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Activating Mutations in the ABCC8 Gene in Neonatal Diabetes Mellitus

Andrey P. Babenko, M.D., Ph.D., Michel Polak, M.D., Ph.D., Hélène Cavé, D. Pharm., Ph.D., Kanetee Busiah, M.D., Paul Czernichow, M.D., Raphael Scharfmann, Ph.D., Joseph Bryan, Ph.D., Lydia Aguilar-Bryan, M.D., Ph.D., Martine Vaxillaire, D. Pharm., Ph.D., and Philippe Froguel, M.D., Ph.D.

ABSTRACT

BACKGROUND

The ATP-sensitive potassium (K\text{ATP}) channel, composed of the beta-cell proteins sulfonylurea receptor (SUR1) and inward-rectifying potassium channel subunit Kir6.2, is a key regulator of insulin release. It is inhibited by the binding of adenine nucleotides to subunit Kir6.2, which closes the channel, and activated by nucleotide binding or hydrolysis on SUR1, which opens the channel. The balance of these opposing actions determines the low open-channel probability, P\text{O}, which controls the excitability of pancreatic beta cells. We hypothesized that activating mutations in ABCC8, which encodes SUR1, cause neonatal diabetes.

METHODS

We screened the 39 exons of ABCC8 in 34 patients with permanent or transient neonatal diabetes of unknown origin. We assayed the electrophysiologic activity of mutant and wild-type K\text{ATP} channels.

RESULTS

We identified seven missense mutations in nine patients. Four mutations were familial and showed vertical transmission with neonatal and adult-onset diabetes; the remaining mutations were not transmitted and not found in more than 300 patients without diabetes or with early-onset diabetes of similar genetic background. Mutant channels in intact cells and in physiologic concentrations of magnesium ATP had a markedly higher P\text{O} than did wild-type channels. These overactive channels remained sensitive to sulfonylurea, and treatment with sulfonylureas resulted in euglycemia.

CONCLUSIONS

Dominant mutations in ABCC8 accounted for 12 percent of cases of neonatal diabetes in the study group. Diabetes results from a newly discovered mechanism whereby the basal magnesium-nucleotide-dependent stimulatory action of SUR1 on the Kir pore is elevated and blockade by sulfonylureas is preserved.
Neonatal diabetes is a form of diabetes mellitus defined by the onset of mild-to-severe hyperglycemia within the first months of life. Permanent neonatal diabetes requires lifelong therapy; transient neonatal diabetes remits early, with a possible relapse during adolescence. More than half of cases of transient neonatal diabetes are associated with abnormalities of an imprinted region on chromosome 6q24. Some cases of permanent neonatal diabetes and rare cases of transient neonatal diabetes are caused by mutations in the KCNJ11 gene encoding the inwardly rectifying potassium-channel subunit (Kir6.2) of the ATP-sensitive potassium (KATP) channel expressed at the surface of the pancreatic beta cell. A few cases of permanent neonatal diabetes are attributed to mutations in the genes that encode glucokinase, insulin promoter factor 1, pancreatic transcription factor 1α, insulin transcription factor 1, or the eukaryotic translation initiation factor 2-alpha kinase 3.

KATP channels of the pancreatic beta cell regulate insulin release. A small number of overactive mutant channels can hyperpolarize the beta cell, reduce calcium influx through voltage-gated calcium channels, and decrease insulin secretion. The beta-cell KATP channel is a hetero-octamer assembled from Kir6.2 and the high-affinity beta-cell sulfonylurea receptor (SUR1, encoded by ABCC8). KATP channels link nutrient metabolism with membrane electrical activity by sensing adenine nucleotides. Nucleotide binding to the tetrameric Kir6.2 pore reduces the mean open-channel probability (Po) whereas magnesium-nucleotide binding or hydrolysis (or both) on SUR1 counterbalances this inhibition to increase Po. Mutations affecting either subunit could alter this balance. Consistent with this mechanism are the findings that mutant Kir6.2 with reduced sensitivity to inhibitory ATP causes neonatal diabetes in mice and humans, whereas mutations in ABCC8 that compromise the stimulatory effect of magnesium-nucleotide binding cause persistent hyperinsulinemic hypoglycemia. Since there are numerous cases of neonatal diabetes of unknown cause, we screened patients with neonatal diabetes for mutations in ABCC8.

