The genetic basis of congenital hyperinsulinism

C James, R R Kapoor, D Ismail, K Hussain

ABSTRACT
Congenital hyperinsulinism (CHI) is biochemically characterised by the dysregulated secretion of insulin from pancreatic β-cells. It is a major cause of persistent hyperinsulinaemic hypoglycaemia (HH) in the newborn and infancy period. Genetically CHI is a heterogeneous condition with mutations in seven different genes described. The genetic basis of CHI involves defects in key genes which regulate insulin secretion from β-cells. Recessive inactivating mutations in ABCC8 and KCNJ11 (which encode the two subunits of the adenosine triphosphate sensitive potassium channels (ATP sensitive K_{ATP} channels)) in β-cells are the most common cause of CHI. The other recessive form of CHI is due to mutations in HADH (encoding for-3-hydroxyacyl-coenzyme A dehydrogenase). Dominant forms of CHI are due to inactivating mutations in ABCC8 and KCNJ11, and activating mutations in GLUD1 (encoding glutamate dehydrogenase) and GCK (encoding glucokinase). Recently dominant mutations in HNF4A (encoding hepatocyte nuclear factor 4α) and SLC16A1 (encoding monocarboxylate transporter 1) have been described which lead to HH. In mutations in all these genes account for about 50% of the known causes of CHI. Histologically there are three (possibly others which have not been characterised yet) major subtypes of CHI: diffuse, focal and atypical forms. The diffuse form is inherited in an autosomal recessive (or dominant manner), the focal form being sporadic in inheritance. The diffuse form of the disease may require a near total pancreatectomy whereas the focal form requires a limited pancreatectomy potentially curing the patient. Understanding the genetic basis of CHI has not only provided novel insights into β-cell physiology but also aided in patient management and genetic counselling.

Congenital hyperinsulinism (CHI) is biochemically characterised by the dysregulated secretion of insulin from pancreatic β-cells. It is a major cause of hypoglycaemia in the newborn and infancy period. The unregulated insulin secretion drives glucose into insulin sensitive tissues (skeletal muscle, liver and adipose tissue) and prevents the generation of alternative energy substrates (such as ketone bodies), thus depriving the brain of both its primary and secondary energy sources. This prevailing metabolic milieu is the main factor leading to hypoglycaemic brain injury and mental retardation in this group of patients.

The incidence of CHI can vary from 1 in 40 000–50 000 in the general population to 1 in 2500 in some isolated communities with high rates of consanguinity. It is a heterogeneous condition with regards to the clinical presentation, the underlying genetic aetiology, molecular mechanisms and histological basis of the disease. The clinical presentation can be heterogeneous ranging from completely asymptomatic, mild medically responsive to severe medically unresponsive disease which may require a near total pancreatectomy. Those patients undergoing a total pancreatectomy have a high risk of developing post-pancreatectomy diabetes mellitus and pancreatic exocrine insufficiency.

Insulin secretion from β-cells is precisely regulated to maintain blood glucose values within the normal range (3.5–5.5 mmol/l). The genetic basis of CHI involves defects in key genes which regulate insulin secretion from β-cells. The most common cause of CHI are recessive inactivating mutations in ABCC8 and KCNJ11 which encode the two subunits of the adenosine triphosphate sensitive potassium channels (ATP sensitive K_{ATP} channels) in the pancreatic β-cell. The β-cell K_{ATP} channels play a key role in transducing signals derived from glucose metabolism to β-cell membrane depolarisation and regulated insulin secretion. The other rare recessive form of CHI is due to mutations in HADH (encoding for-3-hydroxyacyl-coenzyme A dehydrogenase). Dominant forms of CHI are due to inactivating mutations in ABCC8 and KCNJ11, and activating mutations in GLUD1 (encoding glutamate dehydrogenase), GCK (encoding glucokinase), HNF4A (encoding hepatocyte nuclear factor 4α) and SLC16A1 (encoding monocarboxylate transporter 1). Mutations in all these genes account for about 50% of the known causes of CHI, and in some populations mutations in these genes account for only about 20% of CHI cases, suggesting other novel genetic aetiologies.

Histologically there are three major subgroups of the disease: diffuse, focal, and atypical. The diffuse forms of CHI are inherited in an autosomal recessive or dominant manner and the focal form is sporadic in inheritance. The diffuse form of the disease may require a near total pancreatectomy (with a high risk of developing diabetes mellitus) whereas the focal form requires a limited pancreatectomy offering a complete “cure” for the patient. In patients with atypical disease the histological abnormalities are either more extensive while remaining limited, or diffuse with the coexistence of normal and abnormal islets.

