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DNA sequencing to clarify the taxonomical conundrum of the clinical coelomycetes

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Running head: Coelomycetes of clinical interest.

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Summary

The taxonomy of the fungi that produce human infections and that develop asexual fruiting bodies in culture has become very complex. Recent molecular studies have produced dramatic changes in their classification. Currently, the coelomycetes traditionally included in *Sphaeropsidales* and *Melanconiales* are in fact distributed across at least three different classes of the Phylum Ascomycota. Approximately 1,000 genera and 7,000 species have been grouped in the classes *Dothideomycetes*, *Leotiomycetes* and *Sordariomycetes* and their proper identification can only be made by analysing their DNA sequences and comparing them with those corresponding to type strains available in the adequate databases. To facilitate this task for scientists and clinicians involved in the study of these complex, and every day more numerous taxa, we have updated the knowledge about the taxonomy of the commonest coelomycetes of clinical interest with the aim of improving their identification and antifungal treatment.

Keywords: Coelomycetes, *Medicopsis*, mycosis, *Neocucurbitaria*, *Phoma*, *Pyrenochaeta*.

INTRODUCTION

The number of species of coelomycetes involved in human infections has increased enormously in recent years¹⁻⁴. This has been a consequence of the current use of molecular biology approaches in taxonomy that have allowed more stable systematic criteria to be established and a redefinition of modern concepts of genera and species. On that basis, numerous taxa have recently been delimited. For instance, two of the most relevant genera of coelomycetes such as *Phoma* and *Pyrenochaeta* have undergone major changes. The former

has been reduced to only one species within the family *Didymellaceae*; while *Pyrenochaeta* has been excluded from *Cucurbitariaceae* and maintained as *incertae sedis*, its species mainly being distributed into the genus *Neocucurbitaria*.^{5,6} The coelomycetes have been classified, traditionally, by their morphological features.^{3,4} However, its classification turned out to be obsolete, and these fungi have been considered, based on phylogenetic analyses in three different classes, i.e. *Dothideomycetes* (bitunicate ascostromatic-like fruiting bodies), *Leotiomyces* (apothecium-like fruiting bodies), and *Sordariomyces* (unitunicate ascomata-like fruiting bodies) of the phylum Ascomycota.^{4,7-9} Nevertheless, in the clinical setting the term “Coelomycete” is still used to refer to fungi morphologically characterized by producing conidia within fruiting bodies (= conidiomata) of two types, acervular (cup-shaped) or pycnidial (globose to pyriform) conidiomata.^{10,11} Taxonomically, species with clinical prevalence are distributed mainly within the two first classes mentioned above, as was shown by Valenzuela-Lopez *et al.* [4], in a study of a large number of coelomycetous isolates from the USA, which demonstrated that the majority of them were distributed across at least eleven orders, being the *Pleosporales* the most prevalent.

With an ability to cause human infections, the coelomycetes have been involved in numerous opportunistic mycoses ranging from superficial to deep infections, most of them acquired by traumatic implantation of plant material or soil particles mainly in subtropical and tropical areas.^{1,3-4,12-14} The most frequent are reduced to a specific group of taxa that includes *Colletotrichum* spp., *Medicopsis romeroi* and *Neoscytalidium dimidiatum*, although apart from these a huge number of species are occasionally also involved in human pathologies (see Table 1). Approximately 50 species have been reported in human mycoses, mainly causing subcutaneous infections.

Identification of the coelomycetes in the clinical laboratory is not easy because of their difficulty in sporulating. Recognizing and characterizing the most representative morphological structures of these fungi requires some expertise and even then these microorganisms remain sterile in many cases.³ The use of molecular techniques based on the amplification and sequencing of appropriate phylogenetic markers is very important in the identification in this group of fungi.

Treatments are still not established due to the lack of clinical breakpoints for these fungi and to the difficulties in performing antifungal susceptibility testing against these fungi that hardly sporulate. Only few studies on coelomycetes have demonstrated that the use of surgical resection and a few drugs such as amphotericin B and triazoles have shown some efficacy.¹⁴⁻¹⁵

The aim of this paper is to update the current knowledge of the taxonomy of these taxa involved in human infections.

