramoconidia rarely formed. Conidia verrucose, brown to dark brown, non-septate, usually subglobose to globose, less often short-ovoid, narrower at both ends, length : width ratio = 1.2–1.5; (2–)3–4(–6) × (2–)2.5–3(–5) μm [av. (± SD) 3.5 (± 0.7) × 2.7 (± 0.5)]; secondary ramoconidia cylindrical to almost spherical, 0–1-septate, (5–)7–12(–37.5) μm × (2–)2.5–3(–6.5) μm [av. (± SD) 10.3 (± 4.8) × 2.9 (± 0.6)], with up to 4 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.7–1.0(–1.5) μm diam.

Cultural characteristics: Colonies on PDA reaching 27–43 mm diam, olive (2F5), slightly furrowed, often covered with grey secondary mycelium, except at the marginal area where only sporulating structures can be observed. Margin white and regular, with submerged hyphae. Reverse pale green to black. Colonies on OA reaching 29–40 mm diam, olive (2F6), flat, uniform, granule due to profuse sporulation and fasciculate bundles of conidiophores, without sterile mycelium. Reverse dark green to black. Colonies on MEA reaching 18–44 mm diam, highly variable in colour, but mainly olive (2E5), and from flat with regular margin to deeply furrowed with undulate margin. Colony centre wrinkled with crater-shaped appearance. Reverse pale to dark green. Colonies on MEA + 5 % NaCl reaching 24–48 mm diam, olive (3E8), furrowed, velvety, with more pale, undulate margins. Reverse dark green to black.

Maximum tolerated salt concentration: Only 15 % of tested strains develop colonies at 20 % NaCl after 7 d, whereas after 14 d all cultures grow and sporulate.

Cardinal temperatures: No growth at 4 °C, optimum 25 °C (18–44 mm diam), maximum 30 °C (6–23 mm diam). No growth at 37 °C.

Specimen examined: Namibia, from hypersaline water of salters, coll. Nina Gunde-Cimerman, 1 Sep. 2000, isol. P. Zalar, 1 Oct. 2000, CBS H-19734, holotype, culture ex-type EF-572 = CBS 119416.

Habitats and distribution: Hypersaline water in subtropical climates; indoor environments; Arctic ice; contaminant in lesions of humans and animals; plant phyllosphere; rock.

Literature: Haubold et al. (1998), Meiklin et al. (2004).

Differential parameters: Verrucose conidia, short unbranched and non-septate conidiophores which arise laterally alongside erect hyphae.

Strains examined: CBS 191.54, CBS 573.78, CBS 626.82, dH 12862, dH 12991, dH 13191, EXF-228, EXF-380, EXF-565, EXF-567, EXF-571, EXF-572 (= CBS 119416, ex-type strain), EXF-648, EXF-698, EXF-703, EXF-944, EXF-972, EXF-977, EXF-1072, EXF-2372.

Notes: Cladosporium halotolerans strongly resembles C. sphaerospermum. Several strains of this species such as dH 12862, dH 12941, CBS 191.54 and UAMH 7686 have been isolated sporadically from various indoor habitats in Europe, Brazil and the U.S.A. and repeatedly from bathrooms in Slovenia (Table 1). Probably sometimes as uncertain culture contaminations, it has been isolated from plants (GenBank accession no. L25433), inner organs of a diseased frog (AY361982) and human brain (Kantarcioglu et al. 2002). The presence of C. halotolerans species in gypsum sediments entrapped in Arctic ice, the fact that it was repeatedly isolated from hypersaline water and possibly its presence in dolphin skin (see Discussion) suggest that it has a clear preference for (hyper)osmotic habitats. This is supported by its ability to grow at 20 % NaCl.

