Altered Ca\(^{2+}\) Responses in Muscles with Combined Mitochondrial and Cytosolic Creatine Kinase Deficiencies

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Summary

We have blocked creatine kinase (CK)-mediated phosphocreatine (PCr) \(\rightarrow\) ATP transphosphorylation in skeletal muscle by combining targeted mutations in the genes encoding mitochondrial and cytosolic CK in mice. Contrary to expectation, the PCr level was only marginally affected, but the compound was rendered metabolically inert. Mutant muscles in vivo showed significantly impaired tetanic force output, increased relaxation times, altered mitochondrial volume and location, and conspicuous tubular aggregates of sarcoplasmic reticulum membranes, as seen in myopathies with electrolyte disturbances. In depolarized myotubes cultured in vitro, CK absence influenced both the release and sequestration of Ca\(^{2+}\). Our data point to a direct link between the CK-PCr system and Ca\(^{2+}\)-flux regulation during the excitation and relaxation phases of muscle contraction.

Introduction

Creatine kinases (CKs; EC 2.7.3.2) form a small family of isoenzymes that help in keeping cellular ATP/ADP ratios delicately balanced and the ATP pool highly charged. Different CK isoforms exist in mitochondria (dimer octameric sarcosomal and ubiquitous mitCKs) and cytosol (homo- and heterodimeric MM-, BM- and BB-CKs), and occur in a strictly cell type-dependent manner in tissues with large fluctuations in energy metabolism, such as muscle and nerve (Wallimann et al., 1992). Although many concepts have been formulated to explain the involvement of the CK reaction [phosphocreatine \([\text{PCr}^2]\) + MgADP\(^{-}\) + H\(^+\) \(\rightleftharpoons\) creatine \([\text{Cr}]\) + MgATP\(^2\)] in high energy phosphoryl homeostasis (Bessmann and Carpenter, 1985; Wallimann et al., 1992), little is known about its actual role in maintaining the integrity of metabolic energy compartmentalization (Miller and Horowitz, 1986; Saks et al., 1994) and the communication between intracellular sites of ATP consumption and production. It is generally accepted that the CK system helps in setting local concentrations and ratios of ATP and its hydrolysis products ADP, AMP, P\(_1\), and H\(^+\). In turn, these parameters govern the dynamic kinetics of many ATPases in different microenvironments (Rossi et al., 1990; Korge and Campbell, 1994) and may determine the rate of glycolysis and oxidative phosphorylation (OXPHOS; Erecinska and Wilson, 1982; Balaban, 1990).

However, flux distribution of high energy phosphoryl metabolites in different cellular compartments is intriguingly complex and may involve the intertwining of interconversion reactions catalyzed by CKs, adenylate kinases (AKs), nucleoside mono- and diphosphate kinases, hexokinase, or glyceral kinase (Brdiczka and Wallimann, 1994). Individual reaction steps in this complex scheme might well be facilitated by the subcellular clustering of these kinases in multienzyme complexes (Bessmann and Carpenter, 1985).

To assess the importance of CK-catalyzed reactions in this cellular energy network of skeletal muscle, we have generated mice lacking both the mitochondrial CK (ScCKmit) and cytosolic CK (M-CK) by interbreeding ScCKmit\(^{-/-}\) (Steeghs et al., 1996) and M-CK\(^{-/-}\) (van Deursen et al., 1993) mice, and studied the phenotypic consequences in whole muscles in vivo and in cultured myotubes in vitro. We show that the animals are apparently normal but exhibit changes in mitochondrial morphology and composition, contain a hyperproliferative sarcoplasmic reticulum (SR), and show severely impaired force generation. In addition, we found that cultured myotubes exhibit an altered Ca\(^{2+}\) response upon depolarization. Our results suggest that the CK system has a direct role in the regulation of both Ca\(^{2+}\) accumulation and release in skeletal muscle fibers.

Results

Generation of Mice with Combined M-CK and ScCKmit Deficiency

To test whether skeletal muscle development and functioning depend on the continuous access to high energy phosphoryls provided by PCr, we interbred ScCKmit\(^{-/-}\)...
and M-CK\(^{-/-}\) mice to create a loss of function at both the mitochondrial and cytosolic end points of the PCr-CK system. CK\(^{-/-}\) double mutants were identified in offspring from intercrosses between heterozygous ScCKmit\(^{-/+}\); M-CK\(^{-/-}\) animals at approximately the numbers predicted for normal Mendelian segregation with unlinked genes (10 out of 215). Contrary to expectation, they were not overtly different from wild-type or heterozygous inter­mates, bred normally, and had a normal life expectancy. Zymogram assays confirmed the complete absence of muscle-type CK activity and revealed that there was no ectopic expression of any of the other CK family mem­bers, i.e., the brain-type (B-CK) or the ubiquitous mitochondrial CK (UbCKmit) (Figure 1). Residual total CK activity in heart and skeletal muscle extracts was lowered to 0.3% and 2% of wild-type levels, respectively, and can be entirely attributed to the BB-CK and UbCKmit content in capillary or vasculature endothelium and muscle satellite cells. These results provide evi­dence that basal muscle physiology is not dramatically affected by the lack of CK activity.

**Figure 1. Zymogram Gel Analysis of CK-Mutant Muscles**

Activity staining of the different native CK isoenzymes in extracts from skeletal (lanes 1–4) and heart (lanes 5–8) muscle from wild-type (+/+; lanes 1 and 5), M-CK\(^{-/-}\) (lanes 2 and 6), ScCKmit\(^{-/-}\) (lanes 3 and 7), and CK\(^{-/-}\); double-mutant (lanes 4 and 8) mouse. Positions of CK isoenzymes and residual AK activity (noninhibited by Ap5A) are indicated. Note the complete absence of CK activity in (-/-) skeletal muscles.

