

Corrigendum to “Taxonomic re-examination of *Chlamydomonas* strains maintained in the NIES-Collection” [Microbiol. Cult. Coll. 29: 1-12, 2013]

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We discovered errors in our data caused by displacement of 12 strains (NIES-1021, NIES-1022, NIES-2314, NIES-2315, NIES-2316, NIES-2317, NIES-2318, NIES-2319, NIES-2320, NIES-2321, NIES-2322, NIES-2323) in which one strain (NIES-2314) should be removed from the data set in this article. Based on a careful check of the laboratory notebook, we found that displacement of 12 strains had occurred during one PCR procedure. One strain, NIES-2314 was not amplified in that experiment causing the crucial source of the displacement of the above 12 strains. Double-check experiments were conducted for the 12 strains, and we obtained the actual 18S rDNA sequences for the 11 strains. Despite repeated analysis for the NIES-2314, however, we failed to amplify the DNA. The 18S rDNA sequences of the 11 strains were revised in the DDBJ with the same accession number. The accession number of NIES-2314 (AB701519) is now closed in the DDBJ. We express our regret for these errors and have requested that the following corrections be made for this article. The corrected parts are indicated in bold. We would like to apologize for any misunderstanding caused by these errors.

Page 1, right column, line 31 for “**79** *Chlamydomonas* strains” should read “**78** *Chlamydomonas* strains”.

Page 2, left column, line 1 for “**79** strains” should read “**78** strains”.

Page 2, right column, line 11 for “**181** sequences” should read “**180** sequences”.

Page 3, Fig. 2: **Revised figures are attached.** An underline indicates the corrected strains.

Page 4, Fig. 3: **Revised figures are attached.** An

underline indicates the corrected strains.

Page 5, right column, line 1 for “**6** to *Monadinia*” should read “**5** to *Monadinia*”.

Page 5, right column, line 41 for “**49** strains” should read “**48** strains”.

Page 5, right column, line 41 for “**79** NIES strains” should read “**78** NIES strains”.

Page 5, right column, line 47 for “**four** strains” should read “**three** strains”.

Page 5, right column, line 48 for “NIES-**1022**, 1733, **2323** and 2324” should read “NIES-**1021**, 1733 and 2324”.

Page 5, right column, line 49 for “**four** strains” should read “**three** strains”.

Page 5, right column, line 50 for “*Cd. parkeae*” should read “*Cd. parkeae* and *Cd. coccoides*, respectively”.

Page 6, Table 1, for “Table 1 List of **79** NIES strains” should read “Table 1 List of **78** NIES strains”.

Page 6, Table 1, for “*Moewusinia* NIES-1022 *Chlamydomonas* sp. (*Moewusinia*) <*Chlamydomonas parkeae* Ettl <#97 (Moriya, 2002) AB701508” should read “*Moewusinia* NIES-1022 *Chlamydomonas parkeae* Ettl <#97 (Moriya, 2002) AB701508”.

Page 6, Table 1, for “*Moewusinia* NIES-2323 *Chlamydomonas* sp. (*Moewusinia*) <Sa-38 (Suda, 1986) AB701510” should read “*Chlorogonia* NIES-2323 *Chlamydomonas* sp. (*Chlorogonia*) <Sa-38 (Suda, 1986) AB701510”.

Page 7, Table 1, for “*Chlorogonia* NIES-2322 *Chlamydomonas* sp. (*Chlorogonia*) <w-36 (Suda, 1987) AB701515” should read “*Oogamochlamydinia* NIES-2322 *Chlamydomonas* sp. (*Oogamochlamydinia*) <w-36 (Suda, 1987) AB701515”.

