

SUPPORTING INFORMATION

***Elliptochloris*, not *Coccomyxa*, is the photobiont of three lichenized *Multiclavula* species collected in Japan**

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Appendix S3. ITS2 secondary structures of seven *Elliptochloris* strains newly obtained in this study. The barcode region is numbered in white boxes and marked in blue for each helix.

**ITS2 rRNA secondary structure model of
Elliptochloris parasphaerica
 NIES-4523 LC597447**

5.8S/LSU stem

```
---00000-000-0111-11
---12345-678-9012-34
```

```
---23442-154-2453-26
```

```
GUC      C   G   C
  UGCCU  AGC  UCGG  UU->
  |||||  |•|  ||•|  |•
  ACGGA  UUG  AGUC  AG<-
AGA      C   -   C
```

```
-----
->CACCCC
-----
```

Helix I

```
11111
56789
```

```
64444
```

```
--          UU
UCCCCU  CCCUUUCUC  G
•|•|•|•|  |•|•|•|•|•|  |
GGGGGA  GGGAAAGAG  U
          CG          UU
```

```
-----
ACC
-----
```

Helix II

```
22222222223
01234567890
```

```
63367774643
```

```
CGU      CU
UGGU     CUCGGCC  C
•||•     |•|•|•|  |
GCCG     GGGCCGG  A
          CCU      AC
```

```
-----
AAGCACAGA
-----
```

Helix III

```
33333333-344444--4444-----45555-5555--5566-66666666
12345678-901234--5678-----90123-4567--8901-2345678
```

```
33424388-134135--4444-----53345-4136--3361-3431448
```

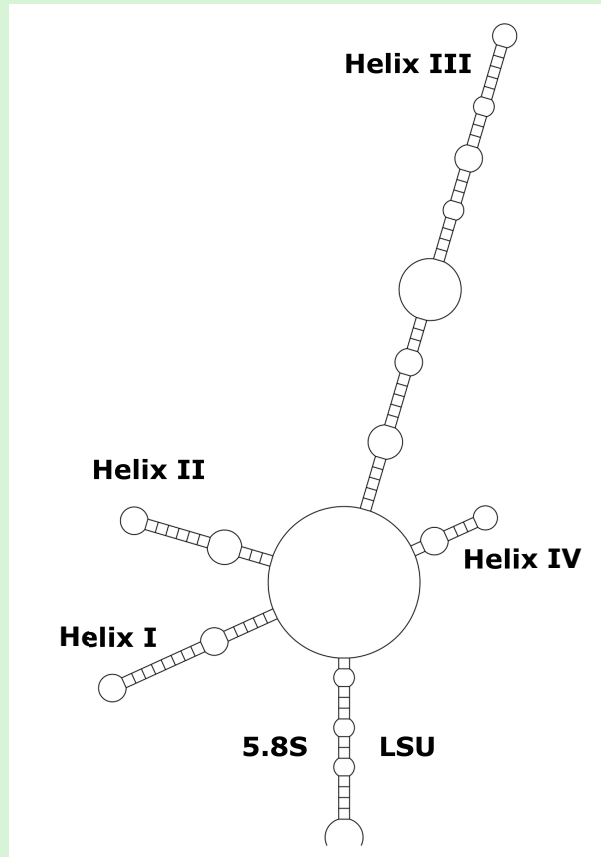
```
---      A-   GUCUCAA   A   CU   G   UC
GGCUCG   AGCAGG  CCCC       GGGCG  CAGU  GGUA  GCGACC  \
|||||   |||||•  ||||       •|||•  |||•  ||•|  |||||  C
CCGAGC   UCGUCU  GGGG       UCCGU  GUCG  CCGU  CGCUGG  /
          CGG     GC     -----   G   --   A   CC
```

```
-----
CGCA
-----
```

Helix IV

```
AA      CC
GG  GUGG  \
||  |||  A
CC  CACC  /
--      UG
```

```
-----
AGUCCACCC->
-----
```



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

**ITS2 rRNA secondary structure model of
Elliptochloris parasphaerica
NIES-4524 LC660438**

5.8S/LSU stem

```

----00000-000-0111-11
----12345-678-9012-34
    
```

```

----23442-154-2453-26
    
```

```

GUC      C  G  C
  UGCCU  AGC  UCGG  UU->
  |||||  |•|  ||•|  |•
  ACGGA  UUG  AGUC  AG<-
AGA      C  -  C
    
```

```

-----
->CACCCC
-----
    
```

Helix I

```

11111
56789
    
```

```

64444
    
```

```

--          UU
UCCCCU  CCCUUUCUC  G
•|||||  |||||  |
GGGGGA  GGGAAAGAG  U
      CG          UU
    
```

```

-----
ACC
-----
    
```