Table 1. Concentrations of Energy Metabolites in CK-Mutant Muscle

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Wild Type</th>
<th>ScCKmit(^{-/-})</th>
<th>M-CK(^{-/-})</th>
<th>CK(^{-/-})</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP (NMR)</td>
<td>5.6 ± 0.9</td>
<td>4.8 ± 0.8</td>
<td>4.5 ± 0.8</td>
<td>8.7 ± 0.5*</td>
</tr>
<tr>
<td>PCr (NMR)</td>
<td>46.5 ± 1.3</td>
<td>46.9 ± 0.7</td>
<td>47.3 ± 1.2</td>
<td>35.6 ± 1.6*</td>
</tr>
<tr>
<td>PCr (chem)</td>
<td>62.1 ± 2.2</td>
<td>64.9 ± 2.6</td>
<td>66.7 ± 3.0**</td>
<td>51.6 ± 5.2*</td>
</tr>
<tr>
<td>Cr (chem)</td>
<td>31.9 ± 2.2</td>
<td>29.1 ± 2.8</td>
<td>25.3 ± 3.0**</td>
<td>42.4 ± 5.2**</td>
</tr>
<tr>
<td>PME (chem)</td>
<td>2.76 ± 0.32</td>
<td>2.26 ± 0.32</td>
<td>2.76 ± 0.45**</td>
<td>1.24 ± 0.27**</td>
</tr>
</tbody>
</table>

Concentrations were either determined by chemical analysis of snap-frozen medial gastrocnemius muscle (given as mean number of \(\mu\)mol/g dry weight ± SD) or calculated from the relative peak areas of phosphate metabolites in fully relaxed NMR spectra (given as percentage of total integral, with ATP as average of the three peaks) of whole hind-limb skeletal muscle of wild-type and CK-mutant mice. Cr and PCr concentrations were normalized for the mean total Cr + PCr content of all muscles. Ratios calculated from the chemical determination and NMR measurements are given individually. In between brackets are the numbers of experiments when the phosphomonoester (PME) signal was clearly above the noise level. The total number of determinations was \(n = 6\) for wild-type and CK\(^{-/-}\); \(n = 5\) for M-CK\(^{-/-}\) animals, and \(n = 4\) or \(n = 6\) for chemical or NMR determination of ScCKmit\(^{-/-}\) animals, respectively. Double asterisks and single asterisks denote significant differences (\(p < 0.01\) and \(p < 0.02\), respectively) between the wild-type group and each of the CK mutants.
Creatine Kinases Modulate Ca\textsuperscript{2+} Homeostasis

Figure 2. \textsuperscript{31}P-NMR Recordings of Changes in Phosphate Metabolites during Muscle Stress

Each spectrum ([A], wild type; [B], CK\textsuperscript{M-} mutant; 48 free induction decays of 70°C pulses, 5 s repetition time) was obtained from lower limb muscle at rest, followed by 8 min of stimulation at 1 Hz, 8 min of recovery, 8 min of stimulation at 5 Hz, and finally, 6 min of rest. (C) (wild type) and (D) (CK\textsuperscript{M-}) (spectra acquired with a scan repetition time of 12 s) show the course of changes in levels of phosphorylated metabolites before (bottom spectra) and during complete anoxia (cardiac arrest) of the animals. P\textsubscript{i}, PCr, and the \(\alpha\), \(\beta\), and \(\gamma\)-ATP peaks are indicated; the PCr peak was set at 0 ppm.

for COX and CS). Evidently, loss of the M-CK isoform is dominant, and additional loss of ScCKmit has no synergistic effects on the mitochondrial machinery.

Next, we applied in vivo \textsuperscript{31}P-NMR to monitor energy conversion processes in intact muscle. Essentially, no differences were observed for fully relaxed \textsuperscript{31}P-NMR spectra from hind-limb muscles of anesthetized wild-type and single-mutant mice. Resting-state spectra of ScCKmit\textsuperscript{M-} muscles confirm the unanticipated presence of PCr, as determined by chemical analysis (Figure 2B). A clear peak appears exactly at the chemical shift position expected for PCr (at 2.44 ± 0.02 ppm from the \(\gamma\)-ATP position) in spectra of CK\textsuperscript{M-} mice. The relative positions of the three ATP resonances in double-mutant skeletal muscle spectra are exactly similar to those in wild-type spectra. Relative peak areas of energy metabolites in ScCKmit\textsuperscript{M-} and M-CK\textsuperscript{M-} single mutants are also similar to those in wild type (Table 1), whereas CK\textsuperscript{M-} mutant muscles show a substantially lower PCr signal (35.6 versus 46.5-47.3) and somewhat higher ATP signals with respect to the total phosphate signal area. Consequently, this results in a 30% lower PCr/ATP ratio. The peak area measurements also show that relative levels of inorganic phosphate (P\textsubscript{i}) and phosphomonoesters (PME) have increased significantly in CK\textsuperscript{M-} muscles, suggesting a rewiring of metabolism via the glycolytic route. Finally, it is important to note that pH calculations yielded similar values for wild-type (7.29 ± 0.07), ScCKmit\textsuperscript{M-} (7.17 ± 0.05), M-CK\textsuperscript{M-} (7.24 ± 0.02) and CK\textsuperscript{M-} (7.21 ± 0.05) mutant muscles.

