

Correction

Correction: Taxonomic and Functional Diversity Provides Insight into Microbial Pathways and Stress Responses in the Saline Qinghai Lake, China

The *PLOS ONE* Staff

An error was introduced during the typesetting process. Figure 3 is incorrect. Please see the correct Figure 3 and its legend here. The publisher apologizes for the error.

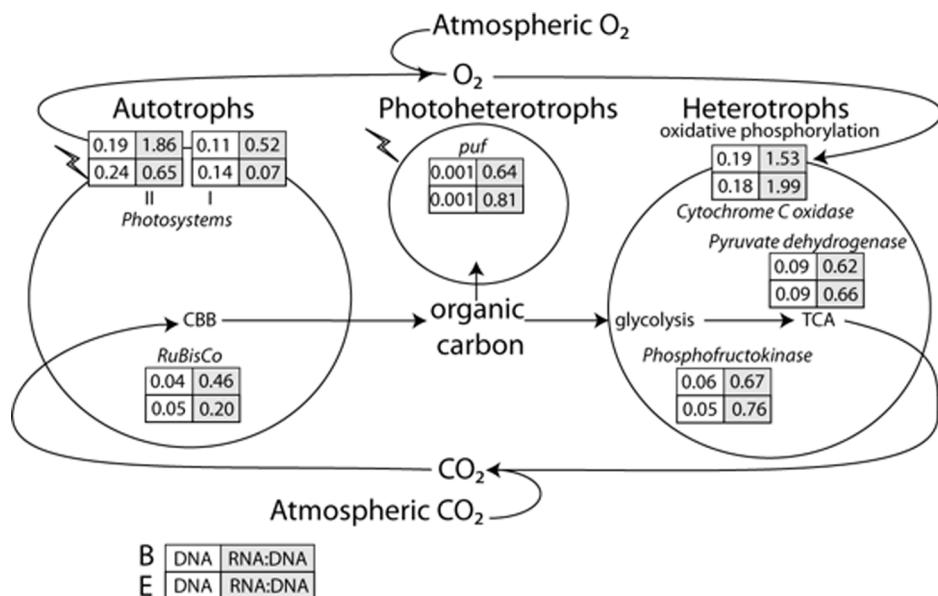


Figure 3. The carbon cycle depicted by a generalized autotroph, photoheterotroph, and heterotroph in Qinghai Lake. The numbers in boxes represent the percentage and the RNA:DNA ratio of reads that were annotated within each metabolic pathway for sites B and E. The key genes used to identify a pathway was Ribulose-bisphosphate carboxylase (RuBisCo): Calvin-Benson-Bassham cycle (CBB), D-glucose 6-phototransferase: glycolysis, pyruvate dehydrogenase: tricarboxylic acid cycle (TCA), and cytochrome C oxidase: oxidative phosphorylation.

Reference

1. Huang Q, Briggs BR, Dong H, Jiang H, Wu G, et al. (2014) Taxonomic and Functional Diversity Provides Insight into Microbial Pathways and Stress Responses in the Saline Qinghai Lake, China. *PLoS ONE* 9(11): e111681. doi:10.1371/journal.pone.0111681.g003

Citation: The *PLOS ONE* Staff (2014) Correction: Taxonomic and Functional Diversity Provides Insight into Microbial Pathways and Stress Responses in the Saline Qinghai Lake, China. *PLoS ONE* 9(12): e116444. doi:10.1371/journal.pone.0116444

Published December 23, 2014

Copyright: © 2014 The *PLOS ONE* Staff. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.