Transgenic Mice Overexpressing Mutant PRKAG2 Define the Cause of Wolff-Parkinson-White Syndrome in Glycogen Storage Cardiomyopathy

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Background—Mutations in the γ2 subunit (PRKAG2) of AMP-activated protein kinase produce an unusual human cardiomyopathy characterized by ventricular hypertrophy and electrophysiological abnormalities: Wolff-Parkinson-White syndrome (WPW) and progressive degenerative conduction system disease. Pathological examinations of affected human hearts reveal vacuoles containing amylopectin, a glycogen-related substance.

Methods and Results—To elucidate the mechanism by which PRKAG2 mutations produce hypertrophy with electrophysiological abnormalities, we constructed transgenic mice overexpressing the PRKAG2 cDNA with or without a missense N488I human mutation. Transgenic mutant mice showed elevated AMP-activated protein kinase activity, accumulated large amounts of cardiac glycogen (30-fold above normal), developed dramatic left ventricular hypertrophy, and exhibited ventricular preexcitation and sinus node dysfunction. Electrophysiological testing demonstrated alternative atrioventricular conduction pathways consistent with WPW. Cardiac histopathology revealed that the annulus fibrosis, which normally insulates the ventricles from inappropriate excitation by the atria, was disrupted by glycogen-filled myocytes. These anomalous microscopic atrioventricular connections, rather than morphologically distinct bypass tracts, appeared to provide the anatomic substrate for ventricular preexcitation.

Conclusions—Our data establish PRKAG2 mutations as a glycogen storage cardiomyopathy, provide an anatomic explanation for electrophysiological findings, and implicate disruption of the annulus fibrosis by glycogen-engorged myocytes as the cause of preexcitation in Pompe, Danon, and other glycogen storage diseases. (Circulation. 2003;107: 2850-2856.)

Key Words: kinases ■ glycogen storage disease ■ excitation ■ arrhythmia ■ hypertrophy

Human mutations in PRKAG2, the gene encoding the γ2 subunit of AMP-activated protein kinase (AMPK), cause cardiomyopathy characterized by ventricular hypertrophy, Wolff-Parkinson-White syndrome (WPW), and progressive conduction system disease.1–5 AMPK, consisting of catalytic (α) and regulatory (γ and β) subunits, is activated in energy-deficiency states and plays a key role in regulation of cardiac metabolism and energy homeostasis.1 In vitro analyses of the biochemical consequences of disease-causing missense mutations in a yeast gene homologue (Snf4) and in transfected COS cells indicated that defects in humans caused constitutive kinase activity.5,6 We have documented vacuolar changes and periodic acid–Schiff (PAS)–positive inclusions, suggesting accumulation of glycogen-related material, in the hearts of affected individuals.5 Although they clearly distinguish this entity from classic hypertrophic cardiomyopathy caused by sarcomere protein gene mutation,7 the exact role played by glycogen stores in disease pathogenesis remains unclear.

An intriguing and poorly understood aspect of this disorder is the conduction system disease associated with PRKAG2 mutations. Affected individuals typically demonstrate ECG

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2850
patterns of ventricular preexcitation and other features associated with WPW.\textsuperscript{2,5,8} WPW is generally thought to be caused by muscular tracts that connect atrium to ventricle outside the specialized conduction tissue such that electrical impulses traversing these tracts bypass the physiological atrioventricular node delay and produce ventricular preexcitation. In most patients with WPW, however, the anatomic substrate for ventricular preexcitation is undefined. Morphological studies of hearts from individuals with PRKAG2 mutations have not been performed, and whether these mutations cause bypass tracts is unknown.

