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Loïc de Pontual[a], Delphine Trochet[a], Franck Bourdeaut[b], Sophie Thomas[a], Heather Etchevers[a], Agnes Chompret[c], Véronique Minard[c], Dominique Valteau[c], Laurence Brugieres[c], Arnold Munnich[a], Olivier Delattre[b], Stanislas Lyonnet[a], Isabelle Janoueix-Lerosey[b], Jeanne Amiel[a,*]

[a] Unité de Recherches sur les Handicaps Génétiques de l'Enfant INSERM U-781, et Département de Génétique, Université René-Descartes,
Faculté de Médecine, Hôpitaux de Paris, Hôpital Necker-Enfants Malades, 149, rue de Sèvres, 75743 Paris Cedex 15, France
[b] Laboratoire de Pathologie Moléculaire des Cancers, INSERM U-830, Institut Curie, Paris, France
[c] Département de Pédiatrie, Institut Gustave Roussy, Villejuif Cedex, France

* Corresponding author: Tel.: +33 1 44495648; fax: +33 1 44495150. E-mail address: amiel@necker.fr (J. Amiel). (currently: Jeanne.amiel@inserm.fr)

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A B S T R A C T
Neuroblastoma (NB), an embryonic tumour originating from neural crest cells, is one of the most common solid tumours in childhood. Although NB is characterised by numerous recurrent, large-scale chromosome rearrangements, the genes targeted by these imbalances have remained elusive. We recently identified the paired-like homeobox 2B (PHOX2B, MIM 603851) gene as disease-causing in dysautonomic disorders including Congenital Central Hypoventilation Syndrome (CCHS), Hirschsprung disease (HSCR) and NB in various combinations. Most patients with NB due to a germline heterozygous PHOX2B gene mutation are familial and/or syndromic. PHOX2B, at chromosome 4p12, does not lie in a commonly rearranged locus in NB. To evaluate the role of PHOX2B in sporadic, isolated NB, we analysed 13 NB cell lines and 45 tumours for expression, mutations of coding and promoter sequences, loss of heterozygosity (LOH), or aberrant hypermethylation of PHOX2B (13 cell lines and 18 tumours). We didn't identify any mutation but LOH in about 10% of the cases and aberrant CpG dinucleotide methylation of the 500 bp PHOX2B promoter region in 4/31 tumours and cell lines (12.9%). Altogether, both germinal and somatic anomalies at the PHOX2B locus are found in NB.

Introduction

Neuroblastoma (NB; MIM 256700) is a tumour of the sympathetic nervous system that accounts for 10% of all cancers in children. Several lines of evidence support the involvement of genetic factors in NB, namely, rare familial cases with vertical transmission and the association of NB with other genetically determined congenital malformations of neural crest origin, such as Hirschsprung disease (HSCR; MIM 142623) and/or Congenital Central Hypoventilation Syndrome (CCHS; MIM 209880).We recently identified the paired-like homeobox 2B (PHOX2B; MIM 603851) gene as the major disease-causing gene in CCHS1 and the first gene for which germline mutations predispose to NB.2–5 PHOX2B is a highly conserved homeotic transcription factor with two alanine tracts of nine and 20 alanines, C terminal to the homeodomain. The vast majority of mutations leading to CCHS result in an expansion of the longer alanine tract. Interestingly, patients harbouring either a missense mutation in the homeodomain or a frameshift mutation are the ones at risk of developing NB, whether or not they have CCHS.6 However, both germline and somatic PHOX2B coding sequence mutations are rare events in sporadic, isolated NB.7,4,8

Epigenetic abnormalities, especially alterations in DNA methylation, are involved in the development of various adult tumours. More recent studies have indicated that epigenetic aberrationsmay also contribute to paediatric cancer pathogenesis. In neuroblastomas, several potential tumour-suppressor genes have been found to be frequently hypermethylated and consequently down-regulated; in particular, genes of the tumour necrosis factor-related apoptosis-inducing ligand (TRAIL) pathway, CASP89 and the DCR receptors (DCR1, DCR2, DCR3 and DCR4.10,11 DNA methylation has been shown to reduce the binding affinity of sequence-specific transcription factors while methylation-dependent gene silencing may also involve alterations in chromatin structure, mediated by methyl binding proteins. Chromosome distribution of the methyl-targeted genes are clustered and the full pattern of methylation may be generated early in tumourigenesis.12,13 Finally, in tumours carrying a germline mutation, a

second-step methylation of the DNA promoter, if present, occurs exclusively on the wild-type allele.

