Using old and new DNA sequencing technology to identify the genetic causes of hyperinsulinism

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Our aim:

A fast, accurate genetic diagnosis for every patient

Because:

- A genetic diagnosis guides treatment
- A genetic diagnosis defines the risk of hyperinsulinism for siblings and future offspring

A genetic diagnosis guides treatment



Jack

- Diagnosed at 1 day
- Diazoxide unresponsive
- Homozygous ABCC8 mutation
- Diffuse disease
- Sub-total pancreatectomy



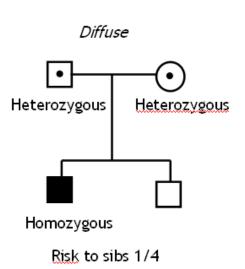
George

- Diagnosed at 1 day
- Diazoxide unresponsive
- Heterozygous ABCC8 mutation
- Focal lesion confirmed by PET-CT scan
- Keyhole lesionectomy

A genetic diagnosis defines the risk for siblings and future offspring

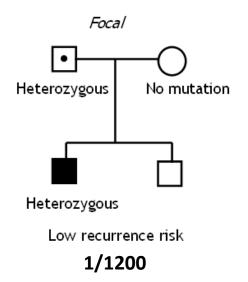


Jack





George



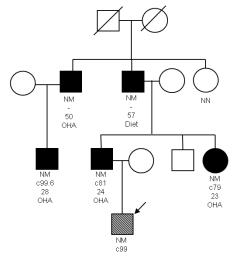
A genetic diagnosis defines the risk for siblings and future offspring



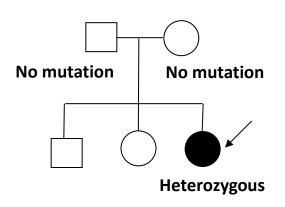
Simon (HNF4A)



Emily (GLUD1)

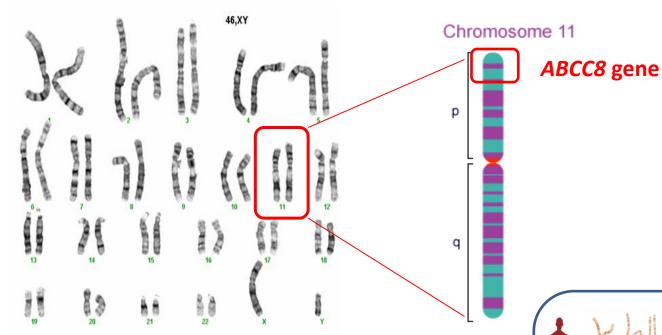


½ risk for siblings and offspring



low risk for siblings (<5%) but ½ risk for offspring

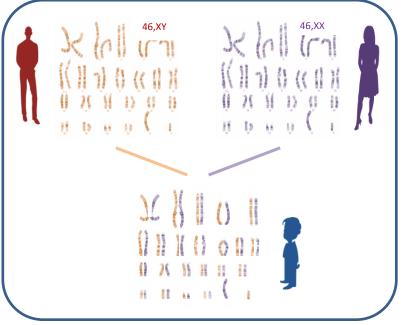
The ABCC8 gene



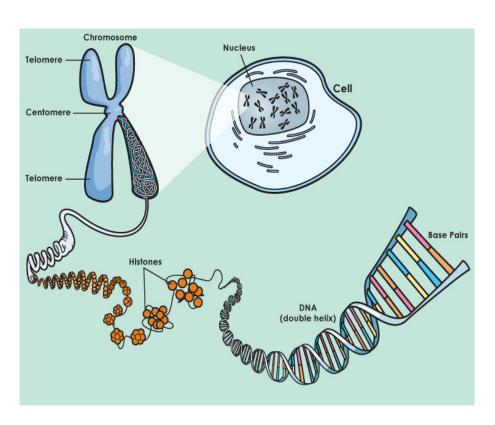
The ABCC8 gene is on chromosome 11

Two copies of the ABCC8 gene:

- One inherited from mother
- One inherited from father



From chromosomes to DNA

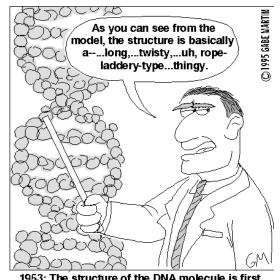


- Each cell contains 23 pairs of chromosomes.
- Chromosomes consist of tightly compacted DNA.