METHODS

Between 1995 and 2005, we studied 73 patients from the French Network for the Study of Neonatal Diabetes Mellitus: 44 had received a diagnosis of transient neonatal diabetes, whereas 29 had received a diagnosis of permanent neonatal diabetes, 3 of whom had associated pancreatic aplasia or hypoplasia. We screened the patients for abnormalities in chromosome 6q24 and mutations in the KCNJ11 gene; glucokinase sequencing was restricted to patients with permanent neonatal diabetes. Alterations in chromosome 6q were found in 25 patients with transient neonatal diabetes (34 percent of the total study group), and mutations in the KCNJ11 gene were found in 13 patients (18 percent of the total study group; 12 with permanent neonatal diabetes and 1 with transient neonatal diabetes). A glucokinase mutation was identified in one patient. We screened the 34 remaining patients (16 with permanent neonatal diabetes and 18 with transient neonatal diabetes) for mutations in the ABCC8 gene using sequence analysis, as described in the Supplementary Appendix (available with the full text of this article at www.nejm.org). We genotyped the parents of each proband with mutated ABCC8, and we confirmed family relationships by genotyping the DNA of probands and their parents with six microsatellite markers. Other members of Family 16 and Family 17, both of which had a history of transient neonatal diabetes, were genotyped to determine whether the mutant alleles segregated with diabetes. The study was approved by the local ethics committees, and all participating patients gave written informed consent. Parental consent was given on behalf of patients younger than 18 years of age; the study was explained to children capable of giving assent, and they provided oral assent.

CLINICAL STUDIES

Probands with mutations of the ABCC8 gene had a thorough clinical examination, and their medical records were reviewed. The two patients with permanent neonatal diabetes underwent a glucagon stimulation test (1 mg was given intravenously, with C-peptide measured 5 and 0 minutes before glucagon administration and 5, 10, and 15 minutes afterward) and glyburide (also known as glibenclamide) stimulation test (0.2 mg per kilogram of body weight). Treatment with sulfonylureas was indicated on the basis of the mutant SUR1-channel response to tolbutamide. The patients with permanent neonatal diabetes and the father of the proband in Family 13 with transient neonatal diabetes received oral glyburide, starting at a dose of 0.2 mg per kilogram per day and gradually increasing the dose during a one-week period.
Molecular Biology and Electrophysiological Analysis

The observed mutations were introduced separately into hamster ABCC8 complementary DNA (cDNA) with the use of standard methods as described in the Supplementary Appendix. Wild-type or mutant SUR1 cDNA, or both, were coexpressed with human Kir6.2 and green fluorescent protein (to mark transfection) in COSm6 cells. Patch-clamp recordings and analyses of the KATP-channel current were carried out as described previously. To compare the responses of the different channels to physiologic nucleotide conditions, the channels in the same patch were recorded in intact cells and inside-out mode immediately after patch isolation and the values were normalized relative to their maximum ligand-independent response and expressed as the fraction of maximal activity (see the Supplementary Appendix).

A homology model of the human SUR1 core was used to map the mutant residues.

Results

ABCC8 Mutations in Patients with Permanent or Transient Neonatal Diabetes

We identified seven heterozygous ABCC8 mutations in 9 of 34 patients with neonatal diabetes: L213R and I1424V in 2 with permanent neonatal diabetes and C435R, L582V, H1023Y, R1182Q, and R1379C in patients with transient neonatal diabetes. The affected amino acids are conserved in the rat, mouse, chicken, and Japanese Takifugu fish; this suggests that they are critical for channel function. We did not observe these mutations on sequencing the relevant exons of 180 patients with diabetes and 140 unrelated white persons of French origin without diabetes. Furthermore, we detected no additional nonsynonymous changes in the ABCC8 exons that were unaffected by mutations in a subgroup of 110 patients with diabetes, including 24 probands with maturity-onset diabetes of the young (MODY) from families without known MODY-associated mutations.