The telemorph of C. halotolerans is predicted to be a Davidiella species. Strain CBS 280.49 was isolated by J.A. van Arx from teleomorph material of a fungus labelled as Mycosphaerella hyperica (Auerw.) Starbäck on Hypericum perforatum in Switzerland. According to Aptroot (2006) this species may belong in Davidiella and produces a Septoria anamorph. In the original herbarium specimen, CBS H-4867, a Mycosphaerella telemorph was present, but no sign of a Cladosporium anamorph. We assume that CBS 280.49 was a culture contaminant.

Cladosporium langeronii (Fonseca, Leão & Nogueira) Vuill., Champ. Paras.: 78. 1931. Fig. 9.
Basionym: Hormodendrum langeronii Fonseca, Leão & Nogueira, Sci. Med. 5: 563. 1927.
≡ Cladosporium langeronii (Fonseca, Leão & Nogueira) Cif., Manuale di Micologia Medica, ed. 2: 488 (1960), comb. superfl.

Mycelium partly submerged, partly superficial; hyphae sometimes enveloped in polysaccharide-like material. Conidiophores erect or ascending, micronematous and macronematous, stipes of variable length, (20–)30–130(–200) × (3–)3.5–4.5(–6.5) μm, dark brown, rough- and thick-walled, regularly septate (cell length 9–22 μm), arising laterally and terminally from submerged or aerial hyphae, branched. Conidial chains dichotomously branched, up to 6 conidia in the unbranched parts. Conidiogenous cells undifferentiated, sometimes seceding and forming ramoconidia. Ramoconidia cylindrical, 0–1 septate, (10–)11–22(–42) × (3–)3.5–4.5(–5) μm, base broadly truncate, 2–3.5 μm wide, slightly thickened and somewhat darkened. Conidia irregularly verrucose to sometimes loosely verrucose, dark brown, non-septate, usually ovoid, length : width ratio = 1.3–1.5; conidial size [3–]4.5–5.8(–8) × (2–)3–4(–5) μm [av. (± SD) 4.8 (± 1.0) × 3.5 (± 0.6)]; secondary ramoconidia cylindrical to almost spherical, mostly 0–1–2-septate, (5–)7.5–12.5(–35.5) × (2.5–)3.4–5.5(–5.5) μm [av. (± SD) 10.7 (± 4.7) × 3.6 (± 0.8)], with 2, rarely 3 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.9–1.5(–2.3) μm diam.

Cultural characteristics: Colonies on PDA, OA and MEA with restricted growth, attaining 2.5–4.5, 1.5–7.0 and 1.0–5.5 mm diam, respectively. Colonies flat or heaped (up to 3 mm), dark green (30F4), with black reverse and slightly undulate margin with immersed mycelium. Sporulating on all media. On MEA + 5 % NaCl growth is faster, colonies attaining 8.5–12.0 mm diam, sporulating and growing deeply into the agar.

Maximum tolerated salt concentration: All strains develop colonies at 17 % NaCl after 14 d.

Cardinal temperatures: No growth at 4 °C, optimum / maximum 25 °C (1.0–5.5 mm diam), no growth at 30 °C.

Specimen examined: Brazil, from man ulcerated nodular mycosis of hand and arm, 1927, coll. and isol. da Fonseca, CBS H-19737, holotype, culture ex-type CBS 189.54.

Habitats and distribution: Polar ice and biomats; conifer wood and growing in polar ice; Herbarium specimen, CBS H-4867, a Mycosphaerella telemorph was present, but no sign of a Cladosporium anamorph. We assume that CBS 280.49 was a culture contaminant.
the strains studied, as well as with a clone from mycorrhizal roots (Menkis et al. 2005). The species is distributed worldwide, without any apparent predilection for a particular habitat. The strains from clinical cases probably were culture contaminants.

**Literature:** da Fonseca et al. (1927a, b).

**Differential parameters:** Restricted growth; lowest salt halotolerance taxon of all *C. sphaerospermum*-like species.

**Strains examined:** CBS 189.54 (ex-type strain), CBS 601.84, CBS 101880, CBS 109868, dH 11736, dH 12459 = EXF-999, dH 13833 = EXF-1933.