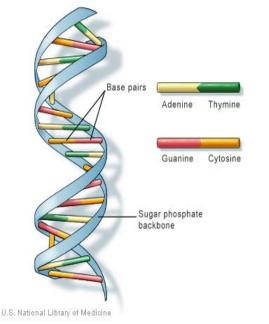
DNA: the genetic code

The information in DNA (Deoxyribonucleic acid) is stored as a code made up of four chemical bases: adenine (A), guanine (G), cytosine (C), and thymine (T).

The order of these bases (A,G,C,T) is the genetic code.



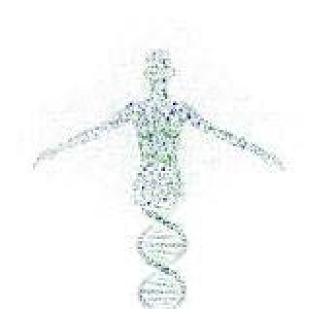
1953: The structure of the DNA molecule is first described.



If you unravel your DNA, it would stretch from here to?

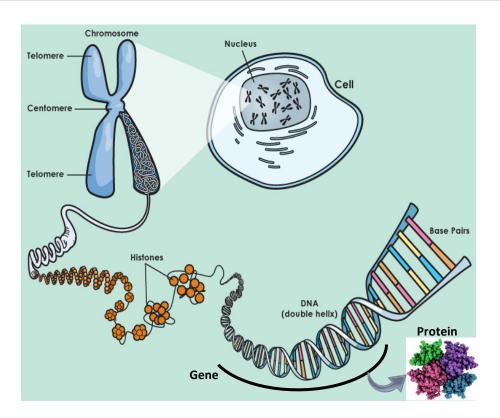
The human genome

- The human genome is made up of 3 billion bases of DNA
- An instruction manual to create and maintain a human being from conception to the end of life



If you typed your genome sequence at 1 base per second, how long would it take?

Genes to proteins



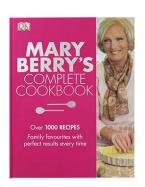
- A gene is a segment of DNA containing the code used to synthesize a protein.
- Humans have approximately 20,000 genes

Nucleus



Chromosomes

Chromosome



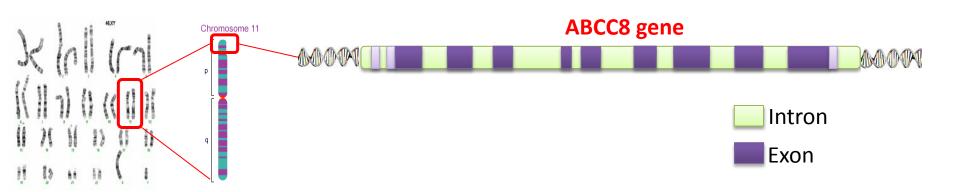
Gene



Protein



The ABCC8 gene

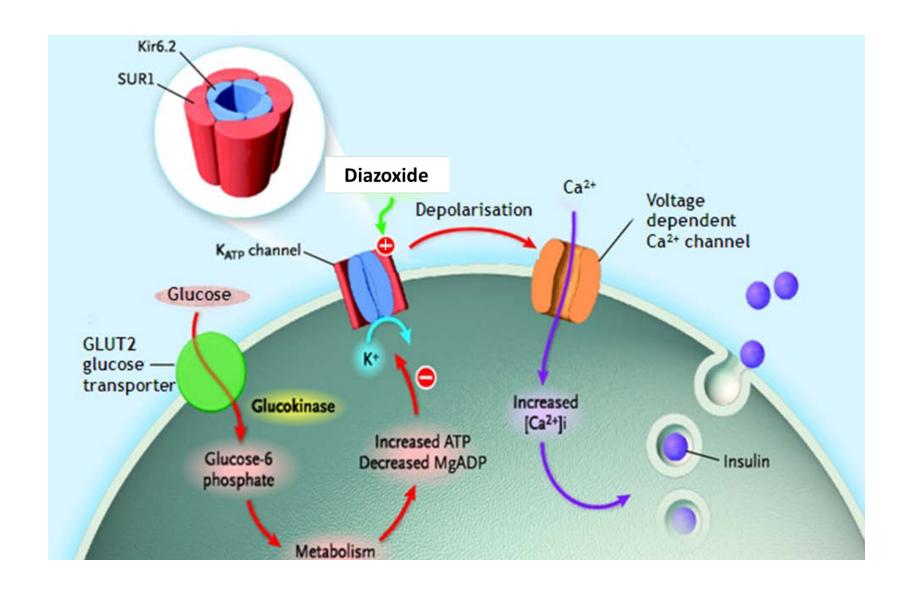


The ABCC8 gene contains 39 exons and 38 introns

- Exons are the 'coding' part of the gene
 - They are the ingredients needed for the cake
- Introns are the 'non-coding' part of the gene
 - They are the cooking utensils needed to make the cake but won't be part of the cake

