INTERACTION BETWEEN RECOMBINANT SERCA HYDROPHILIC DOMAINS AND P-TYPE ATPASES: EFFECTS ON THE ATPASE ACTIVITY OF SERCA, PMCA AND $NA^+ K^+$ ATPASE

Santos, D.F.[1]; Freire, M.M.[1]; Angeli, R.[1]; Cortez, V.F[1]; Albernaz, F.P.[1]; Almeida, W.I.[1]; Verjovski-Almeida, S.[2]; Almeida, F.C.L.[1]; Valente, A.P.[1]; Carvalho-Alves, P.C.[1]

[1]Instituto de Bioquímica Médica, Universidade Federal do Rio de Janeiro.
[2]Instituto de Química, Universidade de São Paulo.

SERCA (sarco(endo)plasmic reticulum Ca-ATPase), PMCA (plasma membrane Ca-ATPase) and Na^+K^+ ATPase are the most important pumps involved in fine tuning the ionic levels inside mammalian cells. SERCA has the better understood molecular mechanism of action, where Ca^{2+} is translocated to the lumen of the endoplasmic reticulum involving major conformational rearrangements among three cytoplasmic domains: actuator (A), nucleotide-binding (N) and phosphorylation (P). The A domain is believed to undergo movement during Ca^{2+} transport coupled to enzyme phosphorylation, interacting with the N and P domains. In previous studies, SERCA A domain recombinant (rSL) stimulated the ATP hydrolysis activity of SERCA1 by uncoupling the Ca^{2+} transport, without changing integrity of the membrane and stimulated PMCA activity three-fold, at saturating [Ca^{2+}], in the absence of CaM. Here we show that rSL is able to stimulate approximately two fold the purified $NA^+ K^+$ ATPase. Because the high homology in A domains, these results suggest a general model for the interplay of N, P and A domains during the catalytic cycle for all three enzymes.

Supported: CNPq and FAPERJ
Key words: P-ATPases, recombinant A domain