PCr Is Not Hydrolyzable in CK\textsuperscript{M-} Muscles

The presence of PCr in CK\textsuperscript{M-} muscles at rest raised the question as to whether this reservoir could still serve as a temporal energy buffer at the onset of exercise. Changes in levels of \textsuperscript{31}P energy metabolites were therefore monitored during and after isometric contraction of lower hind-limb musculature. PCr, P\textsubscript{i}, and ATP profiles of wild-type muscle recorded during periods of stimulation at 1 or 5 Hz and during subsequent recuperation periods were as expected (Figure 2A). In CK\textsuperscript{M-} muscles, levels of PCr and ATP remained apparently constant during and after the exercise period (Figure 2B). Interestingly, also after prolonged exercise periods (20 min; 5 Hz), no significant changes in peak areas of the 3 phosphates of ATP were observed, while intracellular pH responses were comparable to those in wild-type muscle within the time resolution of the experiment. Finally, phosphate metabolites were also monitored under conditions of prolonged severe anoxia. In skeletal muscle of wild-type mice (and ScCKmit\textsuperscript{M-} or M-CK\textsuperscript{M-} mice; data not shown), PCr hydrolysis with a simultaneous fast and steep increase in P\textsubscript{i} levels preceded ATP utilization (Figure 2C). In contrast, the level of PCr in CK\textsuperscript{M-} muscle remained stable, while the complete hydrolysis of ATP occurred with an increase of P\textsubscript{i} (Figure 2D), indicating
that high phosphoryl PCr \rightleftharpoons\text{ATP} exchange is impossible.

**CK Deficiency Reduces Muscle Force Development**

Energy consumption in normal muscle at work is a summation of highly local ATP-hydrolysis events in individual fibers, predominantly supporting SR Ca^{2+} pump (SERCA) and Na^{+}/K^{+} pump activity and cross-bridge cycling for acto-myosin sliding. Since we wished to see whether these activities unite differently in a CK-deficient background, we recorded the contractile behavior of medial gastrocnemius muscles of mutant and control mice upon delivery of a fast and repetitive series of action potentials (producing a tetanus as the Ca^{2+} concentrations in the cytosol level off) [Table 2 and Figures 3A–3C]. Already in response to the second stimulus, and following all subsequent pulses, an impaired force production was seen for CK^{−/−} compared with the wild-type muscle. The force started to decay significantly after the sixth stimulus (60 ms), whereas in wild-type (and ScCK^{−/−}) muscles peak force was not reached before approximately 150 ms of stimulation. Lowering of tetanic force also resulted in lower twitch/twitch force ratios for these mutants (Table 2). In an intermittently repeated isometric contraction series (Figure 3B), there was a clear difference in initial force production between the wild-type and ScCK^{mitf~} group on the one hand and the M-CK^{−/−} and CK^{−/−} group on the other hand. Whereas the force generated by the first repeated contractions initially increased in the wild-type and ScCK^{mitf~} muscles, a large drop in force production (±30%) already occurred in the second twitch of the series in M-CK^{−/−} and CK^{−/−} muscles. Thereafter, force in CK^{−/−} muscles declined further, while M-CK^{−/−} muscles were able to recover slightly. Half-relaxation times of the wild-type, ScCK^{mitf~}, and M-CK^{−/−} muscles remained fairly constant during the first 10 twitches of the series of repeated contractions but increased by 3–5 ms thereafter. In contrast, half-relaxation time increased immediately after the first contractions in the CK^{−/−} muscles, before leveling off later (Figure 3C). Although our measurements integrate all molecular effects on local ATP supply in the entire muscle, comprising different fiber types, our results are most adequately explained by slowed kinetics for Ca^{2+} release instead of uptake. Effects on Ca^{2+}-ATPase-mediated sequestration of Ca^{2+} are not apparent in single mutants but—together with effects on the rephosphorylation of actin-myosin-bound ADP (Cooke and Pate, 1985; Sata et al., 1996)—may dominate the slower relaxation behavior of CK^{−/−} double mutants. In a preliminary approach, we also studied whether there were changes in the myosin heavy chain (MHC) profile of CK-mutant myofibrils, because MHCs are the other principal determinants of shortening velocity and energetic economy of working muscle (Sweeney et al., 1988). As shifts in MHC isotype composition were relatively subtle and occurred in a complex mutation- and fiber type-dependent manner (Steeghs, 1995), they were further neglected in this study.

**Cytomorphic Abnormalities of Structures Involved in ATP and Ca^{2+} Handling**

Having demonstrated the physiological consequences of CK absence, we next examined whether conformational changes in mitochondria and the membraneous structures for Ca^{2+} handling could provide a correlate for altered flux kinetics or compartmentalization of ATP or Ca^{2+}. Ultrastructural and morphometric analysis of diaphragm, intercostal, soleus, gastrocnemius, and heart muscles revealed no changes in the arrangement of outer and inner mitochondrial membranes and cristae, not even in the number of mitochondrial contact sites in the two latter muscles in CK^{−/−} mutants (L. Verdoort et al., submitted). In contrast, the enlarged intermyofibrillar mitochondrial volume that was apparent in fast-twitch fibers of M-CK-deficient gastrocnemius-psoas-soleus (GPS) muscles (van Deursen et al., 1993) was also observed in large fibers of GPS, diaphragm, and intercostal CK^{−/−} muscles. Mitochondria in CK^{−/−} muscles were often packed in rows, and their sizes were highly variable, ranging from extremely large (more than 5 μm in length) to very small. Moreover, mitochondria-rich fibers of all CK^{−/−} muscles, including heart, diaphragm, and large glycolytic skeletal muscles, were distinctly different from other mutants and wild type, in that they contained large(r) numbers of lipid droplets (Figures 4C and 4D). In semithin 1 μm sections, these lipid droplets can often be seen as strings of beads. Electron microscopic examination revealed the lipid droplets to be located immediately adjacent to, and occasionally inside, the intermyofibrillar mitochondria. Association to the subsarcolemmal mitochondrial population was only rarely observed. Furthermore, mitochondria containing glycogen, lipofuscin granules, and other lysosomal structures were present in increased numbers. These deposits are common to diseased muscle and occur to a much lesser extent in normal muscle during aging (Dubowitz, 1985).

