Structural basis of a novel PMF-coupled carbon-concentrating mechanism

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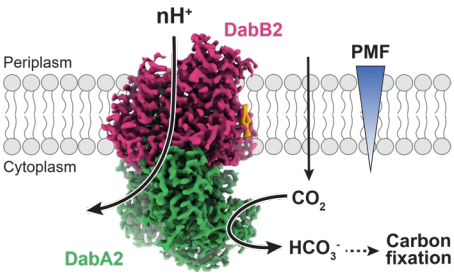

Cryo-EM structure of DAB2 complex

Microbial carbon dioxide (CO_2) fixation is essential for global primary production and forms the basis of food chains in a variety of ecosystems[1]. However, in many natural habitats the process is limited by the scarcity of dissolved CO_2 and the inefficiency of the key CO_2-fixing enzyme ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO)[2]. To overcome this challenge, many autotrophs evolved specialized adaptations, known as CO_2-concentrating mechanisms (CCMs)[3,4]. While cyanobacterial CCMs are relatively well characterized, analogous systems in chemolithoautotrophs, specifically active CO_2 uptake systems have long been overlooked. Here, we present the first cryo-EM structural analysis of the DAB2 complex, an essential membrane-bound CCM for CO_2 uptake in the autotrophic sulfur-oxidizing bacterium *Halothiobacillus neapolitanus*[5]. Our structure reveals a unique β-carbonic anhydrase-like cytoplasmic catalytic subunit (DabA2) and a transmembrane subunit (DabB2) that resembles the proton-conducting subunits of respiratory Complex I. Together with structure-guided mutagenesis and biochemical characterizations, we identified key structural elements possibly couple proton translocation to CO_2 hydration. Our findings establish DAB2 as a prototype of a previously unrecognized family of protonmotive force-coupled vectorial carbonic anhydrases, elucidating a novel strategy for CO_2 capture in non-photosynthetic autotrophs and expanding the mechanistic landscape of bacterial CCMs.

References

1. Hügler, M. & Sievert, S. M. Annual review of marine science 3, 261–289 (2011).
2. Raven, J. A. & Beardall, J. Journal of experimental botany 67, 1–13 (2016).
3. Clement, R., Jensen, E., Prioretti, L., Maberly, S. C. & Gontero, B. Journal of experimental botany 68 (2017).
4. Maberly, S. C. & Gontero, B. Journal of experimental botany 68, 3797–3814 (2017).
5. Desmarais, J. J. et al. Nature microbiology 4, 2204–2215 (2019).