Diabetes caused by Insulin gene (INS) deletion: clinical characteristics of homozygous and heterozygous individuals

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Running title: INS-deletion diabetes

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SUMMARY

Background: Mutations of the preproinsulin gene (INS) account for both permanent neonatal diabetes (PND) and adult-onset diabetes. The molecular mechanism of complete INS-deletion has recently been published and we now add clinical data of homozygous and heterozygous subjects as well as the detailed mapping of the 646 bp deletion of the INS gene.

Methods: Location and size of the INS-deletion was mapped in one case with PND and INS-genotype of the whole family was further characterized by breakpoint-spanning PCR. The phenotype of monoallelic loss of INS was studied in 33 adult family members of the large consanguineous kindred with INS deletion.

Results: The 646 bp deletion was found in two individuals with PND which included exon 1 and exon 2 of the INS gene (chr11: g.2138434_2139080del646) and results in loss of approximately half of the preproinsulin protein. The two boys with homozygous INS-deletion (D/D) presented with reduced birth weight, PND within the first 24 hrs of life and complete absence of c-peptide. Adult family members with the N/D had diabetes onset with earliest 25 yrs, while the oldest subject without diabetes was 45 yrs. INS-deletion-diabetes was initially treated with OADs but then transferred to insulin within 5 to 16 yrs. Overall, N/D-subjects (N=11) had a higher risk to develop insulin-dependent diabetes up to the fifth decade, if compared to normal subjects (N=22).

Conclusion: Complete loss of the human INS gene results in neonatal diabetes, while heterozygous INS-deletion is a strong risk factor for developing insulin-dependent diabetes at adult age.
INTRODUCTION

Diabetes mellitus is characterized by high blood glucose concentrations accompanied by insulin deficiency or impaired insulin function. Genetic factors that play a role in development of diabetes are increasingly recognized and are now established in diagnostic algorithms of autoantibody-negative diabetes (1, 2). Despite this, most diabetes genes act in a polygenetic fashion and few diabetes forms are caused by alterations of single genes (1). Detection and detailed characterization of these gene defects have improved our understanding of human pancreas and islet development and function. Furthermore, variation or mutation of the same gene can cause monogenic diabetes but also contribute to individual risk of the very common, polygenic type 2 diabetes (3-7). Recent studies indicated that autosomal dominant insulin gene mutations can cause permanent neonatal diabetes (PND) but also autoantibody-negative diabetes that is classified then as type-1B or MODY-type diabetes (8-10). The molecular mechanism behind these cases with a MODY-like presentation was suggested to be defective trafficking of proinsulin and increased ER stress (11). Recessive mutations of the preproinsulin (INS)-gene have also been identified as a novel cause of neonatal diabetes and were the commonest cause of isolated PND in the offspring of consanguineous parents (12). In humans, complete loss or inactivation of the two insulin alleles clearly leads to insulin-deficient diabetes from birth, as it has been reported previously from our cases (12). But whether allelic depletion of INS has any human phenotype at all, remains controversial since inactivation of three of four mouse INS-alleles (Ins1−/−/ Ins2+/+) does not lead to diabetes during mouse lifespan (13).

Here we report on the large, consanguineous kindred with the deletion of exons 1 and 2 of the INS gene. The two boys with biallelic INS-deletion had been reported recently (12) and we now add mapping data of the 646 bp deletion resulting in loss of half of the preproinsulin protein and proximal parts of the insulin promoter. Furthermore, we report the phenotype of subjects with a heterozygous INS-deletion and their risk to develop adult-onset and insulin-dependent diabetes.
PATIENTS AND METHODS

