Distinct forms of V H^+-ATPase along the yeast secretory pathway

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We have demonstrated earlier the activity of V H^+-ATPase in various organelles of the secretory pathway of the *Saccharomyces cerevisiae* yeast. To make clear that the ER, Golgi and Golgi-like membranes were efficiently purified from vacuole membranes by sucrose density fractionation we used the respective markers including vacuolar Ca^{2+}-ATPase, Pmc1p::HA. H^+ transport mediated by V H^+-ATPase in ER exhibits higher resistance to bafilomycin (I_{50}=38,4 nM) than that driven by Golgi and vacuolar pumps (I_{50}=0,18 nM), showing, however, similar sensitivity to concanamycin A. It points to a possibility that the V_0 complex of the enzyme in these membranes have different composition of c, c´ and c´´. Additionally organelle forms of the pump presented different coupling efficiency between H^+ transport and ATP hydrolysis. The ratio between a coupling efficiency of the enzyme forms in ER, membranes heavier than ER (probably nuclear envelope), vacuoles and Golgi is 1.0, 2.1, 8.5 and 14 with the highest coupling in the Golgi. Comparative analysis of the initial velocities of H^+ transport in those membranes and immunoreactivity of catalytic subunit A and regulatory subunit B further proved the presence of distinct forms of the V H^+-ATPase in the yeast secretory pathway organelles and/or their selective regulation. Supported by UENF, CNPq, CAPES and FAPERJ.