**Notes:** De Vries (1952) synonymised the isolate identified as *Hormodendrum langeronii* with *C. sphaerospermum*. Strains of this species have often been identified as *C. cladosporioides* (Buzina et al. 2003, Menkis et al. 2005) although it has slightly longer conidia.
**Cladosporium psychrotolerans** Zalar, de Hoog & Gunde-Cimerman, *sp. nov.* MycoBank MB492428. Fig. 10.

**Etyymology:** Refers to its ability to grow at low temperatures.

Mycelium partim submersum; hyphae vagina polysaccharidica carentes. Conidiophora erecta vel adscendentia; stipes (10–350–1000–(150) × (3.5–4.5–7.5) μm, olivaceous-brown, levis, crassitunicatus, complute regulariter septate (cellulis 10–40 μm longis), identidem dichotome ramosus. Conidionum catenae undique divergentes, terminales partes simplices ad 4 conidia continent. Celiae conidiogenae indistinctae. Ramoconidia primaria cylindrical, (18–)19–22–(43) × (2.5)–3.5–(4.5) μm, (0–1)-septata. Condia leves vel lentior verruculosa, dilute brunnea, unicellulare, globosa vel ovaloidea, (2.5–3.5–4.5) × (2–2.5–3–3) μm, long.; lat. 1.3–1.4; ramoconidia secundaria cylindrical, 0–(1–2)-septata, (5–8–16–36) × (2–2.5–3–5) μm, ad 4 cicatrices terminales ferentia; cicatrices inspissatae, conspicue, 0.5–2 μm diam.

**Mycelium** partly superficial partly submerged; hyphae without extracellular polysaccharide-like material. Conidiophores erect or ascending, macronematous, stipes (10–350–1000–(150) × (3.5–4–7.5) μm, olivaceous-brown, smooth or almost so, thick-walled, regularly septate (cell length 10–40 μm), arising laterally from aerial hyphae, repeatedly dichotomously branched. Conidial chains branching in all directions, up to 4 conidia in the unbranched parts. Ramoconidia sometimes formed, cylindrical, (18–19–22–(43) × (2.5)–3.5–(4.5) μm, aseptate, rarely 1-septate, with a broadly truncate base, up to 2 μm wide, unthickened or slightly thickened, somewhat darkened-refractive. Conidia smooth to minutely verruculose, light brown, non-septate, spherical to ovoid, length : width ratio = 1.3–1.4; conidial size (2.5–3–4.5) μm [av. (± SD) 3.4 (± 0.5) × 2.5 (± 0.2)]; secondary ramoconidia cylindrical, 0–(1–2)-septate, (5–8–16–36) × (2–2.5–3–5) μm [av. (± SD) 12.7 (± 0.5) × 3.0 (± 0.5)], with up to 4 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.5–2 μm diam.

**Cultural characteristics:** Colonies on PDA reaching 13–18 mm diam, velvety, olive (3F4) due to profuse sporulation, flat with straight margin. Reverse dark green. Colonies on OA reaching 13–15 mm diam, olive (2F8), of granular appearance due to profuse sporulation, aerial mycelium absent. Colonies either heaped or slightly furrowed, up to 2 μm wide, unthickened or slightly thickened, somewhat darkened-refractive. Conidia smooth to minutely verruculose, light brown, non-septate, spherical to ovoid, length : width ratio = 1.3–1.4; conidial size (2.5–3–4.5) μm, olivaceous-brown, smooth or almost so, thick-walled, regularly septate (cell length 10–40 μm), arising laterally from aerial hyphae, repeatedly dichotomously branched. Conidial chains branching in all directions, up to 4 conidia in the unbranched parts. Ramoconidia sometimes formed, cylindrical, (18–19–22–(43) × (2.5)–3.5–(4.5) μm, aseptate, rarely 1-septate, with a broadly truncate base, up to 2 μm wide, unthickened or slightly thickened, somewhat darkened-refractive. Conidia smooth to minutely verruculose, light brown, non-septate, spherical to ovoid, length : width ratio = 1.3–1.4; conidial size (2.5–3–4.5) μm [av. (± SD) 3.4 (± 0.5) × 2.5 (± 0.2)]; secondary ramoconidia cylindrical, 0–(1–2)-septate, (5–8–16–36) × (2–2.5–3–5) μm [av. (± SD) 12.7 (± 0.5) × 3.0 (± 0.5)], with up to 4 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.5–2 μm diam.

