

Taxonomic revision of the genus *Cutleria* proposing a new genus *Mutimo* to accommodate *M. cylindricus* (Cutleriaceae, Phaeophyceae)

Hiroshi Kawai,^{1*} Keita Kogishi,¹ Takeaki Hanyuda¹ and Taiju Kitayama²

¹Kobe University Research Center for Inland Seas, Kobe, and ²Department of Botany, National Museum of Nature and Science, Amakubo, Tsukuba, Japan

SUMMARY

Molecular phylogenetic analyses of representative *Cutleria* species using mitochondrial *cox3*, chloroplast *psaA*, *psbA* and *rbcL* gene sequences showed that *C. cylindrica* Okamura was not included in the clade composed of other *Cutleria* species including the generitype *C. multifida* (Turner) Greville and the related taxon *Zanardinia typus* (Nardo) P.C. Silva. Instead, *C. cylindrica* was sister to the clade composed of the two genera excluding *C. cylindrica*. *Cutleria* spp. have heteromorphic life histories and their gametophytes are rather diverse in gross morphology, from compressed or cylindrical-branched to fan-shaped, whereas the sporophytes are rather similar. In contrast, the monotypic species *Z. typus* has an isomorphic life history and resembles fan-shaped *Cutleria* in morphology. Morphological comparisons of these taxa revealed that *C. cylindrica* is morphologically distinct from other *Cutleria* spp. and *Z. typus* in having cylindrical gametophytes with multiseriate trichothallic filaments instead of uniseriate filaments (hairs) characteristic of Cutleriales (or Cutleriaceae, Tilopteridales), and in lacking rhizoidal filaments in the crustose sporophytes. Therefore, based on the molecular and morphological data, the establishment of a new genus *Mutimo* to accommodate *C. cylindrica*, and the new combination of *M. cylindricus*, is proposed.

Key words: *Cutleria*, Cutleriaceae, molecular phylogeny, *Mutimo cylindricus*.

INTRODUCTION

The genus *Cutleria*, type of the family Cutleriaceae as well as the order Cutleriales C.E. Bessey 1907, was established based on *C. multifida* (Turner) Greville from England (Turner 1801; Greville 1830). Currently about 10 species are commonly recognized (Guiry & Guiry 2012). *Cutleria* species have two types of gross morphology: (i) dichotomously or more or less irregularly

branched, compressed or cylindrical thalli (e.g., *C. chilosa* (Falkenberg) P.C. Silva, *C. compressa* Kützinger, *C. cylindrica* Okamura and *C. multifida* (Turner) Greville); (ii) flat, fan-shaped thalli (e.g. *C. adspersa* (Mertens ex Roth) De Notaris, *C. hancockii* E.Y. Dawson, *C. kraftii* Huisman and *C. mollis* Allender et Kraft). However, only a sporophytic generation is reported for some taxa and the nature of their gametophytic (erect) thalli are unclear (e.g. *C. canariensis* (Sauvageau) I.A. Abbott et J.M. Huisman and *C. irregularis* I.A. Abbott & Huisman). *Cutleria* species typically show a heteromorphic life history alternating between relatively large dioecious gametophytes of trichothallic growth and small crustose sporophytes, considered characteristic of the order. In contrast, the monotypic genus *Zanardinia*, represented by *Z. typus* (Nardo) P.C. Silva, has an isomorphic life history characterized by flat roundish thalli resembling the gametophytes of the fan-shaped *Cutleria* species (Yamanouchi 1912).

In the present paper, we examined the molecular phylogeny and morphology of *C. cylindrica*, showing its rather distant relationship with other *Cutleria* and *Zanardinia* species, and propose to classify the species in an independent genus.

MATERIALS AND METHODS

For the molecular phylogenetic analyses, specimens of *Cutleria adspersa*, *C. chilosa*, *C. cylindrica* and *C. multifida* were newly collected from Japan, France, Greece, Ireland and Australia, and used for DNA extractions and morphological observations (Table 1). Small fragments of each specimen were quickly dried in silica gel and used for molecular studies. Culture strains of *Halosiphon tomentosus* and *Saccorhiza polyschides* (Tilopteridales) were used for DNA extraction and their DNA

*To whom correspondence should be addressed.

