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Brief report

Clinical and molecular basis of transient neonatal diabetes mellitus in Brazilian children

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ABSTRACT

We report a series of patients with transient neonatal diabetes mellitus (TNDM). Paternal uniparental isodisomy of chromosome 6 and heterozygous KCNJ11 and ABC88 mutation were the mutations found. This first reported series of Brazilian patients expands the geographical data on TNDM contributing to better understanding of its pathophysiology.

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1. Introduction

Transient neonatal diabetes mellitus (TNDM) is now referred to as a unique genetic entity classified as: TNDM1 (OMIM 601410) caused by genetic and epigenetic mutations at chromosome 6q24, TNDM2 (OMIM 610374) caused by ABCC8 mutation(s); and TNDM3 (OMIM 610582) caused by a KCNJ11 mutation (OMIN 600937) [1]. TNDM1 is the most frequent cause of transient neonatal diabetes mellitus, while mutations in the ABCC8 and KCNJ11 genes which encode the SUR1 and KIR6.2 subunits of the pancreatic ATP-sensitive potassium (K-ATP) channel are the second most common cause of the disorder [2].

Due to the rarity of this condition, the present study is aimed to describe, for the first time, a series of Brazilian

children with TNDM, with emphasis on its clinical and molecular aspects.

2. Materials and methods

The medical records of four patients with TNDM treated at a Brazilian university hospital were reviewed.

Laboratory investigation included: glycated hemoglobin (HbA1c), insulin, C peptide, anti-insulin antibody, anti-IA2 antibody, anti-islet cell antibody and anti-GAD antibodies. These tests were performed at the time of diagnosis, at the time of disease remission and at the time of the last assessment.

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Table 1 – Clinical data in Brazilian patients with transient neonatal diabetes mellitus.												
Case	Gender	GA	Pregnancy	BW (centiles)	Physical exam							
					Macroglossia	Umbilical hernia						
#1	M	33 weeks	Arterial hypertension	1190 g (<3th)	Absent	Absent						
#2	M	33 weeks	Premature rupture of membranes	1385 g (3–10th)	Absent	Absent						
#3	F	38 weeks	Urinary tract infection	3250 g (50-90th)	Absent	Absent						
#4	M	38 weeks	Normal	2870 g (10–50th)	Absent	Absent						
M: male; F: female; g: grams; GA: gestational age; BW: birth weight.												

Table 2 – Laboratory data upon diagnosis, remission and follow-up in Brazilian patients with transient neonatal diabetes mellitus.

Exams		Patients									
	Case # 1		Case #2		Case #3		Case #4				
	Diag (1 day)	Rem (4 months)	Diag (1 day)	Rem (2 months)	Diag (15 days)	Rem (7 months)	Diag (50 days)	Rem (3 months)			
Glycemia (70–99 mg/dL)	274	81	463	86	360	78	514				
Insulin (92-25 uUI/mL)	1.3	NP	< 2.0	NP	0.7	NP	NP	< 2.0			
C Peptide (1.1–1.5 ng/mL)	0.2	NP	0.75	NP	0.1	1.1	NP	0.78			
HbA1c (4.5-7.0%)	NP	5.6	NP	5.1	6.5	6.5	NP	6.0			
Anti-GAD (<1.0 U/mL)	0.6	NP	0.5	NP	0.2	NP	NP	0.2			
Anti-IA2 (<0.5 U/mL)	0.2	NP	0.3	NP	0.1	NP	0.2	NP			
Genetic cause for the transient neonatal diabetes		UPD6		UPD6		p.R1183Q (c.3548G > A) ABCC8 mutation		pR50Q (c.149G > A) KCNJ11 mutation			

Diag: age at diagnosis; Rem: age at remission; HbA1c: glycated hemoglobin; anti-GAD: antibody anti-decaborxylase of glutamic acid; anti-IA2: antibody anti-tyrosine phosphatase; NP: not performed; UPD6: paternal uniparental isodisomy of chromosome 6.

Studies to investigate methylation status at chromosome 6q24 were performed at Wessex Regional Genetics Laboratory, Salisbury, UK, as previously described [3]. Studies to investigate the ABCC8 and KCNJ11 mutations were performed at Peninsula Medical School, University of Exeter, UK, as previously reported [2].

This work was approved by the Ethics Research Committee of the participant institution.

3. Results

Table 1 summarizes the main clinical information of the 4 patients (3 males, 1 female). The diagnosis of diabetes mellitus was made between 12 h and 55 days of life. Hyperglycemia was detected in three patients and diabetic ketoacidosis in one patient (Case #1). All patients required transient insulin replacement.

