First occurrence of aprosencephaly/atelencephaly and holoprosencephaly in a family with a SIX3 gene mutation and phenotype/genotype correlation in our series of SIX3 mutations

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RESULTS AND DISCUSSION

Of the 210 patients screened, seven had mutations in the SIX3 gene but none in other HPE causing genes. The findings are illustrated in figs 1, 2, and 3. HPE was associated with AP/AT in three affected sibs carrying a maternally inherited mutation of SIX3.

Aprosencephaly/atelencephaly (AP/AT) refers to rudimentary prosencephalon, while holoprosencephaly (HPE) is a failure of telencephalon cleavage. The question of whether AP/AT results from a disruptive lesion or a growth failure is still debated. At least six causal genes, namely SHH, ZIC2, SIX3, TGIF, PATCHED, and CRIPTO (TDGF1), are linked to HPE and to ventral and dorsal patterning defect of the neural tube.

We report the first occurrence of AP/AT and HPE in a non-consanguineous family with three affected sibs, carrying a maternally inherited mutation of the SIX3 gene. A phenotype/genotype correlation in the series of seven SIX3 mutations found in our cohort of 210 HPE probands is provided.

METHODS

Systematic sequencing of the entire coding region of the SHH, ZIC2, TGIF, and SIX3 genes has been performed in a series of 210 non-chromosomal HPE probands including 56 patients reported previously. Probands were included in the study after brain imaging, karyotyping, and detailed clinicopathological studies, referring to the protocol for fetuses. Mutational analyses were performed as detailed elsewhere.

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Aprosencephaly/atelencephaly (AP/AT) refers to a rare forebrain malformation defined by a lack of prosencephalic derivatives. In aprosencephaly the prosencephalon is absent, while in atelencephaly it exists as a rudimentary median vesicle resembling the diencephalon but without the lateral telencephalic vesicles. Holoprosencephaly (HPE) results from incomplete cleavage of telencephalic vesicles. The only constant finding between the three major forms of HPE (alobar, semi-lobar, and lobar) is the continuity of the dorsal telencephalic midline over the midline (personal observation). Interestingly, craniofacial malformations similar to HPE are found in AP/AT and involve the fronto-nasal eminence (ranging from cyclopia/synophthalmia, cebocephaly, and midline cleft to mild hypotelorism or normal face).

Our neuropathological findings in the probands of family ‘A’ fulfill classical criteria for AP/AT and HPE. Classically in AP/AT and HPE, the midbrain and hindbrain are said to be normal. However, Florell et al stress the existence of abnormal cerebellar hemispheres with “a peculiar mesenchymal proliferation” seen only within the central nervous system. These changes have been linked to the “glomeroid vasculopathy” described in an encephaloclastic vasculopathy leading to hydranencephaly.

We consider thick meninges with persistent embryonic vascular dural plexus to be a common finding in HPE and AP/AT.

During CNS development, sequential specification along anteroposterior (rostrocaudal) and dorsoventral axes occurs even before neural tube closure in Carnegie stage 9. This requires a balance between anteriorising and posteriorising signals ending with the differentiation of the forebrain (prosencephalon), midbrain (mesencephalon), and hindbrain (rhombencephalon) following a general scheme common to vertebrates. By Carnegie stage 11, the rostral most part of the prosencephalon gives rise to the telencephalon medium followed caudally by the diencephalon. At this stage, optic vesicles originate laterally from the diencephalon wall. It is now recognised that the optic primordial appears earlier during development (by Carnegie stage 8) as a single retinal field at the rostral end of the neural plate. The prechordal plate is believed to be responsible for suppressing the median part of the retinal field leading to the emergence of two visual fields.

Key points

- Aprosencephaly/atelencephaly (AP/AT) and holoprosencephaly (HPE) belong to a group of severe forebrain malformations. Neither the occurrence of AP/AT and HPE in the same family nor a common causative gene have ever been documented.
- This is the first report of the occurrence of AP/AT and HPE in a family with three affected sibs carrying a maternally inherited mutation of the SIX3 gene. Phenotype/genotype correlation in this series of SIX3 mutations found a preferential association of HPE with eyes abnormalities.
- Our neuropathological and mutational analysis with phenotype/genotype evaluation provides strong evidence for a link between AP/AT and HPE and the role of the SIX3 gene in the genesis of AP/AT.
- In HPE with eye disorders and no other malformations, we suggest that mutational analysis should start with SIX3 gene screening.
- SIX3 plays an essential role in the patterning of the anterior tate of neuroectoderm and in craniofacial and visual field development.