Email: kawai@kobe-u.ac.jp

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Table 1. List of specimens used for phylogenetic analyses, their collection data, and DDBJ/GenBank accession code of sequences. Sequences newly determined in the present study are indicated in boldface

Species	Locality (collection date, collector and strain number) or literature	Accession code			
		<i>cox3</i>	<i>psaA</i>	<i>psbA</i>	<i>rbcL</i>
<i>Cutleria adspersa</i> (Mertens ex Roth) De Notaris	Onyu Island, Oita, Japan (6 June 2005, S. Arai)	–	AB543565	AB543578	AB545966
	Yakushima Island, Kagoshima, Japan (16 February 2006, T. Kitayama)	AB682740	AB543566	AB543579	AB545967
<i>C. chilosa</i> (Falkenberg) P.C. Silva	Catania, Sicily Island, Italy (8 June 2006, G. Furnari)	AB543500	AB543567	AB543580	AB545968
	Lesbos Island, Greece (4 March 2009, K. Tsiamis & H. Kawai)	AB543501	AB543568	AB543581	AB545969
	Patras, Corinth, Greece (15 April 2011, K. Tsiamis & H. Kawai)	AB682741	AB682743	AB682747	AB682751
<i>C. cylindrica</i> Okamura (= <i>Mutimo cylindricus</i> gen. et comb. nov.)	Shimoda, Shizuoka, Japan (29 April 2005, K. Kogishi)	AB499641	AB543570	AB543583	AB545971
	Shikanoshima, Fukuoka, Japan (25 April 2005, S. Arai)	AB499655	AB543571	AB543584	AB545972
	Otsuku Island, Kumamoto, Japan (March 2005, S. Arai)	AB499663	AB543572	AB543585	AB545973
<i>C. multifida</i> (Turner) Greville	Sekumi, Fukui, Japan (9 June 2005, S. Arai)	AB540623	AB543574	AB543587	AB545975
	Cannes, Provence-Alpes-Côte d'Azur, France (16 April 2008, H. Kawai)	AB540627	AB682744	AB682748	AB682752
	Coobowie, SA, Australia (10 October 2010, H. Kawai)	AB540618	AB682745	AB682749	AB682753
	Carna, Galway, Ireland (13 June 2011, H. Kawai)	AB682742	AB682746	AB682750	AB682754
<i>Halosiphon tomentosus</i> (Lyngbye) Jaasund	Helgoland, Germany (D.G. Müller, KU-1171†)	AB543505	AB543576	AB543589	AB545977
<i>Saccorhiza polyschides</i> (Lightfoot) Batters	Roscoff, Brittany, France (D.G. Müller, KU-1307†)	AB543506	AB543577	AB543590	AB545978
<i>Zanardinia typus</i> (Nardo) P.C. Silva	Silberfeld <i>et al.</i> (2010)	EU681470†	EU681623	EU681664	EU681601

†Culture strain housed in Kobe University Macroalgal Culture Collection (KU-MACC).

sequences were used in phylogenetic analyses as outgroups (Table 1). Genomic DNA was extracted using the DNeasy Plant Mini Kit (Qiagen, Hilden, Germany), following the manufacturer's instructions. Polymerase chain reaction (PCR) amplification and sequencing of the mitochondrial *cox3* (cytochrome oxidase subunit III) gene and the chloroplast *psaA* (photosystem I P700 apoprotein A1), *psbA* (photosystem II reaction center protein D1), and *rbcL* (ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit) genes were performed. Primers for PCR amplification and sequencing are listed in Table 2. PCR was carried out with a TaKaRa PCR Thermal Cycler Dice (Takara Shuzo, Shiga, Japan) using the TaKaRa ExTaq Reaction Kit (Takara Shuzo) or the KOD FX (ToYoBo, Osaka, Japan). After polyethylene glycol purification (Lis 1980), PCR products were sequenced using a CE DTCS Quick Start Kit (Beckman Coulter, Fullerton, CA, USA) and a CEQ8000 DNA Analysis System (Beckman Coulter) following the manufacturer's instructions.

Alignments were prepared using the CLUSTAL X computer program (Thompson *et al.* 1997) and then manually adjusted prior to phylogenetic analyses. In the phylogenetic analyses, the published sequence data of

Zanardinia typus (Silberfeld *et al.* 2010) were used in addition to the sequences determined in this study.