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**Table 2. Force Characteristics of Medial Gastrocnemius Muscles of Wild-Type and CK-Mutant Animals**

<table>
<thead>
<tr>
<th></th>
<th>Wild Type</th>
<th>ScCKmit^{−/−}</th>
<th>M-CK^{−/−}</th>
<th>CK^{−/−}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Twitch force (N)</td>
<td>0.19 ± 0.05</td>
<td>0.17 ± 0.03</td>
<td>0.16 ± 0.03</td>
<td>0.17 ± 0.06</td>
</tr>
<tr>
<td>Tetanic force (N)</td>
<td>0.82 ± 0.22</td>
<td>0.78 ± 0.19</td>
<td>0.55 ± 0.04**</td>
<td>0.56 ± 0.25*</td>
</tr>
<tr>
<td>Tetanic/twitch ratio</td>
<td>4.28 ± 0.36</td>
<td>4.57 ± 0.40</td>
<td>3.41 ± 0.48**</td>
<td>3.39 ± 0.38**</td>
</tr>
<tr>
<td>Time to peak force (ms)</td>
<td>142 ± 4</td>
<td>142 ± 4</td>
<td>72 ± 12**</td>
<td>56 ± 7**</td>
</tr>
<tr>
<td>Half-relaxation time (ms)</td>
<td>5.0 ± 0.5</td>
<td>5.0 ± 0.5</td>
<td>7.2 ± 0.5**</td>
<td>7.5 ± 1.3**</td>
</tr>
</tbody>
</table>

Double asterisks and single asterisk, see Table 1.

* n = 14.
* n = 5.
* n = 4.
* n = 15.
Creatine Kinases Modulate Ca\(^{2+}\) Homeostasis

Figure 3. Contractile Characteristics of Wild-Type and CK-Mutant Muscles

(A) Tetanic and twitch force production in wild-type (full trace) and CK\(^{-/-}\) muscles (dotted trace). Note the similar twitch force in both muscles.

(B) Changes in isometric force production during a series of 20 repeated contractions (intermittent isometric protocol). Successive contractions (duration 170 ms; 1 every 250 ms) were performed in wild-type (open squares, n = 5), and intercostal muscles (closed circles, n = 5), and CK\(^{-/-}\) (open circles, n = 6) muscles. Forces (mean ± SEM) are expressed as a percentage of the force in the first contraction of each series.

(C) Changes in half-relaxation times in a series of 20 repeated isometric contractions. Denotations and numbers of experiments are similar as in (B), except for ScCKmut\(^{+/-}\) where n = 5. Half-relaxation times are mean ± SEM.

Omnipresence of conspicuous darkly staining elongated inclusions within the large fibers of gastrocnemius and intercostal muscles in semithin sections is another distinct feature of CK\(^{-/-}\) animals (Figure 4E). Within the fibers, the inclusions are seen at both subsarcolemmal and intermyofibrillar localizations. Ultrastructural examination of various fibers revealed that the inclusions consist of closely packed longitudinally oriented clusters of membranes known as tubular aggregates (TAs) (Figures 4F and 4G). Besides the well-ordered aggregates, unorganized more dilated membrane structures with variocities containing electron-gray material were also observed (Figure 4H). TAs are a distinct pathological structure in skeletal muscle consisting of aggregated terminal cisternae or longitudinal components of the SR. Figure 4I shows that cisternae of the SR, which are located in the direct surroundings of or connected with tubular inclusions, are indeed heavily dilated. The myofibrillar compartment adjacent to the tubular aggregates showed no structural abnormalities, and triads in those myofibrils also appeared normal. It has been suggested that tubular morphology of longitudinal SR in mature muscle arises as a result of reshuffling of SERCA isoforms (Martonosi, 1996). To test whether a chronic derangement in SERCA content could underly TA formation, we measured its total level in extracts of hind-leg muscles of CK mutants. Semiquantitative immunoblot analysis and in vitro biochemical assays revealed that Ca\(^{2+}\)-ATPase activity (76.5 ± 9.5 in wild type, 75.5 ± 9.8 in M-CK\(^{-/-}\), and 76.6 ± 10.0 mU/mg protein in CK\(^{-/-}\)-mutants) and content (between 94.3 ± 11.0 and 95.2 ± 11.8 pmol/mg protein) were similar, regardless of whether the muscles expressed CKs or not. Also, the levels of calsequestrin, another SR marker, remained constant in all muscle types. For reasons unknown, the content of protein disulphate isomerase (PDI), an SR-lumen marker, was slightly increased in CK\(^{-/-}\) muscles only (Figure 5H). Thus, if SERCAs play a role in the conversion of SR cisternae into TAs, it is most likely the redistribution rather than an overall higher membrane content of these pumps that is involved.