The *ABCC8* gene codes for a protein called SUR1 (Sulphonylurea Receptor 1)

The SUR1 protein controls insulin secretion



When things go wrong...

- Every human genome differs by 3-4 million variants
- Variants can have no effect, they define characteristics like eye colour or they may cause disease (mutation)



 There are different types of mutations, e.g. missense, splicing, small deletions or whole gene deletions





When things go wrong...

No mutation

Decorate with jam, cream and icing sugar

Missense mutation

Decorate with **ham**, cream and icing sugar

Small deletion

Decorate with --- --- icing sugar



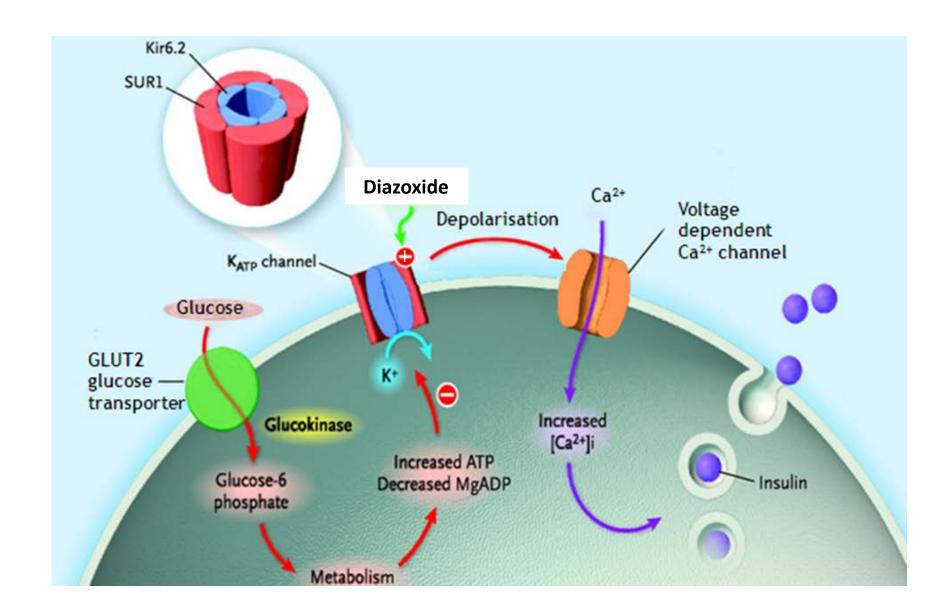
Splicing mutation

Bake the cake with the mixing spoon left in

Gene deletion

No cake!

ABCC8 mutations cause hyperinsulinism

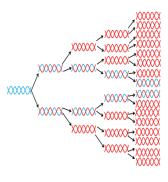


How do we test for ABCC8 mutations?







