

## REVIEW ARTICLE

# Pediatric Disorders with Autonomic Dysfunction: What Role for *PHOX2B*?

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### ABSTRACT

Hirschsprung disease, neuroblastomas, and congenital central hypoventilation syndrome can occur in combination, and familial cases have been reported in all three conditions. This suggests variable expression of a single genetic abnormality as the common cause to these neural crest disorders. Because the *PHOX2B* gene is pivotal in the development of most relays of the autonomic nervous system, including all autonomic neural crest derivatives, it was considered a candidate gene for the above conditions. Recent studies have shown that 1) *PHOX2B* is the main disease-causing gene for congenital central hypoventilation syndrome, an autosomal dominant disorder with incomplete penetrance; 2) *PHOX2B* is the first gene for which germline mutations have been demonstrated to predispose to neuroblastoma; and 3) Hirschsprung disease was associated with an intronic single-nucleotide polymorphism of the *PHOX2B* gene in a case-control study. For clarifying the variable clinical expression of the autonomic nervous system dysfunction observed in neural

crest disorders, international databases of clinical symptoms and molecular test results should be established. Furthermore, the development of genetic mouse models should help to improve our understanding of the molecular mechanisms underlying neural crest disorders. (*Pediatr Res* 58: 1–6, 2005)

### Abbreviations

**ANS**, autonomic nervous system  
**CCHS**, congenital central hypoventilation syndrome  
**HASH-1**, human achaete-scute homologous 1 gene  
**HSCR**, Hirschsprung disease  
**LO-CHS**, late-onset central hypoventilation syndrome  
**MASH-1**, mammalian achaete-scute homologous 1 gene  
**PHOX2B**, paired-like homeobox 2b gene  
**RET**, rearranged after transfection gene  
**SIDS**, sudden infant death syndrome

The neural crest is a multipotent embryonic structure that gives rise to neuronal, endocrine, craniofacial, pigmentary, and conotruncal cardiac tissues (1). Neural crest disorders encompass tumors such as neuroblastomas, birth defects, and variable combinations of single or multifocal abnormalities that affect the above-listed tissues. Hirschsprung disease (HSCR) is a neural crest disorder characterized by the absence of enteric ganglia along a variable length of the intestine (2). Neuroblastoma is a neural crest-derived tumor (3) and accounts for ~10% of all cancers in children. Congenital central hypoventilation syndrome (CCHS), or “Ondine’s curse,” has been classified among the neural crest disorders because it occurs in association with HSCR and neural crest-derived tumors (4,5). Evidence that the paired-like homeobox transcription factor

*Phox2b* is pivotal to the development of the visceral nervous system in mice, including neural crest derivatives that control autonomic ganglia, points to *PHOX2B* as a candidate gene for CCHS, HSCR, and neuroblastoma (6,7). Recent studies have shown that 1) *PHOX2B* is the major disease-causing gene for CCHS (8–12); 2) *PHOX2B* is the first gene for which germline mutations have been found in patients with neuroblastoma (13,14); and 3) two novel intronic single-nucleotide polymorphisms (SNPs) and one deletion mutation in the *PHOX2B* gene have been identified in patients with HSCR, suggesting that *PHOX2B* haploinsufficiency may predispose to HSCR (15,16). Furthermore, studies in transgenic mice have produced data on the homozygous and heterozygous *PHOX2B* knockout phenotypes (17).

