

BIOCHEMICAL CHARACTERIZATION OF AN ATP-SYNTHASE FROM
POLYTOMELLA sp.

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The mitochondrial FoF1-ATP-synthase from the non-photosynthetic alga *Polytomella sp.* presents novel subunits (ASA1-ASA9) structurally unrelated to other ATP-synthases. Some ASA compose the ATPase stator-stalk, while others stabilize the 1600 kDa dimer (Vázquez-Acevedo *et cols.*, 2006, J. Bioenerg. Biomembr. 38, 271-282). We are biochemically characterizing this *Polytomella* ATPase using permeable mitochondrial membranes. ATPase activity measured by hydrolysis of [γ -³²P]ATP (50mM Tris-Cl, pH 8.0, 2mM ATP, 2mM MgCl₂, 0.1mg.mL⁻¹ mitochondrial protein, with/without 100mM KCl) was linear with time (1-60min), and proportional to mitochondria concentration. 0.01-0.1% Triton X-100 did not enhance activity, evidencing membrane permeability, but 0.5 and 1% Triton activated the enzyme by 50% and 30% respectively. KCl and alkaline pH (maximum at pH 8.5) activated the ATPase. Li⁺/Na⁺/K⁺/Cs⁺/NH₄⁺/ChoI-Cl (50-200mM) were equivalent activators. Mg²⁺ at 2mM (maximal rate) was preferred as divalent cation Mg²⁺>Ca²⁺>Zn²⁺>Cu²⁺>Fe²⁺. At 5-10mM Mg²⁺ or Ca²⁺ were quasi-equivalent (90% maximal rate). 100μM DCCD or 100μg.ml⁻¹ oligomycin (ca. 75-80%), 1mM vanadate (ca. 35%), and VO₄+DCCD (>90%) inhibited the ATPase. Resveratrol (100μM) was marginally inhibitory (<20%), while ouabain (1mM), thapsigargin (2μM) and bafilomycin (10μM) were ineffective. Preliminary parameters were V_{MAX}=1050 μmol.mg⁻¹.min⁻¹, K_M=0.90mM in presence and V_{MAX}=720 μmol.mg⁻¹.min⁻¹, K_M= 0.46mM in absence of KCl. Although it presents different subunit structure, *Polytomella* ATP-synthase bears conserved subunits and shares some distinctive functional features with orthodox FoF1-ATPases.

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