Helix II

```

22222222223
01234567890
    
```

```

63367774643
    
```

```

CGU      CU
UGGU  CUCGGCC  C
•||•  |•|||||  |
GCCG  GGGCCGG  A
      CCU      CC
    
```

```

-----
AAGCACAGA
-----
    
```

Helix III

```

33333333-344444--4444-----45555-5555--5566-6666666
12345678-901234--5678-----90123-4567--8901-2345678
    
```

```

33424388-134135--4444-----53341-4136--3361-3431448
    
```

```

---      A-  GUUCAA  A  CU  G  UU
GGCUCG  AGCAGG  CCCC  GGGCA  CAGU  GGUA  GCGACC  \
||||||  |||||•  ||||  •||||  |||•  ||•|  |||||  C
CCGAGC  UCGUCU  GGGG  UCCGU  GUCG  CCGU  CGCUGG  /
      CGG      GC  -----  G  --  A  CC
    
```

```

-----
CGCA
-----
    
```

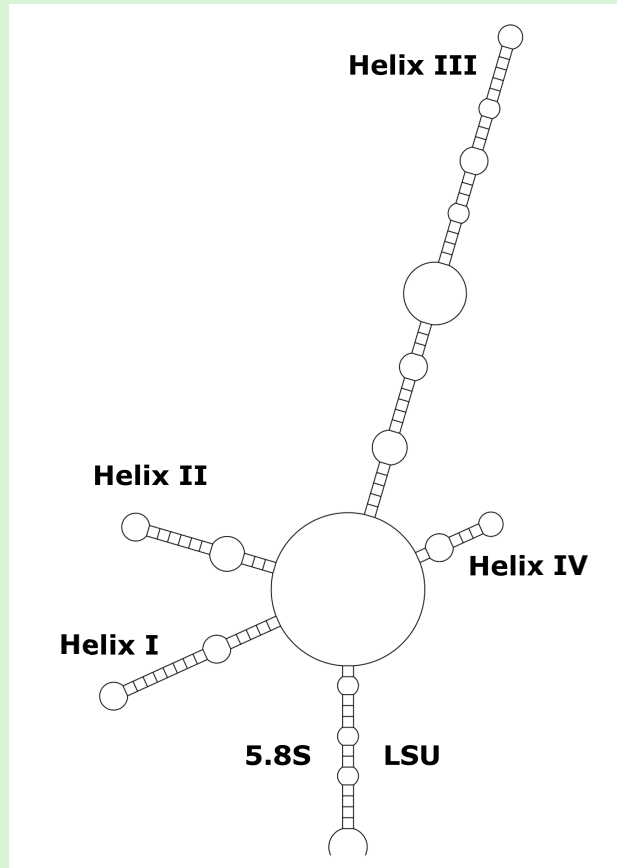
Helix IV

```

AA  CC
GG  GUGG  \
||  |||  A
CC  CACC  /
--  UG
    
```

```

-----
AGUCCACCC->
    
```



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

**ITS2 rRNA secondary structure model of
Elliptochloris subsphaerica
NIES-4526 LC660442**

5.8S/LSU stem

```
---00000-000-0111-11
---12345-678-9012-34
```

```
---23442-154-2453-26
```

```
GUC      C   G   C
  UGCCU  AGC  UCGG  UU->
  |||||  |•|  ||•|  |•
  ACGGA  UUG  AGUC  AG<-
AGA      C   -   C
```

```
-----
->CACCCC
-----
```

Helix I

```
11111
56789
```

```
64444
```

```
      -           U
UCCCCUC CCUUUCUCUUU U
•||||| |·|||·|·|
GGGGGAG GGAAAGAGAAG G
      C           C
```

```
-----
ACC
-----
```

Helix II

```
2222222223
01234567890
```

```
63367774643
```

```
      UGU      CU
UGGU  CUCGCC  C
•||•  |·|||  |
GCCG  GGGCCG  A
      CCU      CC
```

```
-----
AAGCACAGA
-----
```

Helix III

```
33333333-344444--4444-----45555-5555--5566-6666666
12345678-901234--5678-----90123-4567--8901-2345678
```

```
33424388-134133--4444-----53341-4136--3361-3431448
```

