Contribution ID: **129** Type: **not specified**

OPTIMIZING [FEFE]-HYDROGENASE

Monday, 19 December 2022 17:35 (20 minutes)

[FeFe]-hydrogenase is an iron-sulfur protein that catalyzes the chemical reduction of protons into the H2 molecule [1]. This enzyme can be found in cyanobacteria and microalgae organisms. HydA1 enzyme of the unicellular alga Chlamydomonas Rheinhardt is very efficient in reducing protons in water to molecular hydrogen, but it is very sensitive to dioxygen (O2), which irreversibly degrades the enzyme. When O2 becomes concentrated enough, like in intensive photosynthesis, the hydrogenase protein is attacked in the most oxygen sensitive points and the protein becomes non-functioning, unfolded, and suited for degradation pathways. On the other hand, other microalgae strains showed higher resistance to O2. The molecular engineering of hydrogenase has been proposed as a possible workaround to the problem of O2 sensitivity. With this work, we aim at understanding how the hydrogenase (Hyd) variants expressed by these strains can better sustain hydrogen production in the presence of O2. As already performed by other groups, the project begins mapping sequences of hydrogenase expressed in the latter strains to the structure of cyanobacteria Clostridium Pasteurianum H-domain of [FeFe]-hydrogenase. The latter is the unique known structure of Hyd including the position of all atoms in the H-cluster. [FeFe]-hydrogenase is made by two domains: H-domain, within H-cluster principal active site, and F-domain, within secondary active sites. In some microalgae organisms, the evolutionary process guided [FeFe]-hydrogenase protein to lose F-domain and replace it with a smaller disordered domain of variable sequence.
We are focusing on the possible effect of the disordered N-terminal segment of Hyd on the accessibility of dioxygen to the H-cluster [2].

[1] James A. Birrell et al., Coordination Chemistry Reviews 449 (2021) 214191.
[2] Giovanni La Penna, NIC Symposium Proceedings, G. Munster, D. Wolf, M. Kremer 2010

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Session Classification: Session 4 B