

Supplementary Materials

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Supplementary Table 1. Estimates of average evolutionary divergence (%) over sequence pairs within or between species belonging to the Chamo clade

	<i>C. marina</i> var. <i>antiqua</i>	<i>C. marina</i>	<i>C. marina</i> var. <i>ovata</i>
ITS	<i>Chattonella marina</i> var. <i>antiqua</i>	0.086	-
	<i>C. marina</i>	0.043	0.000
	<i>C. marina</i> var. <i>ovata</i>	0.051	0.008
<i>rbcL</i>	<i>C. marina</i> var. <i>antiqua</i>	0.166	-
	<i>C. marina</i>	0.454	0.324
	<i>C. marina</i> var. <i>ovata</i>	0.170	0.425
COI	<i>C. marina</i> var. <i>antiqua</i>	0.950	-
	<i>C. marina</i>	1.326	1.433
	<i>C. marina</i> var. <i>ovata</i>	0.951	1.352

The number of base substitutions per site from averaging over all sequence pairs within or between each species are shown. Analyses were conducted using the maximum composition likelihood model (Tamura et al. 2004). The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). This analysis involved 61 sequences of 555 base pairs (bp) of internal transcribed spacer (ITS), 550 bp of ribulose-1,5-bisphosphate carboxylase / oxygenase large subunit (*rbcL*), and 458 bp of mitochondrial cytochrome c oxidase subunit 1 (COI) regions which are eliminated all positions containing gaps and missing.

REFERENCES

Tamura, T., Nei, M. & Kumar, S. 2004. Prospects for inferring very large phylogenies by using the neighbor-joining method. Proc. Natl. Acad. Sci. U. S. A. 101:11030–11035.