Phylogenetic trees were obtained using maximum likelihood (ML) and Bayesian analyses. With the aid of the Kakusan4 program (Tanabe 2011), the best-fit evolutionary model for each codon position of each gene was determined for each dataset by comparing different evolutionary models via the corrected Akaike Information Criterion (Akaike 1974) for ML analysis, and the Bayesian Information Criterion (Schwarz 1978) for the Bayesian analysis. The ML analysis was performed by the likelihood-ratchet method (Vos 2003), implemented in Phylogears 2.0.2010.08.31 (Tanabe 2010). One thousand sets of 25% site-upweighted data were created using the 'pgresampleseq' command in Phylogears (Tanabe 2010), and trees based on the upweighted data were constructed using Treefinder (Jobb *et al.* 2004) under the maximum likelihood criterion. After eliminating redundant trees from the calculation, the ML tree of the original data was inferred by Treefinder with the best-fit substitution model and by using the trees of upweighted data mentioned above as starting trees. The robustness of the resulting phylogenies was tested by bootstrap analysis (Felsenstein

Table 2. List of primers used for polymerase chain reaction (PCR) and sequencing

Code	F/R	Sequence (5'-3')	Annealing position
trnY-P2	F	GKCAGATTGTAATCTGTTGG	<i>trnY</i> (27–47)
trnY-P1 ^b	F	TCYATCRTAGGTTTGAATCC	<i>trnY</i> (52–71)
cox3-P1 ^b	F	GAYCCWAGTCCMTGGCCWTTAG	<i>cox3</i> (49–70)
cox3-P5.2 ^a	F	KCHCCHGTYTTTAATATTGG	<i>cox3</i> (340–359)
cox3-P6 ^a	R	CDACAATHGCATGATGAGCCC	<i>cox3</i> (478–457)
cox3-Cm1	F	TGGGCTTTTTTACGTCTTC	<i>cox3</i> (316–335)
cox3-Cm2	R	TGCCTAAACCCTGCAGAGCC	<i>cox3</i> (514–495)
cox3-Cm3	F	TCGAATATATGAACGCACCC	<i>cox3</i> (557–576)
cox3-P2 ^b	R	ACAAARTGCCAATACCAAGC	<i>cox3</i> (755–736)
ORF379-P1 ^a	R	CACAATATTTAACTTTATCG	ORF379 (133–114)
psaA130F ^c	F	AACWACWACTTGGATTTGGAA	<i>psaA</i> (132–152)
psaA-P2	R	NCCWGACCAAGMWARACAAC	<i>psaA</i> (645–626)
psaA970R ^c	R	GCYCTARAATYTCTTTCA	<i>psaA</i> (983–965)
psaA-P3	R	GCTGGDTRTARTCAGAACCC	<i>psaA</i> (1259–1239)
psaA1760R ^c	R	CCTCTWCCWGGWCCATCRAWGG	<i>psaA</i> (1742–1720)
psaA-P5	F	CAYCATATHCATGCNTTYAC	<i>psaA</i> (1606–1625)
psaA-P4	R	NGATTCAATHARYTCTTGCC	<i>psaA</i> (2100–2081)
psbA-F ^c	F	ATGACHGCTAYTTTAGAAAAGA	<i>psbA</i> (1–21)
psbA500F ^c	F	CTCTGATGGWATGCCWYTAGG	<i>psbA</i> (504–524)
psbA600R ^c	R	CCAAATACACCAGCAACACC	<i>psbA</i> (620–601)
psbA-R1 ^c	R	GCTAAATCTARWGGGAAGTTGTG	<i>psbA</i> (1031–1009)
rbcL-P2.2	F	CTCGAWTWAAAAGTGAVCGWTAYGAATC	<i>rbcL</i> (26–53)
rbc-F1 ^d	F	CGTTACGAATCWGGTG	<i>rbcL</i> (43–58)
rbc-R2.5 ^e	R	CCTTCATAAACAACACG	<i>rbcL</i> (587–571)
rbcL-Rh3 ^f	F	TTAAYTCTCARCCDTTYATGCG	<i>rbcL</i> (629–650)
Ral-R952 ^g	R	CATACGCATCCATTACA	<i>rbcL</i> (969–952)
rbcL-P1 ^g	F	GKGTWATTTGTAARTGGATGCG	<i>rbcL</i> (944–965)
rbcL-P4	R	AGKTGRGTGCATYGRCCACA	<i>rbcL</i> (1178–1159)
rbcS-P1 ^g	R	GGATCATCTGYCCATTCTACAC	<i>rbcS</i> (122–101)

Annealing positions correspond to the sequences of *Fucus vesiculosus* (*trnY*, *cox3*, and ORF379, AY494079, Oudot-Le Secq *et al.* 2006) and those of *Odontella sinensis* (*psaA*, *psbA*, *rbcL*, and *rbcS*, Z67753; Kowallik *et al.* 1995).