Subjects. The family studied originates from Lebanon and within this family two children with permanent Neonatal Diabetes (PND) have been investigated for anomalies of known genes causing monogenic diabetes including GCK, HNF1A, HNF4A, HNF1B, KCNJ11 and ABCC8 genes. As these showed normal sequences, the insulin gene was investigated and finally loss of the exons 1 and 2 of the INS-gene has been identified as underlying cause and reported recently (12). Extended clinical follow-up studies on the two index patients with permanent neonatal diabetes (PND) were performed at the referring Diabetes Centers. After the bi-allelic deletion was found in both cases with PND, first degree relatives (siblings and parents) of one case agreed in clinical investigation including oral glucose tolerance test and HbA1c measurement. Furthermore, we report on overall 33 adult family members that were available for clinical history, genetic testing, and at least one capillary HbA1c at time of investigation. Informed consent was obtained from all studied individuals and the study has been approved by the local Ethics Committee of the Charité. Oral glucose tolerance tests have been performed in 5 family members according to a standardized protocol including baseline and post-glucose insulin and c-peptide measurements. Insulin and c-peptide was measured by chemiluminescence enzyme immunoassay (Immuliite 2000, Siemens, Germany).

Data and sample collection. Family studies have been performed partially in Lebanon, including collection of clinical data, capillary HbA1c-samples and blood spots on filter paper for genetic testing. Those were done by one adult family member who was specifically trained to interview subjects on concomitant diseases and medication as well as to perform capillary blood tests and store samples appropriately. Classification of diabetes became difficult as onset of insulin deficiency and diabetes symptoms developed slow and showed some variation between subjects. We classified those subjects as having diabetes if firstly, diabetes diagnosis was made by a physician or secondly, if diabetes was yet undiagnosed and HbA1c has been higher than the threshold of 6.1%, indicating at least relevant impaired carbohydrate
metabolism. By this, we tried to compare diabetes status of family members living in European countries and Lebanon. We assume that we missed no cases with diabetes that required treatment or had a relevant HbA1c elevation.

**Mutation Screening.** Samples for genetic testing have been collected as EDTA blood in cases followed in Melbourne and Berlin. In cases from Lebanon, capillary blood was collected on filterpaper (Protein Saver 903®, Whatman, Dassel, Germany) and DNA was subsequently isolated (DNA IQ™ Casework Sample Kit for Maxwell® 16, Promega Corporation, Madison, USA) and analysed. The human INS gene was amplified in three exon specific segments by PCR. We used the following primers: for the noncoding exon 1, forward 5’-ggcaggggttgagaggtag-3’, and reverse 5’-aatcttgagccacctgac-3’; for exon 2 forward 5’-gaagcatgtaggggtagag-3’, and reverse 5’-gctggtcacttttagacgtg-3’, and for exon 3 forward 5’-cctgtcyytcctcctctgt-3’ and reverse 5’-agagacgctggagagacgtg-3’. We used the Mastercycler ep gradient S Amplification System (Eppendorf AG, Hamburg, Germany). The PCR conditions were: 94°C 5 min, 30 cycles of 94 °C for 30 s, 59.5 °C for 30 s, and 72 °C for 30 s; 72 °C for 10 min and 10°C for storage. Breakpoint-spanning PCR to discriminate between heterozygote deletion carriers was performed with the forward primer 5’-ccaggtcaccagacttta-3’, and the reverse primer 5’-gaggaagagtgcctgacgac-3’. PCR products were 977 bp or 331 bp for normal or INS-deleted alleles, respectively. The PCR amplification system and conditions were: Mastercycler ep gradient S Amplification System (Eppendorf AG, Hamburg, Germany) and 94°C 5 min, 30 cycles of 94 °C for 30 s, 58.8 °C for 30 s, and 72 °C for 2 min; 72 °C for 10 min and 10°C for storage.