<i>C. marina</i> _LIMS-PS-2900	ACCACACCGATCCTAAACGGGATCCGTCCTCCATCGTGAACCTGTTTCCGGGCCTTGCCCGC	60
<i>C. marina</i> _CM211006MP1	ACCACACCGATCCTAAACGGGATCCGTCCTCCATCGTGAACCTGTTTCCGGGCCTTGCCCGC	60
<i>C. ovata</i> _COKP9909	-CCACACCGATCCTAAACGGGATCCGTCCTCCATCGTGAACCTGTTTCCGGGCCTTGCCCGC	59
<i>C. subsalsa</i> _CCMP2191	ACCACACCGATCCTAAACGGGATCCGTCCTCCATCGTGAACCTGTTTCCGGGCCTTGCCCGC	60
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<i>C. marina</i> _LIMS-PS-2900	TTGACAGCTTTTACACCATCCAACCA-AACCTCAAACCAAACATTTTGACCCTACCAA	119
<i>C. marina</i> _CM211006MP1	TTGACAGCTTTTACACCATCCAACCA-AACCTCAAACCAAACATTTTGACCCTACCAA	119
<i>C. ovata</i> _COKP9909	TTGACAGCTTTTACACCATCCAACCA-AACCTCAAACCAAACATTTTGACCCTACCAA	118
<i>C. subsalsa</i> _CCMP2191	TTGACATCCTTTACACCATCCAACCAAACCTCAAACCAAACATTTTGACCCTACCAA	120
	***** * *****	
<i>C. marina</i> _LIMS-PS-2900	CCCATTGACTGAACCGTAACGGTTGCTTCTCTGGAAGCAA---TCGGCGATTTAAACAA	176
<i>C. marina</i> _CM211006MP1	CCCATTGACTGAACCGTAACGGTTGCTTCTCTGGAAGCAA---TCGGCGATTTAAACAA	176
<i>C. ovata</i> _COKP9909	CCCATTGACTGAACCGTAACGGTTGCTTCTCTGGAAGCAA---TCGGCGATTTAAACAA	175
<i>C. subsalsa</i> _CCMP2191	CCCATTGACTGAACCGTAACGGCCGCTTCCCTCGGGAGGCAGCCGACGATTTATATCAA	180
	***** * *****	
<i>C. marina</i> _LIMS-PS-2900	ATCATAACGACTTTTACAGCAGCGGATGTCTTGGTTCCACAACGATGAAGAACGCAGCGAAA	236
<i>C. marina</i> _CM211006MP1	ATCATAACGACTTTTACAGCAGCGGATGTCTTGGTTCCACAACGATGAAGAACGCAGCGAAA	236
<i>C. ovata</i> _COKP9909	ATCATAACGACTTTTACAGCAGCGGATGTCTTGGTTCCACAACGATGAAGAACGCAGCGAAA	235
<i>C. subsalsa</i> _CCMP2191	ATCATAACGACTTTTACAGCAGCGGATGTCTTGGTTCCACAACGATGAAGAACGCAGCGAAA	240
	***** * *****	
<i>C. marina</i> _LIMS-PS-2900	TGCGATACGTAATGCGAATTGCGAGAGTCCAGCGAGTCATCAAATGTTTGAACGCACCTGG	296
<i>C. marina</i> _CM211006MP1	TGCGATACGTAATGCGAATTGCGAGAGTCCAGCGAGTCATCAAATGTTTGAACGCACCTGG	296
<i>C. ovata</i> _COKP9909	TGCGATACGTAATGCGAATTGCGAGAGTCCAGCGAGTCATCAAATGTTTGAACGCACCTGG	295
<i>C. subsalsa</i> _CCMP2191	TGCGATACGTAATGCGAATTGCGAGAGTCCAGCGAGTCATCAAATGTTTGAACGCACCTGG	300
	***** * *****	
<i>C. marina</i> _LIMS-PS-2900	CACTTCCGGGATATTCTGGGAGTATGCTTGTAGAGTGTCTGTTGGACCATCTCCCTTG	356
<i>C. marina</i> _CM211006MP1	CACTTCCGGGATATTCTGGGAGTATGCTTGTAGAGTGTCTGTTGGACCATCTCCCTTG	356
<i>C. ovata</i> _COKP9909	CACTTCCGGGATATTCTGGGAGTATGCTTGTAGAGTGTCTGTTGGACCATCTCCCTTG	355
<i>C. subsalsa</i> _CCMP2191	CACTTCCGGGATATTCTGGGAGTATGCTTGTAGAGTGTCTGTTGGACCATCTCCCTCG	360
	***** * *****	
<i>C. marina</i> _LIMS-PS-2900	TTCCCTTCG--GGAAGAAGTGGCGGTAGTTGCCGTACATTTTGCTCTTTGAGCGAGATGAT	414
<i>C. marina</i> _CM211006MP1	TTCCCTTCG--GGAAGAAGTGGCGGTAGTTGCCGTACATTTTGCTCTTTGAGCGAGATGAT	414
<i>C. ovata</i> _COKP9909	TTCCCTTCG--GGAAGAAGTGGCGGTAGTTGCCGTACATTTTGCTCTTTGAGCGAGATGAT	413
<i>C. subsalsa</i> _CCMP2191	TTCCCACTGGGCAACGAGTGGCGGAGTTGCCGTACATTTTGCTCCTGAGCGGGATGAT	420
	**** * * *****	
<i>C. marina</i> _LIMS-PS-2900	CGGTTAAGCACTCGAGATAACAACCGTTGAGTTCAACGGGC-GTGGTAGCGCTGGGCCTC	473
<i>C. marina</i> _CM211006MP1	CGGTTAAGCACTCGAGATAACAACCGTTGAGTTCAACGGGC-GTGGTAGCGCTGGGCCTC	473
<i>C. ovata</i> _COKP9909	CGGTTAAGCACTCGAGATAACAACCGTTGAGTTCAACGGGC-GTGGTAGCGCTGGGCCTC	472
<i>C. subsalsa</i> _CCMP2191	CGGTTAAGCACTCGAGATAACAACCGTTGATTCCGACGGGCGTGGTAGCGCTGGGC--T	478
	***** * *****	
<i>C. marina</i> _LIMS-PS-2900	ATGGCTAAGCACAAATCCTCCCGGTAGAAGTCTCGGTTGATCTAACAGAGGAACTGGAA	533
<i>C. marina</i> _CM211006MP1	ATGGCTAAGCACAAATCCTCCCGGTAGAAGTCTCGGTTGATCTAACAGAGGAACTGGAA	533
<i>C. ovata</i> _COKP9909	ATGGCTAAGCACAAATCCTCCCGGTAGAAGTCTCGGTTGATCTAACAGAGGAACTGGAA	532
<i>C. subsalsa</i> _CCMP2191	TCGGCCAAGCACACATCCTCCCGGCAGAAACCTCGGTTGATCTGACAGAGGAACTGGGT	538
	*** *****	
<i>C. marina</i> _LIMS-PS-2900	GAAGCTTCGGCTGAATCCACTTTTTCAGATCTCTAATCAAGCAAGAAGACCCGC----	586
<i>C. marina</i> _CM211006MP1	GAAGCTTCGGCTGAATCCACTTTTTCAGATCTCTAATCAAGCAAGAAGACCCGC----	586
<i>C. ovata</i> _COKP9909	GAAGCTTCGGCTGAATCCACTTTTTCAGATCTCTAATCAAGCAAGAAGACCCGC----	584
<i>C. subsalsa</i> _CCMP2191	GGCTTCTGC---CGCCTCACTGTTTCAGATCTCCAATCAAGCAAGAAAACCCGCTGAA	592
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Supplementary Fig. S1. The alignment of 185 to 285 ribosomal DNA partial sequences contained the internal transcribed space region, from *Chattonella marina* (LIMS-PS-2900, CM211006MP1), *C. marina* var. *ovata* (COKP9909), and *Chattonella subsalsa* (CCMP2191). Four sequences were simply aligned using Clustal Omega. The asterisks indicate a nucleotide that is not matched by at least one among four sequences. The orange-shaded areas indicate the sequences of forward and reverse primers designed for this study.