We developed transgenic mice overexpressing the PRKAG2 N488I missense mutation to define the mechanisms by which this mutation causes cardiac disease; because human PRKAG2 mutations create a “gain of function,” a transgenic mouse overexpressing the mutant gene appeared to be a suitable model system. The transgenic mice expressed either wild-type or mutant (N488I) PRKAG2 cDNA under control of the cardiac-specific \(\alpha\)-myosin heavy chain (\(\alpha\)-MHC) promoter\textsuperscript{9} (Figure 1A). Transgenic mice carrying the mutant but not wild-type human PRKAG2 cDNA developed both cardiac hypertrophy and ventricular preexcitation. Our analyses of these mice define the anatomic basis for preexcitation in this human cardiomyopathy.

Methods

Transgenic Mice

The PRKAG2 coding region was amplified from human lymphocyte RNA by use of the One-Step reverse transcription–polymerase chain reaction (RT-PCR) kit (Qiagen) with primers 29F, 5‘-GGAGGGGAAAGGGGCGCGAGAC-3’, and 1880R, 5‘-GCAGCCAGTGTTCAAGGGGAAA-3’. An 1851-bp fragment was isolated and subcloned into TOPO TA cloning kit, Invitrogen. The nucleotide sequences of 20 cloned inserts were determined to identify 1 insert that was identical to human PRKAG2 cDNA. A T→A substitution was introduced at nucleotide residue 1553 to encode the Asn→Ile missense mutation (at codon 488, designated N488I). Wild-type and mutant cDNA inserts were released by EcoRI digestion and blunt-end-ligated into the SalI site of pC126 expression vector.\textsuperscript{9} Transgene DNA encoding the \(\alpha\)-MHC promoter, PRKAG2 coding sequence, human growth hormone 3′-UTR, and a polyA signal (Figure 1A) were linearized with BamHI; size-fractionated; purified (QIAquick Gel Extraction Kit, Qiagen); and microinjected into fertilized FVB mouse oocytes.

Genotyping

Transgenic founders were identified by Southern blot analyses of tail DNA as described previously,\textsuperscript{10} except that a 540-bp antisense biotinylated riboprobe (Strip-EZ RNA Kit, Ambion) corresponding to the 3′ end of the cloned cDNA was used to identify the 1000-bp HindIII transgene-specific fragment. Offspring of founder mice were genotyped by PCR amplification of the transgene using primers F, 5′-GCCTGCTTTCAAGAGCGAAG-3′, and R, 5′-GGACGCCAGTGTTGACAGGAA-3′ and a control mouse genomic fragment using primers F, 5′-GAGAAGCTCGGCGATGAG-3′, and R, 5′-ACTCAGCAAGCCCTCCCATCTG-3′, in 1 reaction.

RNA Assessment

Northern blots were performed as described,\textsuperscript{11} using 2 \(\mu\)g total cardiac RNA per gel lane and biotinylated riboprobes prepared as above. Semiquantitative RT-PCR using the above-mentioned PRKAG1 and PRKAG2 primers was performed as described.\textsuperscript{11} Band intensities were quantified by densitometry using NIH Image software.

Protein Analyses

Protein extracts and Western blots were performed as described using 10 to 20 \(\mu\)g of protein lysate per lane. Antibodies specific for the AMPK \(\gamma_2\) peptide (556 to 569 LTPAGAKQKETETE-COOH), \(\alpha_1\), \(\alpha_2\), and pan-\(\beta\) (Upstate Biotechnology) were diluted 1000- to 2000-fold. Horseradish peroxidase–conjugated secondary antibody was used for chemiluminescence detection.
**Biochemical Assays**

Glycogen content was determined by the amylglucosidase digestion method on cardiac tissue that was rapidly excised, instantly immersed in ice-cold PBS, blotted, and freeze-clamped. Glucose was determined with the glucose oxidase kit (Sigma). AMPK activity was assessed by its ability to phosphorylate a synthetic peptide. AMPK complexes were immunoprecipitated from 200 μg protein using α1- or α2-specific antibody and protein A/G Plus-Agarose beads (Santa Cruz Biotechnology). AMPK activity with or without 200 μM AMP was determined by Kirchhoff et al. (1999).