Understanding the genetic basis of CHI has not only provided novel insights into β-cell physiology but also aided in patient management and genetic counselling. In terms of patient management rapid genetic analysis for mutations in ABCC8 and KCNJ11 can help in the genetic diagnosis of diffuse or focal CHI. Prenatal diagnosis of CHI based on the genetic analysis of known family members with mutations in ABCC8 (and KCNJ11) is also now possible permitting immediate medical management at the time of birth.
of β-cell K<sub>ATP</sub> channels in regulating insulin secretion, and then focus in detail on the genetic and molecular basis of CHI due to mutations in the known genes and highlight some of the more recent genetic advances. Table 1 summarises the known genetic causes of CHI.

### THE ROLE OF K<sub>ATP</sub> CHANNELS IN REGULATING GLUCOSE INDUCED INSULIN SECRETION

K<sub>ATP</sub> channels have a key role in the physiology of many cells, and defects either in the channel itself or in its regulation can lead to diseases in humans. Structurally, K<sub>ATP</sub> channels provide a means of linking the electrical activity of a cell to its metabolic state by sensing changes in the concentration of intracellular nucleotides, and in some cases they mediate the regulatory subunit.

The SUR1 (an ATP binding cassette transporter) acts as a regulatory subunit. In the absence of SUR1 subunit, K<sub>ATP</sub> channels can only function if they are assembled and correctly transported to the cell membrane surface (trafficking). The assembly and trafficking of K<sub>ATP</sub> channels are intricately linked processes. Only octameric K<sub>ATP</sub> channel complexes are capable of expressing on the cell membrane surface. For example both Kir6.2 and SUR1 possess an endoplasmic reticulum (ER) retention signal (RRK) that prevents the trafficking of each subunit to the plasma membrane in the absence of the other subunit. Correct assembly of the two subunits masks these retention signals, allowing them to traffic to the plasma membrane. The retention signal is present in the C-terminal region of Kir6.2 and in an intracellular loop between TM11 and NBF-1 in SUR1. Truncation of the C-terminus of Kir6.2 deletes its retention signal, allowing functional expression of Kir6.2 in the absence of SUR1 subunit.

Addition to these retrograde signals, the C-terminus of SUR1 shows a high affinity binding capacity to the sulfonylurea glibenclamide, indicating that SUR1 confers sulfonylurea binding. The sulfonylurea drugs (glibenclamide on November 8, 2022 by guest. Protected by copyright.http://jmg.bmj.com/ J Med Genet: first published as 10.1136/jmg.2008.064337 on 1 March 2009. Downloaded from ABCC8 and KCNJ11 genes are both located on chromosome 11p15.1, separated by only a small stretch of 4.5 kb of DNA. 
channel biogenesis and turnover

molecular basis of recessive inactivating ABCC8 mutations involves multiple defects in KATP channel biogenesis. Heterozygote mutations may result in complex interactions that may respond to treatment with diazoxide.70 Compound some compound heterozygote mutations may be milder and is unresponsive to medical treatment with diazoxide. However, Figure 1 shows a schematic outline of the heter-octameric arrangement of the KATP channel. 

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**Figure 1** (A) Schematic outline of the components of the β-cell KATP channel. The KATP channel is composed of two proteins: SUR1 which consists of 17 transmembrane domains with two intracellular nucleotide binding (NBF) motifs. Two N-linked glycosylation sites are present on amino acids 10 and 1049. Kir6.2 has three transmembrane segments. Common mutations in both of the proteins are highlighted. (B) The hetero-octameric arrangement of the KATP channel. 