Ca\(^{2+}\) Transients Are Altered in CK-Mutant Myotubes In Vitro

Since all (patho)histological and physiological changes in vivo are most easily explained by effects on the Ca\(^{2+}\)-handling machinery, we were prompted next to compare Ca\(^{2+}\) homeostasis in skeletal muscle cells in culture. To this end, satellite cells were isolated from wild-type and mutant animals, and the derived primary myoblasts fused to myotubes in culture. The free cytosolic [Ca\(^{2+}\)], and shape of the transients were measured by digital imaging of single Fura 2-loaded myotubes (Benders et al., 1994). The graphs in Figure 5 show averaged traces of the Ca\(^{2+}\) levels at rest and the Ca\(^{2+}\) transients resulting from acetylcholine- (ACh; 20 µM) or KCl- (125 mM) stimulated depolarizations. The basal [Ca\(^{2+}\)]l level under standard physiological conditions was similar in wild-type and mutant skeletal muscle cells. In contrast, at depolarization by ACh or KCl the amplitude of the Ca\(^{2+}\) responses ([Ca\(^{2+}\)]p) was decreased by about 30% in mutant myotubes, whereas the plateau level ([Ca\(^{2+}\)]p) after stimulation was increased by 35% and 58% in M-CK\(^{-/-}\) and CK\(^{-/-}\) cells, respectively. Moreover, both the half-increase (\(t\)) and the half-decay time...
Figure 4. Morphological Abnormalities in Striated Muscles without CK
(A-D) Diaphragm muscle of wild-type (A and C) and CK^−/− (B and D) animals in 1 μm toluidine blue-stained longitudinal sections (A and B) and in electron microscopy (C and D). Representative areas show increased numbers of electron-gray stained lipid droplets in CK^−/− diaphragm (small arrows, C and D). Similar patterns of lipid droplets were observed in sections of gastrocnemius, soleus, intercostal, and cardiac muscles (data not shown).

(E-I) One-micrometer toluidine blue-stained section (E) and electron micrographs (F-I) of large fibers from gastrocnemius (E, F, H, and I) and intercostal (G) muscles of CK^−/− mice. Several darkly stained inclusions (arrows and asterisks) can be distinguished within two muscle fibers (E). In corresponding electron micrographs (F and G), the inclusions appeared as tightly packed longitudinally oriented tubules known as tubular aggregates (TAs). Intermyofibrillar (arrows in E and F) or subsarcolemmal (asterisks in E and G) accumulations of TAs were found in both gastrocnemius and intercostal muscles. (H) High magnification reveals different aspects of TAs. Apart from regular tubular structures, aggregations of dilated varicosities filled with an electron-gray substance were also present. (I) Electron micrograph demonstrating the sarcoplasmic reticulum origin of the TAs. Arrows point to the gap-spanning foot structures between the T tubule and the SR terminal cisternae (triadic junction). The membranes of both terminal cisternae appear to be “scalloped” along the surface that faces the T tubule. Note that the longitudinal tubules from the A-band region as well as the SR terminal cisternae appear continuous with the tubular aggregate. Bar = 20 μm in (A), (B), and (E), 1 μm in (C), (D), (F), and (G), and 0.5 μm in (H) and (I).

(r2) of the Ca2+ transients were about 1.3- to 1.5-fold higher in the mutant muscle cells. To determine whether the Ca2+ release pathways were the same in all 3 cell types, we examined the effects of nifedipine (5 μM) and ryanodine (10 μM), i.e., specific inhibitors of the voltage-dependent L-type Ca2+ channel (dihydropyridine receptor) and SR Ca2+ release channel (ryanodine receptor), respectively. Both agents completely abolished the depolarization-induced Ca2+ responses (Figures 5C-5F) in all cell types. We interpret this to indicate that there are no other Ca2+ channels effective in our mutants than in the wild type. Likewise, as the SERCA activity and content (13.0 ± 2.6, 12.9 ± 4.8, and 13.6 ± 3.1 mU/mg protein with content ranging between 16.1 ± 3.2 and 17.0 ± 4.0 pmol/mg protein for wild type, M-CK−/−, and CK−/−, respectively), as well as the calsequestrin and PDI levels (Figure 5G), were essentially identical between cell types, we can almost rule out gross alterations of SR composition. Taken together, our results suggest that M-CK deficiency is the direct governing principle in the observed changes in the magnitude and velocity of the Ca2+ fluxes, as various parameters were equal in M-CK−/− and CK−/− cells.

Discussion

The primary observations presented in this paper provide evidence that the CK−PCr system, which is directly coupled to energy transduction, is also intimately connected to the processes for Ca2+ release and storage in skeletal muscle. Unexpectedly, although ATP and Ca2+ are crucial regulators of many physiological processes, we observed no outwardly overt effects on the physiological functioning of voluntary or nonvoluntary muscles in CK−/− mice. This raises the issue of the fate of metabolism and ion homeostasis in the absence of CK.

Redirection of pathways for synthesis and usage of ATP within a muscle fiber may primarily lead to local displacement of AMP/ADP/ATP ratios, change local Mg2+, H+, and inorganic phosphate (P) concentrations, and affect—more indirectly—inosine monophosphate
and lactic acid levels. In turn, these alterations may translate into adaptational shifts in the oxidative or glycolytic metabolic profiles, depending on fiber type (Ventura-Clapier et al., 1995; O’Gorman et al., 1996). Indeed, in our mice with single CK deficiencies, differential compensatory consequences on carbohydrate metabolism were seen in fast-twitch muscle having a relatively high proportion of cytosolic MM-CK and in slow-twitch oxidative muscle being particularly rich in ScCKmit. For single ScCKmit−/− mice, it was previously postulated (Steeghs et al., 1996) that high energy phosphoryl transfers are needed to maintain PCr, a process that could involve a relocation of MM-CK to sites around the mitochondrial periphery. ATP import from circulation or adjacent cells with other CK isoforms most likely, as low level PCr uptake from extracellular space is possible (Down et al., 1983). To conjure a complete picture, further study of PCr levels in myofibrils is warranted to see if and at what age a steady-state situation in accumulation is reached.