LABORATORY IDENTIFICATION

Isolation and morphological identification of clinical coelomycetous isolates

For cultural isolation and characterization the isolates should be inoculated on the following culture media: malt extract agar (MEA; 40 g of malt extract, 15 g of agar-agar, 1 L distilled water), oatmeal agar (OA; 30 g of filtered oat flakes, 15 g of agar-agar, 1 L tap water) and potato dextrose agar (PDA, 4 g of potato infusion, 20 g dextrose, 15 g of agar-agar, 1 L tap water) at $25 \pm 1^\circ\text{C}$ for 14 days in darkness. If the isolate does not sporulate, its incubation under near ultraviolet (UV) light (12 hours light, 12 hours dark) or on carnation leaf agar (CLA) to induce sporulation can be useful.¹⁶⁻¹⁷ For micromorphological characterization, the use of wet mounts prepared in Shear's mounting medium (potassium acetate 3 g, distilled

water 150 mL, glycerin 60 mL, ethanol (95 %) 90 mL) or 85% lactic acid are recommended.

Table 1 summarizes the most relevant morphological features of the most prevalent coelomycetes in the clinical setting.

DNA extraction, amplification, and sequencing

For identification purposes the fungal genomic DNA should be extracted from colonies grown on PDA after 7 days of incubation at $25 \pm 1^\circ\text{C}$, following the protocols by Valenzuela-Lopez *et al.* [4].

Molecular identification of coelomycetes

To this purpose, the fragment of the 28S nrRNA gene (LSU) and internal transcribed spacer region (ITS) should be amplified, and depending on the fungus secondary phylogenetic markers such as beta-tubulin gene (*tub2*) and/or RNA polymerase II subunit 2 gene (*rpb2*) should be additionally tested (see Table 2).

Preliminary identification of coelomycetes can be carried out using the BLAST nucleotide tool of the NCBI (<https://blast.ncbi.nlm.nih.gov/Blast/>), the Westerdijk Fungal Biodiversity Institute (former CBS) (<http://www.westerdijkinstitut.nl/Collections/>) or the Q-Bank (<http://www.q-bank.eu/Fungi/>) databases. For accurate identification of the isolates, the sequences must be compared with those of type or reference strains. It is also recommended to perform an alignment and its phylogenetic analysis using appropriate softwares such as MrBayes, RAxML, MEGA or several other useful programs.¹⁸⁻²⁰

We suggest, depending on the fungi in order to identify, to follow the scheme of figure 1 and the primers listed in Table 2. In general, the genes ITS, LSU, *tub2* and translation elongation factor 1-alpha (*tef1*) are easy to amplify; and also the *rpb2*, which is a bit more difficult to amplify; however, it is one of the most informative marker.⁵⁻⁶ Nowadays, most of ITS and LSU genes of these species are sequenced and available in the public databases. Recently,

additional phylogenetic markers have been sequenced, which increase the possibility of a better taxonomic classification and identification of the fungi.

In figure 2 we provide an example of phylogenetic analysis with a tree performed by using the MEGA software with a set of LSU sequences of clinical coelomycetes available. However, the precise identification always depends on the phylogenetic markers used (see above). Unfortunately, most of the coelomycetes information in public databases it is not updated and in many cases is necessary an exhaustive literature search for a correct taxonomic placement of the fungus.

Recently, the use of matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry for identifying microorganisms in the clinical laboratory has quickly become important.²¹⁻²³ This technique was used previously mostly for yeasts, but more recently it has been also adapted for identifying molds. A recent study by Fraser *et al.* [23] also demonstrated the usefulness of this technique for coelomycetes that produce black grain mycetoma.

Conclusions

The taxonomy of the coelomycetes that have produced human infections is confusing because they are currently distributed across a high number of genera and species. They can only be properly identified by DNA sequencing and comparison with reference strains. However, their identity is crucial for their correct antifungal management, which is still little known.

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CONFLICT OF INTEREST

None to declare.

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Figure legend

Figure 1. Flow scheme showing the phylogenetic markers for coelomycete identification (“?” means that ITS not always it’s an useful tool to resolve the identification at species level).

Data referred to genes are included in Table 2.

