

GENOTYPE AND PHENOTYPE OF 99 VIETNAMES PATIENTS WITH CONGENITAL HYPERINSULINISM

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Background

• Hyperinsulinemic hypoglycemia (HH) is a consequence of unregulated insulin secretion by pancreatic β -cells and is a major cause of hypoglycemic brain injury and mental retardation.

• Congenital HH (CHH) is caused by mutations in genes involved in regulation of insulin secretion, Eight of which have been

Results

Mutations of KCNJ11

➢ 3 Novel paternal inheritance mutation c.482C>T, c.512C>A, c.820G>C in KCNJ11 gene was identified in two unrelated cases.

➢ Homozygous mutation c.185delC in KCNJ11 was identified in 2 siblings.

Phenotype & Genotype correlation:

Results

> 49 cases without identified mutations,

1 case with novel mutations in KCNJ11;

1 case with mutation in HNF4A, & 1

case with maternal mutation in ABCC8

were responsive with diazoxide.

> 47 cases were not responsive with

identified (*ABCC8*, *KCNJ11*, *GLUD1*, *CGK*, *HADH*, *SLC16A1*, *HNF4A* and *UCP2*). Severe forms of congenital HH are caused by inactivating mutations in *ABCC8* and *KCNJ11*, which encode the two components of the pancreatic β -cell ATP-sensitive potassium channel (sulfonylurea receptor SUR1 and the inwardly rectifying ion channel KIR6.2).

Objectives

Our aim is to identify mutations in *ABCC8* and *KCNJ1*1, *HNF4A* and *GLUD* genes, and to describe genotype & phenotype correlations of Vietnamese patients with CHH.

Mutation of HNF4A:

Novel & maternal inheritance mutation c.659T>C in *HNF4A* gene was identified in 1 case.

Table 1. Mutations of ABCC8 & frequency

Genotype with ABCC8 mutations	Number of families
c.3403-1G>A	12
c.3403-1G>A/c.3403-1G>A	1
c.3403-1G>A/c.2995C>T	1
c.2057T>C	2
c.2057T>C/c.2057T>C	1
c.4160_4162del	2

diazoxide including:

• 4 cases with mutations in KCNJ11

 43 cases with homozygous or compound heterozygous or paternal heterozygous mutations in ABCC8.

 * Treatment for cases with unresponsive diazoxide:
 18 cases were preformed near total pancreatectomy by laparoscopy.
 2 cases with paternal heterozygous mutations in *ABCC8* needed focal pancreatectomy by laparoscopy.
 27 cases needed octreotide injection.

Methods

• A case series study including phenotype, genotype characteristics in 99 patients with CHH from 1/2007 to 3/2016 at National Children's Hospital, Hanoi, Vietnam.

 Genomic DNA was extracted from peripheral leukocytes using standard procedures.

All exons of *ABCC8, KCNJ11, HNF4A & GLUD1* was amplified & directly sequenced.
Medical records were reviewed to identify phenotypes.

Results

c.1467+5G>A/c.2800C>T

c.2041-21G>A

c.2041-21G>A/c.3978del c.2041-21G>A/c.2041-21G>A c.2056T>A/c.2057T>C c.2057T>C/c.3403-1G>A c.2057T>C/c.2995C>T

c.2995C>T

c.3293A>G c.3403-1G>A/c.4462C>T c.4415-13G>A c.4610C>T c.655C>A/c.892C>T

Conclusions

Understanding genetic basis of CHI
 provide novel insights into β-cell
 physiology.

Management & genetic counseling:
Genetic analysis for mutation in genes involved in regulation of insulin secretion can help in genetic diagnosis of diffuse or focal CHI and help in treatment.

 Prenatal diagnosis of CHI can help immediate medical management at the time of birth.

Mutations were identified in 50/99 cases (50.5%): ABCC8: 44/99 (44.4%); KCNJ11: 5/99 (5.1%); HNF4A: 1/99 (1.0%). ✤ Mutations of ABCC8: 25/44 cases were compound heterozygous; homozygous or 19/44 paternal/maternal cases were heterozygous. 24 different causative mutations of ABCC8 were identified including **12 novel mutations** and 12 reported mutations.

c.1106A>G/ c.4611G>A

c.1183A>T

c.2056T>A/c.2057T>A

c.3293A>G

c.4061A>G *

c.4135G>A

Deletion of exons 22-26

* Maternal inheritance; other heterozygote cases were paternal inheritance. Red color is novel mutation

References

- Flanagan SE et al. 2009. Human Mutation 30(2): 170–180
- Banerjee I et al. 2011. European Journal of Endocrinology 164: 733–740
- Nessa A et al. 2016. Frontiers in Endocrinology 7 article 29

