Unravelling energy conservation mechanism in sulfate reducing prokaryotes

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Abstract

Sulfate reducing prokaryotes (SRP) are ubiquitous in anoxic sulfate rich environments as marine and fresh sediments or the human gut. These organisms oxidize several carbon sources using sulfate as the electron acceptor, leading to sulfide production. SRP are useful in different processes such as waste water treatments or bioremediation of certain pollutants, but on the other hand, the sulfide produced by their metabolism is highly toxic and corrosive and responsible for material deterioration in some industries or be related with human health problems such as inflammatory bowel diseases, like Crohn's disease and ulcerative colitis. Therefore, understand these organisms metabolism is essential to use them to our benefit.

Dissimilatory sulfate reduction pathway comprises three key enzymes: ATP sulfurylase (Sat), APS reductase (AprAB) and the Dissimilatory Sulfite Reductase (DsrAB/DsrC). Additionally, there are highly conserved membrane complexes, essential to build a proton motive force, required for ATP synthesis. However, in SRP this mechanism is not fully elucidated.

In this project, respiratory membrane complexes from model SRP will be purified, biochemically characterized and reconstituted in liposomes. The obtained proteoliposomes will be characterized in terms of integrity and protein orientation. Further, proteoliposomes will be used in electron transfer experiments with their physiological partners.

This work will contribute to understand SRP energy conservation mechanism and promote the use of these organisms in new (bio)technological applications.