Figure 2. Maximum likelihood tree obtained from the D1-D2 of LSU (588 bp) sequences of 40 coelomycetous isolates. Bootstrap support values of ≥ 70 are indicated on the nodes. The GenBank accession numbers are given for each isolate. *Chaetomella oblonga* ATCC 12718 and *C. zambiensis* CBS 137978 were used to root the tree.

Table 1 Species of coelomycetes of clinical interest and their morphological characteristics

Order & Family	Species (former name)	Human infection	Reference	Conidiomata	Conidia	Other features
Amphisphaeriales						
<i>Bartaliniaceae</i>	<i>Truncatella angustata</i>	Subcutaneous	23	Acervular to pycnidial	Fusiform, 3-septate, 15–23 × 6–8 μm, with apical appendages; basal cell hyaline, obconic, thin-walled; median cells brown, doliiform to subcylindrical, thick-walled	
Botryosphaeriales						
<i>Botryosphaeriaceae</i>	<i>Hendersonula toruloidea</i> synanamorph: <i>Neoscytalidium dimidiatum</i> (<i>Scytalidium hyalinum</i>)	Cutaneous, keratitis, onychomycosis, black grain eumycetoma, endophthalmitis, subcutaneous, Cerebral, systemic	24-31	Pycnidial	Initially hyaline, aseptate, becoming dark brown and septate with age, 12–20 × 4–8 μm	The synanamorph <i>N. dimidiatum</i> produces arthroconidia
	<i>Lasiodiplodia theobromae</i> (<i>Botryodiplodia theobromae</i>)	Keratitis, onychomycosis, endophthalmitis, subcutaneous, pneumonia, sinusitis	32-38	Pycnidial	Initially hyaline, becoming dark brown with longitudinal striations, ellipsoidal, thick-walled, 1-septate, 20–30 × 10–15 μm	Sexual morph on vegetal material. Paraphyses hyaline, cylindrical, septate
	<i>Macrophomina phaseolina</i>	Cutaneous, keratitis, systemic	39-41	Pycnidial	Hyaline, ellipsoid to obovoid, 14–30 × 5–10	Sclerotia on vegetal material

						μm	
	<i>Neodeightonia subglobosa</i> (<i>Sphaeropsis subglobosa</i>)	Keratitis	42	Stromatic	Brown, obovoidal or subspherical to spherical, with truncate base, thick-walled, aseptate, $9\text{--}12 \times 6\text{--}9 \mu\text{m}$		
Diaporthales							
<i>Diaporthaceae</i>	<i>Diaporthe bougainvilleicola</i> (<i>Phomopsis bougainvilleicola</i>)	Bursitis	43	Stromatic	Hyaline, of two types: alpha, ellipsoidal or fusiform, $5\text{--}8.4 \times 1.2\text{--}2 \mu\text{m}$, and beta, filiform, curved, $16\text{--}31 \times 0.5\text{--}0.9 \mu\text{m}$		
	<i>Diaporthe phaseolorum</i> (<i>Phomopsis phaseoli</i>)	Black grain eumycetoma	44	Pycnidial	Hyaline, of two types: alpha, ovoid, $6.7\text{--}7 \times 2.4 \mu\text{m}$, and beta, filiform, $13.3\text{--}22.5 \times 0.5\text{--}0.9 \mu\text{m}$		
	<i>Diaporthe phoenicicola</i> (<i>Phomopsis phoenicicola</i>)	Keratitis	45	Pycnidial	Hyaline, only alpha-conidia, ovoid to fusiform, $8\text{--}12 \times 2\text{--}2.5 \mu\text{m}$		
Glomerellales							
<i>Glomerellaceae</i>	<i>Colletotrichum coccodes</i> (<i>C. atramentarium</i>)	Keratitis, subcutaneous	46-47	Acervular	Hyaline, straight, fusiform, $16\text{--}22 \times 3\text{--}4 \mu\text{m}$	Apressoria brown, clavate, $11\text{--}16.5 \times 6\text{--}9.5 \mu\text{m}$	