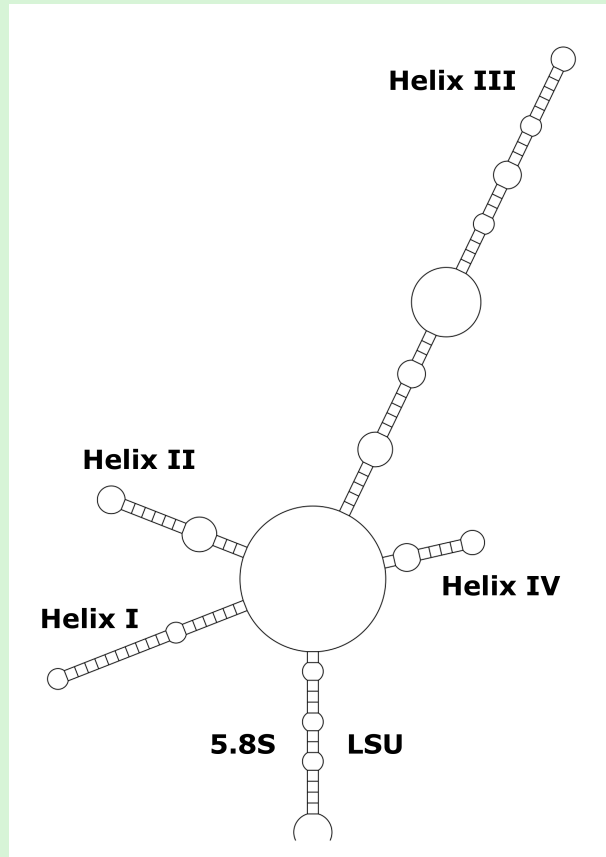
```
      ---      A-      GUUUACAA      A      CU      G      UC
GGCUCG  AGCAGG  CCCC      GGGCA  CAGU  GGUA  GCGACC  \
|||||  |||||  |||      •|||  |||•  ||•  |||||  C
CCGAGC  UCGUCC  GGGG      UCCGU  GUCG  CCGU  CGCUGG  /
      UGG      GC      -----      G      --      A      CC
```

```
-----
CGCA
-----
```

Helix IV

```
      AA      UG
GG  GUGGC  \
||  ||||  C
CC  CACCG  /
      G-      UU
```

```
-----
UUCACCAUUC->
-----
```



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

**ITS2 rRNA secondary structure model of
Elliptochloris subsphaerica
NIES-4532 LC660445**

5.8S/LSU stem

```
---00000-000-0111-11
---12345-678-9012-34
```

```
---23442-154-2453-26
```

```
GUC      C  G  C
  UGCCU  AGC  UCGG  UU->
  |||||  |•|  ||•|  |•
  ACGGA  UUG  AGUC  AG<-
AGA      C  -  C
```

```
-----
->CACCCC
-----
```

Helix I

```
11111
56789
```

```
64444
```

```
-      C  U
UCCCCUC CCUUUCU UUCG \
•|||||  |||||  |||  G
GGGGGAG GGAAAGA AAGC /
      C      A  A
```

```
-----
ACC
-----
```

Helix II

```
2222222223
01234567890
```

```
63367774643
```

```
CGU      CU
UGGU     CUCGGCC  C
•||•     |•|||  |
GCCG     GGGCCGG  A
      CCU      CC
```

```
-----
AAGCACAGA
-----
```

Helix III

```
33333333-344444--4444-----45555-5555--5566-6666666
12345678-901234--5678-----90123-4567--8901-2345678
```

```
73424388-134133--4444-----53341-4136--3361-3431448
```

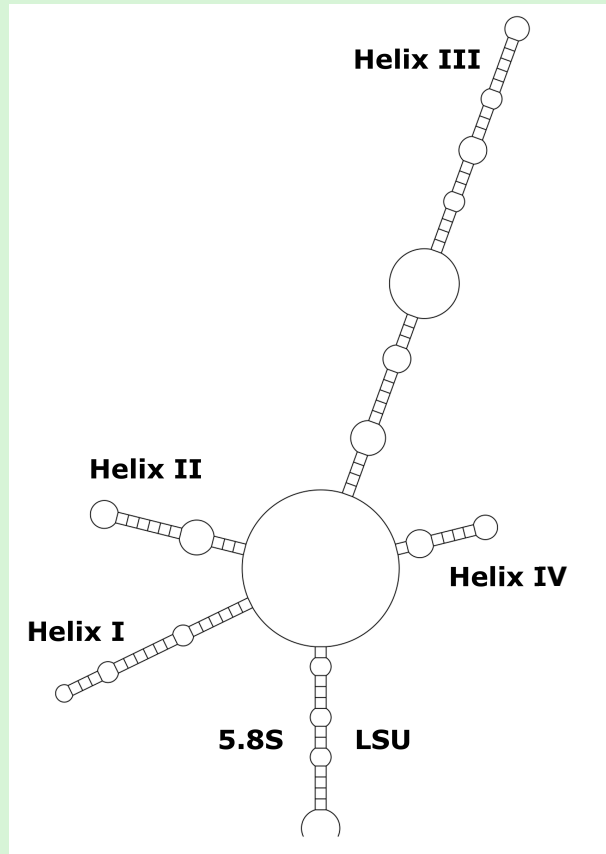
```
G      ---      A-      GUUCACAU      A      CU      G      UC
GCUCG  AGCAGG  CCCC      GGGCA  CAGU  GGUA  GCGACC  \
|||||  |||||  |||      •||||  |||•  ||•|  |||||  C
CGAGC  UCGUCC  GGGG      UCCGU  GUCG  CCGU  CGCUGG  /
A      CGG      GC      -----      G      --      A      CC
```

```
-----
CGCA
-----
```

