

Alternately Spliced cDNAs Encode the Chicken Sarco/Endoplasmic Reticulum Slow Ca²⁺ ATPase

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Two similar forms of the cardiac/slow Ca²⁺ ATPase (SERCA2a and SERCA2b), differing in mobility on SDS-PAGE, are expressed in chicken heart and brain (Kaprielian et al., 1989). However, when the two subtypes of chicken SERCA2 were analyzed by two-dimensional peptide mapping, there was no discernible difference between Ca²⁺ ATPase isolated from brain or heart. In this study, cDNAs encoding each subtype were cloned and sequenced. Chicken SERCA2a is very similar to a variety of Ca²⁺ ATPases (Table I; MacLennan et al., 1985; Burk et al., 1989; Karin et al., 1989; Palmero and Sastre, 1989). The encoding sequence of SERCA2b is identi-

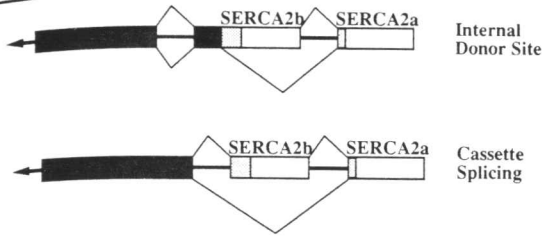
TABLE I
A Comparison of the Deduced Chicken SERCA2a Amino Acid Sequence
against Four Other Ca²⁺ ATPases

	Rabbit SERCA2a	Chicken SERCA1a	Rat SERCA3	<i>Artemia</i>
Chicken SERCA2a	94%	88%	73%	72%

The numbers are the percentage of amino acid identity for each Ca²⁺ pump.

cal to SERCA2a except for the portion encoding the carboxyl terminus, where the final four amino acids of SERCA2a have been replaced with 49 amino acids. This extended carboxyl terminus of chicken SERCA2b is conserved in a variety of mammalian species (Table II; Guntjeski-Hamblin et al., 1988; Lytton and MacLennan, 1988; Lytton et al., 1989). The extended terminus of SERCA2b accounts for the 5-kD shift in apparent M_r as seen on SDS-PAGE. A Kyte/Doolittle hydrophathy plot analysis of the SERCA2b extended terminus suggests that SERCA2b may span the sarco/endoplasmic reticulum membrane an additional time.

Only SERCA2a mRNA is detectable in embryonic and adult heart, while SERCA2b and SERCA2a messages are expressed in adult and embryonic brain. Chicken SERCA2a- and SERCA2b-encoding cDNAs have been cloned into expression vector pRc/RSV (Invitrogen) and transfected into mouse L cells. Using a monoclonal antibody specific for chicken SERCA2 (Kaprielian and Fambrough, 1987), it appears by immunofluorescence microscopy that each Ca²⁺ ATPase subtype



shaded boxes represent the subtype-specific carboxyl termini, while white boxes represent 3' UT regions.

Figure 2. Diagrams depict the two possible alternate splicing mechanisms that might be utilized in chicken SERCA2 primary transcript processing. Boxes represent exons and lines are introns. The black boxes are the common coding portions of SERCA2 and the

SERCA2, as shown in Fig. 2. Further analysis of chicken genomic sequence is underway to determine which of these two splicing mechanisms is utilized in chicken SERCA2 RNA processing.

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