<i>Colletotrichum dematium</i>	Keratitis, endophthalmitis	48-50	Acervular	Hyaline, falcate, acute apex, 20–30 × 3–5 μm	Apressoria brown, clavate to circular, 8–11.5 × 6.5–8 μm
<i>Colletotrichum gigasporum</i> (<i>C. crassipes</i>)	Subcutaneous	51	Acervular	Hyaline, cylindrical with rounded ends, 27–30 × 9–10 μm	Apressoria brown to dark brown, variable in shape including ovoid, clavate or slightly irregular, 15–30 × 7–14 μm
<i>Colletotrichum gloeosporioides</i>	Keratitis, subcutaneous	52-54	Acervular	Hyaline, straight, cylindrical, obtuse at the apex, 9–24 × 3–4.5 μm	Apressoria brown, clavate or irregular, 6–20 × 4–12 μm
<i>Colletotrichum graminicola</i>	Keratitis	55	Acervular	Hyaline, fusiform to falcate, 23–29 × 3.5–5 μm	Apressoria brown, irregular, 17–20 × 12–14 μm
<i>Colletotrichum truncatum</i>	Keratitis	56	Acervular	Hyaline, fusiform, 20–23.5 × 3.5–4 μm	Apressoria light brown, solitary or in groups, ellipsoidal or clavate, 6.5–13 × 5.5–7.5 μm
Hysteriales					
<i>Hysteriaceae</i>					
<i>Rhytidhysterium rufulum</i>	Subcutaneous	57-59	Pycnidial	Hyaline, globose to subglobose, smooth- and thin-walled	Sexual morph on vegetal material

Incertae sedis	<i>Phialemoniopsis ocularis</i> (<i>Sarcopodium oculorum</i>)	Keratitis	60-61	Pycnidial or sporodochial	Hyaline, ellipsoidal, smooth-walled, aseptate, 2–3.5 × 1–1.5 μm	Chlamydospores, brown, thick- and rough-walled, intercallary, solitary or in chains, globose to pyriform, 5–9 × 3–6 μm
Pleosporales						
<i>Cucurbitariaceae</i>	<i>Neocucurbitaria cava</i> (<i>Pyrenochaeta cava</i>)	Subcutaneous	62	Pycnidial	Hyaline, cylindrical to slightly allantoid, smooth- and thin-walled, aseptate, 2.5–3.5 × 1–1.5 μm	Growth at 37°C ^a
	<i>Neocucurbitaria keratinophila</i> (<i>Pyrenochaeta keratinophila</i>)	Keratitis	63-64	Pycnidial	Hyaline, ellipsoidal, smooth- and thin-walled, aseptate, 2.5–3 × 1–2 μm	Growth at 37°C ^a
	<i>Neocucurbitaria unguis-hominis</i> (<i>Pyrenochaeta unguis-hominis</i>)	Onychomycosis	65-67	Pycnidial	Hyaline, cylindrical, smooth- and thin-walled, aseptate, 2–3.5 × 1–1.5 μm	Growth at 37°C ^a
<i>Didymellaceae</i>	<i>Boeremia exigua</i> var. <i>exigua</i> (<i>Phoma exigua</i>)	Lung mass	68	Pycnidial	Hyaline, smooth- and thin-walled, mainly aseptate or 1(–2)-septate, 4.5–8 × 2.5–4 μm	

<i>Didymella glomerata</i> (<i>Phoma glomerata</i>)	Subcutaneous	69	Pycnidial	Hyaline, variable in shape, smooth- and thin-walled, aseptate, 4–8.5 × 1.5–3 µm	Chlamydo spores dark brown, solitary or in chains, multicellular-dictyosporous, 30–65 × 15–25 µm
<i>Epicoccum sorghinum</i> (<i>Phoma sorghina</i>)	Subcutaneous	70	Pycnidial	Hyaline, variable in shape mostly ovoid-ellipsoidal, smooth- and thin-walled, aseptate, 4.5–7 × 2–3 µm	Chlamydo spores dark brown, solitary or in chains, irregular, dictyosporous, 8–35 µm diam.
<i>Juxtiphoma eupyrena</i> (<i>Phoma eupyrena</i>)	Subcutaneous	71	Pycnidial	Hyaline, ellipsoidal, smooth- and thin-walled, aseptate, 4–5.5 × 2–2.5 µm	Chlamydo spores dark brown, barrel shaped, 4–15 µm diam.
<i>Phoma herbarum</i> (<i>Phoma cruris-hominis</i>)	Subcutaneous	69	Pycnidial	Hyaline, ellipsoidal to ovoid, smooth- and thin-walled, aseptate, 4.5–6 × 2–3 µm	
<i>Stagonosporopsis oculi-hominis</i> (<i>Phoma oculi-homini</i>)	Keratitis	72	Pycnidial	Hyaline to brown, cylindrical, smooth- and thin-walled, aseptate (3–7 × 1–2 µm) or 1-septate (9–16 × 3–4.5 µm)	

