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Original article

DNA (cytosine-5)-methyltransferase 3B (*DNMT 3B*) polymorphism and risk of Down syndrome offspring

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ABSTRACT

Down syndrome (DS) is the most common form of human genetic mental retardation. Several polymorphisms in genes coding folic acid cycle enzymes have been associated to the risk of bearing a DS child; however, the results are controversial. S-adenosyl-L-methionine (SAM) is an important intermediate of folic acid pathway and acts as methyl donor and substrate for DNA (cytosine-5)-methyltransferase 3B (*DNMT3B* – EC 2.1.1.37) *de novo* methylation processes during embryogenesis. Recent studies suggest that a functional polymorphism of *DNMT 3B* in maternal genotype may be associated with a decreased risk of having a DS child. We herein investigate the association of this polymorphism with the occurrence of DS in a Brazilian population. We have genotyped 111 mothers of DS infants (MDS) and 212 control mothers (CM) through PCR-RFLP. The observed genotypic frequencies were CC = 0.22; CT = 0.49 and TT = 0.29 in CM, and CC = 0.30; CT = 0.52 and TT = 0.18 in MDS. Allelic frequencies were C = 0.47 and T = 0.53 in CM and C = 0.56 and T = 0.44 in MDS. No deviation of HWE was observed, and both *DNMT 3B* rs2424913 genotype ($\chi 2 = 4.53$; DF = 1; P = 0.03) and allelic ($\chi 2 = 4.90$; DF = 1; P = 0.03) frequencies show significant differences between MDS and CM. The presence of the mutant *DNMT 3B T* allele decreases 30% the risk of bearing a DS child (OR = 0.69; 95% CI: 0.50–0.96; P = 0.03), and the risk is diminished up to 45% in association with the homozygous genotype (OR = 0.54; 95% CI: 0.31–0.96; *P* = 0.04). Our results suggest that women harboring the single nucleotide polymorphism *DNMT 3B* rs2424913 have a decreased risk of a DS pregnancy, and further studies are necessary to confirm this protective effect.

1. Introduction

Down syndrome is the most frequent cause of mental retardation of genetic etiology in humans and occurs in 1/700 stillbirths (Sherman et al., 2007). Failure of segregation machinery during maternal gametogenesis is considered the main cause chromosome 21 missegregation, generating a trisomy 21 zygote. Other causes of DS include chromosomal rearrangements and somatic mosaicism (Hassold and Sherman, 2000). The only validated risk factor associated with DS is advanced maternal age at conception (Allen et al., 2009).

James et al. (1999) published the first report associating a folate pathway gene polymorphism with an increased risk of bearing a DS child. From their original paper to date, several reports have suggested an association between polymorphisms within folate metabolism genes and an increased risk of DS. However, the results are controversial: some reports found an association between DS and folate-related gene polymorphisms, while others failed to find such association. Thus, the association between a given polymorphism and DS varies according to several factors, including nutritional status and genetic background of the studied population (Guéant et al., 2003).

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Cellular processes of nucleotide synthesis and methylation are associated with folic acid cycle, which provides the chemical groups necessary for these reactions. In methylation reactions, DNA (cytosine-5)-methyltransferase 3B (*DNMT3B* – EC 2.1.1.37) uses S-adenosyl-L-methionine (SAM) as methyl donor and substrate for *de novo* methylation during embryogenesis (Bestor, 2000). SAM arises from the methionine generated during homocysteine remethylation and is essential for transmethylation, transsulfuration, and polyamine synthesis (Lu, 2000).

Human DNMT 3B present 23 exons and has been mapped to chromosome 20q11.2 (Xie et al., 1999). Although −149C > T polymorphism has been described as a promoter mutation, it is located in an intronic region according to the SNP databases (NM_006892.3 at NCBI, as well as, ENST00000328111.6 at ENSEMBL). Considering that all the previous publications refer to this polymorphism as a promoter variant 149 base pairs upstream the transcription start site, we adopted dbSNP nomenclature rs2424913. Shen et al. (2002) has described an increased promoter activity *in vitro* in association with this polymorphism.