**Cardinal temperatures:** Minimum at 4 °C (5 mm diam), optimum and maximum at 25 °C (8–15 mm diam).

**Habitats and distribution:** Hypersaline water in the Mediterranean basin.

**Differential parameters:** Growth at 4 °C, maximal NaCl concentration 17 % NaCl, which differentiates it from other species with similar conidia, like *C. sphaerospermum*, *C. halotolerans* and *C. dominicanum*.

**Strains examined:** EXF-326, EXF-332, EXF-391 (= CBS 119412; ex-type strain), EXF-714.

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**Cladosporium salinae** Zalar, de Hoog & Gunde-Cimerman, *sp. nov.* MycoBank MB492438. Fig. 11.

**Etyymology:** Refers to salterns (= Latin *salinae*) as the habitat of this species.

Mycelium partim submersum; hyphae multa rostra lateralia ferentes, hyphae vagina polysaccharidica involutae. Conidiophora vix distincta, lateralia vel terminalia ex hypsis aeris oriunda; stipes longitudine variabilis, [5–]25–50–(60) × (2–2.5–3–4) μm, olivaceous-brown, levis vel lentier verruculosis, crassitunicatus, irregulariter dense septatus (cellulis 6–29 μm longis), simplex, interdum ramosus. Conidionum catenae undique divergentes, terminales ad 6 conidia continent. Celiae conidiogenae nonnumquam integratae, in summum sequentiam sympodialen denticulorum formantes. Conidia levia, interdum lentier verruculosa, dilute brunnea, unicellulata, plerumque fusiformia, (4.5–)5.5–7.5–(10) × (2–2.5–3–3.5) μm, long.; lat. 1.9–2.4; ramoconidia secundaria cylindrical, 0–(1–2)-septata, (7.5–)9.5–13.5–(19) × (2–2.5–3.5–4.5) μm, ad 5 cicatrices terminales ferentia; cicatrices inspissatae, conspicue, protuberantes, 0.7–1.8 μm diam.

**Mycelium** partly superficial partly submerged, with numerous lateral pegs, consistently enveloped in polysaccharide-like material. Conidiophores poorly differentiated, micronematous, stipes (5–)25–50–(60) × (2–2.5–3–4) μm, olivaceous-brown, smooth to often minutely verruculose or irregularly rough-walled, thick-walled, irregularly densely septate (length of cells 6–29 μm), arising laterally and terminally from aerial hyphae, unbranched, occasionally branched. Conidial chains branching in all directions, terminal chains with up to 6 conidia. Conidiogenous cells sometimes integrated, producing sympodial clusters of pronounced denticles at their distal ends. Conidia usually smooth, occasionally minutely verruculose, light brown, aseptate, usually oblong ellipsoidal to fusiform, length : width ratio = 1.9–2.4; (4.5–)5.5–7.5–(10) × (2–2.5–3–5) μm [av. (± SD) 6.7 (± 1.3) × 2.9 (± 0.4)]; secondary ramoconidia cylindrical, 0–(1–2)-septate, (7.5–)9.5–13.5–(19) × (2–2.5–3.5–4.5) μm [av. (± SD) 12.1 (± 3.3) × 3.2 (± 0.6)], with up to 5 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.7–1.8 μm diam.