By use of in vivo NMR analysis, however, we could confirm that PCr no longer can serve to regenerate hydrolyzed ATP in CK−/− double mutants, not even under the most strenuous situations (i.e., complete anoxia). The absence of CK-catalyzed phosphoryltransfer in muscle of CK−/− mutants has been confirmed by monitoring PCr metabolisms in differentiated myotubes from different control or mutant mice by adding 20 μM ACh (A, C, and E) or changing the KCl concentration to 125 mM (B, D, and F). Traces show the averaged [Ca2+] after superimposing all appropriate experiments for wild-type (solid line), M-CK−/− (dashed line), and CK−/− (dotted line) myotubes; numbers examined are given between parentheses. The basal [Ca2+] in myotubes derived from wild-type, M-CK−/−, and CK−/− mice is 122 ± 17 nM (156), 122 ± 10 nM (68), and 126 ± 22 nM (68), respectively. Mean values ± SD for the amplitude ([Ca2+]max or plateau of the Ca2+ responses ([Ca2+]i) and the half-increase (t1/2) or half-decay time (t½) in seconds. Parameters of mutant myotubes differ from those of wild-type myotubes with p < 0.01 (asterisks) or from each other with p < 0.01 (round signs). The effects on depolarization of presence of the dthydropyridine receptor channel blocker nifedipine (C and D) or the ryanodine receptor channel-blocker ryanodine (E and F) are shown in the middle panels. The bottom panels show immunostained signals from SR marker enzymes, SERCA1, calsequestrin, and PDI on strips of Western blots of cultured muscle cells (G) and adult skeletal muscle (H). SERCA1 and calsequestrin signals are present in all lanes (40 μg protein lane, except for M-CK−/− cells, 20 μg lane) but occur at different levels in cell and muscle extracts (note the overstained SERCA signals in all muscle types). Note that the PDI signal is of equal intensity in all lanes but absent in wild-type and M-CK−/− muscle extracts.
the rates of $^{18}$O-phosphoryl appearance in endogenous metabolites, including PCr, of muscle incubated in $^{18}$O-water-enriched medium (N. D. Goldberg, personal communication). Taken together, we consider this strong evidence for all escape routes in ATP $\rightarrow$ PCr conversions being essentially blocked, if we combine nullifying mutations in both end points of the CK–PCr shuttle. Equally important, these data confirm that our previous postulates about redirection of phosphoryl fluxes in single CK mutants were essentially correct. Combined with the observation that PCr can indeed be converted into ATP in the livers of UbCKmin transgenic mice (Koretsky, 1999), our results strongly suggest that the direction of the mitochondrial and cytosolic energy flow in vivo (i.e., toward production or consumption of PCr) is entirely dependent on the physiological state of the cell.

We conclude that the remarkable preservation of basal physiological functions in CK$^{+/−}$ muscles must be based on otherwise cryptic principles of metabolic control and energy homeostasis. Zeleznikar et al. (1995) have provided compelling evidence that AK-meditated ATP $\rightarrow$ ADP exchange is likely involved, as it can partially take over the metabolic energy transfer function. Almost certainly, the fiber type-dependent changes in mitochondrial location and the glycolytic energy flow are other important determinants in the long-term adaptive process in our mutants. An increase in intermyofibrillar—but not subsarcolemmal—mitochondrial volume in fast-twitch fibers was evident in both M-CK$^{+/−}$ and CK$^{+/−}$ mutants, and was described earlier (van Deusen et al., 1993). This phenomenon may serve to preserve adequate ATP delivery and protect the system against kinetically unfavorable substrate-product feedback, which would occur if transcytotic gradients of ATP, ADP, and P$_i$ were simply increased (Gunter et al., 1994). When the overall CK$^{+/−}$ muscle ultrastructure is compared with that of M-CK$^{+/−}$ muscles, however, conspicuous additional pathological manifestations become evident. The presence of lipofuscin granules points to deregulation of metabolism, and the accumulation of lipid in and around the mitochondria in CK$^{+/−}$ mutants may indicate an impaired capacity to utilize fatty acids as substrate for oxidative ATP production (DiDonato et al., 1978). We may expect that unraveling the functional nature of these phenomena will provide more insight into the role of the mitochondrial end of the CK system and its connection to distributed metabolic control. There is now compelling evidence that mitochondrial Ca$^{2+}$ is the most likely candidate for an additional metabolic mediator (Gunter et al., 1994; Hajnóczky et al., 1995), but future studies are necessary to confirm the suggestion that ATP–PCr metabolism and Ca$^{2+}$ homeostasis indeed converge in mitochondria.