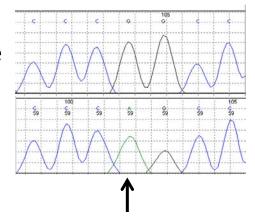


PCR amplify the coding regions of the *ABCC8* gene



Reference

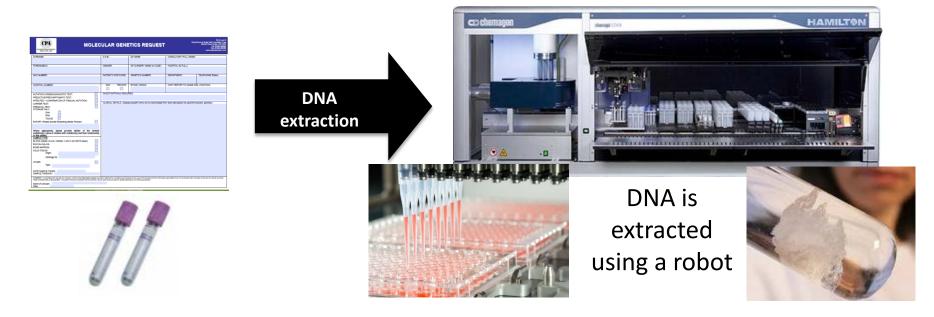
Patient

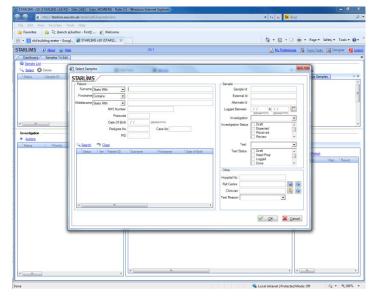


Sequence coding regions of the *ABCC8* gene (10,000 bases)



Laboratory tests are semi-automated







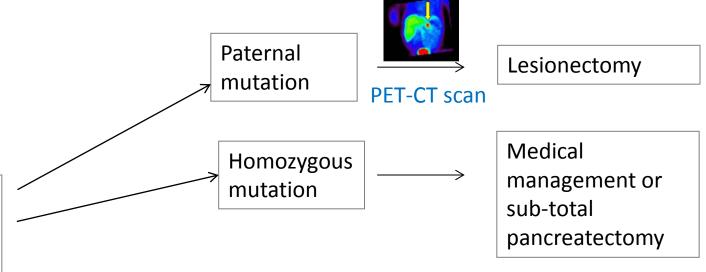
DNA is stored in 2D barcoded tubes

All details stored in password-protected database

Genetic testing for patients with CHI



ABCC8/KCNJ11
Sanger sequencing
test
(1-2 weeks)



Using old and new DNA sequencing technology to identify the genetic causes of hyperinsulinism

Improved DNA sequencing technology

1977

GCCC

TGCC

2000

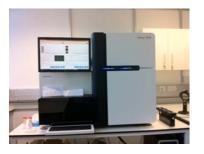


36 0 0 A 1 6 A A 6 C

Radioactive

Fluorescent

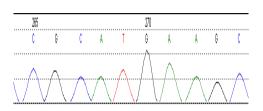
2010

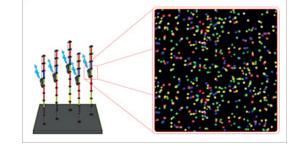




Next generation

From one gene to (nearly) all genes

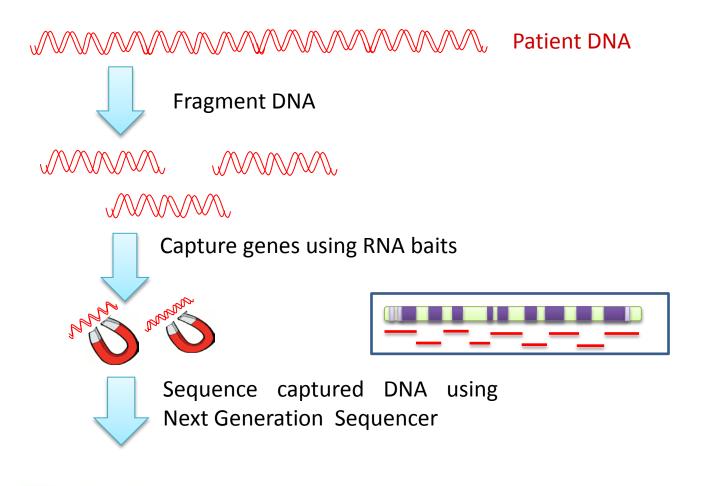




- Sanger sequencing
- Test one gene at a time
- Output 0.5 million bases per day
- Cost £1000 per million bases

- Next generation sequencing
- Test 20,000 genes at once
- Output 5 billion bases per day
- 20p per million bases