**Cultural characteristics:** Colonies on PDA reaching 10–27 mm diam, granular, olive (2E4) due to profuse sporulation, with white undulate margin. Aerial mycelium absent. Colonies either heaped or radially furrowed, in the marginal area growing deeply into the agar. Reverse dark brown to dark green. Colonies on OA reaching 7–20 mm diam, olive (3E6), of granular appearance due to profuse sporulation, aerial mycelium present. Margin either undulate or arachnoid, deeply furrowed. Reverse pale brown to dark green. Colonies on MEA reaching 8–19 mm diam, velvety, reseda-green (2E6), heaped. Margin furrowed, growing deeply into the agar. Colonies on MEA with 5 % NaCl growing much faster than on other media, reaching 25–38 mm diam, of different colours, mostly reseda-green (2E6) and granulate due to profuse sporulation, margin olive-yellow (2D6). Reverse yellow to dark green.

**Cardinal temperatures:** Maximum tolerated salt concentration: MEA + 17 % NaCl after 14 d.

**Habitats and distribution:** Hypersaline water in the Mediterranean basin.

**Differential parameters:** Sympodial conidiogenous cells with pronounced denticles, narrow temperature amplitude.

**Strains examined:** EXF-326, EXF-332, EXF-391 (= CBS 119412; ex-type strain), EXF-714.
Strains examined: EXF-322, EXF-335 (= CBS 119413; ex-type strain), EXF-604.

Notes: Cladosporium salinae morphologically resembles species of the genus Fusicladium because its conidia are oblong ellipsoidal to fusiform and conidiogenous loci of ramoconidia are placed closely together. As any other Cladosporium species, its conidia show typical cladosporioid scar structures, however. Cladosporium salinae seems to have a separate position within the genus Cladosporium since it seems to be distantly related to any other described Cladosporium species or currently known species complex within Cladosporium.
Cladosporium sphaerospermum Penzig, Michelia 2(8): 473. 1882. Fig. 12.

Mycelium partly submerged, partly superficial; hyphae thick, darkly pigmented and densely septate in submerged mycelium, not enveloped in polysaccharide-like material. Conidiophores erect or ascending, micronematous and macronematous, stipes of variable length, (10–)45–130(–300) × (2.5–)3–4(–6) μm, olivaceous-brown, smooth to minutely verruculose, thick-walled, with relatively dense septation (cells mostly 4.5–23 long), septa darkened and somewhat thickened, arising laterally and terminally from immersed or aerial hyphae, either unbranched or branched. Conidial chains branching in all directions, up to 6 conidia in the unbranched parts. Conidiogenous cells not differentiated. Ramoconidia often formed, cylindrical, (11.5–)20.5–40(–48) × (2.5–)3(–3.5) μm, with up to 5 septa, base broadly truncate, 2 μm wide, slightly thickened and somewhat darkened-refractive. Conidia verruculose, brown to dark brown, non-septate, usually subspherical to spherical, less often short-ovoid, narrower at both ends, with length : width ratio = 1.1–1.5; conidial size (2.5–)3–4(–7) × (2–)3–3.5(–4.5) μm [av. (±
SD) 3.8 (± 0.8) × 3.1 (± 0.4); secondary ramoconidia cylindrical to almost spherical, 0–3(−4) septate, (4−)8.5−16 (−37.5) × (2−)3−3.5 (−5) μm [av. (± SD) 13.1 (± 6.3) × 3.2 (± 0.5)], with up to 4, rarely up to 6 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.9–1.1−1.4 μm diam.