Homozygous, compound heterozygous and heterozygous recessive inactivating mutations (missense, frameshift, nonsense, insertions/deletions (macrodeletion), splice site and regulatory mutations) have been reported in ABCC8 and KCNJ11.10–17, 67 68 So far, more than 150 mutations have been reported in ABCC8 and 25 in KCNJ11.69 In the Ashkenazi Jewish population two common mutations (F1388del and c.3992–9G4A) account for 90% of all cases of CHI91 whereas in the Finnish population, two founder mutations have been reported (V187D and E1507K).14 22 Recessive inactivating mutations in ABCC8 and KCNJ11 usually cause severe CHI which in the vast majority of patients is unresponsive to medical treatment with diazoxide. However, some compound heterozygote mutations may be milder and may respond to treatment with diazoxide.29 Compound heterozygote mutations may result in complex interactions resulting in intracellular retention of channel complexes.71 The molecular basis of recessive inactivating ABCC8 and KCNJ11 mutations involves multiple defects in KATP channel biogenesis and turnover, in channel trafficking from the ER and Golgi apparatus to the plasma membrane and alterations of channels in response to both nucleotide regulation and open state frequency. Figure 1 shows a schematic outline of the β-cell KATP channel and locations of the some of the common mutations.

Recessive ABCC8 and KCNJ11 mutations resulting in defects in channel biogenesis and turnover

The mechanisms that control the maturation and assembly of KATP channels are not well understood. Pulse labelling studies have shown that when Kir6.2 is expressed individually, its turnover is biphasic with about 60% being lost with a half life of 36 min.72 The remainder converts to a long lived species (half life 26 h) with an estimated half time of 1.2 h. Expressed alone SUR1 has a long half life of 25.5 h. When Kir6.2 and SUR1 are co-expressed, they associate rapidly and the fast degradation of Kir6.2 is eliminated.72 Two mutations, KCNJ11 (W91R) and ABCC8 (F1388del), identified in patients with the severe form of CHI, profoundly alter the rate of Kir6.2 and SUR1 turnover, respectively.72 Both mutant subunits associate with their respective partners but dissociate freely and degrade rapidly, suggesting that the mutations alter channel biogenesis and turnover.

Recessive inactivating mutations in ABCC8 and KCNJ11 resulting in defects in channel trafficking

Trafficing of KATP channels requires that the ER retention signal, RKR, present in both SUR1 and Kir6.2, is shielded during channel assembly. Some mutations in ABCC8 (such as R1437Q(25X), F1588del and R1359H0) cause a trafficking defect by affecting the exit of channel subunits from the ER compartment.73–75 The R1457Q(25X), mutation in exon 35 of ABCC8 truncates 200 amino acids from the COOH terminal region of the protein, an area that contains the anterograde signalling sequence (L1566, L1567,F1574) and residue L1544 which is part of the cloaking region for the RKR sequence.72 This defect affects the exit of channel subunits from the ER.

The pivotal role played by the RKR signal in allowing the channels to express correctly on the β-cell membrane is illustrated by the fact that when the RKR signal is inactivated by an in-frame deletion (F1388del SUR1AAA), channel activity is impaired, but when surface expression is rescued, the channels function normally.72 Other mutations such as the R1354H (ABCC8) cause a trafficking disorder by effecting retention of mutant proteins in the transit-Golgi network.74

Mutations in KCNJ11 can also cause defective trafficking and truncated non-functional proteins. For example, the Kir6.2 mutation (Y12X) causes the synthesis of a truncated non-functional protein12 whereas another mutation (W91R) leads to defective channel assembly with a rapid degradation in the ER.72 Recently, a new homozygous mutation H259R (KCNJ11) has been shown to lead to a non-functional KATP channels with impaired trafficking to the cell membrane.36

Recessive inactivating mutations in ABCC8 and KCNJ11 resulting in defects of channel regulation

The SUR1 subunit plays a key role in determining the pharmacological regulation of KATP channels with SUR1 acting as a conductance regulator of Kir6.2. The sensitivity of KATP channels to changes in ATP, ADP, and guanosine (GTP, GDP) nucleotides involves both subunits. The functional regulation of KATP Channels is induced by changes in the ATP/ADP ratio. This involves cooperative interactions of nucleotides at both subunits with the actions of ATP induced inhibition of Kir6.2 being countered by the activation of ADP at SUR1. Hence, mutations that affect the regulation of the KATP channels by altering its sensitivity to changes in ADP/ATP will lead to unregulated insulin secretion. Several mutations in ABCC8 (for example, R1420C, T1139M and R1215Q) have now been described that result in the loss of ADP dependent gating properties of the channel.76 77 78 Loss of ADP dependent gating results in the constitutive inhibition of KATP channels by ATP.