Next generation sequencing of all CHI genes

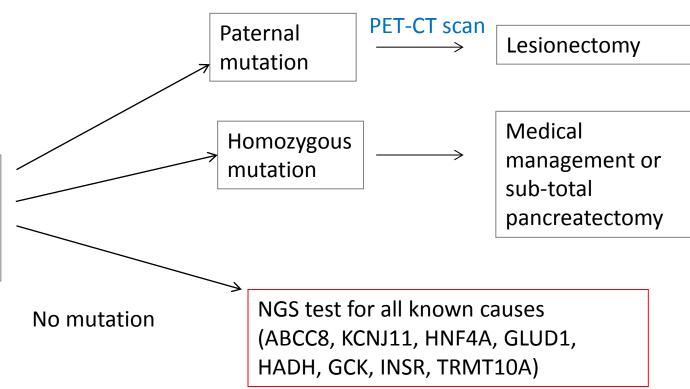




Genetic testing for patients with CHI

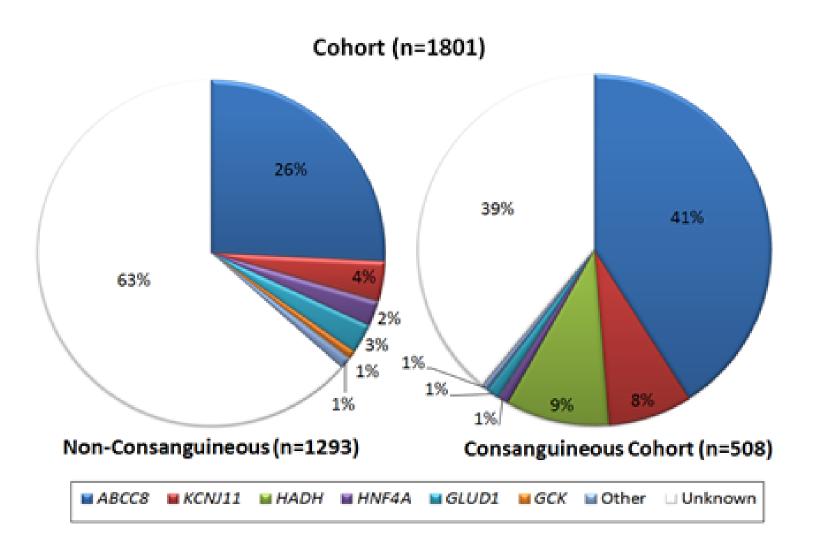


ABCC8/KCNJ11
Sanger sequencing
test
(1-2 weeks)

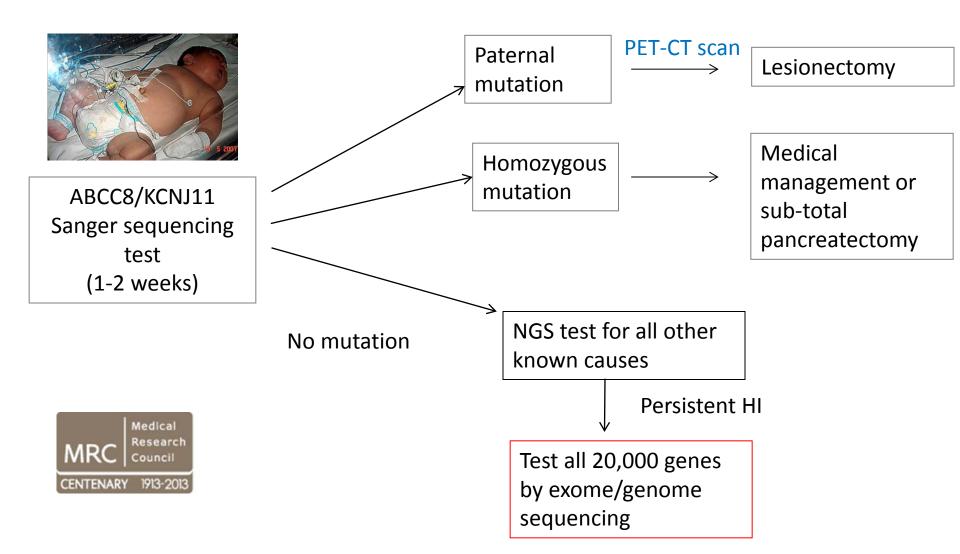




Genetic subtypes in patients with HI

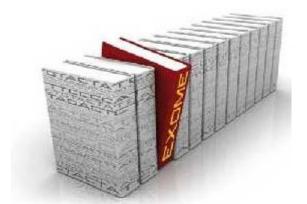


Genetic testing for patients with CHI



Exome sequencing

- Most mutations (>85%) are located within the proteincoding parts (exons) of the genome
- The exons represent ~1% of the genome and can be enriched ("captured") from genomic DNA by hybridisation
- Sequencing all the exons = exome sequencing



Genome sequencing

- Sequencing 3,000,000,000 letters of each person's genetic code
- Sequencing of the first human genome ("finished" in 2003) cost an estimated ~ \$3 billion



