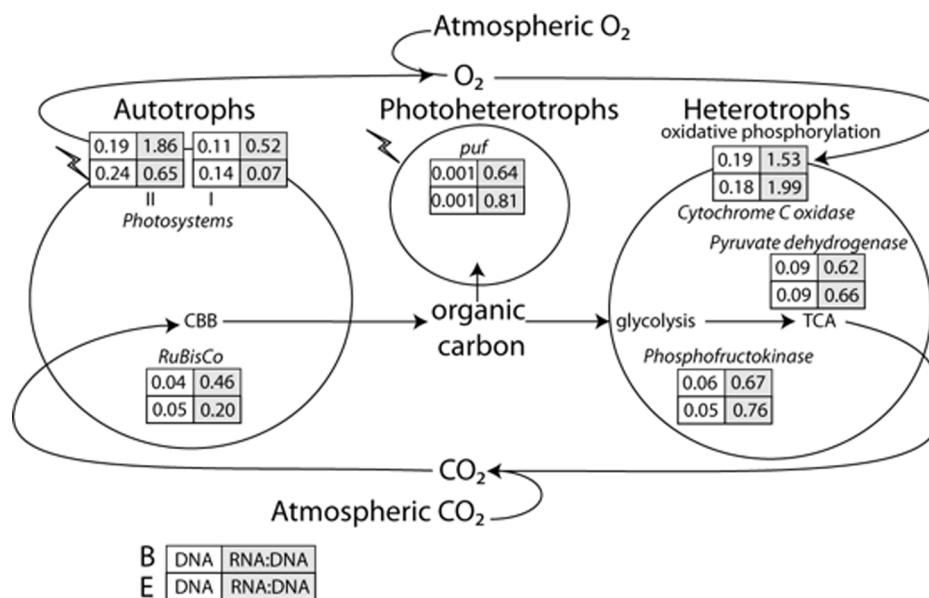


Correction

# 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-phosphotransferase: glycolysis, pyruvate dehydrogenase: tricarboxylic acid cycle (TCA), and cytochrome C oxidase: oxidative phosphorylation. doi:10.1371/journal.pone.0111681.g003

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

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