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Supplementary material

Community Structure of Microorganisms Associated with Reddish-brown Iron-rich Snow

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Table S1. List of Bacterial OTUs detected detected as minor components of the clone library.

OTU	No. of clone	Phylogenetic group	Accession number
OZE-B2	1	Deltaproteobacteria	AB504918
OZE-B4	1	Bacteroidetes	AB504925
OZE-B5	1	Bacteroidetes	AB504926
OZE-B6	2	Bacteroidetes	AB504927, AB504928
OZE-B7	1	Bacteroidetes	AB504929
OZE-B8	1	Bacteroidetes	AB504930
OZE-B10	1	Betaproteobacteria	AB504941
OZE-B12	2	Betaproteobacteria	AB504946, AB504947
OZE-B13	1	Betaproteobacteria	AB504958
OZE-B14	1	Betaproteobacteria	AB504949
OZE-B15	1	Betaproteobacteria	AB504950
OZE-B16	1	Betaproteobacteria	AB504951
OZE-B17	2	Betaproteobacteria	AB504952, AB504953
OZE-B20	1	candidate division OD1	AB504963

Table S2. List of the eukaryotic OTUs detected in this study.

OTU	No. of clone	Closest identified relative ^a (acc. no)	Identities	Accession number
OZE-E1	1	<i>Rhizamoeba saxonica</i> (AY121847)	424/506 (83%)	AB504964
OZE-E2	1	<i>Chytriomycetes</i> sp. AFTOL-ID 1532 (DQ536483)	473/480 (98%)	AB504965
OZE-E3	1	<i>Heteromita globosa</i> (AY496043)	449/485 (92%)	AB504966
OZE-E4	1	<i>Heteromita globosa</i> (U42447)	451/490 (92%)	AB504967
OZE-E5	2	<i>Bodomorpha</i> sp. HFCC57 (DQ211596)	477/485 (98%)	AB504968, AB504969
OZE-E6	1	<i>Heteromita globosa</i> (AY496043)	481/484 (99%)	AB504970
OZE-E7	2	<i>Heteromita globosa</i> (U42447)	461/489 (94%)	AB504971, AB504972
OZE-E8	1	<i>Gymnophrys cometa</i> (AJ514866)	467/484 (96%)	AB504973
OZE-E9	2	<i>Cercomonas metabolicus</i> (DQ211597)	471/482 (97%)	AB504974, AB504975
OZE-E10	1	<i>Heteromita globosa</i> (AY496043)	440/487 (90%)	AB504976
OZE-E11	1	<i>Spongomonas minima</i> (AF411281)	465/486 (95%)	AB504977
OZE-E12	1	<i>Diatoma hyemalis</i> (AB085829)	477/483 (98%)	AB504978
OZE-E13	5	<i>Lacrymaria marina</i> (DQ777746)	457/481 (95%)	AB504979-AB504983
OZE-E14	2	<i>Homalozoon vermiculare</i> (L26447)	467/472 (98%)	AB504984, AB504985
OZE-E15	2	<i>Orthamphisiella breviseries</i> (AY498654)	468/480 (97%)	AB504986, AB504987
OZE-E16	1	<i>Oxytricha longigranulosa</i> (AM412766)	477/479 (99%)	AB504988
OZE-E17	1	<i>Oxytricha granulifera</i> (AM412772)	472/477 (98%)	AB504989
OZE-E18	1	<i>Hypotrichida</i> sp. LPJ-2005 (DQ022066)	466/481 (96%)	AB504990
OZE-E19	1	<i>Pseudokeronopsis bergeri</i> (DQ777742)	469/478 (98%)	AB504991
OZE-E20	2	<i>Bicosoeca petiolata</i> (AY520444)	461/488 (94%)	AB504992, AB504993
OZE-E21	1	<i>Oxytricha granulifera</i> (AM412772)	472/477 (98%)	AB504994
OZE-E22	1	<i>Cryptocaryon irritans</i> (AF351579)	445/479 (92%)	AB504995
OZE-E23	1	<i>Chytridium polysiphoniae</i> (AY032608)	474/484 (97%)	AB504996
OZE-E24	1	<i>Blastocladales</i> sp. TJ-2007a (EF565163)	461/481 (95%)	AB504997
OZE-E25	2	<i>Kriegeria eriophori</i> (DQ419918)	481/481 (100%)	AB504998, AB504999
OZE-E26	1	<i>Pterocystis</i> sp. JJP-2003 (AY268043)	475/490 (96%)	AB505000
OZE-E27	1	<i>Telonema subtilis</i> (AJ564772)	482/485 (99%)	AB505001
OZE-E28	1	<i>Monosiga ovata</i> (AF084230)	459/481 (95%)	AB505002
OZE-E29	2	<i>Rozella</i> sp. AFTOL-ID 16 (AY601707)	432/482 (89%)	AB505003, AB505004
OZE-E30	1	<i>Perkinsus andrews</i> (AY305326)	448/482 (92%)	AB505005
OZE-E31	1	<i>Perkinsus andrews</i> (AY305326)	446/482 (92%)	AB505006
OZE-E32	1	<i>Cytauxzoon felis</i> (AF399930)	173/185 (93%)	AB505007
OZE-E33	2	<i>Komma caudata</i> (U531229)	404/492 (82%)	AB505008, AB505009

a According to the results of BLAST search for representative clones of each OTU.