^aKogishi *et al.* (2010). ^bNi-Ni-Win *et al.* (2008). ^cYoon *et al.* (2002). ^dKawai and Sasaki (2004). ^eKawai *et al.* (2008). ^fHanyuda *et al.* (2004). ^gKawai *et al.* (2007).

1985) using 1000 replications in ML analysis. Bayesian analysis with the selected evolutionary models was done using MrBayes v3.1.2 (Ronquist & Huelsenbeck 2003). The Bayesian analysis was initiated with a random starting tree and ran four chains of Markov chain Monte Carlo iterations simultaneously for 10 000 000 generations, keeping one tree every 100 generations. The first 10 000 trees sampled were discarded as 'burn-in', based on the stationarity of ln L as assessed using Tracer version 1.4.1 (Rambaut & Drummond 2009); a consensus topology and posterior probability values were calculated from the remaining trees.

RESULTS

Phylogenetic analyses among *Cutleria* spp. and *Zanardinia typus*

Maximum likelihood and Bayesian analyses gave essentially the same tree topologies, except for one of the

branching orders within the *C. chilosa* clade. Figure 1 shows a ML phylogenetic tree of *C. multifida*, *C. chilosa*, *C. adspersa*, *C. cylindrica* and *Zanardinia typus* based on combined *cox3*, *psaA*, *psbA* and *rbcL* gene sequences. *C. multifida* and *C. chilosa* were phylogenetically very close, but both formed statistically well-supported monophyletic clades. *C. adspersa* clustered with *Z. typus*, although the bootstrap value was low (<67). The clade composed of *C. multifida* and *C. chilosa* clustered with the clade of *C. adspersa* and *Z. typus*, and the clade of *C. cylindrida* showed a sister relationship with them.

Morphological comparisons of characteristic features among *Cutleria* spp. and *Zanardinia typus*

Characteristic morphological features of *C. multifida* (generic type) and *C. cylindrica* gametophytes (erect thalli) are shown in Figure 2. The medullary layer of

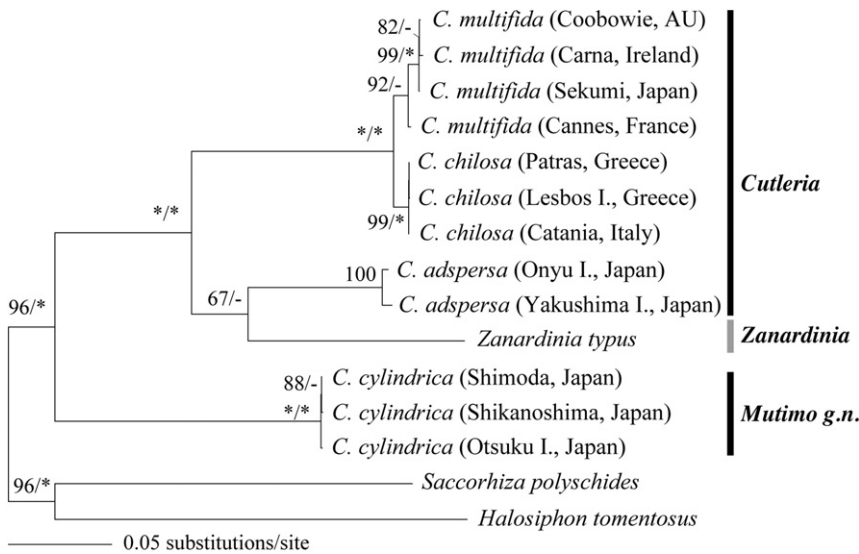


Fig. 1. Maximum Likelihood tree based on the combined dataset (*cox3* (646 bp), *psaA* (1897 bp), *psbA* (944 bp) and *rbcL* (1399 bp)). Numbers at nodes indicate bootstrap values in maximum likelihood (ML) analysis (left) and posterior probabilities (right) for Bayesian analysis. Asterisk (*) indicates 100 (ML) and 1.00 (Bayes). Only posterior probabilities >0.90 and bootstrap values >50% are shown.