The possible involvement of non-coding mutations or promoter methylation of the PHOX2B locus in sporadic neuroblastoma has not been evaluated. In this study, we examined the level of PHOX2B expression and its methylation in NB. PHOX2B was silenced in a subset of 3/13 NB cell lines and loss of expression was associated with aberrant 50CpG dinucleotide methylation of the PHOX2B promoter. PHOX2B promoter methylation was also detected in 2/18 tumuors analysed. Treatment with the demethyling agent 5-Aza-20-deoxycytidine (5-Aza-dC) restored PHOX2B transcription in PHOX2Bnegative cell lines, showing that gene silencing was due to aberrant hypermethylation. We conclude that aberrant CpG dinucleotide methylation of PHOX2B is an alternative mechanism at least as frequent as coding sequence mutations for inactivation of PHOX2B in sporadic NB.

2. Materials and methods

2.1. Patients

13 NB cell lines and 46 sporadic neuroblastic tumours were investigated. Patients were staged according to the International Neuroblastoma Staging System (INSS) and included seven with stage I tumour, ten stage II, seven stage III, 15 stage IV and seven stage IVS. Constitutional and tumour DNA were extracted using standard protocols. We included a patient from a two generation family with predisposition to NB due to a germline PHOX2B gene mutation (NBAF5, Table 1).2

2.2. Sequence analysis

We screened the coding sequence of the PHOX2B gene by direct DNA sequencing, as described elsewhere.1 We studied a 533 bp sequence of the promotor region that is extremely conserved among species (97% between human and chicken at nucleotide level). The primer sequences for PHOX2B promotor region are 5'-GAAGGGGGAAAACACACAC-3' (forward) and 5'-CGTAGGCAGAGGAATTGAGG-3' (reverse). PCR Direct DNA sequencing was performed using the fluorometric method (Big Dye Terminator Cycle Sequencing kit [Applied Biosystems]).

2.3. LOH analysis

Matched constitutional and tumour DNA samples were PCR amplified using microsatellitte markers of the Ge´ne´thon database D4S2974 and D4S1536 flanking the PHOX2B locus. D4S1536 is 4.1Mb centromeric to PHOX2B and D4S2974 is 95 Kb telomeric to PHOX2B. Fluorescent PCR products were electrophoresed and analysed on an automatic sequencer (ABI377, Applied Biosystems, Foster City, USA).

2.4. Cell culture

Cell lines were cultured at 37°C, 5% CO2, in Dulbecco's modified essential medium (DMEM; Invitrogen/Gibco, NY) containing 10% foetal calf serum, 292 μg/ml L-glutamine, 1% 100X MEM (non-essential amino acids medium, Invitrogen/ Gibco), and 0.5% penicillin solution.

Primary human neural crest cells were cultured for 3 weeks in FGF2- and EGF-containing embryonic stem cell medium with modifications available upon request.

2.5. PHOX2B expression in NB cell lines and tumours

Total RNA was isolated from cell lines and tumours by use of RNAzolB (Invitrogen). PHOX2B expression was first obtained from microarray on Affymetrix HG-U133 Plus 2.0 arrays. Data from 55 neuroblastic tumours were normalised using the GCRMA method. Detailed methods will be detailed elsewhere (I. Janoueix-Lerosey and O. Delattre, manuscript in preparation). In addition, RT-PCR detection of PHOX2B mRNA was performed in order to validate these data in 13 NB cell lines and eight tumours (Fig. 1a). First strand cDNA synthesis was performed on 2 μg of total RNA in a volume of 20μl by use of [RNA kit, Applied Biosystems] and oligo(dT) primers. The specific primers used for mRNA amplification were designed within exons 2 and 3, as follows: 5'-GAGGCGCGAGTCCA GGTGTGGTTC-3' (forward) and 5'-CGACAATAGCCTTGGGCCTACCCG- 3' (reverse). Expression analysis was performed in a 25-μl PCR reaction containing 1μl of cDNA, 1 μl dNTPs (2.5 mmol/l each), 0.5 μl of each specific primers (150 ng/μl), and 0.2 μl Taq polymerase (5 U/μl; Invitrogen). PCR conditions were standard with an annealing temperature of 69°C. PCR products were loaded on a 2% agarose gel and directly visualised under UV illumination.

2.6. Analysis of PHOX2B gene hypermethylation by bisulfite DNA sequencing

Genomic DNA was isolated from cell lines and primary tissues by standard procedures. Bisulfite treatment and DNA sequencing were performed as described.14 The primer sequences for PHOX2B are 5'-AAATGTAATTTATAAGATGTTT TTTTTTTG-3' (forward) and 5'-CACACTACTTAAAAATAATAA AAATTAAAT-3' (reverse). PCR conditions were standard with an annealing temperature of 58 _C. PCR products were loaded on a 2% agarose gel and directly visualised under UV illumination. PCR products were cloned in a TA cloning vector (Promega, Madison, WI) and ten individual clones were sequenced for each sample.