**Echocardiography and ECG**

Echocardiography was performed in male mice with a SONOS-4500 Hewlett-Packard echocardiograph as described previously, except that mice were anesthetized before hair removal. ECG recordings, electrophysiologic studies, and continuous ECG recordings (Holter monitor) were performed as described previously.

**Histopathology**

Mouse hearts were fixed and stained as described previously. Sections for immunohistochemistry were deparaffinized, incubated with AMP kinase γ, antibody and fluorescein-conjugated secondary antibody, and examined under a fluorescence microscope. For electron microscopy, 1-μm sections fixed in glutaraldehyde were embedded in Epon 812 and stained with toluidine blue. Hearts were analyzed for accessory atrioventricular connections by serial analyses (see text). All data are presented as mean±SD and analyzed by Student’s t test.

**Results**

A full-length human PRKAG2 cDNA, which encodes a 569-amino-acid polypeptide and is 95% similar to the mouse homologue, was amplified from lymphocyte RNA and used as a transgene (see Methods and Figure 1A). A second transgene was created by mutating codon 488 from Asn to Ile. Seven independent transgenic lines expressed robust amounts of wild-type PRKAG2 RNA (denoted TG<sup>wt</sup>), and 8 independent lines expressed abundant N488I<sup>PRKAG2</sup> RNA (denoted TG<sup>488I</sup>). Levels of cardiac glycogen were compared with levels found in nontransgenic controls, but cardiac glycogen was markedly greater in TG<sup>488I</sup> than TG<sup>wt</sup> mice. Cardiac anatomy of TG<sup>488I</sup> mice showed only

### Data Analysis

Preliminary studies of TG<sup>wt</sup> lines 4656, 4657, and 4671 and TG<sup>488I</sup> lines 4623, 4625, 4636, 4645, and 4649 indicated that all lines shared phenotypic features (ie, heart size, glycogen content, histopathology). Lines 4657 and 4623 and control littermates were selected for detailed analyses (see text).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Wild-Type</th>
<th>TG&lt;sup&gt;wt&lt;/sup&gt;</th>
<th>TG&lt;sup&gt;488I&lt;/sup&gt;</th>
<th>TG&lt;sup&gt;wt&lt;/sup&gt; vs WT</th>
<th>TG&lt;sup&gt;488I&lt;/sup&gt; vs TG&lt;sup&gt;wt&lt;/sup&gt;</th>
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</thead>
<tbody>
<tr>
<td>HW/BW, mg/g</td>
<td>4.8±0.2</td>
<td>7.0±0.4</td>
<td>11.5±1.4</td>
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<td>Water/HW, %</td>
<td>77.0±1.6</td>
<td>74.7±0.7</td>
<td>75.0±1.3</td>
<td>0.03</td>
<td>NS</td>
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<td>Protein/HW, %</td>
<td>14.6±5.7</td>
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<td>15.6±3.8</td>
<td>NS</td>
<td>NS</td>
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<tr>
<td>Glycogen/HW&lt;sup&gt;*&lt;/sup&gt;</td>
<td>1.6±0.7</td>
<td>10.1±1.2</td>
<td>52.9±3.4</td>
<td>&lt;0.001</td>
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<td>Echocardiography</td>
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<tr>
<td>Heart rate, bpm</td>
<td>607±82</td>
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<td>NS</td>
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</tr>
<tr>
<td>LWT, mm</td>
<td>0.90±0.08</td>
<td>0.99±0.08</td>
<td>1.22±0.23</td>
<td>0.05</td>
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<td>LVEDD, mm</td>
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<td>2.51±0.49</td>
<td>3.15±0.45</td>
<td>NS</td>
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<td>FS, %</td>
<td>67.2±7.1</td>
<td>75.5±5.7</td>
<td>56.9±9.3</td>
<td>0.03</td>
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<td>20 Weeks</td>
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<td>Heart rate, bpm</td>
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<td>484±47</td>
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<td>LWT, mm</td>
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<td>NS</td>
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<td>LVEDD, mm</td>
<td>2.49±0.25</td>
<td>2.74±0.50</td>
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<td>NS</td>
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</tr>
<tr>
<td>FS, %</td>
<td>78.1±4.8</td>
<td>76.3±6.2</td>
<td>34.4±7.8</td>
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HW/BW indicates ratio of wet heart weight to body weight; LWT, maximum left ventricular wall thickness; LVEDD, left ventricular end-diastolic diameter; and FS, fractional shortening. Data (mean±SD) reflect 4–10 mice evaluated in each group. *Micrograms per milligram wet weight.