### PHOX2B Is Essential for the Development of Neural Crest Derivatives in Mice

Neural stem cells in the developing nervous system can give rise to a wide variety of distinct neuronal subtypes. Consider-

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able progress has been made in identifying the molecular signals that control neuronal specification and differentiation. For example, the generation of autonomic neurons from neural crest cells is induced by an extrinsic signal (bone morphogenic proteins) that elicits the expression of a network of transcription factors, which, in turn, control autonomic neuron differentiation (18). This network includes *Mash-1* (Ascl1-Mouse Genome Information), the mammalian homologue of the *Drosophila* archaete scute gene complex, and the paired homeodomain transcription factor *Phox2b*. *Phox2b* and its paralogue, *Phox2a*, bind to the promoter of the subtype-specific noradrenergic marker genes tyrosine hydroxylase and dopamine- $\beta$ -hydroxylase, activating their transcription. *Mash-1* and *Phox2b* can induce the differentiation of noradrenergic neurons from neural crest precursor cells (19–22) and are essential determinants of the noradrenergic phenotype, both central and peripheral (6,7,23,24). Depending on the subtype of noradrenergic neuron, they can act in different epistatic orders and interact with distinct transcription factors in various noradrenergic cell types (18,25). Furthermore, *Mash-1* and *Phox2b* work in concert during the generation of parasympathetic cholinergic (26) and serotonergic neurons (27,28).

Homozygous *Phox2B*-deficient mice die shortly after mid-gestation (6). The cause of death is complete absence of noradrenergic neurons, including those of the locus coeruleus in the CNS (6). Homozygous *Phox2b*-deficient embryos lack sympathetic, parasympathetic, and enteric ganglia (6). Furthermore, *Phox2b* controls the development of peripheral chemoreceptors and afferent visceral pathways (17). In homozygous *Phox2b*-deficient mice, the neural crest-derived carotid body degenerates, as do the three epibranchial placode-derived visceral sensory ganglia (geniculate, petrosal, and nodose), whereas the nucleus of the solitary tract, which integrates all visceral information, never forms (17).

Heterozygous *Phox2b* newborn mice develop normally after birth. Nevertheless, they have abnormal function of chemical respiratory control and dysgenesis of the petrosal chemoreceptors, which may underlie the neonatal respiratory phenotype (17) characterized by an abnormal duration of sleep apneas during the first days of life (J.G., personal observations). Therefore, the respiratory phenotype of heterozygous *Phox2b* partly models the respiratory phenotype of CCHS patients.

### **PHOX2B, the Major Disease-Causing Gene for CCHS**

**Clinical features of CCHS.** CCHS is a very rare disorder with an estimated prevalence of 1 in 200,000 live births (29). Sleep-dependent hypoventilation, especially during non-rapid eye movement sleep, is the hallmark of CCHS (4,5). Clinical onset occurs in the first few postnatal days in most patients, in the absence of neuromuscular disorders, heart or lung disease, or identifiable brain lesions. There is considerable within- and between-patient variability in the severity of hypoventilation. Hypoventilation is present during wakefulness in the most severe cases. A functional characteristic of CCHS patients is absence or marked blunting of the ventilatory response to sustained hypercapnia. CCHS patients also have a depressed ventilatory response to sustained hypoxia. Peripheral chemo-

receptors are functional in the milder cases (4). In addition to respiratory abnormalities, CCHS patients have functional disorders of autonomic nervous system (ANS) control with abnormalities in heart rate, blood pressure, and pupil diameter control (4,5,30,31). Furthermore, the enteric nervous system may be abnormal, with ~15–20% of patients having Hirschsprung disease (HSCR) (4,5,29). It is interesting that most of the CCHS patients with HSCR have aganglionosis extending proximal to the sigmoid (29). Neural crest-derived tumors such as neuroblastoma, ganglioneuroblastoma, and ganglioglioma are present in ~5% of patients with CCHS (3). Finally, a few patients exhibit central hypoventilation syndrome during infancy or early childhood (4). Although late-onset central hypoventilation syndrome (LO-CHS) is very probably a heterogeneous condition, relationships between a subgroup of LO-CHS and CCHS have been debated.

**Genetic basis for CCHS.** A genetic basis for CCHS is supported by several lines of evidence: 1) although CCHS is usually a sporadic disorder, familial cases have been reported in monozygotic twins, female siblings, and male–female half-siblings (4,5); 2) concomitant presence of genetically determined conditions, *i.e.* HSCR and neuroblastoma, has been described (3–5); and 3) more important, vertical transmission of CCHS has been reported (32,33). In addition, a child with CCHS was born to a mother who had a neural crest tumor, suggesting differences in the clinical expression of neural crest disorders (34). Furthermore, investigations in parents of CCHS patients have found a high prevalence of dysautonomic symptoms (35,36).