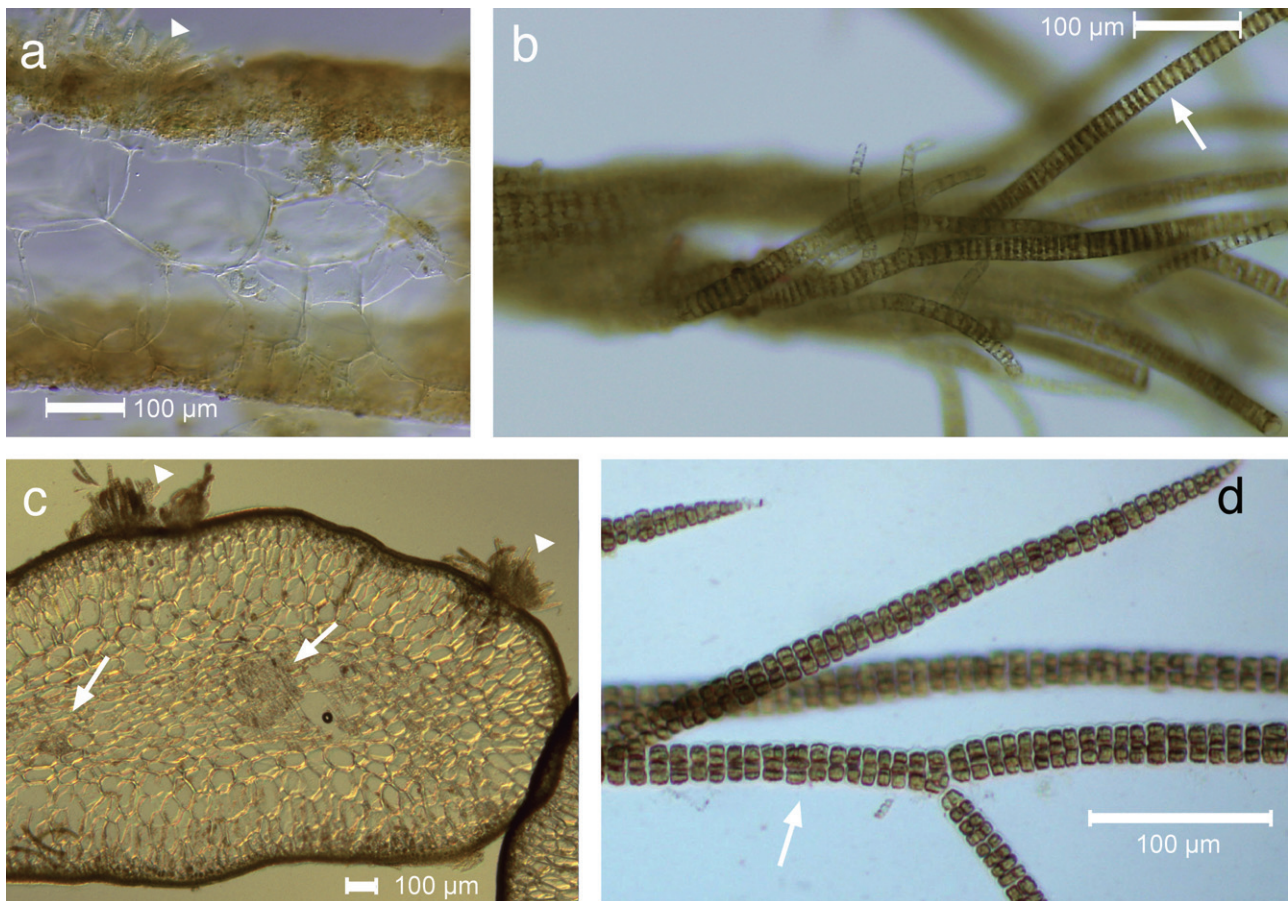


Fig. 2. Characteristic sporophyte morphology of *Cutleria multifida* (a, b) and *Mutimo cylindricus* (c, d). (a) Cross section showing solid medullary layer composed of large inner cells. Arrowhead shows sori with paraphyses. (b) Uniseriate trichothallic filaments (arrow) at the tip of the thallus. (c) Cross section showing partly hollow medullary layer with inner rhizoidal filaments (arrows). Arrowheads show sori with paraphyses. (d) Partly multiseriate assimilatory filaments (arrow) at the tip of thallus.