**Characteristics of Wild-Type, TG<sup>wt</sup>, and TG<sup>488I</sup> Hearts**

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**Parameters**

- HW/BW: Heart Weight to Body Weight
- Water/HW: Water Content to Heart Weight
- Protein/HW: Protein Content to Heart Weight
- Glycogen/HW: Glycogen Content to Heart Weight
- Echocardiography: Heart Rate, Left Wall Thickness, Left Ventricular End-Diastolic Diameter, Fractional Shortening

**Values**

- HW/BW: Normal
- Water/HW: Normal
- Protein/HW: Normal
- Glycogen/HW: Elevated

**Results**

A full-length human PRKAG2 cDNA, which encodes a 569-amino-acid polypeptide and is 95% similar to the mouse homologue, was amplified from lymphocyte RNA and used as a transgene (see Methods and Figure 1A). Seven independent transgenic lines expressed robust amounts of wild-type PRKAG2 RNA (denoted TG<sup>wt</sup>), and 8 independent lines expressed abundant N488I<sup>PRKAG2</sup> RNA (denoted TG<sup>488I</sup>). Levels of cardiac glycogen were compared with levels found in nontransgenic controls, but cardiac glycogen was markedly greater in TG<sup>488I</sup> than TG<sup>wt</sup> mice. Cardiac anatomy of TG<sup>488I</sup> mice showed only increased heart size and glycogen content.
mild morphological changes despite significantly increased glycogen content. Cardiac weight and left ventricular wall thickness were increased compared with wild-type mouse hearts (Table), but TGwt hearts had neither histopathological changes (Figure 2) nor cardiac dysfunction associated with glycogen storage. In contrast, TGN488I mice had strikingly abnormal cardiac morphology and histology. Cardiac mass and left ventricular wall thickness were markedly increased in TGN488I mice compared with nontransgenic controls or TG wt mice (Figure 2, A–C, and Table). Histological analyses (Figure 2, D–I) showed myocyte hypertrophy; PAS staining revealed abundant glycogen throughout the myocardium. Ventricular but not atrial myocytes contained vacuoles, which were similar to those observed in cardiac histopathology of humans bearing a PRKAG2 mutation.5 Electron microscopy revealed that vacuoles contained pooled, non–membrane-bound glycogen, which displaced contractile elements and distorted the overall cell morphology (Figure 2K). Neither interstitial fibrosis nor lipid deposition was evident.

The cardiac function of TGN488I mice deteriorated over time. Echocardiograms of TGN488I mice showed cardiac hypertrophy with near-normal fractional shortening at 8 to 10 weeks, but by 20 weeks of age, contractile function was reduced and chamber dilation was evident (Table). Cardiac hypertrophy was associated with a proportional increase in protein content (Table) and augmented ventricular expression of hypertrophy-related genes: atrial natriuretic peptide (ANP), brain natriuretic peptide (BNP), and α-skeletal actin (Figure 3). ANP, BNP, and α-skeletal actin RNA in TGwt hearts were 6-, 3-, and 4-fold greater than in nontransgenic hearts, respectively (3 to 4 mice per group; P<0.05), whereas these RNAs were 20-, 10-, and 8-fold greater in TGN488I than in nontransgenic hearts. ANP and BNP RNAs were expressed at a significantly higher level in TGN488I than in TGwt hearts (P<0.025).