**Statistical analysis.** Clinical numeric data is given as median and range, where appropriate. Clinical characteristics of subjects were compared by Mann Whitney-U or Chi-Square test (frequency of diabetes) using the statistical package PASW version 18 (Chicago, USA).
RESULTS

Identification of insulin gene deletion in the family. During the course of our studies of neonatal diabetes, we identified a consanguineous family (figure 1) in which diabetes at adult age appeared to segregate as a dominant trait, while neonatal diabetes occurred in a recessive way. Screening for INS mutation in these two cases resulted in a lack of the PCR-product of the coding exon 2 and the non-coding exon 1, while exon 3 and the neighbouring tyrosine hydroxylase gene (TH) were well amplified (11). Thus, sequencing with several primer sets within the region between INS and TH was performed to characterize size and exact location of the deletion. We found a small deletion of 646 bp including the proximal promoter region and exons 1 and 2 of the insulin gene (chr11:g.2138434_2139080del646). The deletion results in loss of all protein structures encoded by exon 2, namely signaling peptide, A chain and half of c-peptide, but also of the proximal transcription factor binding sites G1, CRE3, CRE4 and the TATA box of the INS promoter (figure 2).

For family screening, a breakpoint spanning PCR was established and we identified other subjects in the family with a heterozygous deletion of the INS exons 1 and 2. Overall, 33 adult family members with complete clinical data and HbA1c were analysed to calculate the diabetes risk associated with the N/D genotype, including 22 cases without deletion and 11 cases with the N/D genotype (table 1 and figure 1).

Patients with a homozygous INS-gene deletion. Neonatal diabetes in the two cases with complete INS-deletion was diagnosed within the first hours of life and treated directly with insulin. In keeping with the severe insulin deficiency, both children also had significant intrauterine growth retardation and birth weight was markedly reduced (table 3). Following insulin treatment, postnatal growth of both children was normal and caught up into growth percentiles of unaffected siblings. Apart from neonatal diabetes, neither boy had any other organ abnormality nor did both have impaired mental development.
Subjects with a heterozygous INS-gene deletion. We tried to compare the diabetes status in family members living in Germany or in Lebanon, respectively. The status “diabetes” in this study was defined as diagnosis made by a following physician (oGTT) or as increased HbA1c above 6.1 % as the normal range cut off. This was largely applied in many family members from Lebanon as they had not been regularly screened for diabetes. In the 33 adult family members that were available for genetic and clinical testing, diabetes was more frequent (p<0.05) in those with N/D genotype (5 of 11) than with normal N/N (3 of 22) genotype (table 1). Diabetic N/D subjects had been diagnosed between 25 and 47 yrs of age and were initially treated with oral antidiabetic drugs (OADs). With a delay of 3 to 16 yrs, diabetes treatment was then changed to insulin in all cases with diabetes. Some cases with bad metabolic control also died of severe micro- and macrovascular complications (subjects A 3.3 and A 3.7). The three subjects with normal genotype and diabetes (figure1, subjects no. B 3.1.1, 2.2, and 2.4) had mild symptoms at onset and were diagnosed approximately two decades later than N/D subjects (table 1 and table 3).

Clinical investigation and oGTTs were performed in the index family with three members with N/D genotype and one index case with complete deletion (D/D; A4.4 in Figure 1). The case with complete deletion (D/D) and neonatal diabetes from birth and displayed complete loss of c-peptide. In contrast, the N/D-cases of the index family had no clinical signs of diabetes and displayed normal insulin sensitivity and insulin resistance as characterized by insulin sensitivity index (ISI) and HOMA-IR (table 3).

As mentioned, birth weight was reduced in the D/D case as a result of reduced insulin secretion in utero, but whether heterozygous deletion carriers have a lower birth weight is not clear, as birth weights have not been documented in most adult family members born in Lebanon.
CONCLUSIONS

We report on a large family with subjects showing complete or heterozygous loss of the insulin gene. Complete loss results in neonatal diabetes, reduced birth weight and complete absence of c-peptide. Furthermore, heterozygous subjects have a relevant risk of developing insulin deficiency and diabetes with advanced age.

As reported recently, recessive preproinsulin (INS) mutations are a novel cause of permanent or transient neonatal diabetes (12). In humans, the phenotype of monoallelic loss of INS could be discussed controversial as in mice; a heterozygous null genotype at the Ins2 locus is insufficient to cause diabetes, no matters whether alone or in combination with a homozygous null genotype at the Ins1 locus (13).