C. multifida is solid and composed of large inner cells lacking rhizoidal filaments (Fig. 2a), whereas *C. cylindrica* is sometimes hollow, and forms inner rhizoidal filaments (Fig. 2c). Because of the larger inner cells, fresh specimens of *C. multifida* tend to be fragile, whereas, *C. cylindrica* composed of smaller and denser inner cells are rather rough. In addition, the trichothallic filaments of *C. multifida* are uniseriate (Fig. 2b) but those of *C. cylindrica* are uniseriate at the base, but becoming multiseriate at the distal end (Fig. 2d).

Table 3 represents the comparisons of selected morphological features covering the majority of *Cutleria* spp. (AlgaeBase, Guiry & Guiry 2012) and *Z. typus*. Figure 3 shows a schematic representation of two different morphological types shown in Table 3 focused on the morphology of trichothallic filaments and anatomy of gametophytes, and the anatomy of sporophytes. As to the gametophyte morphology, *C. multifida* (generitype), *C. adpersa*, *C. chilosa*, *C. hancockii*, *C. kraftii*, and *C. mollis* share compressed or fan-shaped gametophytes terminated with uniseriate trichothallic filaments characteristic of the genus (Fig. 3a,b). In contrast, *C. cylindrica* has solid, cylindrical gametophytes, and the trichothallic filaments are multiseriate (polystichous) (Fig. 3d,e). As to the sporophyte morphology, *C. cylindrica* is also unique in having asexual plurilocular zoidangia (Kitayama *et al.* 1992) and in the absence of rhizoids issuing from the bottom layer of the crustose sporophytes (Fig. 3f). *Zanardinia typus* differed from *Cutleria* species including *C. cylindrica* in having an isomorphic life history alternating between flat spherical or fan-shaped thalli, but common to *Cutleria multifida* and other taxa excluding *C. cylindrica* it has uniseriate trichothallic filaments, and rhizoids in the central region of the thalli (Fig. 3a–c).

DISCUSSION

In the molecular phylogenetic analyses, *C. cylindrica* was shown to be a sister to the clade composed of *C. adpersa*, *C. chilosa*, *C. multifida* (type of the genus) and *Zanardinia typus*. Morphologically, as compared in Table 3, *C. cylindrica* has distinctive features and is distinguishable from the rest of the *Cutleria* species and *Zanardinia typus*: *Cutleria* species generally have compressed, branched or flat fan-shaped gametophytes with uniseriate trichothallic hairs at the tip, and the inner part of the thalli is filled with large medullary (inner) cells, and remains solid. In contrast, gametophytes of *C. cylindrica* have cylindrical thalli ending in polystichous trichothallic filaments, and the thalli occasionally become hollow by the thickening of the thalli and formation of inner rhizoidal filaments. The polystichous trichothallic filament of the erect thalli in *C. cylindrica* is not a ‘hair’ in the strict sense. In addition, the *Aglaozonia*-stage (sporophyte) of *C. multifida* and

Table 3. Comparisons of selected morphological features among major *Cutleria* taxa and *Zanardinia typus*

Taxa	<i>C. cylindrica</i> Okamura 1902 (= <i>Mutimo</i> <i>cylindricus</i> c.n.)	<i>C. multifida</i> (J.E. Smith) Greville 1830	<i>C. adpersa</i> (Mertens ex Roth) De Notaris 1842	<i>C. chilosa</i> (Falkenberg) P.C. Silva 1957	<i>C. hancockii</i> E.Y. Dawson 1944	<i>C. kraftii</i> Huisman 2000	<i>C. mollis</i> Allender and Kraft 1983	<i>Zanardinia typus</i> (Nardo) P.C. Silva in W. Greuter 2000
Life history pattern	Heteromorphic	Heteromorphic	Heteromorphic	Heteromorphic	Heteromorphic	Heteromorphic	Heteromorphic	Isomorphic
Gametophyte	Cylindrical	Compressed	Compressed	Compressed	Flabellate	Flabellate	Flabellate	Flabellate, flattened spherical
Growth mode	Trichothallic with multiseriate apical filaments	Trichothallic with uniseriate apical filaments	Trichothallic with uniseriate apical filaments	Trichothallic with uniseriate apical filaments	Marginal trichothallic with uniseriate filaments	Trichothallic, with simple filaments	Marginal trichothallic with uniseriate filaments	Marginal trichothallic with uniseriate filaments
Sporophyte								
Asexual plurilocular zoidangia	Present	Absent	Unknown	Unknown	Unknown	Unknown	Unknown	Absent
Rhizoidal filament	Absent	Present	Present	Present	Present	Unknown	Present	Present