The partial pedigrees of families carrying mutations of ABCC8 are shown in Figure 1. The L213R, H1023Y, and I1424V were noninherited mutations, as were the L582V and R1379C mutations in one family each. The L582V and R1397C mutations were also inherited in one family each, as were the C435R and R1182Q mutations. In these four families, the father of each proband was heterozygous for the mutation and the mutant alleles cosegregated with diabetes. The father of the proband with a C435R mutation in Family 13 was given a diagnosis of diabetes mellitus at 13 years of age; after he was found to have the C435R mutation, he discontinued insulin (after 24 years of treatment) after a successful response to glyburide (10 mg per day). An oral glucose-tolerance test showed that the father of the proband with an R1182Q mutation in Family 34 had diabetes; he is currently being treated with diet alone. In Family 16 with a history of transient neonatal diabetes, family members II-3 and II-4 were given a diagnosis of diabetes after 30 years of age on the basis of the results of an oral glucose-tolerance test and are currently being treated with diet alone. Diabetes developed in the father of the proband (with an R1379C mutation) in Family 17 when he was 32 years old, and he is receiving glyburide. The R1379C allele was also identified in the proband’s paternal grandmother who had had gestational diabetes and is currently being treated with diet and in a maternal great-aunt who was given a diagnosis of diabetes at 44 years of age and is currently being treated with sulfonylureas.

We found mutations of ABCC8 in 9 of the 34 patients with neonatal diabetes in our case series in whom no genetic defect had previously been identified. These 9 patients account for 12 percent of the 73 patients with neonatal diabetes included in the study. Of the 29 patients with permanent neonatal diabetes in the study, 12 had KCNJ11 mutations (41 percent), 2 had ABCC8 mutations...
(7 percent), and 15 had no apparent mutations (52 percent). Fifty-seven percent of the 44 cases of transient neonatal diabetes were attributable to anomalies of chromosome 6q, 2 percent to mutations of \( \text{KCNJ11} \), and 15 percent to mutations of \( \text{ABCC8} \). The cause of 11 cases of transient neonatal diabetes remains to be determined.

**Diabetes**

Table 1 summarizes the clinical characteristics of probands with mutant \( \text{SUR1} \). Diabetes mellitus was diagnosed in patients at a median of 32 days of age (range, 3 to 125) with hyperglycemia leading to polyuria and polydipsia in five patients and ketoacidosis in two patients. Probands in Family 17 and Family 34 had low birth weights and hyperglycemia. There were no detectable anti-islet antibodies, and ultrasonography revealed no pancreatic abnormalities. Initial insulin treatment was required for 1, 2.5, 3, 4, 4, 8.5, and 10 months in probands with transient neonatal diabetes in Families 16, 34, 17, 19, 13, 36, and 28, respectively. The last documented dose of insulin varied from 0.12 to 1.2 U per kilogram per day, with a mean of 0.67 U per kilogram per day. After identification of the mutations in the patients with permanent neonatal diabetes, glyburide therapy was initiated and found to be successful and insulin was discontinued after 2 days in the proband from Family 12 and after 15 days in the proband from

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**Figure 1. Diabetes and \( \text{ABCC8} \) Mutations in Nine Families with Neonatal Diabetes.**

Panel A shows the pedigrees of seven families with \( \text{ABCC8} \) mutations. Panel B shows the extended pedigrees of two additional families. In each panel, the mutation identified in each family is given in parentheses, and the \( \text{ABCC8} \) alleles are indicated: N denotes wild-type, M mutant, and NA not available for testing. Squares represent male family members, circles female family members, symbols with a slash deceased family members, gray symbols family members with neonatal diabetes, black symbols family members with type 2 diabetes occurring later in life, and hatched symbols family members with remitting diabetes. In Family 19 and Family 28, both of which had a history of transient neonatal diabetes, the age (in years) at relapse of transient neonatal diabetes is indicated within the gray symbols. In Family 17 with a history of transient neonatal diabetes (Panel B), Patient III-3 was given a diagnosis of gestational diabetes (indicated by cross hatching). In Families 13, 16, and 17, the proband with transient neonatal diabetes is indicated by an asterisk.
The current doses of glyburide are 0.59 and 0.22 mg per kilogram per day, respectively. Two of the patients with transient neonatal diabetes required insulin again later in life. Hyperglycemia recurred in the proband from Family 28 at 16 years of age; this patient was treated with insulin and then was given glipizide (0.16 mg per kilogram per day). The proband from Family 19 required insulin at 11 years of age, and when he was 16 years of age, his treatment was switched to glyburide (0.28 mg per kilogram per day). These doses are at the high end of, or exceed, doses of glipizide and glyburide currently recommended by the Food and Drug Administration for treating type 2 diabetes in adults.

Neurologic Features

The proband with permanent neonatal diabetes from Family 12 presented with developmental delay, but in contrast to some persons carrying a mutation of KCNJ11, did not have seizures or muscle weakness. His parents reported that he had motor and spatial dyspraxia. None of the other index patients had the facial features associated with some mutations of KCNJ11. None of the other index patients had abnormal cognitive function or development.

