

1 Kuhns et al (2016) provide evidence that the gastric pathogen *Helicobacter pylori* can use molecular  
2 hydrogen as an energy source. Increased growth yields and inorganic carbon incorporation both support  
3 the ability of *H. pylori* to gain metabolically useful energy from hydrogen. However, the use of the  
4 term *chemolithoautotrophic* to describe these findings is not correct.

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6 The term *chemolithoautotrophy* is accurately defined as a metabolic mode that derives energy from  
7 chemical compounds (*chemo*-; as opposed to light or *photo*-), electrons from inorganic sources (*-litho*-)  
8 and carries out *net* fixation of inorganic carbon (*-autotrophy*; (2)). While the *-litho*- portion of this term  
9 has been used to describe heterotrophic organisms that oxidize inorganic compounds to supplement  
10 their metabolism (3), the *-autotroph* portion of this term can only be applied where carbon dioxide can  
11 serve as the predominant source of carbon for biosynthesis.

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13 Since abundant organic carbon was present in the growth medium, it is unclear if CO<sub>2</sub> accounted for  
14 the main source of carbon for *H. pylori*. In addition, although the authors do observe CO<sub>2</sub> uptake into  
15 biomass this does not prove that autotrophic carbon fixation occurred. *Anaplerotic* carbon fixation  
16 occurs as a series of carboxylation reactions that replenish intermediates in the citric acid cycle (4) or  
17 during fatty acid synthesis (5). As a normal process during heterotrophic growth, it explains the  
18 observed incorporation of CO<sub>2</sub> in the absence of hydrogen. While such carboxylating enzymes do  
19 indeed incorporate inorganic carbon into biomass, the growth mode of an organism can only be  
20 considered autotrophic if they have complete pathways for using inorganic carbon as the main source  
21 for cellular biosynthesis (6).

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23 This point is illustrated considering the importance of the higher activity and abundance of the acetyl-  
24 CoA carboxylase enzyme in the presence of hydrogen observed by Kuhns et al (2016). While this  
25 enzyme is indeed responsible for the carboxylation of acetyl-CoA to malonyl-CoA, the CO<sub>2</sub> thus

26 incorporated is lost during the condensation of malonyl-CoA subunits during lipid synthesis (5). Its  
27 higher activity may therefore simply be the result of higher levels of lipid synthesis associated with  
28 increased growth in the presence of hydrogen.

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30 It should be simple to clarify whether autotrophic carbon fixation likely occurred during these  
31 experiments. The authors could estimate how much carbon was needed to support the observed  
32 increase in cell density, and compare this estimate with the amount of inorganic carbon incorporated  
33 into biomass. Unless the amount of inorganic carbon fixed represents a dominant fraction of *H. pylori*'s  
34 cell carbon, *chemolithoheterotrophic* would be a more accurate term for the results observed by Kuhns  
35 et al (2016). Indeed, such *chemolithoheterotrophic* growth with hydrogen has been previously observed  
36 in other organisms (7).

37

38 A final point is worth mentioning. True autotrophs are well-known among the Epsilonproteobacteria  
39 (6,8), which employ the reverse tricarboxylic acid (rTCA) cycle for carbon fixation (9). Therefore, the  
40 absence of RuBisCO reported by Kuhns et al (2016) is not surprising given that autotrophic  
41 Epsilonproteobacteria do not use this enzyme for carbon fixation. The key enzyme that allows the  
42 rTCA cycle to run in a reductive direction is ATP-citrate lyase (6); however, the genes encoding this  
43 enzyme are absent in *H. pylori* strain 26695 (10). Since it lacks this enzyme and is thought to have a  
44 complete (albeit non-canonical) oxidative citric acid cycle (11), the current genomic evidence also  
45 argues against the possibility of autotrophic carbon fixation in *H. pylori*.

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54 References:

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56 1. **Kuhns LG, Benoit SL, Bayyareddy K, Johnson D, Orlando R, Evans AL, Waldrop GL,**

57 **Maier RJ.** 2016. Carbon Fixation Driven by Molecular Hydrogen Results in

58 Chemolithoautotrophically Enhanced Growth of *Helicobacter pylori*. *Journal of Bacteriology*

59 **198:1423–1428.**

60 2. **Canfield DE, Erik Kristensen, Bo Thamdrup.** 2005. Thermodynamics and Microbial

61 Metabolism, p. 65–94. *In* Donald E. Canfield, EK and BT (ed.), *Advances in Marine Biology.*

62 Academic Press.

63 3. **Muyzer DG, Kuenen PJG, Robertson DLA.** 2013. Colorless Sulfur Bacteria, p. 555–588. *In*

64 Rosenberg, E, DeLong, EF, Lory, S, Stackebrandt, E, Thompson, F (eds.), *The Prokaryotes.*

65 Springer Berlin Heidelberg.

66 4. **Kornberg HL.** 1965. Anaplerotic Sequences in Microbial Metabolism. *Angew Chem Int Ed*

67 *Engl* **4:558–565.**

68 5. **Voet D, Voet JG.** 2010. *Biochemistry* 4<sup>th</sup> edition. Wiley, Hoboken, NJ.

69 6. **Hügler M, Sievert SM.** 2011. Beyond the Calvin Cycle: Autotrophic Carbon Fixation in the

70 Ocean. *Annu Rev Marine Sci* **3:261–289.**

71 7. **Kiessling M, Meyer O.** 1982. Profitable oxidation of carbon monoxide or hydrogen during

72 heterotrophic growth of *Pseudomonas carboxydoflava*. *FEMS Microbiology Letters* **13:333–**

73 **338.**

74 8. **Campbell BJ, Engel AS, Porter ML, Takai K.** 2006. The versatile  $\epsilon$ -proteobacteria: key

75 players in sulphidic habitats. *Nature Reviews Microbiology* **4:458–468.**

- 76 9. **Hügler M, Wirsén CO, Fuchs G, Taylor CD, Sievert SM.** 2005. Evidence for Autotrophic  
77 CO<sub>2</sub> Fixation via the Reductive Tricarboxylic Acid Cycle by Members of the  $\epsilon$  Subdivision of  
78 Proteobacteria. *J Bacteriol* **187**:3020–3027.
- 79 10. **Tomb J-F, et al.** 1997. The complete genome sequence of the gastric pathogen *Helicobacter*  
80 *pylori*. *Nature* **388**:539–547.
- 81 11. **Kather B, Stingl K, van der Rest ME, Altendorf K, Molenaar D.** 2000. Another Unusual  
82 Type of Citric Acid Cycle Enzyme in *Helicobacter pylori*: the Malate:Quinone Oxidoreductase.  
83 *J Bacteriol* **182**:3204–3209.