The candidate-gene approach has been used to identify gene mutations in CCHS. *PHOX2B* is a candidate gene for CCHS. The *PHOX2B* gene in humans is located on chromosome 4p12 and encodes a highly conserved homeobox domain transcription factor (314 amino acids), with two short and stable polyalanine repeats of nine and 20 residues, respectively (37). Recent studies have shown *PHOX2B* mutations in the majority of CCHS patients (Table 1) (8–12). Most of the mutations consisted in alanine expansions within the polyalanine stretch of *PHOX2B* exon 3 (Table 1). Importantly, in individuals who are heterozygous for length variants of the polyalanine stretch of *PHOX2B* exon 3, the largest allele is prone to unsuccessful amplification by DNA polymerase, indicating a need for improving methodologic approaches (11). *PHOX2B* polyalanine expansion mutations have also been identified in some patients with LO-CHS (Table 1) (11,12,38), suggesting a genetic link between CCHS and LO-CHS. Of particular interest is a recent case report of an adult who received a diagnosis of LO-CCHS at 35 y of age and carried an alanine *PHOX2B* mutation and had two daughters with LO-CHS and the same *PHOX2B* mutation as their father (39). The function of polyalanine stretches is largely unknown in humans (40). Nevertheless, there is growing evidence for a common disease-causing mechanism resulting from heterozygous polyalanine expansions and consisting of a protein misfolding leading to cytoplasmic aggregation of both mutant and wild-type proteins and therefore loss of nuclear transactivation function (40). Further evidence that *PHOX2B* is the primary CCHS gene comes from a few case reports of children who have CCHS and have no polyala-

**Table 1.** Molecular analysis of *PHOX2B* mutations in patients with CCHS and with LO-CHS

	<i>PHOX2B</i> Mutation		Investigators (Reference)
	Poly-Ala Expansion	Other Mutations	
CCHS probands (no. of cases)			
29 CCHS	16	2 frameshift	Amiel <i>et al.</i> (8)
10 CCHS	4	1 frameshift	Sasaki <i>et al.</i> (9)
67 CCHS	65	1 nonsense	Weese-Mayer <i>et al.</i> (10)
27 (24 CCHS and 3 LO-CHS)	22	3 frameshift	Matera <i>et al.</i> (11)
188 (179 CCHS and 9 LO-CHS)*	174	10 frameshift 3 missense	Trochet <i>et al.</i> (12) Trochet <i>et al.</i> (12)
Inherited <i>PHOX2B</i> Mutation			
CCHS probands with affected offspring (no. of familial cases)			
3	Poly-Ala expansion		Weese-Mayer <i>et al.</i> (10)
2	Poly-Ala expansion		Matera <i>et al.</i> (11)
	Frameshift		Matera <i>et al.</i> (11)
2	Poly-Ala expansion		Trochet <i>et al.</i> (12)
<i>PHOX2B</i> Mutation			
Unaffected parents of CCHS patients (no. of parents†)			
8	None		Amiel <i>et al.</i> (8)
67	4 somatic mosaicism		Weese-Mayer <i>et al.</i> (10)
27	1 poly-Ala expansion		Matera <i>et al.</i> (11)
	1 frameshift		Matera <i>et al.</i> (11)
124‡	10 somatic mosaicism		Trochet <i>et al.</i> (12)

Poly-Ala, polyalanine.

\* Including the 29 CCHS patients from Amiel *et al.* (8).

† Unaffected parents for whom blood samples were available.