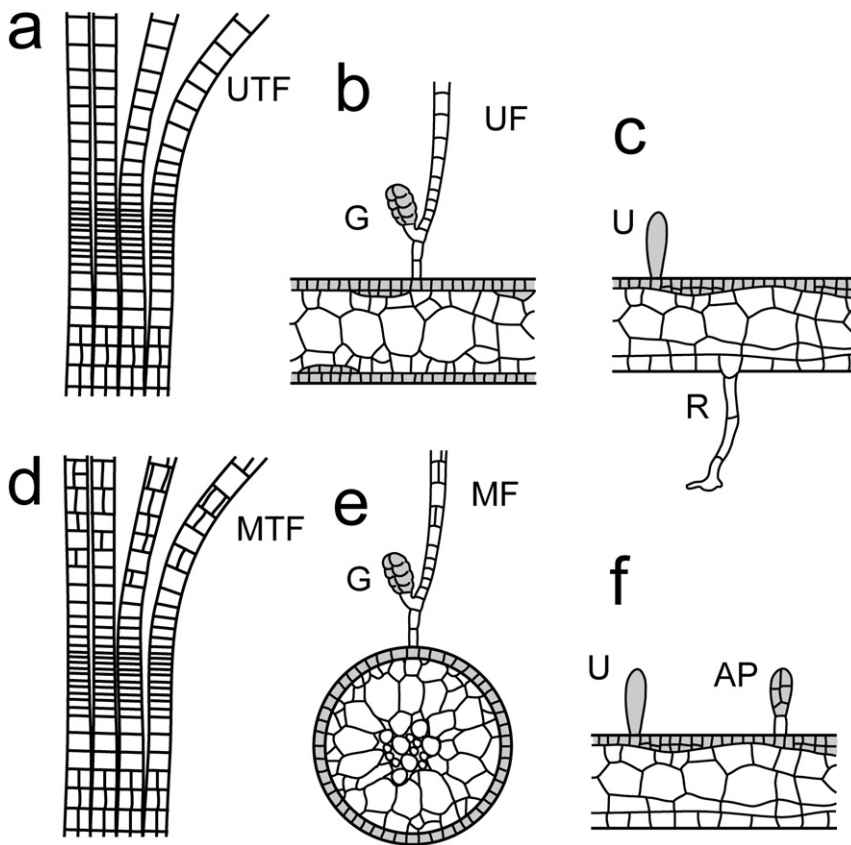


Fig. 3. Comparisons of characteristic morphological features between *Cutleria* and *Zanardinia* (a–c) and *Mutimo* (d–f). Please note that the figures are considerably simplified and are not proportional among the figures. (a) uniseriate trichothallic filaments at the tip of gametophytes; (b) cross section of fertile gametophyte; (c) cross section of fertile sporophyte; (d) multiseriate trichothallic filaments; (e) cross section of fertile gametophyte; (f) cross section of fertile sporophyte. AP, asexual plurilocular zoidangia; G, gametangia; MF, multiseriate filament; MTF, multiseriate trichothallic filament; R, rhizoid, U, unilocular zoidangia; UF, uniseriate filament; UTF, uniseriate trichothallic filament.

some other species is reported to have rhizoids at the bottom surface (Fritsch 1945; Fletcher 1987), but the crustose sporophyte of *C. cylindrica* is tightly attached to the substrates and forms no rhizoids. In conclusion, it is clear that *C. cylindrica* is conspicuously anomalous in the genus *Cutleria*, and therefore we consider that it is necessary to place the species in its own genus, and we propose the establishment of a new genus, *Mutimo* Kawai et Kitayama, to accommodate the species.

Zanardinia differs from *Cutleria* in having an isomorphic life history, but the basic morphology of the thalli resembles the gametophytes of *Cutleria* (Yamanouchi 1912, 1913). In addition, the thalli (gametophyte/sporophyte) of *Zanardinia* appear to have intermediate morphological features between the erect gametophytic thalli (especially those of *C. adspersa*) and crustose sporophyte (*Aglaozonia* stage) of *Cutleria*: the young marginal portion of the thalli resembles the terminal portion of flabellate *C. adspersa* gametophytes, but the inner developed portion is prostrate with rhizoids and resembles an *Aglaozonia* stage.