Dominant inactivating ABCC8 and KCNJ11 mutations causing CHI

Dominant inactivating mutations in ABCC8 and KCNJ11 have been described which lead to CHI.22–27 However, the phenotype of patients with dominant inactivating mutations in ABCC8 and KCNJ11 seems to be much milder than that of patients...
with recessive inactivating ABC8 and KCNJ11 mutations. Patients with dominant mutations seem to be responsive to medical treatment with diazoxide, may present later than those with recessive mutations, and do not require a pancreaticectomy. In one large study of 16 families with dominant CHI caused by mutations in ABC8 or KCNJ11, all of the mutations were conservative single amino acid changes, allowing for normal channel formation at the plasma membrane. Whereas recessive mutations cause near absence of KATP channel activity (to have defects in channel biogenesis or trafficking of mature functional channels to the plasma membrane), dominant mutations demonstrate normal channel assembly with their respective wild type partner and normal trafficking of assembled channels to the plasma membrane when expressed in vitro.

A dominant missense CHI causing mutation F55L (KCNJ11) has been shown to greatly reduce the open probability of KATP channels in intact cells without affecting channel expression. It was shown that the low channel activity was due to reduced channel response to membrane phosphoinositides and/or long chain acyl-CoAs, as application of exogenous PIP2 or oleoyl-CoA restored channel activity similar to that seen in wild type channels. These electrophysiological observations provide a link between KATP channels and their regulation by membrane phosphoinositides and/or long-chain acyl-CoAs.

DOMINANT ACTIVATING MUTATIONS IN GLUD1

The GLUD1 gene is located on chromosome 10q23.3 and contains 15 exons coding for a 505 amino acid mature enzyme, glutamate dehydrogenase (GDH). GDH is a mitochondrial matrix enzyme which is expressed at high levels in the liver, brain, kidney, pancreas, heart and lungs. This enzyme catalyses the oxidative deamination of glutamate to α-ketoglutarate and ammonia using NAD+ and/or NADP+ as co-factors. In the β-cell α-ketoglutarate enters the tricarboxylic acid cycle and leads to an increase in the cellular ATP. This increases the ATP/ADP ratio which triggers closure of the KATP channels and leads to an increase in the cellular ATP. This increases the ATP/ADP ratio which triggers closure of the KATP channels and leads to an increase in the cellular ATP.

Figure 2 Schematic representation of the mutations in the GLUD1 gene known to cause congenital hyperinsulinism. Mutations are described to occur in three domains: the allosteric binding domain (exons 11 and 12), the catalytic domain (exons 6 and 7), and the antenna region (exon 10).
pancreas, liver, and brain. The presence of tissue specific promoters allows differential regulation and transcription of different transcripts giving rise to three different sized versions of exon 1 (a, b, and c). In the pancreas the upstream promoter is functional, while in the liver the downstream promoter is used. Exon 1a is expressed in the pancreatic β-cells whereas exons 1b and 1c are expressed in the liver.

Glucokinase (hexokinase IV or D) is one member of the hexokinase family of enzymes. The name, glucokinase, is derived from its relative specificity for glucose under physiologic conditions. Glucokinase is a key regulatory enzyme in the pancreatic β-cells. It operates as a monomer and phosphorylates glucose on carbon 6 with MgATP as a second substrate to form glucose-6-phosphate (G6P) as a first step in the glycolytic pathway. It plays a crucial role in the regulation of insulin secretion and has been termed the pancreatic β-cell sensor on account of its kinetics, because the rate of phosphorylation of glucose in the pancreatic β-cells is directly related to the concentration of glucose over a range of physiologic glucose concentrations (4–15 mmol/l). These kinetic characteristics are the enzyme’s low affinity for glucose (concentration of glucose at which the enzyme is half maximally activated, S0.5, 5–10 mmol/l), cooperativeness with glucose (Hill number of 1.7), and lack of inhibition by its product G6P. The enzyme has at least two clefts, one for the active site, binding glucose and MgATP, and the other for a putative allosteric activator. Glucokinase activity is closely linked to the KATP and calcium channels of the β-cell membrane, resulting in a threshold for glucose stimulated insulin release of approximately 5 mmol/l, which is the set point of glucose homeostasis.

