Crouzon syndrome is not linked
craniosynostosis loci at 7p and 5qter

W Reardon, L van Herwerden, C Rose, B Jones, S Malcolm, R M Winter

Abstract
Evidence for linkage has been sought, in
four pedigrees with Crouzon syndrome, between polymorphic markers known to
be linked to the Saethre-Chotzen locus on
7p and another form of autosomal domi-
nant craniosynostosis on 5q. The data we
present exclude Crouzon syndrome as an
allelic variant at either of these known
craniosynostosis loci.

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The craniosynostoses comprise a clinically and genetically heterogeneous group of disorders characterised by premature fusion of the skull bone sutures. Several recognisable entities are identifiable within this broad group, among them Crouzon, Apert, Pfeiffer, and Jackson-Weiss syndromes.1 Originally described by Crouzon in a mother and son in 1912, the syndrome which bears his name (MIM No 123500) is principally characterised by cranio-
synostosis, shallow orbits, ocular proptosis, and maxillary hypoplasia, although a host of other clinical features have been identified.12 Although variability in gene expression within families is well documented, and indeed craniosynostosis has occasionally been absent in obligate gene carriers, the phenotype of the autosomal dominant mode of transmission is not in doubt.5-7

While Crouzon syndrome is clinically distinct from other autosomal dominant craniosyn-
Tosis syndromes, the aetiological relationship between these disorders remains unclear. Two such conditions have recently been mapped, the locus for Saethre-Chotzen syndrome being localised by mapping and cytogenetic evidence to 7p218-10 and a family with autosomal domi-
nant craniosynostosis of possibly undescribed type being assigned to 5qter using linked markers.11,12

Among our population of patients with Crouzon syndrome, we have identified four pedigrees suitable for linkage studies. We have sought evidence for linkage of Crouzon syn-
drome to the known craniosynostosis loci on
7p and 5qter as described. The purpose of this report is to present these data and to emphasise the locus heterogeneity that is likely to under-
lie the autosomal dominant craniosynostosis
syndromes.

Materials and methods

PATIENTS
The four pedigrees are shown in the figure.
These were identified through the craniofacial
and reconstructive surgery department as well
as through old records within the genetics
department at the Hospital for Sick Children,
Great Ormond Street, London. All four pedi-
grees were phenotypically characteristic of Crouzon syndrome, the predominant clinical
features being marked proptosis and craniosyn-
ostosis. Blood was obtained from 24 affected
and 28 normal subjects for the study.

LABORATORY STUDIES
DNA was extracted from lymphocytes using
standard methods.13 This was amplified in
the polymerase chain reaction (PCR) using
primers flanking short tandem repeat poly-
morphisms, D5S211 on 5q and D7S488 on 7p.
Details of primers are available elsewhere.14
Each PCR reaction contained 50 ng genomic
dNA, 10 mmol/l Tris, pH 8-3, 1-5 mmol/l MgCl,2 50 mmol/l KCl, 200 μmol/l each
dGTP, dATP, dTTP, and 20 μmol/l dCTP,
0-7 μCi α 32p-dCTP, 25 pmol of each primer,
and 0-5 units Taq polymerase (Bioline) in a final
volume of 20 μl. The products of amplification
were separated by denaturing polyacrylamide
gel electrophoresis and autoradiographed.
The data were analysed using the Linkage pro-
gram, version 5-03.14

Results
The results of the analysis are presented in
the table. Each pedigree showed at least one
recombination between the disease and both
test loci.

Discussion
The preliminary approach to mapping the locus
for Saethre-Chotzen syndrome was greatly
facilitated by an array of cytogenetic data from
unrelated patients with craniosynostosis in
whom 7p deletions were observed,15 thus iden-
tifying this region as a possible candidate for
syndromic craniosynostosis. Confirmation of
linkage between 7p markers and several families
with the Saethre-Chotzen phenotype followed.8
This observation has subsequently been con-
ﬁrmed by more detailed mapping studies and,
most recently, by the report of the Saethre-
Chotzen phenotype in a patient with a de novo
translocation involving 7p21.16 No such cyto-
genetic pointers have been reported for Crouzon
syndrome and likely candidate loci for this
form of craniosynostosis are not widely recog-
nised. For this reason, and because it has been
suggested that allelic mutations at the 5qter
craniosynostosis locus might be the basis of

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The four pedigrees used in the study are detailed.

Lod scores for Crouzon syndrome against D5S211 and D7S488

<table>
<thead>
<tr>
<th>Locus</th>
<th>$\theta = 0$</th>
<th>0.01</th>
<th>0.02</th>
<th>0.03</th>
<th>0.04</th>
</tr>
</thead>
<tbody>
<tr>
<td>D5S211</td>
<td>$-\infty$</td>
<td>-11.86</td>
<td>-3.23</td>
<td>-1.09</td>
<td>-0.23</td>
</tr>
<tr>
<td>D7S488</td>
<td>$-\infty$</td>
<td>-14.61</td>
<td>-4.25</td>
<td>-1.69</td>
<td>-0.57</td>
</tr>
</tbody>
</table>

other autosomal dominant craniosynostosis syndromes, it is important to investigate the possibility of linkage between Crouzon syndrome and known craniosynostosis loci. D7S488 has been shown to be tightly linked to the Saethre-Chotzen gene with a maximum lod score of 5.574 at $\theta = 0.05$. In these Crouzon pedigrees there is a lod score of -2 at 19 cM, excluding the possibility that Crouzon
and Saethre-Chotzen syndromes are allelic forms of craniosynostosis.

A further family with a previously undescribed form of craniosynostosis has shown tight linkage with the probe D5S211 on 5qter, with a maximum lod score of 4.82 at θ = 0. The negative lod scores with this marker in the Crouzon families (−2 at θ = 0.15) mean that Crouzon syndrome is not allelic with the 5q craniosynostosis locus.

The data we present conclusively exclude linkage of Crouzon syndrome within 10 cM on either side of the markers linked to the known craniosynostosis loci and dismiss the possibility of Crouzon syndrome representing an allelic variant of either of these forms of craniosynostosis. Further efforts to map Crouzon syndrome are under way.

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