Cultural characteristics: Colonies on PDA reaching 21–44 mm diam, velvety, olive (2F5) due to profuse sporulation, either with white and regular, or exceptionally undulate margin. Aerial mycelium sparse. Colonies flat or rarely radially furrowed with elevated colony centre. Exudates not prominent, some strains release green soluble pigments into the agar. Reverse blackish blue to pale green. Growth deep into the agar. Colonies on OA reaching 21−38 mm diam, olive (2F8), of granular appearance due to profuse and uniform sporulation, almost no aerial mycelium. Margin either regular or arachnoid, deeply radially furrowed. Reverse black. Colonies on MEA reaching 15–35 mm diam, velvety, linden-green (2C5), radially furrowed. Colony centre wrinkled, forming a crater-like structure; margin furrowed, lighter in colour, consisting of
submerged mycelium. Reverse pale to dark brown. Colonies on MEA with 5 % NaCl growing faster than on other media, reaching 31–60 mm diam, mainly olive (2D4), either being almost flat or radially furrowed, with margin of superficial mycelium; sporulation dense. Reverse ochraceous or dark green.

Maximum tolerated salt concentration: On MEA + 20 % NaCl 89 % of all strains tested develops colonies after 7 d, 96 % after 14 d.

Cardinal temperatures: No growth at 4 °C, optimum 25 °C (15–35 mm diam), maximum 30 °C (2–15 mm diam). No growth at 37 °C.

Specimen examined: Netherlands, from nail of man, 1949, coll. and isol. R.W. Zappey, CBS H-19738, neotype designated here, incorrectly selected by de Vries (1952) as ‘lectotype’, culture ex-neotype CBS 193.54 = ATCC 11289 = IMI 049637.

Habitats and distribution: Hypersaline water in mediterranean and tropics; soil and plants in temperate climates; indoor wet cells; humans. The species does not seem to have any particular preference. Human isolates were probably culture contaminants.

Literature: Penzig (1882), de Vries (1952), Ellis (1971), de Hoog et al. (2000), Samson et al. (2002).

Diagnostic parameters: Thick-walled, melanised, densely septate mycelium, almost spherical, verruculose to verrucose terminal conidia, growth on 20 % NaCl after 7 d.

Strains examined: CBS 109.14, CBS 122.63, CBS 190.54, CBS 192.54, CBS 193.54 (ex-neotype strain), CBS 102045, CPC 10944, EXF-131, EXF-328, EXF-385, EXF-446, EXF-455, EXF-458, EXF-461, EXF-464, EXF-465, EXF-598, EXF-644, EXF-645, EXF-649, EXF-715, EXF-738, EXF-739, EXF-781, EXF-962, EXF-965, EXF-1061, EXF-1726, EXF-1732.

Fig. 13. Cladosporium spinulosum. Macro- and micromorphological characters. A–D. Colony surface grown on PDA (A), OA (B), MEA (C) and MEA plus 5 % NaCl (D) of strains incubated for 14 d at 25 °C in darkness. E. Habit of conidiophores. F–J. Conidiophores. K–L. Conidia (also visible in I–J). All from 7-d-old SNA slide cultures. A–L, from EXF-334 (ex-type strain). Scale bars A–D = 10 mm, E = 100 µm, F = 30 µm, G–L = 10 µm.
Cladosporium spinulosum Zalar, de Hoog & Gunde-Cimerman, *sp. nov.* MycoBank MB501099. Fig. 13.