Our molecular data suggest that *Zanardinia* is included in the clade of *Cutleria*, so that it is considered that the isomorphic life history of *Zanardinia* might have evolved secondarily in the *Cutleria* lineage. However, changes of life history patterns in relation to the morphology of gametophytes and sporophytes are

often seen even among relatively close phylogenetic taxa in brown algae: In the order Ralfsiales, most members have an isomorphic life history with crustose thalli, but *Analipus* spp. have isomorphic life histories with terete thalli, and *Heteroralfsia* has a heteromorphic life history with terete sporophyte and crustose gametophyte (Kawai 1989; Lim *et al.* 2007). Similarly, most members of Scytosiphonales (or Scytosiphonaceae in Ectocarpales *s.l.*) have a heteromorphic life history with terete gametophyte and crustose sporophyte, but *Melanosiphon* and *Myelophycus* have an isomorphic life history with terete thalli (Wynne 1969; Kogame *et al.* 1999; Cho *et al.* 2003). Furthermore, considerably different life history patterns are found within the genus *Syringoderma*, although taxonomic revision at the generic level might be necessary (Henry 1984; Kawai & Yamada 1990).

As to the phylogenetic position of Cutleriaceae in higher taxonomic ranks and their ordinal assignment, recent molecular phylogenies suggest its close relationship with *Sacchorhiza*, *Tilopteris* and *Halosiphon*, and some authors placed the family in the order Tilopteridales (Phillips *et al.* 2008; Silberfeld *et al.* 2010). Our own analyses support these results, and the independence of Cutleriaceae at the ordinal rank is challenged. *Microzonia* has been traditionally included in Culteriales, but it is currently included in Syringoder-

matales (Bittner *et al.* 2008). As to the genus level taxonomy of *Cutleria* and *Zanardinia*, although the generic independence of *Zanardinia* is questioned, we would like to suspend any conclusion until the phylogenetic relationships among more taxa become clarified.

Mutimo gen. nov. H. Kawai et T. Kitayama

Gametophyta flava vel fusca brunnea, parenchymata cylindrica ramosa, plerumque epilithica, solitaria vel caespitosa, haptero parvo discoideo affixa, dichotome vel lateraliter ramosa, caespitibus filamentorum polystichorum terminata; e strato medullario et corticali constantia, strato medullario e cellulis aliquot magnis incoloratis constante, strato corticali e cellulis parvis pigmentosis in stratis 1 vel 2 dispositis constante. Quaque cellula chloroplastos multos disciformes sine pyrenoidibus continens. Trichomata phaeophyceana praesentia, plerumque aggregata. Gametophyta plerumque dioecia, gametangia plurilocularia dispersa super facie thallorum efferentia; gametangia feminea loculis multo majoribus quam loculis gametangiorum masculorum. Thalli sporophytici crustosi parenchymati cellulis marginalibus meristematis, zoidangia sessilia cylindrica unilocularia in facie formantes. A *Cutleria* gametophytis cylindricis filamentis polystichis terminatis distinguendo.

Gametophytes yellowish to dark brown in color, parenchymatous, cylindrical, branched, mostly epilithic, solitary or caespitose, attached with a small discoid holdfast, dichotomously or laterally branched, terminated with tufts of polystichous filaments; composed of medullary layer consisting of several large, colorless cells and cortical layer consisting of 1–2 layers of small pigmented cells. Each cell containing many disc-shaped chloroplasts without pyrenoids. Phaeophycean hairs present, usually grouped. Gametophytes normally dioecious, forming plurilocular gametangia scattered on the surface of the thalli. Locules of female gametangia are significantly larger than those of male gametangia. Sporophytic thalli crustose, parenchymatous, with marginal meristematic cells, forming sessile, cylindrical unilocular zoidangia on the surface. Distinguished from *Cutleria* in having cylindrical gametophytes terminating with polystichous filaments.

Etymology: The generic name originates from the Japanese name of the type species based on its whiplash-shaped gametophytic thalli.

Mutimo cylindricus (Okamura) H. Kawai et T. Kitayama comb. nov.

Basionym: *Cutleria cylindrica* Okamura 1902.

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