

Molecular basis of salinity tolerance in the halotolerant alga *Dunaliella*

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Dunaliella is a unicellular green alga that is unique in its ability to adapt to some of the harshest environments known on earth. Most *Dunaliella* species tolerate extreme salinities, *D. acidophila* grows optimally at pH 0-1, *D. bardawil* tolerates exceptionally high irradiance and *D. antarctica* thrives at subzero temperatures.

Our laboratory focuses on understanding the molecular mechanisms that enable *Dunaliella* to adapt to extreme environments, particularly high salinity. Our aims are: to identify proteins associated with halotolerance and to clone their corresponding genes, to clarify the structural basis enabling proteins/enzymes to function at high salt concentrations and to utilize genes from *Dunaliella* to generate transgenic plants with enhanced salinity tolerance.

Salt-induced proteins

We have identified two major plasma membrane proteins which were induced by high salt in *D. salina*. The proteins are homologous to eucaryotic carbonic anhydrase and to human transferrin, the first transferrin identified in plant systems. Functional analyses showed that the transferrin-like protein mediates uptake of Fe^{3+} ions whereas the carbonic anhydrase is involved in CO_2 acquisition. The results established that iron and CO_2 acquisition are major rate limiting steps for survival in hypersaline environments. Both proteins share unique functional and structural features: they are resistant to high salt and function in low salt as well as in high salt, and both are acidic proteins and possess internal repeats (2 or 3). A comprehensive differential analysis of salt-induced proteins in *Dunaliella* is carried out by 2D gels combined with biotin tagging, mass spectroscopic analysis and sequencing (M. Ortal-Schwarz, T. Versano, collaboration with A. Zamir).

Na^+ elimination

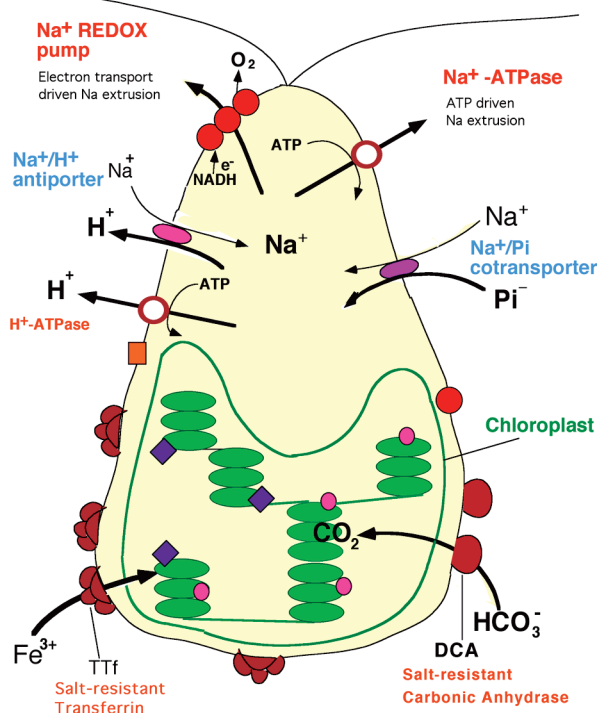
Dunaliella has an exceptional ability to eliminate Na^+ ions, a detrimental factor for survival in hypersaline solutions. We have identified a novel redox-driven Na^+ pump, responsible for Na^+ elimination in *Dunaliella* (A. Katz). We have shown that *Dunaliella* utilizes the large electrochemical Na^+ gradient ($G_{\text{Na}^+} = 180\text{--}220\text{ mV}$) also for energization of phosphate and sulfate uptake via Na^+/Pi and Na^+/SO_4 symporters (M. Weiss). These

results suggested that *Dunaliella* recycles Na^+ ions across the plasma membrane as the main ion in transport processes (see scheme).

Cold-acclimation

Following acclimation at 7°C , *Dunaliella* salina cells acquire resistance to freezing down to -40°C . We have shown that the primary target of freezing damage in the photosynthetic system is PS-II and that it is protected by cold-acclimation. Cold-acclimation is associated with increased desaturation level of fatty acids in the plasma and thylakoid membranes. A glycine-rich RNA binding protein which is induced at low temperature was identified and cloned (S. Zchut and M. Weiss).

Ion transporters involved in salt-resistance in *Dunaliella*



Iron acquisition

Iron availability is a major limiting factor in global biomass productivity in aquatic environments. We have cloned the first known algal Fe transporter (algal transferrin) and demonstrated that it functions in uptake of Fe^{3+} ions. Recently we cloned two additional proteins which are induced under iron deprivation: a different plasma membrane transferrin and a unique chlorophyll a/b binding protein. These studies indicate that *Dunaliella* copes with iron deprivation by overexpression of iron transporters and by extensive modification of the photosynthetic system (M.Ortal-Schwarz, T. Versano).

Selected Publications

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- Weiss, M., Haimovitch, G. and Pick, U. (2001) Phosphate and sulfate uptake in the halotolerant alga *Dunaliella* are driven by Na^+ -symport mechanism. J. Plant Physiol. (in press).
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