Metabolic Tests

The baseline fasting levels of C-peptide in the proband from Family 12 and Family 16 were low (0.24 and 0.30 ng/mL, respectively) but increased by 388 percent and 432 percent, respectively. After treatment with oral glipizide, C-peptide levels increased by 22 percent and 11 percent, respectively.

Table 1. Clinical Characteristics of Probands with Neonatal Diabetes with Mutant SUR1.*

<table>
<thead>
<tr>
<th>Family No.</th>
<th>Mutation</th>
<th>Sex</th>
<th>Wk of Gestation</th>
<th>Birth Weight g (percentile)</th>
<th>Age at Diagnosis</th>
<th>Weight g</th>
<th>Presentation</th>
<th>Glucose mmol/liter</th>
<th>Age at Metabolic Testing</th>
<th>Height cm (SD)</th>
<th>Weight kg (percentile)</th>
<th>Insulin U/kg/day</th>
<th>Current Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Permanent neonatal diabetes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>L213R</td>
<td>Male</td>
<td>41</td>
<td>3065 (22)</td>
<td>125</td>
<td>5320</td>
<td>Polyuria, polydipsia</td>
<td>28.6</td>
<td>4.75</td>
<td>107.5 (0)</td>
<td>17 (50)</td>
<td>0.12</td>
<td>Glb, 10 mg/day</td>
</tr>
<tr>
<td>16</td>
<td>I1424V</td>
<td>Male</td>
<td>40</td>
<td>3080 (25)</td>
<td>33</td>
<td>3360</td>
<td>Ketoacidosis</td>
<td>66</td>
<td>16.5</td>
<td>178 (+0.9)</td>
<td>69 (85)</td>
<td>0.88</td>
<td>Glb, 15 mg/day</td>
</tr>
<tr>
<td><strong>Transient neonatal diabetes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
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<td></td>
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<td></td>
</tr>
<tr>
<td>13</td>
<td>C435R</td>
<td>Male</td>
<td>40</td>
<td>3040 (25)</td>
<td>32</td>
<td>3575</td>
<td>Polyuria, polydipsia</td>
<td>44.5</td>
<td>4.75</td>
<td>108.8 (+0.5)</td>
<td>17.5 (75)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>L582V</td>
<td>Male</td>
<td>40</td>
<td>3350 (50)</td>
<td>15</td>
<td>3210</td>
<td>Polyuria, polydipsia</td>
<td>51.4</td>
<td>5.25</td>
<td>117 (+1.9)</td>
<td>18.4 (50)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>R1379C</td>
<td>Female</td>
<td>40</td>
<td>2050 (−3)</td>
<td>3</td>
<td>2100</td>
<td>Hyperglycemia</td>
<td>6.9</td>
<td>5.25</td>
<td>114.5 (+1.6)</td>
<td>19.5 (82)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>R1379C</td>
<td>Female</td>
<td>40</td>
<td>2330 (−3)</td>
<td>60</td>
<td>4900</td>
<td>Polyuria, polydipsia</td>
<td>22</td>
<td>15.7</td>
<td>158 (−0.8)</td>
<td>54 (70)</td>
<td>1.2</td>
<td>Glb, 10 mg/day</td>
</tr>
<tr>
<td>28</td>
<td>H1023Y</td>
<td>Male</td>
<td>40</td>
<td>3400 (55)</td>
<td>21</td>
<td>NA</td>
<td>Ketoacidosis</td>
<td>37.8</td>
<td>16</td>
<td>180 (+1.2)</td>
<td>59.5 (60)</td>
<td>0.5</td>
<td>Glp, 10 mg/day</td>
</tr>
<tr>
<td>34</td>
<td>R1182Q</td>
<td>Male</td>
<td>34</td>
<td>1830 (8)</td>
<td>4</td>
<td>1680</td>
<td>Hyperglycemia</td>
<td>13.6</td>
<td>2</td>
<td>82 (−1.5)</td>
<td>10.3 (8)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>36</td>
<td>L582V</td>
<td>Male</td>
<td>40</td>
<td>3570 (67)</td>
<td>74</td>
<td>6100</td>
<td>Polyuria, polydipsia</td>
<td>34</td>
<td>1.8</td>
<td>92 (+2)</td>
<td>92 (90)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* Glb denotes glyburide, NA not available, and Glp glipizide. To convert values for glucose to milligrams per deciliter, divide by 0.05551.
† Values in parentheses are the standard deviation from the norm.
6 were low, with the birth weight of 20 of 25 in the lowest 3 percent of the population, as compared with 3 of 7 patients with transient neonatal diabetes caused by mutant SUR1 (P=0.01) (Table 1, and the Supplementary Appendix). Macroglossia was present in 4 of the 25 probands with transient neonatal diabetes related to an anomaly in chromosome 6q24 region, but not in the patients with transient neonatal diabetes associated with a SUR1 mutation. Diabetes was diagnosed earlier in patients in the former group than in the latter group (mean of 4.0 vs. 29.9 days, P<0.05), which probably reflects, at least in part, the lower birth weights of the patients in the former group (20 vs. 2 with low birth weights, P=0.02), since patients with a low birth weight are more likely to have systematic glucose monitoring. Other clinical features, including developmental delay and the frequency and time of recurrence of diabetes, did not differ significantly between the groups. Anomalies of chromosome 6 were not associated with permanent neonatal diabetes.