**Etymology:** Refers to its conspicuously digitate conidia.

Conidiophora erecta vel adscendentia; stipites longitudine variabili, (15–)25–50(–155) × (2.5–)3–4(–5) μm, olivaceo-brunneus, levis, crassitunicatus, 0–6(–9)-septatus (cellulis 6–20 μm longis), ex hyphis submersis vel aeriis lateraliter vel terminaliter oriundus, simplex vel ramosus. Conidiorum catenae undique ramosae, ad 4 conidiis in partibus linearibus continuis cohaerentibus. Cellulae conidiogenae integratae vel discretae, acervos distales denticulorum conspicuorum sympodialium proferentes. Conidia echinulata vel digitata, brunnea vel fusca, continua, vulgo subglobosa vel globosa, (4.5–)5.5–7(–8) × (3–)4–4.5(–5) μm, long.: lat. = 1.1–1.6, digiti 0.6–1.3 μm longi; ramoconidia secundaria etiam digitata, cylindrica vel subglobosa, 0(–1)-septata, (6–)6.5–8(–18) × (4–)4.5–5(–5.5) μm, 1–3 cicatrices distales ferentia. Cicatrices inspissatae, conspicuae, protuberantes, 0.8–1.2 μm diam. Hyphae nonnumquam polysaccharide-like material. Hyphae sometimes enveloped in polysaccharide-like material. *Conidiophores* erect or ascending, stipes of variable length, (15–)
25–50(–155) × (2.5–)3–4(–5) μm, olivaceous-brown, smooth, sometimes irregularly rough-walled to verrucose near the base, thick-walled, 0–6(–9)-septate (cells mostly 6–20 μm long), arising laterally and terminally from immersed or aerial hyphae, either unbranched or branched, somewhat tapering towards the apex. Conidial chains branching in all directions, up to 4 conidia in the unbranched parts. Conidiogenous cells sometimes integrated, producing sympodial clusters of pronounced denticles at their distal ends. Ramoconidia rarely formed. Conidial wall ornamentation conspicuously digitate, with up to 1.3 μm long projections having parallel sides and blunt ends. Conidia brown to dark brown, aseptate, usually subspherical to spherical, length : width ratio = 1.1–1.6; conidial size (4.5–)5.5–7(–8) × (3–)4–4.5(–5) μm [av. (± SD) 6.2 (± 1.0) × 4.2 (± 0.5)]; secondary ramoconidia ornamented as conidia, cylindrical to almost spherical, 0(–1)-septate, (6–)8(–)10 μm × (4–)4.5–5(–5.5) μm [av. (± SD) 8.6 (± 4.0) × 4.8 (± 0.4)], with up to 3 distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0.8–1.2 μm diam.

Cultural characteristics: Colonies on PDA reaching 20–30 mm diam, velvety, dull green (29E4) to dark green (29F6) due to profuse sporulation, either with white and regular, or undulate margin. Aerial mycelium sparse. Colonies flat or radially furrowed with elevated colony centre. Growth deep into the agar. Exudates not prominent. Colonies on OA reaching 20–25 mm diam, dull green (29E4) to dark green (29F6), sometimes olive (3D4), of granular appearance due to profuse and uniform sporulation; almost without aerial mycelium. Margin arachnoid. Reverse pale brown to black. Colonies on MEA reaching 17–28 mm diam, velvety, dull green (29E4) to dark green (29F6), either flat or radially furrowed. Colony centre wrinkled, forming a crater-like structure; margin furrowed, paler in colour, consisting of submerged mycelium only. Reverse pale to dark green. Colonies on MEA with 5 % NaCl reaching 12–18 mm diam, of different colours, greenish grey (29D2), greyish green (29D5) to dark green (29F6); colony appearance variable, mostly either being almost flat with immersed colony centre or radially furrowed, with white to dark green margin consisting of superficial mycelium; sporulation dense. Reverse pale to dark green.

Maximum tolerated salt concentration: On MEA + 17 % NaCl, two of three strains tested developed colonies after 14 d.

Cardinal temperatures: Growth at 4 °C, optimum and maximum at 25 °C (17–28 mm). No growth at 30 °C.

Specimen examined: Slovenia, from hypersaline water of Sečovlje salterns, coll. and isol. S. Sonjak, Feb. 1999, CBS H-19796, holotype, culture ex-type CBS 119907.

Habitats and distribution: Hypersaline water in temperate climate.

Diagnostic parameters: Conidia and ramoconidia with a digitate ornamentation.

Strains examined: EXF-334 (= CBS 119907; ex-type strain), EXF-382.