Abbreviations: AP/AT, aprosencephaly/atelencephaly; HPE, holoprosencephaly; WG, weeks gestation
bilateral optic primordial. Lack of inhibition of the median component leads to a single eye (cyclopia) and to its variant synophthalmy. The neurohypophysial anlage rises from the ventral diencephalon and may be deficient in AP/AT as well as in HPE. The future cerebral hemispheres become identifiable during Carnegie stage 14, rising laterally from the telencephalon medium. In terms of timing, AP/AT may be considered as an early failure of the neural tube in forming a normal prosencephalon, while HPE results from the incapacity of the telencephalon to split into two hemispheric vesicles. One can postulate that in addition to cyclopia, HPE may result from lack of suppression of a presumptive “medial telencephalic field”.

The aetiology of AP/AT is still debated. Classically, AP/AT has been reported as a sporadic event due to an encephaloclastic process. In our family, the mutation of SIX3, an HPE causing gene, supports the hypothesis of a link between AP/AT and HPE. The SIX3 gene has been isolated from the HPE2 region on chromosome 2p21. This gene belongs to the human SIX family which contains several
genes (SIX1/SIX2, SIX3/SIX6, and SIX4/SIX5) exhibiting strong amino acid sequence homology. This amino acid sequence of the SIX3 gene has mainly two DNA binding regions called the SIX domain and the homeodomain. Both share a complete amino acid sequence homology with the mouse Six3 gene and almost complete homology with optix, a Drosophila gene (expressed in eye primordia). In addition, the mouse Six3 gene has been found to be expressed in the retina and lens of developing eyes as well as in the hypothalamus and pituitary. In human, expression of SIX3 has only been studied in the retina and was detected from embryonic weeks 5–7 until adulthood. Interestingly, in Six3−/− mice the prosencephalon is severely truncated, telencephalic vesicles are lacking, and eyes and olfactory placodes are malformed.

Our mutational analysis of the SIX3 gene in 210 HPE patients found seven SIX3 mutations in both highly conserved regions, two frameshift, and five missense. The new frame-shift mutation led to a truncated protein in the homeodomain. This is additional evidence for the involvement of the SIX3 gene in HPE. The five new missense mutations concerned both the SIX domain and the homeodomain. Interestingly, another missense mutation, c.Arg257Pro, has been also reported in association with semi-lobar HPE, microphthalmia, and iris coloboma. The missense mutations could be related to HPE for two main reasons: they are localised in highly conserved regions (residues Pro231 and Arg257 which are conserved in the optix gene) and there is adequate segregation between the mutation and the associated malformations in all tested families (the mutation was not found in 100 normal chromosomes from unrelated Caucasian individuals).

Genotype/phenotype correlations in our series of seven SIX3 mutations with HPE found three cases with a spectrum conserved regions, two frameshift, and five missense. The new frameshift mutation led to a truncated protein in the homeodomain. This is additional evidence for the involvement of the SIX3 gene in HPE. The five new missense mutations concerned both the SIX domain and the homeodomain. Interestingly, another missense mutation, c.Arg257Pro, has been also reported in association with semi-lobar HPE, microphthalmia, and iris coloboma. The missense mutations could be related to HPE for two main reasons: they are localised in highly conserved regions (residues Pro231 and Arg257 which are conserved in the optix gene) and there is adequate segregation between the mutation and the associated malformations in all tested families (the mutation was not found in 100 normal chromosomes from unrelated Caucasian individuals).

Genotype/phenotype correlations in our series of seven SIX3 mutations with HPE found three cases with a spectrum
of eye anomalies (from synophthalmia/cyclopia to hypotelorism). Eye abnormalities are consistent with the pattern of SIX3 expression during embryonic development in mice or in humans. Anterior encephalocele found in one case with HPE may be linked to abnormality of ectomesenchymal tissue of the cephalic pole. In contrast to other HPE causing genes (SHH, ZIC2, and TGIF), in this series no other malformations, usually associated with the limbs and heart, were found. We suggest that mutational analysis starts with screening of the SIX3 gene in cases of HPE associated with severe disorders but no other malformations.

In conclusion, the occurrence of HPE and AP/AT and our mutational and neuropathological analysis provides strong evidence of a link between AP/AT and HPE which may form part of a continuum of forebrain patterning defects. These results support the hypothesis that SIX3 is central in the patterning of the anterior fate of the neuroectoderm by inhibiting posteriorising (diencephalic) signals, including, but probably not limited to, Wnt signalling. Further studies, especially of the timing and pattern of SIX3 gene expression during early human development, should help understanding of the mechanism of AP/AT and HPE.

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