Page 7, Table 1, for “*Monadinia* NIES-1021

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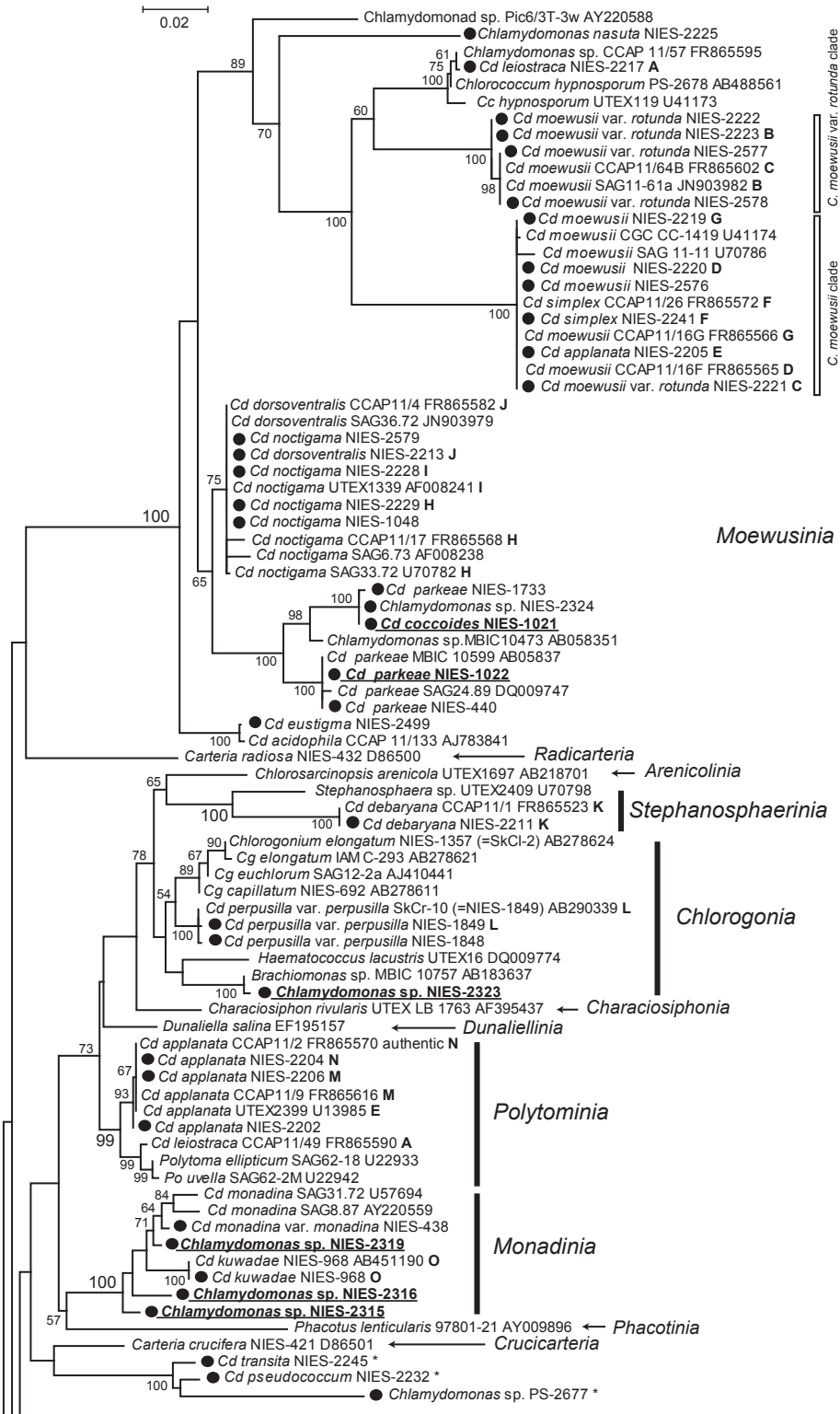


Fig. 2 Details of the ML tree obtained based on 18S rDNA sequences. *Moewusinia*, *Stephanosphaerinia*, *Chlorogonia*, *Polytominia*, and *Monadinia* are shown with representative strains of *Radicarteria*, *Arenicolinia*, *Characiosiphonia*, *Dunaliellinia*, *Phacotinia*, and *Crucicarteria*. Bootstrap values of more than 50% are shown on each branch. Sequences analyzed in the present study are indicated in filled circles. The same alphabetical characters (A-O) indicate strains of the same origin. An underline indicates the corrected strains.