2.7. Treatment of NB cells with 5-Aza-dC

Cells were seeded, allowed to attach over a 24 h period, and treated for 72 h with the demethyling reagent 5-Aza-dC (Sigma) at a final concentration of 1 lM. After the treatment period the medium was removed and RNAs were extracted.

3. Results

3.1. Mutation and LOH at the PHOX2B locus in neuroblastoma

As previously reported, a heterozygous frameshift mutation was identified in the SK-N-SH cell line (721-740del20nt,3). No mutation, either somatic or germinal, of the PHOX2B coding sequence and promoter conserved region were identified in the other 12 NB cell lines and the 45 individuals with sporadic NB. A heterozygous missense mutation (R100L) was identified in patient NBAF5 originating from a family predisposed to NB over three generations. No second molecular event could be identified in tumoural DNA (Table 1). We detected three known

synonymous base substitutions, 552C > T(S184S), 750G > A (A250A) and 870C > A (P290P). In one patient, the P290P variant was heterozygous in constitutional DNA and homozygous in tumoural DNA. LOH was confirmed in this patient and identified in four other tumours (5/46 tumours, 10.8 %) with fluorescent microsatellite markers.

3.2. PHOX2B expression in NB cell lines and tumours

PHOX2B expression levels were obtained from Affymetrix HG U133 Plus 2.0 arrays. High level of PHOX2B expression was found in 10/13 cell lines and 15/17 tumours whereas no expresion could be detected in three cell lines and two tumours (Table 1). PHOX2B expression was examined by RT-PCR in 13 NB cell lines and eight tumours and two neural crest-derived tissues: adrenal gland medulla (MSR) and human trunk-level neural crest cells. These primary, non-transformed cells were derived from a human embryo at 28 days of development with a normal karyotype. Loss of expression was confirmed by the absence of PHOX2B mRNA transcripts in 3/13 cell lines (SK-N-SH, SK-N-BE and GIMEN) whereas PHOX2B cDNAs were visualised in all other cell lines and non-cancerous adrenal (MSR) and neural crest cells (NC) (Fig. 1a). PHOX2B was silenced in three tumours: one ganglioneuroma (NBAF21), one ganglioneuroblastoma (NBAF38) and one NB (NB10) (Fig. 1a).

3.3. Methylation and silencing of PHOX2B in NB cell lines and tumours

Promoter-associated CpG islands of PHOX2b were analysed by methyl sequencing in a panel of 13 cell lines, 18 tumours and two neural crest-derived tissues: adrenal gland medulla (MSR) and human trunk-level neural crest cells. All 12 CpG dinucleotides were 100% methylated (10/10 clones) in 2/13 cell lines (SK-N-BE and GIMEN) and in 2/18 tumours (NBAF21 and NB10 (Fig 1b). As sequencing of the PCR products showed that cytosines outside the CpG sites were converted to thymine, an incomplete bisulfite conversion could be ruled out.

3.4. Restoration of PHOX2B expression in negative cell lines by 5-Aza-dC

5-Aza-dC, a methyltransferase inhibitor, was used to investigate whether PHOX2B expression could be restored cell lines for which PHOX2B was not expressed. PHOX2B mRNA expression levels, analysed by RT-PCR, were restored in SK-N-BE and GIMEN cell lines, while no re-expression was observed for SKN- SH.

4. Discussion

This study of a series of 13 cell lines and 46 neuroblastic tumours aimed to determine the role of PHOX2B in sporadic NB. PHOX2B, not known so far for being either a tumour-suppressor gene or a proto-oncogene, is the first predisposing gene identified in NB. Most mutations occur in familial and syndromic NB cases. A heterozygous germline mutation was found in about 20% of published pedigrees and reached 50% when HSCR is associated with NB either in the index case or relatives.2,5,7,4 However, germline PHOX2B mutations are rare in sporadic isolated NB (1/215 cases in the series reported by Van Limpt and 2/86 in the series reported by McConville).3,8 Somatic PHOX2B mutations have also been described in NB.3 In the series of 45 sporadic NB cases we report, no PHOX2B gene mutations were identified either in the coding sequence or the promoter region. LOH at the PHOX2B locus could be detected in 5/46 cases.