Most association studies involving *DNMT 3B* polymorphism are related to cancer development; DNA methylation of promoter regions is one of the major regulatory mechanisms of gene expression (Shen et al. 2002) and aberrant DNA methylation may contribute to carcinogenesis through deamination of 5-methyl cytosine to thymine, increasing mutation rates (Lee et al., 2005). Also, an abnormal supply of folic acid cycle intermediates could unbalance the availability of SAM, the main donor of methyl groups for methylation reactions, leading to centromeric hypomethylation and chromosomal nondisjunction (James et al., 1999).

To determine the association of DNA (cytosine-5)-methyltransferase 3 beta rs2424913 polymorphisms over DS pregnancy risk we have performed a case-control study in a population from Rio de Janeiro, a state located in the Southeast region of Brazil.

2. Materials and methods

2.1. Subjects

Mothers of Down syndrome children (MDS) were selected from Genetics Service of IPPMG (Portuguese acronym for Martagão Gesteira Childcare and Pediatrics Institute) at Federal University of Rio de Janeiro and control mothers (CM) were enrolled through Pediatric Clinic from the same Institution. A total of 111 MDS and 212 CM were included in this study and maternal age varied from 14 to 49 years old in MSD and 14 to 43 years old in CM. The inclusion criterion for MDS was give birth to a karyotipically confirmed trisomy 21 child. Preset inclusion criteria for CM were a medical history free of chronic disorders associated to *DNMT 3B rs2424913*, no previous miscarriage and give birth to healthy children without congenital defects. Both case and control subjects were inhabitants of the Rio de Janeiro. MDS and CM were asked to answer a socioeconomic questionnaire and donate a buccal epithelial cell sample. The study protocol was approved by the Ethics Committee of Federal University of Rio de Janeiro (UFRJ) and written informed consent was obtained from all subjects. A total of 111 MDS and 212 CM agreed to participate and were included in this study.

2.2. DNA extraction and DNMT 3B rs2424913 genotyping

Genomic DNA was isolated from buccal epithelial cells by standard procedure (Aidar and Line, 2007) and quantified by spectrophotometry. Genotypes were determined by PCR amplification followed by digestion with restriction endonuclease (PCR-RFLP) as described by Xiao et al. (2008) with minor modifications. Conditions used to amplify a 380 bp fragment containing the polymorphism are shown in Table 1. Reactions were carried out in a final volume of 15 μL containing 50ηg genomic DNA, 1X Green GoTaq™ Reaction Buffer (with 1.5 mM $MgCl_2$), 9 pmol each primer, and 1 U GoTaq™ Polymerase (Promega). PCR products were digested with XmaJI endonuclease (Thermo Fischer Scientific) according to supplier recommendations, and the digested products were resolved in 2% agarose gel, ethidium bromide stained and visualized under UV light. Genotypes are identified according to the band pattern as shown in Table 1.

2.3. Statistical analysis

Deviation from the Hardy–Weinberg equilibrium was determined by Chi-square and Fischer's exact test was used to compare allelic and genotypic distributions. The possible association of *DNMT 3B* rs2424913 and DS pregnancy risk was determined as odds ratios (OR) estimates with 95% confidence intervals (95% CI). The effect associated with the presence of the mutant allele was assessed in co-dominant (TT vs. CC and CT vs. CC), dominant (TT or CT vs. CC) and recessive (TT vs. CT or CC) models. Significance was achieved at $P < 0.05$. All statistical analyses were performed using GraphPad InStat Version 3.06 (GraphPad Software, San Diego, CA).