Cost of sequencing has dropped to \$1000

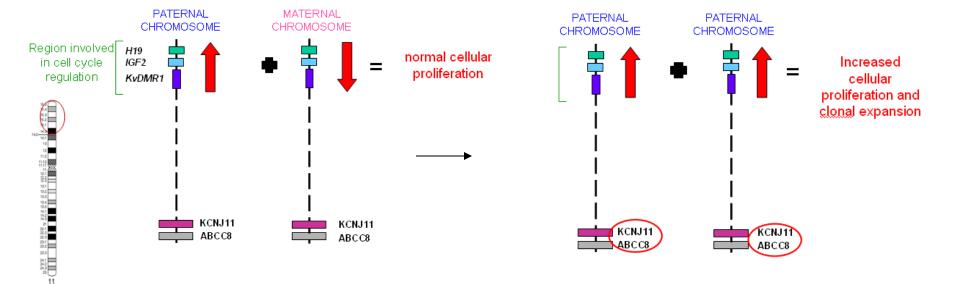


Uses of new DNA sequencing technology

- 1) Test all known CHI genes in one test (targeted NGS)
- 2) Identify new genetic causes of CHI (exome or genome sequencing)
- Find new CHI causing mutations in non-coding DNA of known genes

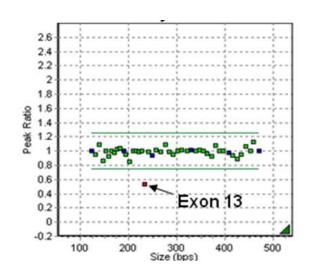
Focal hyperinsulinism is due to a paternal K_{ATP} mutation and somatic patUPD of 11p15

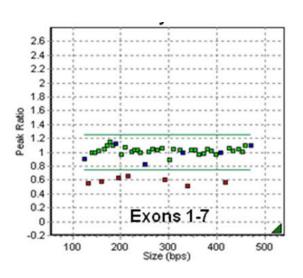




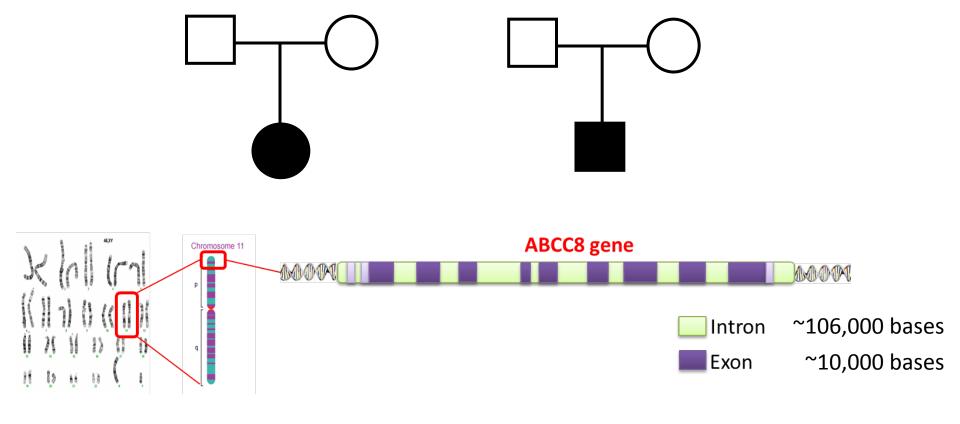
Genetic testing results for focal CHI

- 1) Sanger sequencing of *KCNJ11* and *ABCC8* identified mutations identified in 35/39 confirmed focal cases
- Dosage analysis by MLPA detected partial gene deletions in
 2/39 cases
- 3) Two patients with focal disease but no mutation