Because human PRKAG2 missense mutations caused ventricular preexcitation and progressive conduction system disease,2,5,8,20 cardiac electrophysiology was studied in transgenic mice. Surface ECGs (Figure 4A) showed that ≈50% of TGN488I mice had shortened PR intervals, indicative of a reduction in the physiological time delay between atrial and ventricular electrical activation, and delta waves, suggestive
of ventricular preexcitation. Concurrent ECGs and 2D echocardiography indicated that preexcitation was associated with asynchronous left ventricular contraction. Preexcitation was not found in any TGWT mice (n \( \geq 200 \)) or in TGWT mice.

Invasive electrophysiological studies (Figure 4B) confirmed preexcitation in 2 independent TGN488I lines. Two distinct pathways for atrioventricular conduction were observed with different coupling intervals and different ventricular morphologies of excitation (our unpublished results). Continuous ECG recordings showed that multiple patterns of ventricular activation coexisted in the same animal (Figure 4C), analogous to electrophysiological observations in human patients with PRKAG2 mutations and WPW.8 TGN488I mice had a lower basal heart rate (Table), and on continuous ECG monitoring (n=6), all exhibited deterioration of the conduction system with frequent spontaneous episodes of sinus bradycardia (<300 bpm) and various escape rhythms, including paroxysmal supraventricular tachycardia and atrial fibrillation (Figure 4D). Stress (induction of anesthesia and/or manipulation) resulted in syncope and led to sudden death in 5 TGN488I mice; ECG monitoring of stressed TGN488I mice suggested severe and persistent sinus bradycardia as the cause of death. Spontaneous mortality, associated with severe left ventricular dysfunction, was observed in TGN488I mice 20 to 40 weeks old (Figure 5A). Continuous ECG recording in 3 old mice (>30 weeks old) (Figure 5B) demonstrated severe sinus bradycardia but not tachyarrhythmia or atrioventricular block before death.

To examine the specialized cells of the conduction system, TGN488I mice were crossed with minK-LacZ mice,17 which transcribe \( \beta \)-galactosidase mRNA under control of the minK promoter so that \( \beta \)-galactosidase was expressed in cardiac conduction system cells. Compound mutant mice (MinK/TG N488I ) had no evidence of gross abnormalities in the cardiac conduction system compared with wild-type MinK mice (data not shown). Although the gross organization of the conduction system was normal, serial histological examination of the atrioventricular junction in TGN488I mice showed important differences (Figure 6). The annulus fibrosis, which normally insulates the atria from the ventricles, was a continuous structure in both wild-type and TGWT hearts. However, in hypertrophied TGN488I hearts, the annulus fibrosis was thinned, stretched, and disrupted, most notably at the atrioventricular junction above the interventricular septum. This region contained many vacuolated, glycogen-loaded

- ANF
- BNP
- Sk Actin
- 28S

WT TGWT TG N488I

Figure 3. Expression of hypertrophy-associated genes in cardiac ventricles of 8-week-old wild-type (WT) and transgenic (TGWT and TG N488I ) animals. Northern blots were probed with ANP (ANF), BNP, and \( \alpha \)-skeletal actin (Sk actin) cRNA probes.
myocytes. However, all TG<sup>N488I</sup> hearts studied (n=5) showed loss of fibrous separation between atrial and ventricular myocardium in the anterior septum lateral to the aortic outflow tract and adjacent to the tricuspid annulus (the region defined by surface ECG criteria as the locus of preexcitation). Furthermore, 2 TG<sup>N488I</sup> hearts also showed disruption of annulus fibrosis in the posterior septal region, consistent with multiple accessory AV connections, as suggested by continuous ECG monitoring (Figure 4C). No distinct bypass tracts were observed.