‡ Including 105 pairs of parents and 19 single parents.

nine repeat expansion but exhibit other *PHOX2B* mutations, such as frameshift mutation (8,11,12), nonsense mutation (10), or missense mutation (8,12) (Table 1). Finally, direct sequencing of the *PHOX2B* coding sequence, the intron-exon boundaries, and the 530 bp of the promoter region failed to detect a nucleotide variation in a small percentage of CCHS cases (12). However, two unaffected mothers of CCHS patients carried a frameshift *PHOX2B* mutation and an alanine *PHOX2B* mutation, respectively (11) (Table 1).

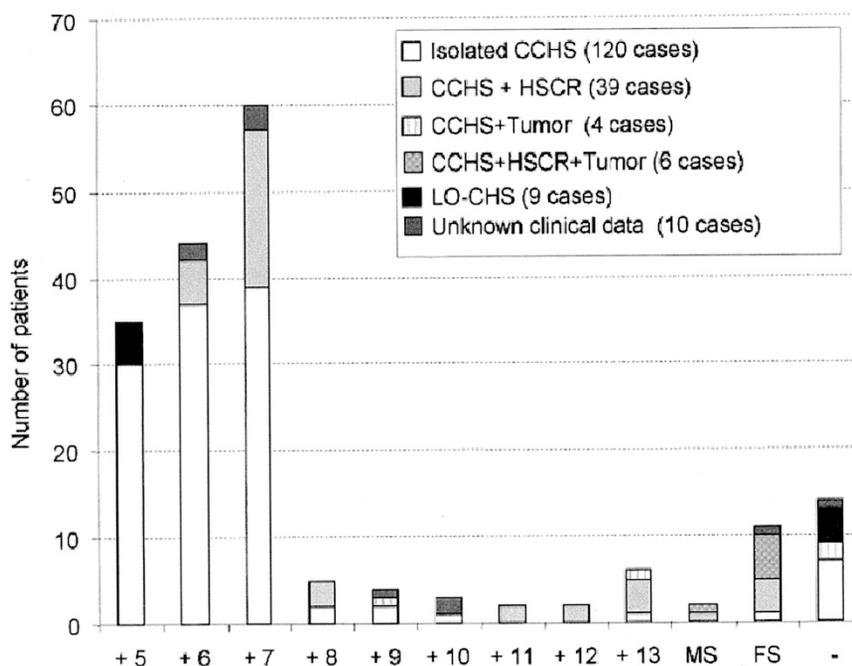
**Inheritance of CCHS.** The mode of inheritance is autosomal dominant. Indeed, most of the mutations found so far in affected probands with unaffected parents occurred *de novo* (8,10–12). When the alanine expansion is transmitted from an affected parent to his or her affected child, the expansion remains stable. However, the mutation identified in the proband can be detected in DNA extracted from peripheral leucocytes of an asymptomatic parent (10,12). A somatic mosaicism was detected in 4.5% of parents (Table 1) (10,12). This has important implications for genetic counseling. The recurrence risk cannot be predicted accurately, as the percentage of germline mosaicism is unknown. Nevertheless, the risk may be as high as 50%; consequently, prenatal diagnostic investigations should be offered in the event of a subsequent pregnancy (10,12).

**Genotype/phenotype correlations.** Genotype/phenotype correlations have been described in CCHS patients. Weese-Mayer *et al.* (10) reported an association between the number of *PHOX2B* repeats and the number of ANS dysfunction symptoms. Furthermore, a larger number of repeats may be associ-

ated with long sinus pauses in patients with CCHS (author observations). Matera *et al.* (11) reported a genotype/phenotype correlation between the number of *PHOX2B* repeats and the severity of the respiratory disorders. Trochet *et al.* (12) reported that the distribution of alanine expansion patterns differed among patient subgroups in a series of 188 CCHS cases (Fig. 1). The smallest alanine expansion was the only pattern identified in LO-CHS but was not found in any of the patients with CCHS and HSCR. However, although patients with CCHS and HSCR tend to have longer alanine expansions than do patients with isolated CCHS, the phenotype cannot be predicted accurately from the genotype, because the +7 alanine expansion is the most common pattern in both the isolated CCHS and the CCHS-plus-HSCR populations. Finally and very important, studies of genotype/phenotype interactions strongly support the possibility that CCHS patients who develop malignant neural crest-derived tumors harbor either a missense or a frameshift heterozygous mutation in the *PHOX2B* gene (9,10,12). Thus, the results of *PHOX2B* molecular testing identify a subset of CCHS patients who are at very high risk for developing malignant tumors (12).

