- 17 Jackson CE, Weiss L, Reynolds WA, Formas TF, Peterson JA: Craniosynostosis, midface hypoplasia, and foot abnormalities: An autosomal dominant phenotype in a large Amish kindred. J Pediatr 1976;88:963–968.
- 18 Meyers GA, Day D, Goldberg R, Daentl DL, Przylepa KA, Abrams LJ, Graham JM, Feingold M, Moeschler JB, Rawnsley E, Scott AF, Jabs EW: FGFR2 exon IIIa and IIIc mutations in Crouzon, Jackson-Weiss and Pfeiffer syndromes: Evidence for missense changes, insertions, and a deletion due to alternative RNA splicing. Am J Hum Genet 1996;58:491–498.
- 19 Miller SA, Dykes DD, Polesky HF: A simple salting out procedure for extracting DNA from human nucleated cells. Nucleic Acids Res 1988;16:1215.
- 20 Cohen SR, Dauser RC, Gorski JL: Insidious onset of familial craniosynostosis. Cleft Palate Craniofac J 1993;30:401-405.
- 21 Kreiborg S: Crouzon syndrome. Scand J Plast Reconstr Surg Suppl 1981;18:1–198.
- 22 Rousseau F, El Ghouzzi V, Delezoide AL, Legeai Mallet L, Le Merrer M, Munnich A, Bonaventure J: Missense FGFR3 mutations create cysteine residues in thanatophoric dwarfism type I (TDI). Hum Mol Genet 1996;5:509– 512.
- 23 Williams AF, Barclay AN: The immunoglobulin superfamily – domains for cell surface recognition. Annu Rev Immunol 1988;6:381– 405.
- 24 Shiang R, Thompson LM, Zhu Y, Church DM, Fielder TJ, Bocian M, Winokur ST, Wasmuth JJ: Mutations in the transmembrane domain of FGFR3 cause the most common genetic form of dwarfism, achondroplasia. Cell 1994;78: 335-342.
- 25 Rousseau F, Bonaventure J, Legeai-Mallet L, Pelet A, Rozet J, Maroteaux P, Le Merrer M, Munnich A: Mutations in the gene encoding fibroblast growth factor receptor-3 in achondroplasia. Nature 1994;371:252-254.

Erratum

.....

Due to a technical failure a portion of the text under 'Results' was omitted in the paper 'Tetrasomy 18p de novo: Parental Origin and Different Mechanisms of Formation' by Bugge et al., Eur J Hum Genet 1996;4:160– 167. Printed below is the complete text for 'Results'. We apologize for any inconvenience this may have caused.

Tetrasomy 18p de novo: Parental Origin and Different Mechanisms of Formation

Merete Bugge^a, Elisabeth Blennow^b, Ursula Friedrich^c, Michael B. Petersen^{a, g}, Florence Pedeutour^h, Aspasia Tsezou¹, Alena Ørum^d, Stig Hermann^e, Troels Lyngbye^f, Catherine Sarri^g, Dimitrios Avramopoulos^h, Sofia Kitsiou¹, Jean Claude Lambert¹, Michèle Guzda¹, Niels Tommerup^a, Karen Brøndum-Nielsen^a

^a Department of Medical Genetics, The John F. Kennedy Institute, Glostrup, Denmark,

- ^b Department of Molecular Medicine, Clinical Genetics Unit, Karolinska Institute, Stockholm, Sweden,
- ^c Institute of Human Genetics, University of Aarhus, Denmark,
- ^d County Center for Multiply Handicapped Adults in Copenhagen, Søborg, Denmark,
- e County Center for Multiply Handicapped Children in Copenhagen, Gentofte, Denmark,
- Department of Pediatrics, University Hospital of Aarhus, Denmark,
- ^g Department of Genetics, Institute of Child Health, Athens, Greece,
- ^h Laboratoire de Génétique, Hôpital Pasteur, Nice, France,
- ¹ 2nd Department of Pediatrics, 'Kyriakou' Children's Hospital, Athens, Greece,

¹ Unité de Génétique, Hôpital de Cimiez, Nice, France

Results

Parental Age Distribution

Range for mothers 24–39 years, mean maternal age 29 years; range for fathers 25–45 years, mean paternal age 32.1 years (table 1).

Chromosome analysis revealed 47 chromosomes in all 9 cases; the size and banding pattern of the extra small metacentric chromosome were compatible with an isochromosome of the short arm of chromosome 18. All cases were nonmosaic. All parental karyotypes were normal.

In situ hybridization with a chromosome 18 centromere-specific probe showed a monocentromeric signal on the marker chromosome in all cases. FISH using an 18pspecific library showed labeling of the short arms of chromosomes 18 and the whole of i(18p). No labeling of the marker chromosome was observed after FISH with an 18q-specific library (fig. 1).

DNA analysis indicated that all nine i(18p) chromosomes were of maternal origin (table 2, fig. 2). A uniparental origin of the normal chromosomes 18 could be excluded. In 6 cases (cases 1–6), the 18p markers showed that the maternal heterozygous alleles were reduced to homozygosity in the proband in the pericentromeric region, while they remained heterozygous (nonreduced) in the telomeric region. In cases 7 and 8, all informative markers in the proband were nonreduced and in case 9, 6 informative markers showed reduction to homozygosity for maternal alleles (table 2).