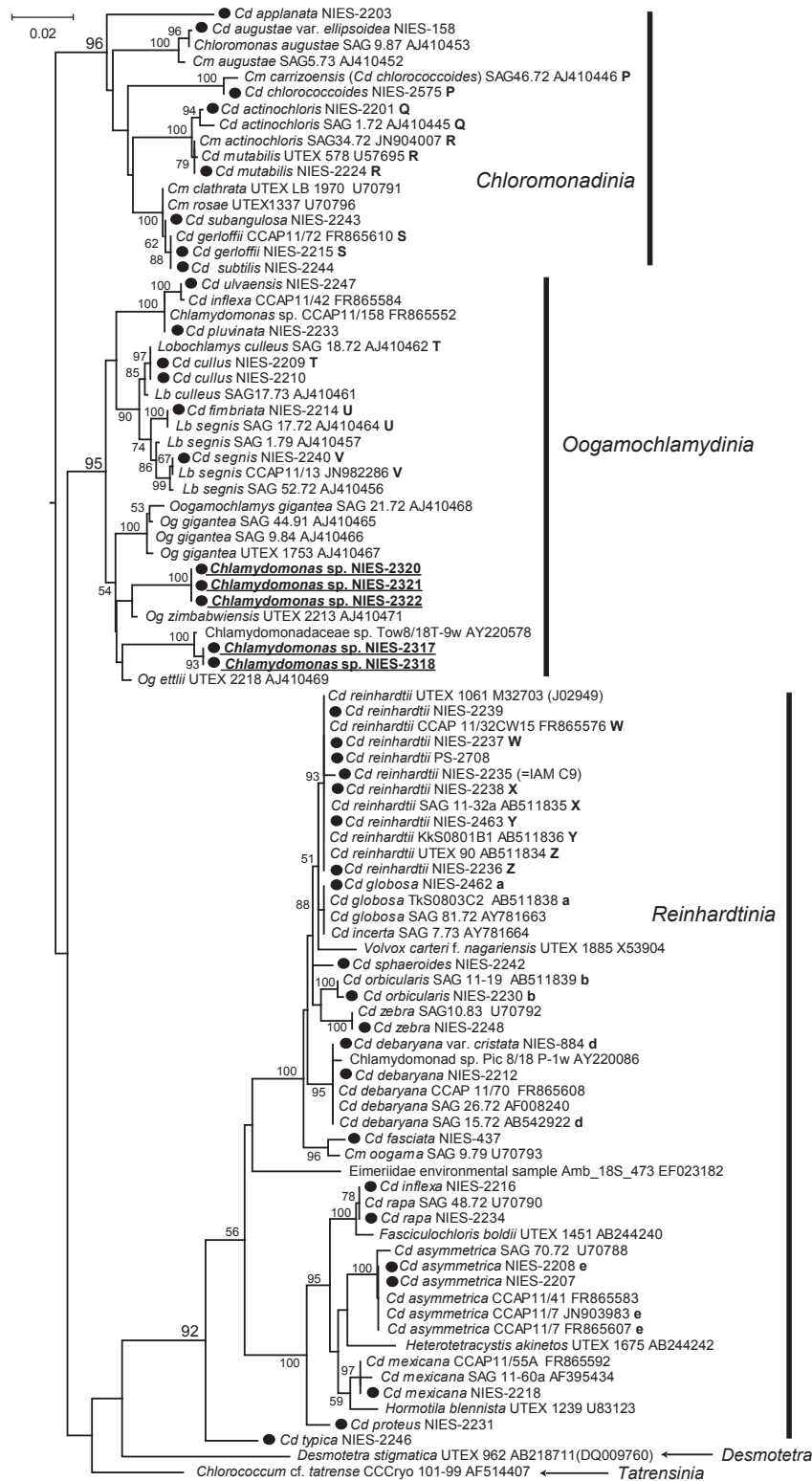


Fig. 3 Details of the ML tree obtained based on 18S rDNA sequences. *Chloromonadina*, *Oogamochlamydia*, and *Reinhardtina* are shown with representative strains of *Desmotetra*, and *Tatrensina*. Bootstrap values of more than 50% are shown on each branch. Sequences analyzed in the present study are indicated in filled circles. The same alphabetical characters (P-e) indicate strains of the same origin. An underline indicates the corrected strains.

Chlamydomonas kuwadae Gerloff < *Chlamydomonas coccooides* Butcher <#95 (Moriya, 2002) AB701517" should read "***Moewusinia*** NIES-1021 *Chlamydomonas* sp. (***Moewusinia***) < *Chlamydomonas coccooides* Butcher <#95 (Moriya, 2002) AB701517".

Page 7, Table 1, "***Monadinia*** NIES-2314 *Chlamydomonas* sp. (***Monadinia***) <SIS-ch (Suda, around 1986) AB701519" to be deleted.

Page 7, Table 1, for "***Monadinia*** NIES-2318 *Chlamydomonas* sp. (***Monadinia***) <KZ-5-17 (Suda, around 1986) AB701521" should read "***Oogamochlamydinia*** NIES-2318 *Chlamydomonas* sp. (***Oogamochlamydinia***) <KZ-5-17 (Suda, around 1986) AB701521".

Page 8, Table 1, for "***Oogamochlamydinia*** NIES-2316 *Chlamydomonas* sp. (***Oogamochlamydinia***) <CChla (Suda, around 1986) AB701528" should read "***Monadinia*** NIES-2316 *Chlamydomonas* sp. (***Monadinia***) <CChla (Suda, around 1986) AB701528".

Page 8, Table 1, for "***Oogamochlamydinia*** NIES-2319 *Chlamydomonas* sp. (***Oogamochlamydinia***)

<H-3-6 (Suda, 1986) AB701530" should read "***Monadinia*** NIES-2319 *Chlamydomonas* sp. (***Monadinia***) <H-3-6 (Suda, 1986) AB701530"

Page 10, left column, line 4 for "NIES-2319, 2320 and 2321" should read "NIES-2320, 2321 and **2322**".

Page 11, left column, line 33 for "**15** strains" should read "**14** strains".

Page 11, right column, line 3 for "**Two strains of *Cd. parkeae*, NIES-1022 and 1733,** were downgraded" should read "***Cd. coccooides* NIES-1021 and *Cd. parkeae* NIES-1733** were downgraded".

Page 11, right column, line 6 for "**two other strains, NIES-2323 and 2324,**" should read "**another strain, NIES-2324,**".

Page 11, right column, line 25-30, "***Monadinia: Chlamydomonas coccooides* NIES-1021 was revised to *Cd. kuwadae* because this strain was shown to be included in a subclade that consisted of *Cd. kuwadae* with high bootstrap support (100% in the ML tree, Fig. 2, and 99% in the NJ tree) based on the results of phylogenetic analyses.**" to be deleted.