As compared with 9 patients with neonatal diabetes caused by mutant SUR1, 13 patients with neonatal diabetes caused by mutant Kir6.2 had a similar frequency of low birth weight, similar distribution of age at diagnosis, and similar glucose levels at presentation. Ketoacidosis was more frequently associated with diabetes caused by mutant Kir6.2 than with diabetes caused by mutant SUR1 (9 of 13 patients vs. 2 of 9), but this difference was not significant (P=0.09), possibly because of the small number of patients in each group. The prevalence of developmental delay was not significantly different (3 of 13 patients vs. 1 of 9) and epilepsy was diagnosed in 1 of 13 patients with neonatal diabetes caused by mutant Kir6.2, but in none of the patients with neonatal diabetes caused by mutant SUR1. Dyspraxia was observed in two patients with neonatal diabetes caused by mutant Kir6.2 and in one patient with neonatal diabetes caused by mutant SUR1. In our case series, mutations of $KCNJ11$ were mainly associated with permanent neonatal diabetes (12 of 13), whereas most mutations of $ABCC8$ (7 of 9) were linked to transient neonatal diabetes.

**EFFECT OF $ABCC8$ MUTATIONS ON $K_{ATP}$ CHANNEL ACTIVITY**

The amino acids of SUR1 affected by mutation are at positions consistent with the mutations that affect protein function (see the Supplementary Appendix). To determine whether mutations in the $ABCC8$ gene changed the $P_o$ through a change in the intrinsic effect of SUR1 on channel activity or by amplifying the stimulatory effect of magnesium ATP, we compared the activities of mutant and wild-type channels in intact mammalian cells and under controlled nucleotide conditions. Measurements were made on the same patch in the intact cells and in the excised, inside-out configuration at a quasi-physiologic concentration of ATP in the presence and absence of physiologic concentrations of magnesium (free magnesium concentration, 0.7 mM) (examples of currents are provided in Fig. S2 of the Supplementary Appendix). Figure 2 shows that the normalized activities of mutant channels (containing the I1424V or H1023Y variant) in intact cells and in 1 mM magnesium ATP are nearly four and seven times as great, respectively, as those of wild-type channels under similar nucleotide conditions. A similar concentration of submembrane nucleotides (1 mM) in simian kidney cells has been gauged by others. In the absence of magnesium, and in the presence of 1 mM ATP, the $P_o$ of the mutant and wild-type channels did not differ significantly.

To test the effect of heterozygosity, we mixed both wild-type and mutant SUR1 with Kir6.2 and found that the average mean activities (in intact cells and in the presence of 1 mM magnesium ATP) were significantly greater than those of wild-type channels (P<0.001), although somewhat lower than those of “homozygous” mutant channels. In addition, the channels associated with neonatal diabetes were more active than wild-type channels at other concentrations of magnesium ATP ≥0.1 mM (see Fig. S3 of the Supplementary Appendix). These findings suggest that the heterozygous mutations of $ABCC8$ overactivate beta-cell $K_{ATP}$ channels by overstimulating the pore. To exclude the possibility that overactivity of the mutant I1424V and H1023Y channels is caused by either a gain in the intrinsic, ligand-independent, activity or by attenuation of the inhibitory action of ATP on Kir6.2, we measured the mean ligand-independent $P_o$ values and steady-state ATP-inhibitory curves (i.e., without magnesium) (Fig. 3). The maximal $P_o$ ($P_o$ MAX) values and the ATP-inhibitory curves for both mutant channels overlapped those of wild-type channels. We conclude that mutant I1424V and H1023Y channels overactivate beta-cell $K_{ATP}$ channels under physiologic magnesium-nucleotide conditions by increasing the magne-
sium-nucleotide–dependent stimulatory action of SUR1 on the pore.