AMPK activity, with and without AMP stimulation, was measured in cardiac extracts from young TG<sup>wt</sup> and TG<sup>N488I</sup> mice after immunoprecipitation with α1 subunit–specific antibodies (Figure 7). AMP stimulation produced a modest (<2-fold) increase in α<sub>1</sub> or α<sub>2</sub> subunit–associated AMPK activity in wild-type or transgenic heart extracts. Both α<sub>1</sub> and α<sub>2</sub> subunit–associated basal AMPK activity was increased in TG<sup>N488I</sup> mice compared with TG<sup>wt</sup> mice. In TG<sup>N488I</sup> hearts, AMPK activity associated with the α<sub>2</sub> subunit demonstrated a much more dramatic increase (≈8-fold versus <2-fold) than the increase in α<sub>1</sub> subunit–associated AMPK activity in these same mice (Figure 7).

Discussion
We demonstrate that transgenic mice overexpressing mutant PRKAG2 exhibit the cardiomyopathy and electrophysiological abnormalities found in humans with this mutation.2–5 Transgenic mice expressing mutant PRKAG2 demonstrated increased cardiac enzyme activity and cardiac glycogen storage. In contrast, overexpression of wild-type PRKAG2 produced only mild glycogen accumulation, mild cardiac hypertrophy, and no conduction system disease. These data establish PRKAG2 mutations as a glycogen storage cardiomyopathy and confirm for the first time the direct relationship between PRKAG2 mutations, AMPK activation, glycogen storage, and the features of human disease. Analyses of the atrioventricular junction of these mice explain the preexcitation found in mice and presumably humans with these mutations.

Increased cardiac expression of either wild-type or mutant PRKAG2 cDNA led to increased glycogen storage. Pharmacological activation of AMPK has previously been shown to increase glycogen.21,22 Intermediate glycogen levels observed in TG<sup>wt</sup> mice were presumably a result of a small, undetectable increase in AMPK activity (Figure 7).<sup>6,23</sup> By age 5 weeks, TG<sup>N488I</sup> hearts contained 5-fold more glycogen than TG<sup>wt</sup> hearts and 30-fold more glycogen than nontransgenic wild-type hearts, consistent with the significant increases in AMPK activity detected in the transgenic animals (Figure 7).

Comparison of the pathophysiology of PRKAG2 mutations with other glycogen storage diseases provides useful clues to the mechanism of cardiomyopathy and conduction system disease. Cardiac hypertrophy is a common feature of several other inherited disorders of glycogen metabolism.24–26 Mice lacking the α-glucosidase gene, a model of Pompe’s disease, show progressive accumulation of glycogen (up to 140 μg/mg protein) and cardiac hypertrophy.27,28 Quite like TG<sup>N488I</sup> mice, thereby supporting the concept that glycogen accumulation per se accounts for cardiac hypertrophy.

Many glycogen storage disorders also cause conduction system disease, and some have ECG patterns suggestive of preexcitation. Although an ECG pattern of WPW is sometimes found in Pompe disease,15,25 it is more frequently observed with Danon disease, a cardiac and skeletal myo-
athy with encephalopathy, preexcitation, and bradyarrhythmias.26 Because no histologically defined bypass tracts have been identified, these individuals are often presumed to have accelerated AV nodal conduction or abnormal fasciculoventricular connections.15,16,20 Disruption of annulus fibrosis by glycogen-filled myocytes, rather than distinct bypass tracts, is the likely mechanism for preexcitation in these diseases. Distinguishing between WPW caused by muscular bypass tracts rather than disruption of the annulus fibrosis may have clinical significance, particularly with regard to ablation therapies.

Our studies also suggest an explanation for the cardiac conduction defects caused by glycogen accumulation.5,5,15,24,26 Glycogen accumulation after conduction system development is complete leads to remodeling of atrioventricular conduction pathways in TG\(^{-}N488I\) mice. Whether glycogen accumulation in humans bearing these mutations occurs during or after conduction system development is unclear. Perhaps postnatal reversal of glycogen accumulation will restore normal cardiac conduction. Analyses of transgenic mice bearing mutant PRKAG2 whose expression can be controlled will answer this question.

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