Phenotypic expression of the fibroblast growth factor receptor 3 (FGFR3) mutation P250R in a large craniosynostosis family

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Abstract
The craniosynostosis syndromes are a heterogeneous group of sporadic, autosomal dominant disorders with significant clinical overlap. Recently, we described a large family with autosomal dominant craniosynostosis suggestive of Saethre-Chotzen syndrome, in which linkage to the Saethre-Chotzen syndrome loci on 7p had been excluded.

We now report the presence of a mutation in the fibroblast growth factor receptor 3 (FGFR3) in this family. The mutation, P250R, had been previously reported in 10 patients with non-syndromic craniosynostosis. Variable expression of this mutation is evident especially in two additional members of this family, one of whom is severely affected with pancraniosynostosis. The family provides a further example of genetic heterogeneity and variable expression of the craniosynostosis syndromes and broadens the phenotypic spectrum associated with the FGFR3 mutation P250R. In addition, we found a polymorphism (F354L) in the transmembrane domain of FGFR3 which occurs with a frequency of 3% in the Turkish population but is uncommon among Germans.

Keywords: craniosynostosis; Saethre-Chotzen syndrome; FGFR3

The craniosynostosis syndromes are characterised by marked genetic and allelic heterogeneity. Mutations in two out of four known fibroblast growth factor receptor (FGFR) genes account for various forms of craniosynostosis, such as Crouzon, Apert, Jackson-Weiss (FGFR2), and Pfeiffer (FGFR1, FGFR2) syndromes. Recently, a single recurrent mutation in the FGFR3 gene, P250R, was reported to cause non-syndromic craniosynostosis. FGFR3 was previously shown to be mutated in various forms of dwarfism and Crouzon syndrome with acanthosis nigricans.

Here we report the presence of the mutation P250R in FGFR3 in a large German family (family 1) (fig 1) with craniosynostosis and additional features suggestive of Saethre-Chotzen syndrome. The phenotype of eight affected subjects has been described previously. They show unilateral (4/8) or bilateral (4/8) coronal synostosis of varying degree and a low frontal hairline (8/8). Other features include hypertelorism (7/8), facial asymmetry (5/8), strabismus (3/8), ptosis (2/8), partial cutaneous syndactyly (3/8), and brachydactyly (1/8). Characteristics of other craniosynostosis syndromes, such as midface hypoplasia, osseous syndactilies, and broad big toes and thumbs were absent. In the meantime two further affected family members were born. Subject IV.9 presents with unilateral coronal synostosis, marked facial asymmetry,
and deviation of the nasal septum (fig 2), like her affected sibs. Subject IV.10 (fig 3) is severely affected with craniosynostosis, ocular proptosis, and downward slanting palpebral fissures. The “cloverleaf skull” was detected prenatally by ultrasound in the 30th week of gestation. Both IV.9 and IV.10 have normal hands and feet.

Using linkage analysis we mapped the disease locus to a 30 cM interval on 4p16 which includes the FGFR3 gene. Mutation analysis using SSCP of the transmembrane domain (for primers Shiang et al.) showed a TC transition at nucleotide position 1150 of FGFR3 in the affected subject IV.6, his unaffected sister IV.7, and the unaffected father, who is of Turkish descent. T1150C predicts the amino acid exchange F384L and creates a MnlI restriction site. MnlI restriction digest in 50 healthy subjects each of German and Turkish descent showed the heterozygous presence of F384L in three out of the 50 Turkish controls but none of the Germans. F384L lies between the common achondroplasia mutation (G380R) and the recurrent mutation in Crouzon syndrome with acanthosis nigri-