**Inhibition of Mutant Channels by Sulfonylureas**

A key issue in the treatment of neonatal diabetes is whether mutant channels are inhibited by sulfonylureas; if they are, they could be used in place of insulin. We used tolbutamide (which binds SUR1 specifically and is more rapidly reversible than gliburide and glipizide) to assess the sensitivity of the mutant recombinant channels (Fig. 4A and 4B). A concentration of 200 μM tolbutamide, which saturates the high-affinity binding site of wild-type SUR1, inhibited wild-type and mutant channels (containing the I1424V or H1023Y variant) to a similar degree in the absence of magnesium nucleotides (Fig. 4A). This inhibition indicated that tolbutamide binding to SUR1 and its functional coupling to the Kir6.2 pore were not altered by the I1424V or H1023Y mutations.

To determine whether the increased stimulatory activity of the mutant receptor compromised the ability of a pharmacologic concentration of sulfonylureas to abolish the stimulatory action of magnesium nucleotides, we assessed the effect of 50 μM tolbutamide under magnesium-nucleotide conditions that maintain substantial steady-state KATP currents in inside-out patches, where accurate detection of zero current level is possible (Fig. 4B). We observed the normal, enhanced inhibition of both permanent neonatal diabetes and mutant channels of transient neonatal diabetes in the presence of magnesium nucleotides. On the basis of these results, treatment with sulfonylureas, gliburide, and glipizide, respectively, was initiated in patients with permanent neonatal diabetes and transient neonatal diabetes and has proved effective.

**Discussion**

Our results indicate that heterozygous activating mutations in ABCC8, encoding the SUR1 regulatory subunit of the ATP-sensitive potassium channels found in beta cells, cause both permanent and transient neonatal diabetes. Although the molecular mechanisms of the ABCC8 and KCNJ11 mutations are distinct, the cellular mechanism reducing insulin release is common to both (Fig. 4C, 4D, 4E, and 4F). Our results are consistent with a report that neonatal diabetes develops in transgenic mice expressing a mutant Kir6.2 subunit with
reduced sensitivity to inhibitory ATP and that some cases of permanent neonatal diabetes and transient neonatal diabetes are caused by mutations in KCNJ11. These studies underscore the key role of KATP channels in coupling beta-cell membrane potential (and thus the requirement for calcium to release insulin-containing granules) with nutrient metabolism. The common pathway accounts for the direct overlap of the clinical features related to abnormal insulin release secondary to mutations in ABCC8 and KCNJ11. As compared with patients with neonatal diabetes related to a SUR1 mutation, patients with neonatal diabetes related to a Kir6.2 mutation revealed no significant differences in the prevalence of low birth weight, age at diagnosis, or severity of hyperglycemia or accompanying ketoacidosis. Mutations of KCNJ11 are typically associated with permanent neonatal diabetes, whereas most mutations of ABCC8 are associated with transient neonatal diabetes, perhaps reflecting a less severe form of diabetes.

Previous reports have highlighted a heterogeneity of symptoms associated with neonatal diabetes caused by mutant Kir6.2, which may reflect the sharing of the Kir6.2 pore by both SUR1–Kir6.2 neuroendocrine channels and sarcolemmal SUR2A–Kir6.2 channels. The neurologic features of several persons with neonatal diabetes related to a mutant SUR1 channel imply that SUR1-containing KATP channels can control the membrane potential of neuronal cells, such as inhibitory motor neurons.

Our data show that the net inhibitory action of ATP on two types of neonatal diabetes caused by a mutant SUR1 channel was unchanged (as compared with wild-type SUR1) and that the increased activity of the channels, under physiologic conditions, was caused by an increase in the magnesium-dependent stimulatory action of SUR1 on the pore. The position of the mutations that we have described, together with further investigations, should provide insight into the stimulatory mechanism. This finding is at variance with that of a recent study showing an alteration in the inhibitory action of ATP on a mutant SUR1 channel.