In humans, some heterozygous mutations of the INS gene are known to cause diabetes, if the resulting, mutant proinsulin is misfolded and thus leads to increased ER stress and finally a dominant-negative effect on pancreatic survival beta cell function (11). Diabetes in these patients with heterozygous INS mutations shows a broad spectrum of clinical phenotypes suggesting that different INS-mutations behave differently. Experiencing these patients and Ins1/Ins2 ko animal observations (13) the hypothesis was stressed that in humans, only dominant-negative INS-mutations are able to cause diabetes, while loss of one allele was suggested to be without clinical impact (14,15). Given the recessive inheritance, heterozygous offspring are much more frequent; however less is known about the clinical impact of monoallelic impairment of the INS gene.

The two boys with biallelic INS-deletion had undetectable c-peptide levels and absent insulin function. Sequencing of the region between TH and INS gene indicated a very small 646 bp deletion that only affects parts of the insulin promoter, the non-coding exon 1 and the coding exon 2 of the INS gene. In detail, we have found that next to exons 1 and 2 basal promoter elements including the transcription factor binding sites G1, CRE3, CRE4 and the TATA box of the proximal INS promoter are lost. The basal approx. 100 bp promoter provides an assembly platform for the RNA polymerase II initiation complex and therefore next to exon 2,
fundamental elements of regular INS transcription are also lost (16). CRE3 and CRE4 predominantly can interact with transcription factors activated by cAMP and diacylglycerol (DAG) that can operate as activators, nonactivators or suppressors (17). Mutagenesis experiments have shown that all four CRE sites of the human INS promoter are transcriptionally active (18). The human INS promoter G1 box (5’GTAGGGGA) binds the transcription factor Pur-1/MAZ and is specifically found in the primate INS promoter region (19).

Diabetes caused by heterozygous loss of one INS gene in our family was different from type 2 diabetes and characterized by normal or decreased BMI and early need of insulin treatment. Therefore, heterozygous subjects show characteristics of a late-onset MODY-like or type 1B-like diabetes that resembles in some ways other monogenic diabetes forms that are associated with gene alterations of GCK, HNF1A, HNF1B or HNF4A. This may suggest that sequencing and deletion analysis of INS should be included into diagnostic work up, if monogenic diabetes is assumed.

In summary, complete loss of the human INS gene results in neonatal diabetes, reduced birth weight and complete absence of c-peptide protein and insulin function. Furthermore, heterozygous INS deletion is a strong risk factor for developing diabetes at older age despite normal BMI. As heterozygous offspring might be frequent in a general population, genetic testing for INS gene alterations should be considered, if subjects are primarily insulin deficient and not obese.
DECLARATION OF INTERESTS

The authors have nothing to disclose.

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REFERENCES


20. Matsuda M & DeFronzo RA. Insulin sensitivity indices obtained from oral glucose tolerance testing: comparison with the euglycemic insulin clamp. *Diabetes Care* 1999 **22** 1462-1470.
FIGURE LEGENDS:

Figure 1: Pedigree of the family, genotype of tested subjects without deletion (N/N), with biallelic (D/D) or allelic (D/N) loss of INS are indicated. Filled symbols mark the two index cases with PND and hatched symbols those with adult-onset diabetes. The underage (<18 yrs) subjects A4.2, A4.3, A4.4 and B4.6 are indicated in this pedigree to give a complete picture of the index families but they are not included into statistical analyses reported in table 1. The insert shows gel electrophoresis of PCR products using primers spanning the 646 bp breakpoint on example of one patient with neonatal diabetes and his siblings (upper band approx. 1000 bp, lower band approx. 350 bp).