<i>Didymosphaeriaceae</i>	<i>Paraconiothyrium cyclothyrioides</i>	Systemic	73	Stromatic	Initially hyaline, yellowish brown with age, cylindrical, thin-walled, aseptate, $3-4.2 \times 1.2-1.5 \mu\text{m}$	
	<i>Paraconiothyrium fuckelii</i> (<i>Coniothyrium fuckelii</i>)	Systemic	74	Pycnidial	Pale brown, cylindrical, smooth- and thin-walled, aseptate, $2.5-4 \times 1.5-2 \mu\text{m}$	
<i>Incertae sedis</i>	<i>Medicopsis romeroi</i> (<i>Pyrenochaeta romeroi</i>)	Cutaneous, black grain eumycetoma, subcutaneous	11,75-77	Pycnidial	Hyaline, cylindrical to ellipsoidal, smooth- and thin-walled, aseptate, $2-2.8 \times 1.2-1.5 \mu\text{m}$	Growth at 37°C ^a
<i>Macrodiplodiopsidaceae</i>	<i>Pseudochaetosphaeronema larense</i> (<i>Chaetosphaeronema larense</i>)	Black grain eumycetoma	78	Pycnidial	Hyaline, cylindrical, smooth- and thin-walled, aseptate, $2-3 \times 1-1.8 \mu\text{m}$	
	<i>Pseudochaetosphaeronema martinelli</i>	Subcutaneous	79			Culture sterile
<i>Melanommataceae</i>	<i>Pleurophomopsis lignicola</i>	Subcutaneous, sinusitus	80-81	Pycnidial	Hyaline, ellipsoidal, smooth- and thin-walled, aseptate, $2-3 \times 0.5-1 \mu\text{m}$	
<i>Nigrogranaceae</i>	<i>Nigrograna mackinnonii</i> (<i>Pyrenochaeta mackinnonii</i>)	Black grain eumycetoma	82	Pycnidial	Subhyaline, ellipsoidal, smooth, aseptate, $2.5-3 \times 1.5-2 \mu\text{m}$	

<i>Phaeosphaeriaceae</i>	<i>Tintelnotia destructans</i>	Onychomycosis	83	Pycnidial	Hyaline to pale brown, ellipsoidal, smooth- and thin-walled, aseptate, 2–3.2 × 1–2 μm	Growth at 37°C ^a
<i>Sporormiaceae</i>	<i>Westerdykella minutispora</i> (<i>Phoma minutispora</i>)	Subcutaneous	84	Pycnidial	Hyaline, subglobose to ellipsoidal, smooth- and thin-walled, aseptate, 2–2.5 × 1.5–2 μm	Chlamydospores dark brown, subglobose or irregular, solitary mostly terminally on hyphae, 6–15 μm diam. Can produce sexual morph
<i>Thyridariaceae</i>	<i>Parathyridaria percutanea</i> (<i>Rousoella percutanea</i>)	Subcutaneous	85	Pycnidial	Hyaline to pale brown, ellipsoidal, smooth- and thin-walled, aseptate, 1.2–2 × 0.7–0.9 μm	Growth at 37°C ^a
<i>Trematosphaeriaceae</i>	<i>Emarellia grisea</i>	Black grain eumycetoma	86			Culture sterile
	<i>Emarellia paragrisea</i>	Black grain eumycetoma	86			Culture sterile
	<i>Trematosphaeria grisea</i> (<i>Madurella grisea</i>)	Black grain eumycetoma	11,87-88	Pycnidial	Hyaline to pale brown, clavate to ellipsoidal, smooth- and thin-walled, aseptate, 4–5.4 × 2–2.4 μm	Growth at 37°C ^a