It is interesting that a subset of CCHS patients with the *PHOX2B* gene mutation are characterized by mutations in other rearranged after transfection gene (*RET*) pathway genes, including *RET*, *GDNF*, and the human ortholog of Mash-1 (*HASH-1*) (8,41). Therefore, mutations in other genes may contribute to the considerable variability in CCHS phenotypes.

Finally, recent advances in functional imaging have allowed investigations of functional brain deficits during respiratory



**Figure 1.** *PHOX2B* mutations among subgroups of patients with CCHS or LO-CCHS. The mutation types are reported on the x axis. Alanine expansions are symbolized by a plus sign (+) followed by the number of extra alanines. MS, missense mutations; FS, frameshift mutations. The minus sign (-) represents the group of patients ( $n = 14$ ) with no identified *PHOX2B* mutation. Clinical subgroups are listed in the graph key. Reprinted with permission from Trochet *et al.*, *Am J Hum Genet*, 76:421–426, ©2005 by The American Society of Human Genetic.

and cardiovascular challenges in CCHS patients (42,43). Functional deficits have been found in brainstem areas targeted by *PHOX2B* expression. However, functional deficits were also observed in other areas that are not known to be targeted by *PHOX2B*, such as limbic structures and deep cerebellar nuclei. It is unclear whether these functional deficits are secondary to hypoxic or perfusion sequelae of abnormal developmental *PHOX2B* expression or reflect other unknown genetic deficits in CCHS patients.

#### ***PHOX2B* Haploinsufficiency May Predispose to HSCR**

HSCR is the main genetic cause of functional intestinal obstruction, with an incidence of 1/5000 live births. Patients can be classified as having short-segment HSCR (80% of cases), in which the aganglionic segment does not extend beyond the upper sigmoid, or long-segment HSCR, with extension proximal to the sigmoid; long-segment disease is the more common pattern in CCHS patients (29). HSCR is characterized by incomplete penetrance, a marked gender-related difference in clinical expression, and variation in penetrance affecting the extent of aganglionosis. As mentioned above, HSCR can occur in combination with CCHS and also with neuroblastoma (44). It is interesting that some patients with HSCR have impaired cardiovascular and pupillary control (45) and abnormal breathing during sleep (H.T., unpublished data), suggesting that dysfunction of the autonomic component of cardiovascular, pupillary, and breathing control can be present in patients with HSCR. So far, there have been no reports of CCHS with HSCR in one of the parents.

HSCR is a complex genetic disorder that requires the interaction of multiple genes for disease expression (46–48). Mu-

tations of eight susceptibility genes that belong to the RET and endothelin pathways have been identified (2). Studies in two-locus mouse models of HSCR have shown that interactions between *Ret* and *EDNRB* (endothelin receptor B) genes are central to this complex disorder (47). However, even with extensive mutation screening, a *RET* mutation is identified in only 50% of familial and 15–20% of sporadic HSCR cases and an *EDNRB* mutation in approximately 5% of cases (2). Recently, the contribution of *PHOX2B* to the HSCR phenotype was investigated in patients with HSCR. Garcia-Barcelo *et al.* (15) showed an association between HSCR and an intronic SNP in a case-control study. However, Benailly *et al.* (16) reported a deletion mutation in the *PHOX2B* gene in a girl with syndromic short-segment HSCR. These new findings suggest that *PHOX2B* haploinsufficiency may predispose to HSCR.