Figure 2: Schematic of the proximal INS gene showing the deletion above the gene. Transcription factor binding sites of the proximal promoter region are indicated at their respective position; a part of the preproinsulin protein that is coded by exon 2 and lost by the deletion is indicated below the nucleotide sequence. The nomenclature of the deletion is based on the coding sequence where nucleotide 1 represents translational start site.
Fig. 1
Fig. 2

Proximal insulin gene promoter

Exon1

Exon2

Exon3

-65_581del646

signaling peptide (24 AA)  B-chain (30 AA)  C-peptide (31 AA)  A-chain (23 AA)
<table>
<thead>
<tr>
<th>Genotype</th>
<th>N/D</th>
<th>N/N</th>
</tr>
</thead>
<tbody>
<tr>
<td>N (male / female)</td>
<td>11 (6/5)</td>
<td>22 (10/12)</td>
</tr>
<tr>
<td>Diabetes / All</td>
<td>5/11#**</td>
<td>3/22#</td>
</tr>
<tr>
<td>Age [yrs]</td>
<td>44.5 (22 - 55)</td>
<td>37.7 (18 - 73.8)</td>
</tr>
<tr>
<td>Diabetes onset (yrs)</td>
<td>44.0 (25 - 47)**</td>
<td>65 (63 - 67)</td>
</tr>
<tr>
<td>BMI [kg/m²]</td>
<td>23.1 (19.9 – 32.7)</td>
<td>25.1 (16.0 – 38.5)</td>
</tr>
<tr>
<td>HbA1c [%]</td>
<td>5.9 (4.8 – 12.3)*</td>
<td>5.2 (4.3 – 6.9)</td>
</tr>
</tbody>
</table>

Values are median (minimum - maximum), significant differences: *p<0.05, **p<0.01 (N/N vs N/D with or without diabetes), # Chi-Square test.
<table>
<thead>
<tr>
<th>Subject (gender)</th>
<th>Present age</th>
<th>Genotype</th>
<th>Most recent HbA1c (%)</th>
<th>Most recent BMI (kg/m^2)</th>
<th>Diabetes Age at onset</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>A3.2 (male)</td>
<td>54 yrs</td>
<td>D/N</td>
<td>12.3</td>
<td>21.5</td>
<td>33 yrs</td>
<td>33 – 34 yrs diet, 34 – 49 yrs OADS, since 49 yrs insulin</td>
</tr>
<tr>
<td>A3.3 (male)</td>
<td>53 yrs</td>
<td>D/N</td>
<td>12.2</td>
<td>20.2</td>
<td>40 yrs</td>
<td>40 – 49 yrs OADs, since 50 yrs insulin</td>
</tr>
<tr>
<td>A3.4 (male)</td>
<td>51 yrs</td>
<td>D/N</td>
<td>6.5</td>
<td>26.2</td>
<td>42 yrs</td>
<td>42 yrs - OADs</td>
</tr>
<tr>
<td>A3.7 (female)</td>
<td>44 yrs</td>
<td>D/N</td>
<td>8.8</td>
<td>20.1</td>
<td>25 yrs</td>
<td>25 – 33 yrs OAD, since 34 yrs insulin</td>
</tr>
<tr>
<td>B3.1 (female)</td>
<td>50 yrs</td>
<td>D/N</td>
<td>6.9</td>
<td>27.8</td>
<td>47 yrs</td>
<td>47 – 50 yrs OAD</td>
</tr>
<tr>
<td>2.2 (female)</td>
<td>74 yrs</td>
<td>N/N</td>
<td>6.7</td>
<td>32.3</td>
<td>65 yrs</td>
<td>diet no OADs</td>
</tr>
<tr>
<td>B3.1.1 (male)</td>
<td>72 yrs</td>
<td>N/N</td>
<td>6.7</td>
<td>28.3</td>
<td>67 yrs</td>
<td>diet no OADs</td>
</tr>
<tr>
<td>2.4 (male)</td>
<td>64 yrs</td>
<td>N/N</td>
<td>6.6</td>
<td>38.5</td>
<td>63 yrs</td>
<td>diet no OADs</td>
</tr>
</tbody>
</table>

OADs: oral antidiabetic drugs
Table 3: Clinical and genetic characteristics of the two index families, numbers of subjects are from figure 1.