Table 2 summarizes the main laboratory information obtained at the time of diagnosis and TNDM remission.

4. Discussion

4.1. Molecular aspects

The genetic origin for more than 90% of the cases of TNDM is established. Disruption of the imprinted TNDM locus on chromosome 6 is the most common etiology [4,5].

Three types of abnormalities involving 6q24 cause TNDM1: (1) paternal uniparental disomy of chromosome 6 (UPD6), either complete or segmental [6]; (2) duplication of the imprinted TNDM1 region on chromosome 6q24 [7]; and (3) epimutations (maternal hypomethylation of the TNDM differentially methylated region in the absence of any detectable chromosome anomaly) [4]. The common underlying effect of these abnormalities is overexpression of genes in the TNDM locus [8]. The TNDM locus is genomically imprinted, with restriction of gene expression from the maternally inherited allele. However, since the ZAC/PLAGL1 has biallelic expression in white blood cells, this makes it difficult to demonstrate the relaxation of imprinting as a mechanism that causes TNDM through analysis of the blood of patients with this phenotype, since there is scarce availability of samples of other tissues, for obvious ethical reasons [9]. In a subset of TNDM patients, imprinting is disrupted at diverse chromosome locations throughout the genome, in a widespread DNA methylation defect of genomic imprinting [3,10].

The paternal isodisomy of chromosome 6 seen in patients 1 and 2, with homologous chromosomes 6 in all the loci, is consistent with paternal chromosomal duplication after fertilisation of maternal gamete nullisomic for chromosome 6; this is a sporadic event, with low recurrence risk [5]. In the present study, 2 of the 4 patients had paternal isodisomy of chromosome 6, in accordance with the published prevalence of UPD6 [11].

Flanagan et al. [2] identified K-ATP channel genes mutations in 25/28 patients (12 KCNJ11 and 13 ABCC8) with TNDM in

whom methylation defects at chromosome 6q24 had been excluded. In their study the phenotype associated with mutations in the two genes was similar, contrasting with the group of 6q24 patients, who had a lower birth weight, earlier diagnosis and disease remission.

Besides the defects previously described, TNDM may also be caused by mutations in the INS gene and, more rarely, in the HNF1B gene [1].

4.2. Clinical aspects

The clinical manifestations of TNDM begin in the first weeks of life. Polyuria, dehydration and low weight gain are the most frequent symptoms [8]. The patients are generally born at term, being small for gestational age and looking malnourished [12].

Apparently, there is no major phenotypic difference between patients with UPD6, duplication of 6q24, methylation defect, and no identifiable anomaly of chromosome 6, to support the hypothesis that most patients share the same genetic mechanism [13]. Nevertheless, among patients with TNDM, those with 6q24 abnormalities showed more marked intrauterine growth retardation. Consistently with such data, in the present report, the two patients with UPD6 were premature, and one was small for gestational age. In this report, remission of hypoglycemia occurred earlier in the patients with isodisomy when compared to the patients with KCNJ11 and ABCC8 mutations. Since our patients are still young, they will need long-term follow up, until puberty, for assessment of diabetes recurrence.

In general, diagnostic investigation shows hyperglycemia, glycosuria, moderate or absent ketonuria, insulinopenia, reduction in the serum C-peptide levels, slight increase in glycated hemoglobin and negative results for anti-insulin, anti-islet and anti-GAD [13,14]. All these laboratory findings were present in our patients.

Although insulin replacement is the first choice for neonatal diabetes, the identification of an activating mutation(s) in the KCNJ11 or ABCC8 genes is clinically important, because of a favorable response sulfonylureas therapy (oral hypoglycemiants that inhibit the potassium ATP channel, increasing insulin release), that not only improves glucose control but also reduces the risk of hypoglycemia [15,16].

5. Conclusions

The genetic basis of TNDM in Brazilian patients, first reported in this paper, is similar to molecular defects previously reported in the literature [17,18]. This information is important to assist in genetic counseling on recurrence of the disease and is essential to understand the role of genetics and epigenetics in the pathophysiology of TNDM.

Contributors

CA participated in the conception and design of the study and the data acquisition, wrote the initial the draft and revised the final version; SF and SE tested the ABCC8 and KCNJ11 mutations and contributed to the final version of the paper; DM tested the UPDS and contributed for the final version of the paper. All authors acknowledge that they have participated sufficiently in the work to take responsibility for its content approving its final version.

Conflicts of interest

There are no conflicts of interest.

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