3. Results and discussion

Due to its high frequency, Down syndrome has great importance for public health worldwide. Although the genetic cause of DS has been discovered decades ago, the molecular mechanism underlying chromosome missegregation remains unknown. Both genetic and environmental factors are related to trisomy 21 and advanced maternal age is the only currently validated risk factor for DS. It has been shown that nutritional components can modulate epigenetic status of mammalian cells (Yen et al., 1994), and maternal polymorphisms in genes coding enzymes involved with folic acid cycle may act as potential risk factors for DS by centromeric hypomethylation and chromosomal nondisjunction secondary to the alteration of maternal folic acid metabolism (James et al., 1999).

DNA methylation is a chemical modification involved in regulation of gene expression that is important for several cellular processes, and DNA methyltransferase family is involved in both the maintenance of imprinted patterns and *de novo* methylation (Okano et al., 1999; Bestor, 2000). Disturbance in epigenetic mechanisms have been implicated in cancer development and several syndromes.

DNMT 3B is a nuclear protein involved in *de novo* methylation processes and it has been proposed that this protein interacts with

Table 1
PCR-RFLP conditions and genotypes observed for DNMT3B −149C > T polymorphism.

Primers (5′-3′)*	PCR conditions	Band pattern (bp)
F: 5′-TGCTGTGACAGGCAGAGCAG-3′ R: 5′-GGTAGCCGGGAACTCCACGG-3′	94 °C for 5 min, followed by 32 cycles of 94 °C for 30 s, 60 °C for 50 s, and 72 °C for 1 min, and a final elongation step at 72 °C for 4 min	CC: 380 CT: 380, 207 and 173 TT: 207 and 173

* As described by Xiao et al. (2008).

a constitutive centromere protein (CENP-C) to regulate the histone code in centromeric and pericentromeric regions that are essential for chromosome condensation and the fidelity of segregation (Gopalakrishnan et al., 2009). Another evidence that links DNMT 3B to chromosomal disjunction arises from the loss of DNA methylation from centromeric and pericentromeric repeat regions observed in Immunodeficiency, Centromere instability, Facial anomalies (ICF) syndrome patients (Erlich et al., 2006).

Several studies showed that some of SNPs in the *DNMT3B* gene may influence *DNMT3B* activity on DNA methylation, and one common *DNMT 3B* polymorphism located within an intronic region (rs2424913) is associated with an increased activity (Shen et al., 2002) and a higher expression of the protein was observed in carriers of heterozygous genotype (Fonseca-Silva et al., 2012).

DNMT 3B rs2424913 allelic distribution varies according to genetic background. The highest frequency of the mutant allele was described in China (T = 0.96–0.99) while the lowest frequency was observed in the Greek population (T = 0.26). Frequencies ranging from 0.42 to 0.48 were observed in Australia, USA, Poland, Netherlands and Great Britain (Jaiswal et al., 2015). The reported frequency in Italy is 0.32 (Coppède et al., 2013) while in India a frequency of 0.74 was observed (Jaiswal et al., 2015). In Brazil, Fonseca-Silva et al., 2012 observed a low frequency of the mutant allele (T = 0.25), however the sample size was small (N = 24). On the other hand, the frequency reported by Succi et al., 2014 (T = 0.51) was similar to our findings.

The frequency of the mutant *DNMT 3B* rs2424913 allele was 0.53 in CM and 0.44 in MDS. Genotype frequencies in CM were 0.22; 0.49 and 0.29 for CC; CT and TT, respectively, and 0.30; 0.52 and 0.18 for CC; CT and TT, respectively, in MDS. Genotypic distributions observed for both MDS and CM were according to those expected for Hardy Weinberg equilibrium ($\chi^2 = 0.05$; P = 0.98 for CM and $\chi^2 = 0.39$; P = 0.82 for MDS). Analysis of allele and genotype frequencies of *DNMT 3B* rs2424913 have revealed significant differences between cases and controls (P = 0.03 and P = 0.027, respectively). A summary of allele and genotype frequencies of the polymorphism in MDS and CM is shown in Table 2.