Heterozygous inactivating mutations in GCK cause maturity onset diabetes of the young (MODY), homozygous inactivating in GCK mutations result in permanent neonatal diabetes, whereas heterozygous activating GCK mutations cause CHI. So far seven activating GCK mutations (V455M, A456V, Y214C, T65I, W99R, G68V, S64Y) have been described that lead to CHI (fig 3). Activating GCK mutations increase the affinity of GCK for glucose and alter (reset) the threshold for glucose stimulated insulin secretion. All reported activating mutations cluster in a region of the enzyme, which has been termed the allosteric activator site and is remote to the substrate binding site. The allosteric site of GCK is where small molecule activators bind, suggesting a critical role of the allosteric site in the regulation of GCK activity. Both GCK activators and activating mutations increase enzyme activity by enhancing the affinity for glucose as described by a decrease in K0.5. There is no evidence to suggest that over-expression of GCK (increased gene dosage effect) is a likely cause of CHI.

The clinical symptoms and course of patients with GCK mutations cover a broad spectrum from asymptomatic hypoglycaemia to unconsciousness and seizures, even within the same family with the same mutation, implicating a complex mechanism for GCK regulation. Patients with activating GCK mutations may present with postprandial hyperinsulinaemic hypoglycaemia. Most of the GCK mutations reported to date cause mild diazoxide responsive CHI. However, a “de novo” mutation in GCK (Y214C) was described in a patient with medically unresponsive CHI. This mutation was located in the putative allosteric activator domain of the protein and functional studies of purified recombinant glutathionyl S transferase fusion protein of GK-Y214C showed a sixfold increase in its affinity for glucose, a lowered cooperativity, and increased kcat. The relative activity index of GKY214C was 150, and the threshold for glucose stimulated insulin secretion was predicted by mathematical modelling to be 0.8 mmol/l, as compared with 5 mmol/l in the wild-type enzyme. In the largest study performed to date on a pool of patients who were negative for mutations in the ABCC8 and KCNJ11 genes, the prevalence of CHI due to mutations in GCK was estimated to be about 7%.

**RECESSIVE MUTATIONS IN HADH**

Mitochondrial fatty acid β-oxidation constitutes the essential physiological response to energy depletion caused by fasting, severe febrile illness or increased muscular activity. The process of β-oxidation results in production of acetyl-CoA by the sequential oxidation and cleavage of straight chain fatty acids. Importantly, hepatic β-oxidation provides the source of energy for extrahepatic tissues through ketone body formation upon fasting. HADH encodes for the enzyme L-3-hydroxyacyl-coenzyme A dehydrogenase (HADH) (previously known as short-chain L-3-hydroxyacyl-CoA dehydrogenase (SCHAD)), which is an intra-mitochondrial enzyme that catalyses the penultimate step in the β-oxidation of fatty acids, the NAD+ dependent dehydrogenation of 3-hydroxyacyl-CoA to the corresponding 3-ketoacyl-CoA. Human HADH encodes a 314 amino acid protein with eight exons and spans approximately 49 kb. It is composed of a 12 residue mitochondrial import signal peptide and a 302 residue mature HADH protein with a calculated molecular mass of 34.5kD.

Loss-of-function mutations in the HADH gene are associated with CHI. The clinical presentation of all patients reported is heterogeneous, with either mild late onset intermittent HH or severe neonatal hypoglycaemia. All reported cases have presented with increased 3-hydroxylglutarate in urine and hydroxybutyrylcarnitine in blood which may be diagnostically useful markers for HADH deficiency. In the first patient reported sequencing of the HADH genomic DNA from the fibroblasts showed a homozygous mutation (C773T) changing proline to leucine at amino acid 258. Analysis of blood from the parents showed they were heterozygous for this mutation. Western blot studies showed undetectable levels of immunoreactive HADH protein in the patient’s fibroblasts. Expression studies showed

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**Figure 3** Schematic representation of the mutations in the GCK gene known to cause congenital hyperinsulism.
that the P258L enzyme had no catalytic activity. This patient presented with intermittent hypoglycaemia at 4 months of age.

A novel, homozygous deletion mutation (deletion of the six base pairs CAGGTC at the start of HADH exon 5) was found in the second patient who presented with severe neonatal hypoglycaemia. The mutation affected RNA splicing and was predicted to lead to a protein lacking 30 amino acids. The observations at the molecular level were confirmed by demonstrating greatly reduced HADH activity in the patients' fibroblasts and enhanced levels of 3-hydroxybutyryl-carnitine in their plasma. Urine metabolite analysis showed that HADH deficiency resulted in specific excretion of 3-hydroxyglutaric acid by fibroblasts (possibly reflecting additional post-transcriptional regulation of MCT1 levels in extrapancreatic tissues). These studies suggest that activating mutations in SLC16A1 lead to pyruvate and lactate uptake and pyruvate stimulated insulin release despite ensuing hypoglycaemia.22

RECENT ADVANCES IN THE GENETIC AETIOLOGY OF CHI

A further mechanism of hyperinsulinaemia is hypoglycaemia has been described whereby strenuous physical exercise causes an inappropriate burst of insulin release that can lead to hypoglycaemia. This work led to the identification of the molecular basis of exercise induced CHI (due to mutations in SLC16A1). Mutations in HNF4A have been recently reported to cause both transient and persistent hyperinsulinaemic hypoglycaemia associated with macrosomia and a family history of maturity onset diabetes of the young.