<table>
<thead>
<tr>
<th>Subject no.</th>
<th>B3.4</th>
<th>A3.9</th>
<th>A4.1</th>
<th>A4.2</th>
<th>A4.3</th>
<th>A4.4</th>
<th>B4.6</th>
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</thead>
<tbody>
<tr>
<td>Genotype</td>
<td>N/D</td>
<td>N/D</td>
<td>N/D</td>
<td>N/N</td>
<td>N/N</td>
<td>D/D</td>
<td>D/D</td>
</tr>
<tr>
<td>Diabetes</td>
<td>no</td>
<td>no</td>
<td>no</td>
<td>no</td>
<td>no</td>
<td>PND</td>
<td>PND</td>
</tr>
<tr>
<td>present age in yrs (gender)</td>
<td>44 (m)</td>
<td>37 (f)</td>
<td>21 (f)</td>
<td>17 (m)</td>
<td>8a (f)</td>
<td>12 (m)</td>
<td>6 (m)</td>
</tr>
<tr>
<td>HbA1c (%)</td>
<td>5.9</td>
<td>5.1</td>
<td>4.8</td>
<td>4.9</td>
<td>5.2</td>
<td>8.7</td>
<td>7.9</td>
</tr>
<tr>
<td>Fasting glucose (mg/dl)</td>
<td>96</td>
<td>76</td>
<td>74</td>
<td>82</td>
<td>70</td>
<td>166</td>
<td>220</td>
</tr>
<tr>
<td>Fasting insulin (mU/l)</td>
<td>8.7</td>
<td>4.5</td>
<td>6.2</td>
<td>9.7</td>
<td>4.4</td>
<td>&lt;0.5*</td>
<td>nd</td>
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<tr>
<td>HOMA-IR</td>
<td>2.1</td>
<td>0.8</td>
<td>1.1</td>
<td>2.0</td>
<td>0.8</td>
<td>nd</td>
<td>nd</td>
</tr>
<tr>
<td>ISI*</td>
<td>3.4</td>
<td>12.7</td>
<td>9.2</td>
<td>6.2</td>
<td>10.8</td>
<td>nd</td>
<td>nd</td>
</tr>
<tr>
<td>BMI (kg*m⁻²)</td>
<td>27.3</td>
<td>22.8</td>
<td>19.9</td>
<td>24.2</td>
<td>19.2</td>
<td>18.9</td>
<td>17.4</td>
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<tr>
<td>SD</td>
<td>1.61</td>
<td>0.43</td>
<td>-0.6</td>
<td>0.85</td>
<td>1.6</td>
<td>0.3</td>
<td>0.5</td>
</tr>
<tr>
<td>birth weight (g)</td>
<td>nd</td>
<td>nd</td>
<td>2500</td>
<td>3170</td>
<td>3000</td>
<td>1650</td>
<td>1290</td>
</tr>
<tr>
<td>SD</td>
<td>nd</td>
<td>nd</td>
<td>-0.7</td>
<td>+1.3</td>
<td>+0.6</td>
<td>-3.0</td>
<td>-3.5</td>
</tr>
<tr>
<td>(gestational age, weeks)</td>
<td>(36.0)</td>
<td>(35.5)</td>
<td>(36.5)</td>
<td>(36.0)</td>
<td>(35.0)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>present height (cm)</td>
<td>160.3</td>
<td>148.2</td>
<td>147.8</td>
<td>176.7</td>
<td>122.3</td>
<td>144.7</td>
<td>115.8</td>
</tr>
<tr>
<td>SD</td>
<td>-3.0</td>
<td>-3.2</td>
<td>-3.3</td>
<td>-0.6</td>
<td>-0.4</td>
<td>-0.9</td>
<td>-0.5</td>
</tr>
</tbody>
</table>

# c-peptide, nd: not done, birth weights not known. * Insulin sensitivity index published by Matsuda et al (20)