Notes: Cladosporium spinulosum is a member of the C. herbarum species complex (Figs 2–4) although its globose conidia are reminiscent of C. sphaerospermum. Within Cladosporium, the species is unique in having conspicuously digitate conidia and ramoconidia. The two strains are differing in the size of conidia. The average size of conidia in EXF-334 is 6.2 (± 0.9) × 4.2 (± 0.5) μm, and in EXF-382 it is 3.9 (± 0.6) × 3.3 (± 0.4) μm.

Cladosporium velox Zalar, de Hoog & Gunde-Cimerman, sp. nov. MycoBank MB492435. Fig. 14.

Etymology: Refers to the quick growth of strains of this species.

Cladosporium velox partum submersum: hypheae vagina polysaccaridica carentes. Conidiophora erecta, lateralia vel terminalia ex hyphs aeris oriunda; stipes (10–)25–150(–250) × (2.5–)3–4(–4.5) μm, olivaceous-bruneus, leiva, cassisculentus, ad 7-septatus (cellula 10–60 μm longis), identidentem dichotome ramosus. Conidiorum catenae undique divergentes, terminales partes simplices ad 5 conidia continentes. Cellulae conidigenae indistinctae. Conidia leiva vel leniter verruculosa, dilute brunnea, unicellularia, ovoidae, (2,3–)4(–5) μm × (1,5–)2–2.5(–3) μm, long. : lat. 1,4–1,7; ramoconidia secundaria cylindrica, 0–1-septata, (3,5–)5,5–19(–42) μm × (2,5–3–4(–5) μm, ad 4–5 cicatrices terminales ferentia: cicatrices inspissatae, protuberantes, conspueae, 0,5–1,5 μm diam.

Cladosporium velox partum superficially partly submerged; hypheae without extracellular polysaccharide-like material. Conidiophores erect, stipes (10–)25–150(–250) × (2,5–)3–4(–4,5) μm, slightly attenuated towards the apex, olivaceous-brown, smooth- and thick-walled, arising terminally and laterally from aerial hyphae, dichotomously branched [up to 5(–7)-septate, cell length 10–60 μm]. Ramoconidia rarely formed. Conidial chains branching in all directions, terminal chains with up to 5 conidia. Conidia smooth to very finely verruculose, pale brown, non-septate, ovoid, length : width ratio = 1,4–1,7; (2–)3–4(–5,5) μm × (1,5–)2–2.5(–3) μm [av. (± SD) 3,6 (± 0,6) × 2,3 (± 0,2)]; secondary ramoconidia cylindrica, 0–1-septata, (3,5–)5,5–19(–42) μm × (2,5–3–4(–5) μm [av. (± SD) 13,4 (± 10,2) × 2,8 (± 0,5)], with up to 4(–5) distal scars. Conidiogenous scars thickened and conspicuous, protuberant, 0,5–1,5 μm diam.

Cultural characteristics: Colonies on PDA reaching 35–45 mm diam, velvety, dark green due to profuse sporulation, on some parts covered with white sterile mycelium, flat with straight white margin. Reverse dark green to black. Colonies on OA reaching 30–43 mm diam, dark green, mycelium submerged, aerial mycelium sparse. Margin regular. Reverse black. Colonies on MEA reaching 30–42 mm diam, pale green, radially furrowed, with raised, crater-shaped central part, with white, undulate, submerged margin. Sporulation poor. Colonies on MEA with 5 % NaCl reaching 35–45 mm diam, pale green, velvety, flat with regular margin. Reverse pale green. Sporulation poor.

Maximum tolerated salt concentration: 20 % NaCl after 14 d.

Cardinal temperatures: Minimum at 10 °C (9 mm diam), optimum at 25 °C (30–42 mm diam) and maximum at 30 °C (5–18 mm diam).

Specimen examined: India, Chandij, isolated from Bambusa sp., W. Gams, CBS H-19735, holotype, culture ex-type CBS 119417.

Habitats and distribution: Hypersaline water in Slovenia; bamboo, India.

Strains examined: CBS 119417 (ex-type strain), EXF-466, EXF-471.

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