

Redox control on basal animal behavior and metabolism

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Ecosystems require oxic conditions to support a high number of metazoan trophic levels [1], including a diversity of predatory bilaterian taxa [2]. Hypoxic conditions, however, are still known to support various free-living facultative anaerobic bilaterians [3], thin aerobic bilaterians [4], and at least one species of sponge [5]. Sponges, in particular, are non-bilaterian filter feeders that largely consume picoplankton and dissolved organic matter, and, by virtue of their collared feeding cells, are arguably analogous to the earliest animals with respect to their trophic ecology and cell biology [6] [7]. By quantifying the response of modern sponge taxa to low oxygen conditions, we can constrain the feedbacks thought to have existed between the first animal ecosystems and the redox evolution of the Neoproterozoic environment, 1,000-541 million years ago [8].

Tethya wilhelma is a tropical demosponge capable of motility, contraction, and asexual reproduction (via budding) under laboratory conditions. Preliminary survey of the *T. wilhelma* transcriptome suggests the presence of at least 50% of the described enzymes involved in anaerobic energy metabolism in eukaryotes, in accordance with at least seven other sampled sponge taxa [9]. We experimentally investigated the control of dissolved oxygen concentrations – down to levels below 1% of modern atmospheric saturation – on the respiration, contraction, gene expression, and metabolism of *T. wilhelma*. To our knowledge, our efforts represent the first attempt to detect transcriptomic changes in sponges kept under low oxygen. Our results reiterate the need to more carefully consider the biology of non-bilaterian animals when attempting to reconstruct the biogeochemical dynamics of the Neoproterozoic earth system.

[1] Fenchel & Finlay (1995) *Ecology and Evolution in Anoxic Worlds*, Oxford Univ. Press. [2] Sperling *et al.* (2013) *PNAS* **110**, 13446-13451. [3] Müller *et al.* (2012) *Microbiol. Mol. Biol. Rev.* **76**, 444-495. [4] Sperling *et al.* (2013) *EPSL* **371-372**, 143-155. [5] Mills *et al.* (2014) *PNAS* **111**, 4168-4172. [6] Richter & King (2013) *Annu. Rev. Genet.* **47**, 509-537. [7] Wörheide *et al.* (2012) *Adv. Mar. Biol.* **61**, 1-78. [8] Mills & Canfield (2014) *BioEssays* **36**, 1145-1155. [9] Mentel *et al.* (2014) *BioEssays* **36**, 924-932.