In sarcoplasm, [Ca$^{2+}$], exerts a dominant regulatory control on the excitation–contraction coupling (Ebashi, 1976) and acts as a second messenger to modulate cellular function. The proposal of local Ca$^{2+}$ alterations being the principal reporter and regulator for metabolic, physiological, and cytoarchitectural changes in CK-deficient muscles is therefore consistent with the observation that M-CK$^{+/−}$ and CK$^{+/−}$ mutants, besides ultrastructural features, share striking similarities in tetanic force profiles and Ca$^{2+}$-release/uptake characteristics in vivo and in vitro. Based on the idea that the altered CK activity influences [Ca$^{2+}$], the quick and significant drop in force generation seen in intermittently stimulated M-CK$^{+/−}$ and CK$^{+/−}$ muscles can be most easily explained by a drop in the magnitude of Ca$^{2+}$ release and a lesser recruitment of fibers (Edwards et al., 1975; de Haan et al., 1989). Comparison of the Ca$^{2+}$ transients in cultured wild-type and mutant myotubes suggests a more complicated model, whereby the response amplitude, speed of release ($\tau_0$), and sequestration ($\tau_1$) of Ca$^{2+}$ have been changed. To date, little is known regarding the reliability of extrapolating data from the in vitro to the in vivo situation, especially as the cytoarchitectural arrangement of the plasma membrane, myofilaments, and SR vesicles in muscle cells may differ from the situation in vivo (Flucher and Frazinzi-Armstrong, 1996). We observed that the depolarization-induced Ca$^{2+}$ transients are prevented by inhibition of the Ca$^{2+}$ channels in both cultured wild-type and mutant muscle cells (Figures 5E and 5F), suggesting that a "skeletal muscle type" of excitation–contraction coupling mechanism is operational. Likewise, we know that a similar mechanism for uptake of Ca$^{2+}$ in sequestering SR vesicles exists in developing and adult fibers, underscoring the validity of comparing in vitro and in vivo findings. Still, for an adequate interpretation of our results it is important to stress that our cultured myotubes contain a significant level of BB-CK activity, the early embryonic CK isoform in muscle. On average, 28% ± 10% (n = 10) of total CK activity in cultured wild-type cells resulted from BB-CK activity, while the absolute level of BB-CK in mutant cells was similar to that in wild type. We thus have to conclude that BB-CK cannot fully substitute MM-CK in counteracting [Ca$^{2+}$] changes at depolarization, although this is not relevant for in vivo physiology per se, as B-CK expression is switched off completely during development (Wallimann et al., 1992) (Figure 1).

What could be the mechanisms by which CK absence affects both the amplitude and kinetics of release and uptake in Ca$^{2+}$ transients? Impaired PCr $\rightarrow$ ATP exchange could influence the speed and magnitude of Ca$^{2+}$ release by setting a local change in the cytosolic ([Ca$^{2+}$]) and SR luminal [Ca$^{2+}$], owing to impaired SERCA action. In turn, this may affect the open probability (P$_0$) of the ryanodine receptor and thus influence quantal Ca$^{2+}$ release from the SR (Hidalgo and Donoso, 1995; Klein et al., 1996). ATP availability can also influence the P$_0$ more directly. Local depletion of [ATP], and the accompanying increase in free [Mg$^{2+}$] near the channel, can lead to a reduction in Ca$^{2+}$ release in skeletal muscle fibers (Owen et al., 1996) and influence the filling state of the internal Ca$^{2+}$ stores (Hofer et al., 1996). Furthermore, local changes in [ATP] could induce changes in the protein phosphorylation status and thus the activities of dihydropyridine receptor and ryanodine receptor clusters (Valdivia et al., 1995). It is also conceivable that the function of the Na$^+$/K$^+$ pump (Wallimann et al., 1992) and/or ATP-sensitive potassium channels (Olson et al., 1996) in the sarcolemma membrane might be severely disregulated by alterations in local [ATP] and affect depolarization characteristics in cells and muscles alike. Clarifying whether one or a combination of these factors is involved represents an important issue for future investigations.
Fortunately, there is more consistent information on the possible mechanisms for altered Ca\(^{2+}\) uptake. Our data confirm predictions based on in vitro studies and provide more general evidence for a specific and direct functional coupling between MM-CK, ScCKmit, and the Ca\(^{2+}\)-handling machinery at stages of advanced muscle development. Coupling to M-CK and ScCKmit may tune the regulation of Ca\(^{2+}\) release, as well as the role of Ca\(^{2+}\) sequestration in cytosolic and mitochondrial compartments, and does so differently in different muscle fibers. In turn, the compartmentalized [Ca\(^{2+}\)] may act as a second messenger in adapting the cellular organization to physiological demand. Further analysis of the embedding of CK protein and the catalyzed phosphoryl transfer reaction in different microenvironments under different physiological challenges is necessary to understand the details on the coupling of PCR-ATP supply and these spatial and temporal events in Ca\(^{2+}\) homeostasis in muscle.

Experimental Procedures

Generation and Genotyping of CK-Deficient Mice

Procedures involved in the generation and genotyping of M-CK\(^{-/-}\) and ScCKmit\(^{-/-}\) nullizygous mice have been described in detail elsewhere (Van Deursen et al., 1995; Steeghs et al., 1996). ScCKmit\(^{-/-}\) and M-CK\(^{-/-}\) mice were crossed to obtain animals heterozygous for both CK isoforms. Sibling matings of these mice resulted in the generation of ScCKmit and M-CK double-mutant CK\(^{-/-}\) mice. All wild-type and CK-mutant mice had a mixed inbred (50%-50% C57BL/6 \times 129/Sv) background. Breeding was carried out under standard housing conditions in the KUN Central Animal Facility.

CK Isoenzyme, Ca\(^{2+}\)-ATPase, and SR Marker Determination and Fiber Typing

Muscle extracts were prepared and diluted 1:5 in 30 mM Na\(_2\)PO\(_4\) buffer (pH 7.4) containing 0.05% (v/v) Triton X-100, 0.3 mM diithio­tol, and 0.3 mM phenyl methanesulphonyl fluoride (Steeghs, 1995). Total CK-specific activity was measured using a CBR-CK NAC­activated kit (Boehringer GmbH, Mannheim, Germany, No. 475742).