Helix IV

```
AA      UG
GG  GUGGC  \
||  |||||  C
CC  CACCG  /
G-      UU
```

```
-----
UUCACCAUUC->
-----
```



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

**ITS2 rRNA secondary structure model of
Elliptochloris subsphaerica
S-200-PL-015A LC660441**

5.8S/LSU stem

```
---00000-000-0111-11
---12345-678-9012-34
```

```
---23442-154-2453-26
```

```
GUC      C  G  C
  UGCCU  AGC  UCGG  UU->
  |||||  |•|  ||•|  |•
  ACGGA  UUG  AGUC  AG<-
AGA      C  -  C
```

```
-----
->CACCCC
-----
```

Helix I

```
11111
56789
```

```
64444
```

```
-          U
UCCCCUC  CCUUCUCUUU  U
•|||||  |||||•|
GGGGGAG  GGAAAGAGAAG  G
          C          C
```

```
-----
ACC
-----
```

Helix II

```
22222222223
01234567890
```

```
63367774643
```

```
UGU      CU
UGGU     CUCGGCC  C
•||•    |•|||||  |
GCCG     GGGCCGG  A
          CCU      CC
```

```
-----
AAGCACAGA
-----
```

Helix III

```
33333333-344444--4444-----45555-5555--5566-6666666
12345678-901234--5678-----90123-4567--8901-2345678
```

```
33424388-134133--4444-----53341-4136--3361-3431448
```

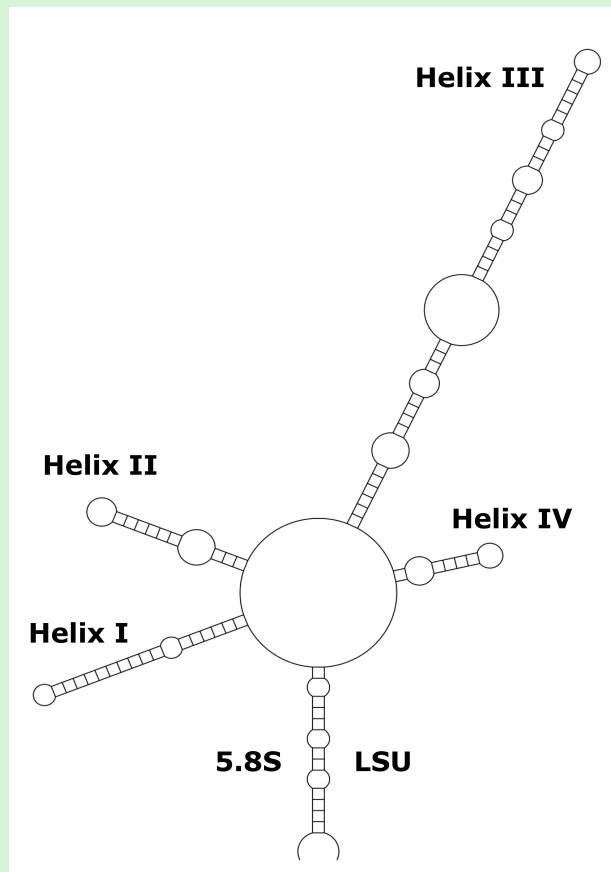
```
---      A-      GUUUACAA      A      CU      G      UC
GGCUCG   AGCAGG   CCCC           GGGCA  CAGU   GGUA  GCGACC  \
|||||    |||||    ||||         •||||  |||•  ||•|  |||||  C
CCGAGC   UCGUCC   GGGG           UCCGU  GUCG   CCGU  CGCUGC  /
          UGG      GC      -----      G      --      A      CC
```

```
-----
CGCA
-----
```

Helix IV

```
AA      UG
GG  GUGGC  \
||  ||||  C
CC  CACCG  /
G-    UU
```

```
-----
UUCACCAUUC->
-----
```



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases