A Novel HLXB9 Mutation in a Chinese Family with Currarino Syndrome

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Introduction

Currarino syndrome (CS), first described in 1981,1 is a congenital malformation typically associated with sacral agenesis, anorectal malformations, and a presacral mass. Patients affected by CS display a phenotypic variability, whereby the spectrum of phenotypes ranges from a severe triad to asymptomatic features.2,3

A familial tendency with autosomal dominant inheritance was noted by Yates et al in 1983.4 Ross et al. further reported that mutations in the homeobox gene HLXB9 are the major cause of CS.5 Mutations in the HLXB9 gene have been identified in almost all reported cases of familial CS, and in approximately 30% of patients with sporadic CS.6

The HLXB9 gene is essential for proper pancreatic development and for the differentiation of motor neurons in the spinal cord.7,8 It has 3 exons and encodes a 403-amino acid transcription factor HB9 protein. The HB9 protein contains a homeodomain preceded by a highly conserved 82-amino acid domain and a poly-alanine region.9

In this article, we report a new HLXB9 gene mutation identified in a Chinese family with members suffering from CS, together with the clinical characteristics of the affected individuals.

Patients and Methods

The cases of 2 members of a family diagnosed with CS were analyzed for clinical findings. Blood samples were taken from the patients and their relatives and screened for DNA mutations in the HLXB9 gene. The Isl1 and Lim3 genes, known to be involved in the same pathways as the HLXB9,9,10 were also screened. After having obtained informed consent, DNA was extracted from peripheral blood using a TIANamp Genomic DNA Kit in accordance with manufacturer’s instructions (Tiangen Biotech, Beijing, China). Polymerase chain reaction (PCR) amplification and direct sequencing were performed to screen for DNA mutations. The primers used to screen HLXB9 and Lim3 genes were as described in the literature.5,11 The Isl1 gene primers were designed by us (information available on request). Direct sequencing was performed using an ABI 3730 automatic sequencer (Applied Biosystems, Carlsbad, CA, USA).

Results

Clinical Findings

Patient 1 was an 11-year-old girl. She was admitted due to a recurrent presacral mass for 1 year. She was born with an imperforate anus (low type) and subsequently underwent anoplasty. No magnetic resonance imaging (MRI) was performed at the time, so whether she had a presacral mass or not was not identified. Constipation persisted even after the operation. At the age of 3, a rectal biopsy showed the absence of ganglion cells, consistent with a diagnosis of Hirschsprung’s disease. During a radical macrosigmoid operation, a presacral mass was discovered, and she also underwent excision of the mass. Histological examination of the mass showed it to be a dermoid cyst. The presacral mass reoccurred during the follow-up period. MRI of the lumbosacral spine revealed sacrococygeal hypoplasia and a presacral mass (6.8 × 6.4 × 9.1 cm; Fig. 1), all of which are consistent with the diagnosis of Currarino syndrome. The mass was removed again. A subsequent histological examination determined the mass to be a dermoid cyst.

Patient 2 was a 3-year-old boy, the younger brother of patient 1. He was born with a rectoperineal fistula and consequently underwent anoplasty at the local hospital. Constipation persisted and he was admitted to our hospital. Barium enema suggested the possibility of Hirschsprung’s disease, but subsequent rectal biopsy excluded the diagnosis. An MRI of the lumbosacral spine showed a lipomyelomeningocele, a tethered cord, and sacral agenesis (Fig. 2), all leading to the diagnosis of Currarino syndrome. The child underwent repair of the myelomeningocele and release of the tethered cord. Postoperatively, the patient was still constipated and was managed with enemas for constipation.
Genetic Analysis
Using the methods described above, we identified a novel HLXB9 heterozygous non-sense mutation (c.552C → G; p.Tyr184X) affecting the highly conserved domain. The 2 patients, their mother, as well as their maternal grandmother presented with the same heterozygous p. Tyr184X mutation (Fig. 3). The mother and maternal grandmother, who did not show any clinical features and did not undergo any X-ray or MRI examinations, were regarded as asymptomatic carriers. No mutation was present in the other members of the family. The screening of the Isl1 and Lim3 genes revealed no mutation in those genes in any members of the family.

Discussion
Currarino syndrome is mainly caused by HLXB9 mutations attributed to a haploin-sufficiency. To date, a total of 69 HLXB9 mutations (including cytogenetic anomalies) have been identified. The phenotypic variability observed in this study among the family members carrying the same mutation can be best explained by the existence of other modifier genes, which may affect the HLXB9 protein partners or transcriptional regulators. Candidate genes may include those known to be involved in the same pathways as HLXB9. We screened the Isl1 and Lim3 genes, both of which are regulators of HLXB9 gene expression during the development of the motor neurons in other vertebrates. In the case of the family studied, however, there were no mutations in the Isl1 and Lim3 genes in any family member. It will be necessary to screen more candidate genes to explain the presence of CS.

The identification of the HLXB9 gene mutation confirms the CS diagnosis, and it is suggested that mutational analysis should be performed in patients suspicious for CS. It is still difficult to offer precise genetic counseling, due to the lack of genotype-phenotype correlations and the variability of expression in carriers.

Conflict of Interest
None

References