Most studies of *DNMT 3B* rs2424913 concerns the association of this polymorphism with different cancer types (Zhu et al., 2015) and the results are controversial. To date there are only two studies evaluating DS risk in association with DNMT3B rs 24224913 polymorphism. Coppede at al. (2013) have evaluated the role of DNMT 3B −579 G > T and rs2424913 polymorphisms in DS risk and found a protective effect associated with −579 GT and GT + TT genotypes in an Italian population. No independent significant association of rs2424913 and the risk of having a DS child were observed. However, a jointed analysis have revealed a statistically significant decreased DS risk associated with GT/CC haplotype (OR = 0.22; CI 95% 0.08–0.64; P = 0.003) (Coppède et al., 2013) probably due to −579 G > T polymorphism. Jaiswal et al. (2015) suggested that, although no independent association of these two polymorphisms have been identified in an Indian cohort, it might be possible that combinations involving −579 G and −149 T alleles might be considered maternal risk factors for DS.

Table 3
Association between maternal *DNMT 3B* −149C > T genotype and Down syndrome pregnancy risk among Down syndrome mothers (DSM; n = 111) and control mothers (CM; n = 212).

Model	Overall		
	OR	95% CI	P
TT vs. CC	0.47	0.24–0.92	0.03*
CT vs. CC	0.79	0.46–1.38	0.49
TT vs. CT or CC	0.54	0.31–0.96	0.04*
TT or CT vs. CC	0.67	0.40–1.13	0.14
T vs. C	0.69	0.50–0.96	0.03*

* Significant at p < 0.05.

We calculated the OR with 95% CI to assess the possible effect of the polymorphism over DS pregnancy risk (Table 3). The presence of the mutant allele (T vs. C) reduces in 30% the risk of a DS pregnancy (OR = 0.69; 95% CI: 0.50–0.96; P = 0.03). We have observed an excess of mutant homozygous genotype among CM compared to MDS, indicating a decrease in DS pregnancy risk associated with this genotype. In a recessive model (TT vs. CT or CC) an OR of 0.54 was observed (95% CI: 0.31–0.96; P = 0.04), representing a 45% reduction in the risk. Also, a >50% reduction was associated with TT genotype in contrast to wild type homozygous genotype (OR = 0.47; 95% CI: 0.24–0.92; P = 0.03) in a co-dominant model (TT vs. CC).

Our data revealed a significant independent decreased risk associated with the presence of allele T in both the co-dominant (TT vs. CC) and recessive (TT vs. CT or CC) models. Assuming the increased activity of the promoter and a higher expression level of the protein associated with this polymorphism (Shen et al., 2002; Fonseca-Silva et al., 2012) we could imagine a cellular scenario in which the presence of the mutant allele, mostly in homozygous state, should counteract an impaired DNA methylation of pericentromeric regions essential to normal segregation, avoiding DNA hypomethylation and allowing a decreased risk of having a DS child. Our results add to mounting evidence for the protective effect of *DNMT 3B* rs2424913 polymorphism on DS risk, and additional studies are necessary to establish the relationship between this polymorphism and the risk of bearing a DS child.

4. Conclusion

Our data indicate a protective effect of *DNMT 3B* rs2424913 polymorphism on DS offspring risk and further studies are mandatory to clarify the underlying mechanism, allowing this polymorphism to be taken into account in association studies related to

Table 2
Allelic and genotype frequencies of *DNMT 3B* −149C > T polymorphism in Down syndrome mothers (DSM) and control mothers (CM).

	Down syndrome mothers		Control mothers		P
	N	%	N	%	
Allele					
C	124	55.85	198	46.70	0.03*
T	98	44.15	226	53.30	
total	222	100.00	424	100.00	
Genotype					
CC	33	29.73	47	22.17	0.03*
CT	58	52.25	104	49.06	
TT	20	18.02	61	28.77	
total	111	100.00	212	100.00	

* Significant at P < 0.05.

the contribution of folate metabolism to the maternal risk of having a DS child.

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