DOMINANT MUTATIONS IN SLC16A1 CAUSING EXERCISE INDUCED CHI

In the glycolytic pathway glucose is metabolised to pyruvate which then enters in the mitochondria. Pyruvate can be converted into lactate or enters into the tricarboxylic acid cycle, generating reducing equivalents. This leads to stimulation of the respiratory chain and ATP synthesis. The transport of monocarboxylates such as lactate and pyruvate is mediated by the SLC16A1 family of proton linked membrane transport proteins known as monocarboxylate transporters (MCTs). Fourteen MCT related genes have been identified in mammals and of these seven MCTs have been functionally characterised. Despite their sequence homology, only MCT1–4 have been demonstrated to be proton dependent transporters of monocarboxylic acids.

The SLC16A1 gene encodes for MCT1 that mediates the movement of lactate and pyruvate across cell membranes. The SLC16A1 gene maps to chromosome 1p13.2-p12, spans approximately 44 kb, and is organised as five exons intervened by four introns. The first of these introns is located in the 5’ UTR-encoding DNA, spans >26 kb, and thus accounts for approximately 60% of the entire transcription unit. Analysis of a 1.5 kb fragment of the MCT1 5’ flanking region shows an absence of the classical TATA-Box motif. However, the region contains potential binding sites for a variety of transcription factors.

Studies in whole rat and mouse islets have shown that pyruvate and lactate cannot mimic the effect of glucose on insulin secretion despite active metabolism. This is postulated to be due to low expression of MCT in β-cells. However, over expression of lactate dehydrogenase (LDH) and MCT1 leads to pyruvate induced insulin secretion. In exercise induced CHI there is increased expression of MCT1 transporter in β-cells due to dominant mutations in SLC16A1. In these patients anaerobic physical exercise induces HH that is preceded by an inappropriate increase in the concentration of circulating insulin. Affected patients become hypoglycaemic within 30 min after a short period of anaerobic exercise. A pyruvate load test causes a brisk increase in the serum insulin concentration suggesting that pyruvate metabolism or transport is in some way involved in signalling insulin secretion from β-cells in these patients. A genome scan performed on two families with 10 affected patients first mapped the gene to chromosome 1. Mutations in the promoter region of SLC16A1 gene were confirmed in all patients. Studies on cultured fibroblasts from affected patients showed abnormally high SLC16A1 transcript levels, although the MCT1 transport activity was unchanged in fibroblasts (possibly reflecting additional post-transcriptional control of MCT1 levels in extrapancreatic tissues).

Two of the SLC16A1 mutations identified in separate pedigrees resulted in increased protein binding to the corresponding promoter elements and marked (5- or 10-fold) transcriptional stimulation of SLC16A1 promoter-reporter constructs. Some of the mutations were in the binding sites of several transcription factors (nuclear matrix protein 1, albumin negative factor (ANF) and AML-1a, simian-virus-40-protein-1 (Sp1), upstream stimulatory factor (USF), myeloid zinc finger 1 (MZF1), and GATA-1 binding site). These studies suggest that activating mutations in the promoter region of SLC16A1 could induce increased expression of MCT1 in the β-cell (where this gene is not usually transcribed) allowing pyruvate uptake and pyruvate stimulated insulin release despite ensuing hypoglycaemia.

DOMINANT HETEROZYGOUS MUTATIONS IN HNF4A

Hepatocyte nuclear factor 4α (HNF4α) is a transcription factor of the nuclear hormone receptor superfamily and is expressed in liver, kidney, gut, and pancreatic islets. In combination with other hepatocyte nuclear factors, HNF4α has been proposed to form a functional regulatory loop that regulates the development and function of the pancreas and the liver. In β-cells, HNF4α has been shown to be the most widely acting transcription factor and regulates several key genes involved in glucose stimulated insulin secretion.