For zymogram analyses, extracts were diluted in Tris-barbital buffer (pH 8.0), and CK proteins (in 2.2-4.0 \(\mu\)g extract protein) were resolved on agarose gels using the Universal Ge 8 system from CIBA Corning (Alameda, CA). Enzyme activities were visualized using the catalytic phosphokinase isoenzymes colorimetric detection kit (Sigma Diagnostics) according to the manufacturer’s instructions (Procedure no. 715-EP). Staining by AK activity was prevented by including 10 \(\mu\)M of the specific inhibitor P\(_{\text{H2}}\)-di(adenine-5')-penta­phosphate (Ap5A) in all staining mixtures.

Procedures for determining activity and concentration of SR Ca\(^{2+}\)-ATPase have been described previously (Benders et al., 1994). For visualization of SR constituents, extracts from muscles or cells (20-40 \(\mu\)g protein per lane) were fractionated on 10.5% (w/w) polyacrylamide-SDS gels and electroblotted to nitrocellulose membranes. Separate strips of the blot were incubated with monoclonal antibodies against calsequestrin (1:1 diluted; SanverTech, Breda, The Netherlands), anti-mouse alkaline phosphatase-conjugated secondary antibody (PDI (1:1000; kind gift of Dr. N. Bui leid), followed by (goat or rabbit) anti-mouse alkaline phosphatase-conjugated secondary antibody (1:1000; Sigma, St. Louis, MO), and stained following routine methods. Electrophoretic analysis of MHC composition, and determinations of cytochrome COX and CS activities, were as described pre­viously (Steeghs, 1995).

Chemical Analysis of Metabolite Concentrations

Procedures for the measurements of creatine and adenosine metab­olites in medial gastrocnemius muscles of mice have been described (van Deursen et al., 1993; Steeghs et al., 1996).

\(^{31}P\)-NMR Spectroscopy

In vivo \(^{31}P\)-NMR spectra of mouse hind-limb muscles were recorded on an Oxford Instruments magnet (4.3 T) equipped with a S.M.I.S. In vivo.
spectrum and working at 73 MHz. Probe characteristics and experimental conditions for the 31P-NMR spectroscopy at rest and during lower limb muscle contraction, as well as for inversion transfer, were essentially as described previously (Heerschap et al., 1988; van Deursen et al., 1984). Spectra in muscles at work were acquired with a 5 s pulse interval [to avoid excessive saturation of PCR resonance in double-mutant muscle] in blocks of 48 scans each, giving a time resolution of 240 s per spectrum. After acquisition of a spectrum at rest, 2 spectra were obtained during 8 min of electrostimulation at 1 Hz (square pulses of 2 ms at 15 V). The muscles were allowed to recover for 8 min, during which 2 additional spectra were acquired, before another 8 min stimulation period of 5 Hz was applied. Subsequent muscle recovery was monitored for variable lengths of time. pH values were calculated from the chemical shift of the Pi signal.

Physiological Measurements of Skeletal Muscle Function
Contractions characteristics and force measurements of medial gastrocnemius muscles were performed as described previously (de Haan et al., 1989). Muscle optimum length (L0) was first estimated using twitch contractions at different lengths of the muscle-tendon complex and further assessed using 3 tetani (duration, 150 ms; stimulation frequency, 100 Hz). Subsequently, the muscle performed 2 fatiguing exercise protocols: one long duration (5 s) isometric tetanus at L0 and a series of 20 repeated isometric contractions (duration 170 ms) within 5 s at L0. Force signals were digitized (1000 Hz) and analyzed for peak force, time to peak force, and half time of relaxation (time for force to fall from half to a quarter at the end of stimulation; Edwards et al., 1975).

Electron Microscopy and Histochemical Fiber Typing
Mice were anesthetised intraperitoneally (using 2,2,2-tibromoethanol) prior to the removal of the MPS muscle complex, heart, diaphragm muscle, and intercostal muscles. Sample preparation, pre- and postfixation, and Epon embedding were essentially as described (van Deursen et al., 1993). For light microscopic analysis, semithin 1 μm sections were cut and stained with toluidin blue following routine procedures. Subsequently, ultrathin sections were cut, double contrasted with uranyl acetate, and examined in a Philips electron microscope EM 301 or a JEOL TEM 1010. For routine histochemical examination, cross-sections of the MPS muscle groups were stained as described (Van Deursen et al., 1993).

[Ca2+] Measurements in Cultured Skeletal Muscle Cells
Hind-leg muscle from 10- to 25-day-old wild-type and homozygous mutant animals was dissociated, and the isolated satellite cells were grown on collagen-coated glass coverslips (25 mm diameter) in serum-containing media for 2 days (Benders et al., 1984). Cells were allowed to differentiate for 4 days, loaded with 10 μM Fura 2 for 1.5 hr, and single-cell fluorescence intensity ratios (240/390 nm) were collected using conventional video microscopy and converted to [Ca2+] as previously described (Benders et al., 1994). For calibration, Ca2+-saturated or Ca2+-free dye was set by 2 μM ionomycin in the presence of 1.8 mM Ca2+ (pH 7.5) or 20 mM EGTA (pH 8.0), respectively. Under these conditions, the myotubes remain attached to the coverslip. The calibration parameters did not differ between the wild-type, M-CX1−, and CK−− muscle cells.

Statistics
The unpaired t test was used to compare between wild-type animals and each of the mutant groups. Significance was set at p < 0.01 or 0.05.

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