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# The gene encoding sarcoplasmic reticulum calcium ATPase-1 (*Atp2a1*) maps to distal mouse Chromosome 7

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***Species:*** Mouse
***Locus name:*** ATPase, $Ca^{2+}$ transporting, cardiac muscle fast twitch 1
***Locus symbol:*** *Atp2a1*
***Map position:*** Chr 7: cen–. . . *Atp2a1*–1.6 (0.2–5.7)–*Fgfr2*–9.1 (4.5–16.2)–*Fgf3*–
***Method of mapping:*** Interspecific backcross of the type: (C57BL/6 × *Mus spretus*)$F_1$ × C57BL/6, N = 140 [1,2].
***Molecular reagents:*** The mouse genomic DNA sequences corresponding to the *Atp2a1* and *Fgfr2* loci were identified by hybridizing Southern blots to $^{32}P$-labeled probes. In the case of *Atp2a1,* we used a 648-bp cDNA fragment of the coding region [3] to probe the blots. In the case of *Fgfr2,* we used a 670-bp cDNA fragment also of the coding region [4]. The genomic sequence corresponding to the *Fgf3* gene was identified by amplification of DNA samples from the parental strains C57BL/6 and *Mus spretus* (SEG/Pas) by the polymerase chain reaction (PCR). Primers designed from the mouse cDNA sequence of *Fgf3* were as follows:

5′ GTGACAATACATTCCTGCTGT 3′ forward, and
5′ CTCAGATCTTATCTCTAGCAC 3′ reverse

***Allele detection:*** Genomic DNA samples of the offspring of the interspecific backcross were digested with *Eco*RI, separated by electrophoresis in 0.8% Tris-borate/EDTA buffered agarose gels, blotted to nylon membranes (Amersham™), and probed with a radio-labeled *Atp2a1* cDNA probe under conditions of high stringency. Under such conditions, we found that the above-mentioned *Atp2a1* probe hybridizes to a 7.5-kb fragment with C57BL/6 DNA and to a 4.0-kb fragment with *Mus spretus* DNA. The *Fgfr2* alleles were identified by a method reported by Avraham and associates [5], where it was found that the *Fgfr2* probe hybridizes to a 6.4-kb fragment with C57BL/6 DNA and to a 4.7-kb fragment with *Mus spretus* DNA. The *Fgf3* locus was typed by comparing the size of the PCR products: 161 bp with C57BL/6 DNA versus 165 bp with *Mus spretus* DNA.
***Discussion:*** Mammalian $Ca^{2+}$-ATPases of the sarcoplasmic reticulum occur in different isoforms which are encoded by at least three different structural genes in human [6,7]. ATP2A1 encodes the adult and neonatal fast skeletal isoform, ATP2A2 encodes slow skeletal and cardiac or ubiquitous isoforms, and ATP2A3 encodes ATPases that are expressed in a great variety of muscular and nonmuscular cells. Two of these genes have been localized on different chromosomes in human: ATP2A1 maps to Chromosome (Chr) 16p11.2-12.1, while ATP2A2 maps to Chr 12q23-24.1 [8]. Given that, in human, the locus homologous to *Fgfr2* (FGFR2) maps to the q25.3-q26 region of Chr 10 [5] we confirm that the homology breakpoint between human Chrs 10 and 16 on mouse Chr 7 is centromeric and very close to the *Fgfr2* locus.
***Technical comments:*** The PCR reactions were performed in a final reaction volume of 25 µl. Final concentrations were: 10 mM Tris pH 8.4; 50 mM KCl; 0.1% Tween 20; 200 µM dATP, dCTP, dGTP, dTTP, and 2 mM $MgCl_2$. Each reaction was performed with 100 ng of genomic DNA and 0.6 U of *Taq* DNA polymerase (Amersham™). 35 cycles of 40 s at 94°C, 40 s at 55°C) were run. They were preceded by an initial denaturation step (3 min at 94°C) and followed by a final elongation step of 3 min at 72°C. PCR products were analyzed by 4% Tris-borate/EDTA-buffered agarose gel electrophoresis.

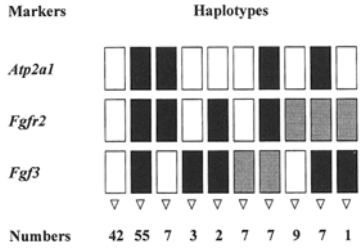


**Fig. 1.** Segregation data of *Atp2a1, Fgfr2,* and *Fgf3* shown as haplotype schemes. *Atp2a1* was placed on mouse Chr 7 with DNA samples prepared from the offspring of an interspecific backcross of the type: (C57BL/6 × *Mus spretus*)$F_1$ × C57BL/6. Each column represents the observed genotypes in a total of 140 mice. Black boxes represent homozygosity for the C57BL/6 allele, white boxes represent heterozygosity for the *Mus spretus* allele, and grey boxes indicate that the genotype is not known at the corresponding locus. The number of mice inheriting each genotype is indicated at the bottom of each column.

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