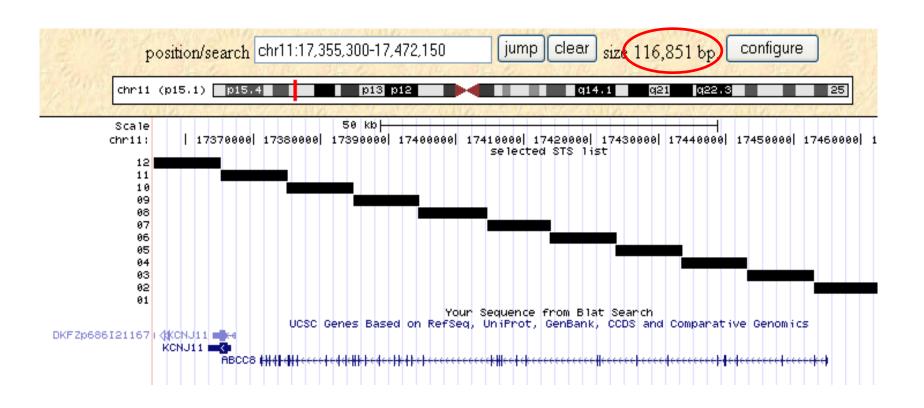


The hunt for intronic mutations causing focal hyperinsulinism

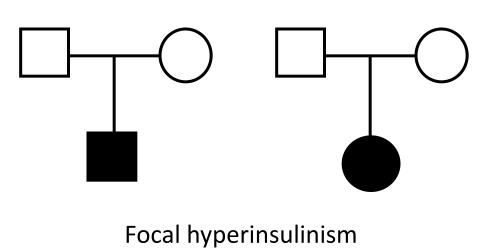


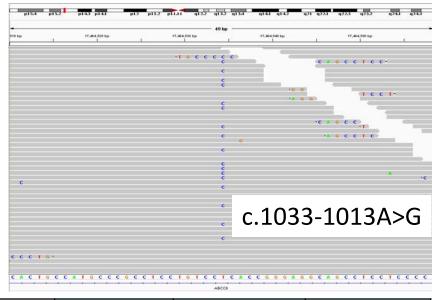
Sequence the entire ABCC8 gene (116,000 bases) by next generation sequencing

ABCC8 long range PCR



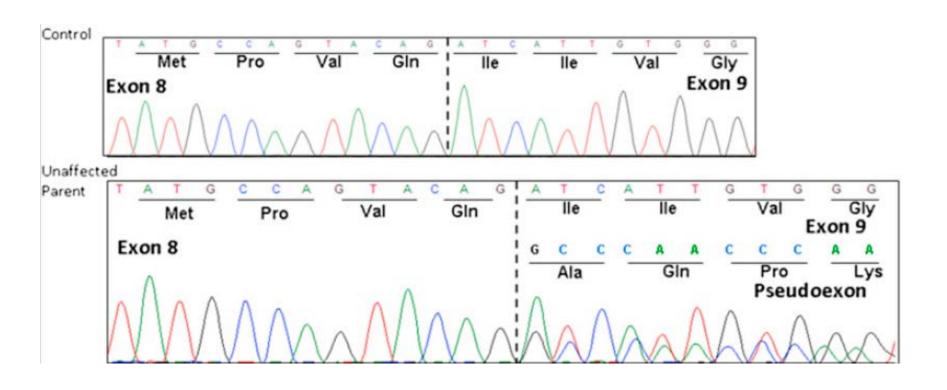
Results – ABCC8 variants





	Patient 1	Patient 2	Shared
Heterozygous variants	90	225	83
Exclude variants in 1000 genomes or dbSNP132	9	10	9
Exclude indels in homopolymer tracts	3	4	1
Predicted to create cryptic splice site	1	1	1

Father's blood sample shows abnormal splicing



Further testing

- ABCC8 mutation identified in 3 additional focal cases (12%) and one diffuse case
- This is a founder mutation in patients from the Republic of Ireland
- This discovery allowed a couple whose first child died of CHI to have a prenatal test in their next pregnancy

REPORT

Next-Generation Sequencing Reveals Deep Intronic Cryptic ABCC8 and HADH Splicing Founder Mutations Causing Hyperinsulinism by Pseudoexon Activation

AJHG 2013

Sarah E. Flanagan,¹ Weijia Xie,¹ Richard Caswell,¹ Annet Damhuis,² Christine Vianey-Saban,³ Teoman Akcay,⁴ Feyza Darendeliler,⁵ Firdevs Bas,⁵ Ayla Guven,⁶ Zeynep Siklar,⁷ Gonul Ocal,⁷ Merih Berberoglu,⁷ Nuala Murphy,⁸ Maureen O'Sullivan,^{9,10} Andrew Green,^{11,12} Peter E. Clayton,¹³ Indraneel Banerjee,^{13,14} Peter T. Clayton,¹⁵ Khalid Hussain,^{16,17} Michael N. Weedon,¹ and Sian Ellard^{1,2,*}

Thank you: 2102 probands from 77 countries