The HNF4α gene is located on human chromosome 20q13.1–13.2. The gene consists of at least 12 exons and spans 30 kb. The HNF4A gene has two promoters, P1 and P2, with P2 being upstream to P1. The distant upstream P2 promoter represents the major transcription site in β-cells, and is also used in hepatic cells. Transfection assays with various deletions and mutants of the P2 promoter revealed functional binding sites for HNF4A, HNF1β, and IPF1. The HNF4α protein consists of an N-terminal ligand independent transactivation domain (amino acids 1–24), a DNA binding domain containing two zinc fingers...
(amino acids 51-117), and a large hydrophobic portion (amino acids 163-368) composed of the dimerisation, ligand binding, co-factor binding, and ligand dependent transactivation domain.116

Heterozygote mutations in the human HNF4A gene classically lead to maturity onset diabetes of the young subtype 1 (MODY1), which is characterised by autosomal dominant inheritance and impaired glucose stimulated insulin secretion from pancreatic ß-cells.117 These mutations in the HNF4A gene cause multiple defects in glucose stimulated insulin secretion and in expression of HNF4A dependent genes.117 118 Recently mutations in the HNF4A gene were reported to cause macrosomia and both transient and persistent HH. Hence, it is unclear how heterozygous mutations in the HNF4A gene cause HH in the newborn period followed by the opposite phenotype of MODY-1 in young adulthood. Figure 4 summarises the genetic causes of CHI.

THE GENETIC BASIS OF FOCAL CHI

CHI presents as three (probably more, but these have not been fully defined yet) different morphological forms: a diffuse form with functional abnormality of islets throughout the pancreas; an atypical form where the pathophysiology is unclear; and a focal form with focal islet cell adenomatous hyperplasia, which can be cured by partial pancreatectomy.121 Focal CHI is characterised by nodular hyperplasia of islet-like cell clusters, including ductuloinseral complexes and giant ß-cell nuclei.122 The genetic aetiology of focal CHI is distinct from that of diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region within the focal region results in paternal isodisomy and a paternally inherited mutation in ABCC8/KCNJ11 encoding the KATP channel.123–128 The specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutional diffuse CHI. Focal adenomatous hyperplasia involves the specific loss of the maternal 11p15 region and a constitutio
imprinted.\textsuperscript{127} The 11p15.5 chromosome region involved contains an imprinted domain, including several imprinted genes characterised by mono-allelic expression.\textsuperscript{120–135} These include four maternally expressed genes (H19, a candidate tumour suppressor gene; P57KIP2, a negative regulator of cell proliferation; KVLQIT1, the gene coding for the potassium channel involved in the long QT syndrome; HASH2, a transcription factor; and one paternally expressed gene, the insulin-like growth factor 2 (IGF2).\textsuperscript{128} 152–156

The imbalance between imprinted genes (increased IGF2 and diminished H19 and P57KIP2) gives rise to the increase in proliferation of β-cells, a striking feature of focal adenomatous hyperplasia not observed in the diffuse form.\textsuperscript{128} H19 seems directly or indirectly to modulate cytoplasmic levels of the product of the IGF2 allele and thus the H19 gene seems to be an antagonist to IGF2 in trans.\textsuperscript{128} Figure 5 illustrates the genetic aetiology of a focal lesion.

The probability for this somatic chromosomal event occurring in a fetus carrying a heterozygous mutation of ABCB8/KCNJ11 of paternal origin is about 1%.\textsuperscript{128} Recently it was demonstrated that individual patients with focal CHI may have more than one focal pancreatic lesion due to separate somatic maternal deletion of the 11p15 region\textsuperscript{129} and that some focal pancreatic lesions have a duplication of the paternal allele on chromosome 11.\textsuperscript{129}

SUMMARY

CHI is a major cause of hypoglycaemia in the newborn and infancy period. So far mutations in seven different genes have been reported which lead to dysregulated insulin secretion. Recent advances have identified the molecular basis of exercise induced CHI (due to mutations in SLC16A1) and highlighted the intriguing link between transient (or persistent HH) and maturity onset diabetes of the young (due to mutations in HNF4α). Rapid genetic analysis for mutations in ABCB8 and KCNJ11 can be used as a powerful tool for differentiating between focal and diffuse disease in some patients and thus aid in patient management. Further genetic studies are required to understand the molecular basis of CHI in patients where no mutations are found in the genes described so far.

Competing interests: None declared.

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