Experiments designed to approximate the heterozygous condition by expression of 1:1 mixtures of mutant with wild-type subunits resulted in average mean activities, under physiologic magnesium-nucleotide conditions, intermediate to those of wild-type and mutant channels. The maximal activity of mixed KATP channels declines exponentially as the number of wild-type subunits (with the less stable active conformation) increases in the complex. Therefore, the overactivating effect of a mutation is expected to drop off rapidly with the inclusion of wild-type subunits. The results imply that a small subpopulation of pure mutant channels can make a considerable contribution to the hyperpolarization of beta cells and perhaps of some neurons with electrically tight membranes whose potential is dominated by a small number of channels.

In clinical practice, there is no way to distin-
**Normal Beta Cell**

**Without Nucleotides**

<table>
<thead>
<tr>
<th>Channel Type</th>
<th>Relative Activity in 200 µM Tlb</th>
</tr>
</thead>
<tbody>
<tr>
<td>I1424V Mutant</td>
<td>0.45</td>
</tr>
<tr>
<td>Wild-Type</td>
<td>0.40</td>
</tr>
<tr>
<td>H1023Y Mutant</td>
<td>0.35</td>
</tr>
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</table>

**With 0.5 mM Magnesium ATP and 0.5 mM ADP**

<table>
<thead>
<tr>
<th>Channel Type</th>
<th>Relative Activity in 50 µM Tlb</th>
</tr>
</thead>
<tbody>
<tr>
<td>I1424V Mutant</td>
<td>0.40</td>
</tr>
<tr>
<td>Wild-Type</td>
<td>0.35</td>
</tr>
<tr>
<td>H1023Y Mutant</td>
<td>0.30</td>
</tr>
</tbody>
</table>

**Mutant Beta Cell in the Presence of Sulfonylurea**

**Increased glucose**

**Mutant SUR1**

- ATP
- Ca²⁺

**Increased Ca²⁺ influx**

**Decreased insulin secretion**

**Hyperglycemia**

**Stimulatory action of magnesium nucleotides (low ATP:ADP ratio)**

**Stimulatory action of magnesium nucleotides (elevated ATP:ADP ratio)**

**Reduced stimulatory action of magnesium nucleotides (elevated ATP:ADP ratio)**

**Stimulates insulin secretion**

**Decreased Ca²⁺ influx**

**Decreased insulin secretion**

**Stimulates insulin secretion**

**Stimulates insulin secretion**
Figure 4 (facing page). Effect of SUR1 Mutations on Response to Tolbutamide (Tlb).

The mean (±SE) activity of each type of channel is shown in response to 200 μM tolbutamide in magnesium-free conditions (Panel A) and to 50 μM tolbutamide in the presence of 0.5 mM magnesium ATP and 0.5 mM magnesium ADP (Panel B). The data were derived from six experiments for each condition and type of channel. Representative current records are provided in Figure S5 of the Supplementary Appendix. Panel C shows how ATP inhibits beta-cell K
ATP channels through its interaction with Kir6.2 in a control subject. When glucose levels are low, this inhibitory action is balanced by the stimulatory action of magnesium nucleotides on SUR1 (indicated by the large green arrow), which increases channel activity. Membrane depolarization activates voltage-dependent calcium channels, and calcium influx stimulates insulin secretion. An increase in glucose metabolism increases the ratio of ATP to ADP and thereby reduces the stimulatory action of SUR1 (Panel D). In a patient with neonatal diabetes, the enhanced stimulatory action of the mutant receptor is sufficient to keep K
ATP channels open even at an elevated ratio of ATP to ADP, thus attenuating insulin release and producing hyperglycemia (Panels E and F). The data presented in Panels A and B, however, suggest that a sulfonylurea (tolbutamide) counters the stimulatory effect of the mutation to stimulate insulin release. This result is confirmed by the response of patients with permanent neonatal diabetes and transient neonatal diabetes to glyburide and glipizide.

The diagnosis of diabetes in fathers with ABC8 mutations is consistent with adult-onset type 2 diabetes mellitus or a mild form of transient neonatal diabetes. Systematic blood screening in French newborns makes the latter unlikely, and we propose that mutations of the ABC8 gene may give rise to a monogenic form of type 2 diabetes with variable expression and age at onset. The potential contribution of overactive ABC8 mutations to familial early-onset type 2 diabetes remains to be evaluated, but our findings emphasize how molecular understanding of a rare pediatric form of diabetes may illuminate the more common form of the disease.

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