FUNCTIONAL CONSEQUENCES OF ALTERATIONS TO W854 AND W855 LOCATED IN THE M7-M8 LOOP OF THE CA²⁺-ATPASE OF SARCOPLASMIC RETICULUM

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Ca²⁺-ATPase of sarcoplasmic reticulum (SR) is a membrane-bound enzyme that sustains active transport of Ca²⁺ from the cytosol to the lumen, coupled to utilization of ATP. Functional analysis of two tryptophan of Ca²⁺-ATPase, located in the M7-M8 lumenal loop (W854 and W855), was performed changing tryptophans to either alanine (A) or phenylalanine (F). W854A and W855F mutations allow good expression, but produced strong inhibition of Ca²⁺-ATPase activity. The main defect produced by these mutations is strong interference with enzyme phosphorylation by ATP in the presence of Ca²⁺, and also by Pi in the absence of Ca²⁺. The phosphoenzyme of mutants appeared unable to react with ADP, suggesting that ADP-insensitive E2P had accumulated at steady state. Mutants were analyzed with respect to their sensitivity to 1,3-dibromo-2,4,6tris(methylisothiouronium)-benzene (Br₂-TITU) inactivation. Higher levels of phosphoenzyme formed from ATP and Ca²⁺ were accumulated for wild-type and W854 mutants in the presence than in the absence of Br₂-TITU. In contrast, W855 mutants lost Br₂-TITU inhibition. These results indicate that the inhibition of Ca²⁺-ATPase by Br₂-TITU occurs through the interaction with W855 that is conserved in all Ca²⁺-ATPases and Na⁺,K⁺-ATPases. Functional and structural analysis of the experimental data has pointed to two tryptophan residues playing a critical role in the catalytic cycle of the SR Ca^{2+} -ATPase. Supported by FAPESP and CNPq.