^aspecies that was previously tested at different temperature conditions

Table 2 Primers used for coelomycetes identification

Gene	Product name	Primer	Direction	Sequence (5'-3')	Reference	Used in
Internal transcribed spacer (complete)	ITS	ITS-5	Forward	GGA AGT AAA AGT CGT AAC AAG G	White <i>et al.</i> ⁸⁹	All coelomycetes
		ITS-4	Reverse	TCC TCC GCT TAT TGA TAT GC	White <i>et al.</i> ⁸⁹	
28S ribosomal RNA	LSU	LR0R	Forward	GTA CCC GCT GAA CTT AAG C	Rehner & Samuels ⁹⁰	All coelomycetes
		LR5	Reverse	TCC TGA GGG AAA CTT CG	Vilgalys & Hester ⁹¹	
Actin	ACT	ACT-512F	Forward	ATG TGC AAG GCC GGT TTC GC	Carbone & Kohn ⁹²	<i>Colletotrichum</i> , <i>Didymella</i> , <i>Phoma</i>
		ACT-783R	Reverse	TAC GAG TCC TTC TGG CCC AT	Carbone & Kohn ⁹²	
Beta-tubulin	TUB2	T1	Forward	AAC ATG CGT GAG ATT GTA AGT	O'Donnell & Cigelnik ⁹³	<i>Colletotrichum</i> , <i>Diaporthe</i>
		Bt-2b	Reverse	ACC CTC AGT GTA GTG ACC CTT GGC	Glass & Donaldson ⁹⁴	
		TUB2Fd	Forward	GTB CAC CTY CAR ACC GGY CAR TG	Woudenberg <i>et al.</i> ⁹⁵	<i>Didymellaceae</i> , Pleosporalean coelomycetes
		TUB4Rd	Reverse	CCR GAY TGR CCR AAR ACR AAG TTG TC	Woudenberg <i>et al.</i> ⁹⁵	
Calmodulin	CAL	CAL-228F	Forward	GAG TTC AAG GAG GCC TTC TCC C	Carbone & Kohn ⁹²	<i>Colletotrichum</i> , <i>Diaporthe</i>
		CAL-737R	Reverse	CAT CTT TCT GGC CAT CAT GG	Carbone & Kohn ⁹²	
Chitin synthase 1	CHS-1	CHS-79F	Forward	TGG GGC AAG GAT GCT TGG AAG AAG	Carbone & Kohn ⁹²	<i>Colletotrichum</i>

		CHS-354R	Reverse	TGG AAG AAC CAT CTG TGA GAG TTG	Carbone & Kohn ⁹²	
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	GDF1	Forward	GCC GTC AAC GAC CCC TTC ATT GA	Guerber <i>et al.</i> ⁹⁶	<i>Colletotrichum</i>
		GDR1	Reverse	GGG TGG AGT CGT ACT TGA GCA TGT	Guerber <i>et al.</i> ⁹⁶	
Histone H3	HIS3	CYLH3F	Forward	AGG TCC ACT GGT GGC AAG	Crous <i>et al.</i> ⁹⁷	<i>Colletotrichum</i>
		CYLH3R	Reverse	AGC TGG ATG TCC TTG GAC TG	Crous <i>et al.</i> ⁹⁷	
RNA polymerase II second largest subunit	RPB2	fRPB2-5F	Forward	GAY GAY MGW GAT CAY TTY GG	Liu <i>et al.</i> ⁹⁸	All coelomycetes
		fRPB2-7R	Reverse	CCC ATW GCY TGC TTM CCC AT	Liu <i>et al.</i> ⁹⁸	
Translation elongation factor 1-alpha	TEF	EF1-728F	Forward	CAT CGA GAA GTT CGA GAA GG	Carbone & Kohn ⁹²	<i>Diaporthe</i>
		EF1-986R	Reverse	TAC TTG AAG GAA CCC TTA CC	Carbone & Kohn ⁹²	
		TEF1-983F	Forward	GCY CCY GGH CAY CGT GAY TTY AT	Schoch <i>et al.</i> ⁹⁹	All coelomycetes
		TEF1-2218R	Reverse	AT GAC ACC RAC RGC RAC RGT YTG	Schoch <i>et al.</i> ⁹⁹	



