ERRATA

Revised Taxonomy of the Methanotrophs: Description of *Methylobacter* gen. nov., Emendation of *Methylococcus*, Validation of *Methylosinus* and *Methylocystis* Species, and a Proposal that the Family *Methylococcaceae* Includes Only the Group I Methanotrophs

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Volume 43, no. 4, p. 750, column 1, line 18: “*Methylobacter capsulatus*” should read “*Methylococcus whittenburyi*.”

Ch2, a Novel Halophilic Archaeon from an Australian Solar Saltern

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Volume 43, no. 2, p. 731, column 1: Figure 3 should appear as shown below.

0 ATTCCGGTTGATCCTGCCGGAGGCCATTGCTATTGGGATCCGATTTAGCCATGCTAGTCGCACGAGTTCAGACTCGTGCGGAATAGCTCAGTAACACGTG
100 GCCAACTACCCCTTCGGAACACAATACCCTCGGGAACTGTGTATACCATACCACCAC'TGGAATGAGTGGTATGCCAAACGCTCCGGCGCAGGCTAATAA
200 CGAAGGATGTGGCTGCGGCCGATTAGGTAGACGGTGGGTAACGGGCCACCGTGCCAATAATCGGTATGGGTTCATGAGAGTGAGAACCCAGAGACGGAA
300 CTGAGACAAGATTCCGGGCCCTACGGGGCGCAGCAGGCGCGAAACCTTTACACTGCACGACAGTGCGATAGGGGGATCCCAAGTGACACAGGCATAGCGCC
400 TGTGCTTTTCGGTACCCTAAGCGGTACCAGAATAAGGGCTGGGCAAGACCGGTGCCAGCCGCCCGGTAATAACCGGCAGCCCAAGTGATGGCCGATCTT
500 ATTGGGCCTAAAGCGTCCGTAGCTGGCCGCGCAAGTCCATCGGGAAATCCACCTGCTCAACAGGTGGGCGCCCGGTAGAAACTGCGTGGCTTGGGACCGG
600 AAGGCGCGACGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGACCGCCGATGGCGAAAGCACGTGCGGAGAACGGATCCGACAGTGAGG
700 GACGAAAGCCAGGTCTCGAACCAGGATTAGATACCCGGGTAGTCTGGCCGTAAACAATGTCTGCTAGGTGTGGCCCCCACTACGAGTGGGTGCTGTGCC
800 GTAGGGAAGCCGCTAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATGAAACTTAAAGGAATTGGCGGGGAGCACTACAACCGAGGAGCCTGCGGTT
900 TAATTGGACTCAACGCCGGACATCTCACCAGCATCGACTGTAATAATGACGACCAGGTTGATGACCTTGTCCGAGTTTCAGAGAGGAGGTGCATGGCCGC
1000 CGTCAGCTCGTACCGTGAGGCGTCTGTTAAGTCAGGCAACGAGCGAGACCCGACCCCTTACTTGCCAGCAGTACCGCGAGGTAGCTGGGGACAGTAGGG
1100 GGACCGCCGTGGCTAACACGGAGGAAGGAACGGCAACGGTAGGTCAGTATGCCCCGAATGTGCTGGGCAACACGCGGGCTACAATGGTCGAGACAAAGG
1200 GTTCCTACTCCGAAAGGAGACGGTAATCTCAGAACTCGATCGTAGTTCGGAGGTTGGGCTGCAACTCGCCACATGAAGCTGGATTCCGGTAGTAATCGC
1300 GTGTCACAAGCGCGCGGTGAATACGTCCCTGCTCCTTGCAACACCGCCCGTCAAAGCACCCGAGTGAGGTCCGGATGAGGCGTTCCACGAACGTGGAAT
1400 CTGGCTTCGCAAGGGGGCTTAAGTCGTAACAAGGTAGCCGTAGGGGAATCTGCGGCTGGATCACCTCCT

FIG. 3.