Figure legends

Figure S1. Phylogenetic relationships of form I RuBisCO clones obtained in this study.

The clones sharing more than 252 amino acid in 256 sites were grouped into the same OTU. This minimum evolution tree was constructed with 207 amino acid sites. For the OTUs with plural clones, the numbers of clones are presented in parentheses. Numbers on nodes are percentage values of 1000 bootstrap resampling (values larger than 50 are shown). The names of OTUs defined in this study are prefixed with “OZE-L”.

Figure S2. Phylogenetic relationships of form II RuBisCO clones obtained in this study.

The clones which have identical peptide sequences were grouped into the same OTU. This minimum evolution tree was constructed with 113 amino acid sites. For the OTUs with plural clones, the numbers of clones are presented in parentheses. Numbers on nodes are percentage values of 1000 bootstrap resampling (values larger than 50 are shown). The names of OTUs defined in this study are prefixed with “OZE-M”.

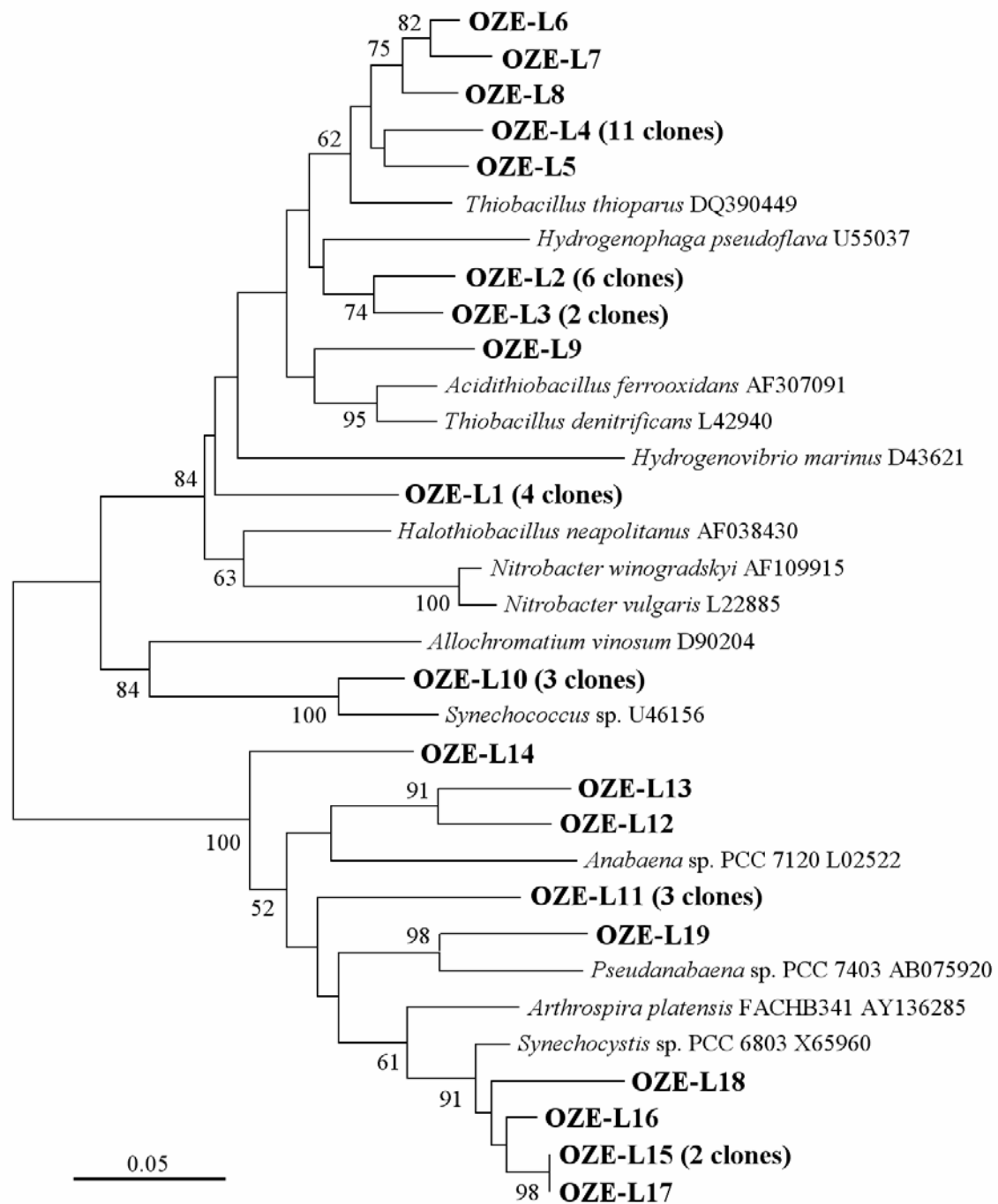


Figure S1 Kojima et al.

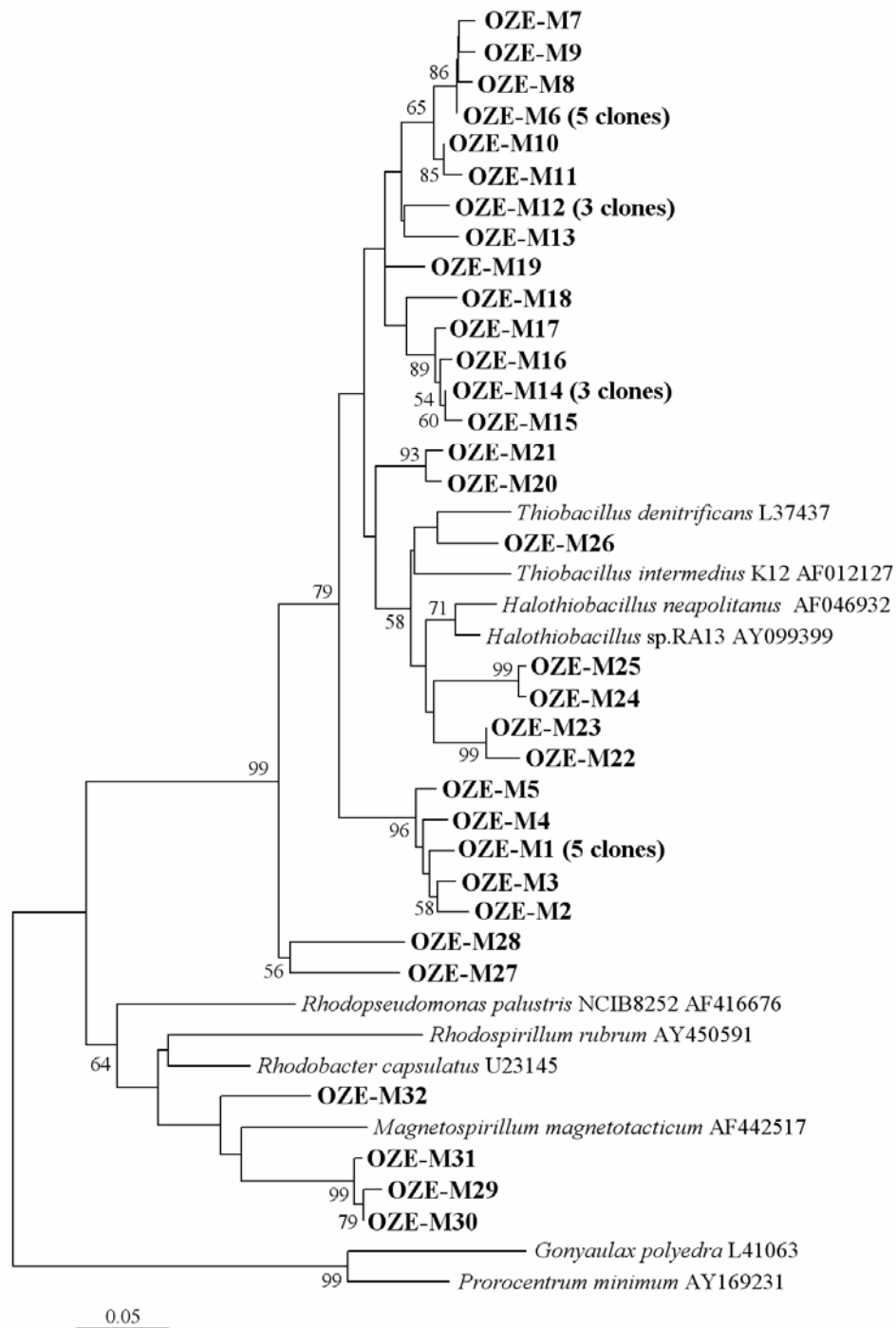


Figure S2 Kojima et al.