This ratio of about 10% has to be balanced with the known high rate of chromosomal rearrangement in NB. It is worth noting that LOH of the short arm of chromosome 4 is found in roughly 20% of NB, but PHOX2B is centromeric to the smallest region of overlap (SRO).15,16

We subsequently asked the question of epigenetic events at the PHOX2B locus and identified clonal aberrant CpG island methylation of the promoter in 2/13 NB cell lines and 2/18 tumours (ganglioneuroma in one case and NB stage II in one case). The demethylating drug 5-Aza-dC re-induced PHOX2B expression in NB cell lines, suggesting that PHOX2B methylation correlates with gene silencing. Moreover, it is well established that DNA demethylating agents as 5-Aza-dC induce adrenergic differentiation in NB cell lines17 and have an antiproliferative effect in mouse NB models.18 Hypermethylation and downregulation of potential tumour-suppressor genes such as genes involved in cell-cycle control or apoptosis is often associated with a poor outcome in NB.9,19,20

We first considered PHOX2B as a potential tumour-suppressor gene since, i) at least some mutations identified in syndromic or familial NB cases (i.e. missense mutations of the homeodomain) are likely loss-of-function mutations, ii) a 'second hit' model has been proposed in NB21 and, iii) some constitutional LOH at chromosome 4p encompass the PHOX2B locus.4 However, in patients with germinal PHOX2B mutation, neither a secondmutation nor LOH or aberrant promoter hypermethylation in the tumours have been identified as reported earlier.2

PHOX2B has been shown to promote differentiation by controlling G1-S transition during cell cycle of sympathetic neuroblast precursors22 and is an essential regulator of normal autonomic nervous system development.23 Mice with a homozygous inactivation of Phox2b fail in proper differentiation of the sympathetic nervous system. A gain-of-function or a dominant negative effect of PHOX2B frameshift mutations is not, however, ruled out. When tested, mutant transcripts were present and stable.2 While mutant proteins localised to the nucleus, we observed some ability to bind DNA for two of the three PHOX2B frameshift mutations tested in vitro, although transactivation of the dopamine betahydroxylase promoter was always severely impaired.24 Moreover, Bachetti and coworkers reported an increased transactivation of the PHOX2A promoter for proteins resulting from frameshift mutations when compared to the wild type protein. 25 PHOX2B is expressed not only in neural crest cells but also in mature sympathetic tissue of adrenal gland (Fig. 1a and1). Methylation-associated repression of PHOX2B could result in a differentiation block of sympathetic neuroblasts.

Interestingly, NB10 patient had HSCR. We found aberrant homozygous PHOX2B promoter methylation on the tumour sample DNA while neither a mutation nor a deletion could be identified on either germinal or tumour DNA. Interestingly, PHOX2B was not methylated on lymphocyte DNA. We could speculate that PHOX2B methylation occurred during embryonic development and is responsible for both HSCR and NB development. As malignant transformation of cells could happen at different stages of tissue maturation, aberrant methylation may contribute to the diversity that characterises NB and other genes of the RET-PHOX2B pathway could be implicated. Interestingly, aberrations in the p53/MDM2/ p14 (ARF) pathway have recently been described in the two NB cell lines where PHOX2B was found methylated26; a p53 mutation in SKNBE(2)C and aberrant p14 (ARF) methylation in GIMEN.

Promoter methylation is not only implicated in silencing tumour-suppressor genes but also in regulation of developmental pathways during embryogenesis.27 Abnormal methylation in NB could result from abnormalities in this process in a self-renewing multipotent stem cell becoming the malignant progenitor of this neural crest cancer.Within a single tumour, cell phenotypes are characteristic of embryonic structures, particulary neuroblasts, Schwann cells and melanocytes. Cellular heterogeneity and maturation stage correlate with clinical stage and prognosis of the disease.

However, down-regulation of PHOX2B was not always associated with hypermethylation. In SK-N-SH, the mutation is heterozygous and no PHOX2B expression could be detected. This result is discordant with the one reported by van Limpt and coworkers who observed the expression of both wild-type and mutant cDNAs in this cell line. However, they observed a PHOX2B gene silencing in the SHEP cell line, a stable subclone of SK-N-SH and also carrying the frameshift mutation. One could speculate on aberrant hypermethylation outside of the promoter region studied. However, it is worth noting that no expression of H-ASH1 could be detected either in the SK-N-SH cell line or in NBAF38 tumour (data not shown). This could also contribute to PHOX2B down-regulation. Finally, one can speculate on the effects of other mechanisms such as micro RNAs Fig. 2.

Genetic heterogeneity in predisposition to neuroblastic tumours is likely. The high reocurence of loss of heterozygosity for chromosomes 1p36 and 11q23 supported the existence of putative tumour-suppressor genes within these regions. However, these loci do not segregate with NB in most familial cases. On the other hand, linkage analysis has focused attention on 16p12-13 and 4p16.28,16 Several studies have clearly demonstrated that PHOX2B is a major predisposing gene in syndromic NB cases (i.e. associated with other autonomic dysfunction).6,3,29 Aberrant methylation of the PHOX2B promoter seems to be an alternative mechanism as frequent as mutation in sporadic NB cases and argues that loss-of-function by haploinsufficiency is the NB-predisposing mechanism.

Conflict of interest statement
None declared.

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