#### ***PHOX2B*, the First Gene for Which Germline Mutations Have Been Shown to Predispose to Neuroblastoma**

Neuroblastoma is a tumor of the sympathetic nervous system. Although no predisposing genes have been identified so far, several lines of evidence support the involvement of genetic factors: a few familial cases with vertical transmission and multifocality have been reported (49,50), and neuroblastoma occasionally arises in patients with genetically determined congenital neural crest disorders such as HSCR and CCHS (3). The recent identification of *PHOX2B* as the major disease-causing gene in CCHS pointed to *PHOX2B* as a candidate gene for both familial and syndromic neuroblastoma (13). Trochet *et al.* (13) reported missense *PHOX2B* mutations in both a familial case of neuroblastoma and a patient with neuroblastoma and HSCR. In a study of families with neuro-

blastoma, Mosse *et al.* (14) identified a frameshift *PHOX2B* mutation in one family but found no evidence for mutations in this gene in eight other families. These data suggest that *PHOX2B* mutations may be involved in neuroblastoma tumorigenesis but that germline mutational events in this gene may not be present in all hereditary neuroblastoma cases. Studies in larger numbers of patients will help to determine the frequency of *PHOX2B* mutations in genetic and sporadic forms of neuroblastoma. Further work is needed to clarify whether 1) *PHOX2B* mutations in patients with neuroblastoma result in gain or loss of function and 2) *PHOX2B* is a partner of alternative genetic events that predispose to tumorigenesis. Finally, it should be borne in mind that a child with CCHS was born to a mother with neuroblastoma, suggesting variable clinical expression of a single genetic disorder (34).

### Is PHOX2B a Candidate Gene for Sudden Infant Death Syndrome?

Abnormalities in ANS control have been shown to contribute to the vulnerability of some infants to sudden infant death syndrome (SIDS) (51). Kinney *et al.* (52) suggested that SIDS may be related to a developmental abnormality in the medullary serotonergic network. However, the prevalence of SIDS is high in CCHS families, suggesting that these two disorders may share developmental abnormalities in ANS control (53). The recent demonstration that Mash-1 and Phox2b transcription factors are involved in the development of central serotonergic neurons in mice (27,28), the recent identification of *PHOX2B* as the major disease-causing gene of CCHS, and the presence of *HASH-1* mutations in addition to *PHOX2B* mutations in three patients with CCHS (8,41) point to *PHOX2B* and *HASH-1* as candidate genes for SIDS. However, no *HASH-1* or *PHOX2B* polyalanine expansion mutations were found in a group of 92 SIDS victims (54). Similarly, Kijima *et al.* (55) found no *PHOX2B* gene mutations in 23 SIDS victims. Further genetic studies are needed in SIDS to clarify the interactions between SIDS and abnormal ANS development.

**In summary.** Candidate gene approaches have brought new insights into the molecular mechanisms of neural crest disorders such as CCHS, HSCR, and neuroblastoma. The finding that *PHOX2B* is the major disease-causing gene for CCHS allows genetic counseling and prenatal diagnosis. Information on the potential transmission of CCHS must be disseminated to CCHS families, obstetricians, and pediatricians. Moreover, meticulous attention should be paid to infants whose mother or father has CCHS or neuroblastoma. *PHOX2B* is the first gene for which germline mutations have been shown to predispose to neuroblastoma. Nevertheless, the molecular events that lead to neuroblastoma need further investigation. Furthermore, the presence of frameshift or nonsense *PHOX2B* mutations in CCHS patients who developed malignant neural crest-derived tumor warrants careful follow-up of patients who carry such mutations. Among the complex genetic interactions reported so far in HSCR, *PHOX2B* haploinsufficiency may play a role in the variable clinical expression of HSCR. Finally, further genetic investigations in SIDS victims and their families should further explore the *PHOX2B* signaling pathway. Inter-

national databases of clinical symptoms and molecular analyses should be organized to clarify the variable clinical expression of the ANS dysfunction observed in neural crest disorders. Furthermore, development of genetic mouse models is useful for improving our understanding of the molecular mechanisms underlying neural crest disorders.

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