Lack of chromosomal imbalances in adamantinomatous and papillary craniopharyngiomas

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Cranioopharyngiomas are among the most common paediatric tumours and are thought to arise from embryonic remnants of Rathke's pouch. The molecular mechanisms involved in their formation remain elusive and little is known about chromosomal imbalances that could suggest the locations of tumour suppressor or proto-oncogenes involved in the pathogenesis. The paucity of published data on the molecular basis of such tumours prompted this investigation of 20 adamantinomatous and nine papillary craniopharyngiomas for genetic abnormalities by comparative genomic hybridisation (CGH). CGH revealed no DNA copy number changes in any of the 29 primary craniopharyngiomas, regardless of their histological subtype. These data suggest that chromosomal imbalances are a rare event in both adamantinomatous and papillary craniopharyngiomas.

CGH analysis
DNA was isolated by phenol-chloroform extraction according to standard protocols. CGH analysis was undertaken as described previously. Briefly, tumour DNA was labelled with biotin-16-dUTP (Boehringer Mannheim, Mannheim, Germany) and reference DNA from a healthy male donor with digoxigenin-11-dUTP (Boehringer Mannheim) in a standard nick translation reaction. The DNAse concentration in the labelling reaction was adjusted in order to reveal an average fragment size of 200–500 base pairs. The labelled DNA fragments were purified from remaining nucleotides by column chromatography. For CGH, 500 ng of tumour DNA, 300 ng of reference DNA, and 30 μg of human Cot1 DNA (Gibco, Karlsruhe, Germany) were co-precipitated and redissolved in 10 μl of hybridisation buffer. Denaturation of DNA (75°C for five minutes) was followed by a preannealing time of 45 minutes at 37°C. Target metaphase spreads (46,XY), which had been prepared following standard procedures, were denatured separately in 70% formamide/2×SSC for two minutes at 72°C.

Hybridisation was allowed to proceed for three to four days. Post-hybridisation washes were carried out to a stringency of 50% formamide/2×SSC (NaCl/sodium citrate) at 45°C and 0.1×SSC at 60°C. Biotinylated and digoxigenated sequences were detected simultaneously using avidin-FITC (Boehringer Mannheim, 1:200) and anti-digoxigenin-rhodamine (Boehringer Mannheim, 1:40). The slides were counterstained with DAPI and mounted in an antifade solution (Vectorashield, Vector Laboratories).

Microscopy and digital image analysis
Separate digitised grey level images of DAPI, FITC, and rhodamine fluorescence were taken with a CCD camera connected to a Leica DMRBE microscope. The image processing was carried out by use of Applied Imagining software. Average green-red ratios were calculated for each chromosome in at least 10 metaphases.

Chromosomal regions with CGH ratio profiles surpassing the 50% CGH thresholds (upper threshold 1.25, lower threshold 0.75) were defined as loci with copy number gains or losses. For the assignment of these gains to chromosomal bands, the signal intensities were compared to the DAPI banding on individual chromosomes. As tumour specimens and normal DNA were not sex matched, X and Y chromosomes were excluded.

RESULTS
CGH revealed no DNA copy number changes in any of the 29 primary craniopharyngiomas, regardless of their histological subtype. Successful completion and the quality of CGH investigation in each case was established by checking the narrowness of the 95% confidence interval as well as the loss of the Y and gain of the X chromosome in tumour material from female patients hybridised on metaphase spreads of a male donor (internal positive control).
Craniopharyngiomas are benign tumours that show a bimodal age distribution and arise in two distinct clinicopathological variants: the adamantinomatous and the papillary subtypes. The molecular mechanisms involved in craniopharyngiomas remain elusive. While a genetic susceptibility is not known, there are reports describing the occurrence of craniopharyngiomas in consanguineous siblings as well as in a mother and daughter. To date, cytogenetic (that is, karyotypic) data on only 11 craniopharyngiomas have been published, and have shown multiple chromosomal abnormalities in two cases, both of which involved chromosomes 2 and 12, while the other nine cases presented with normal karyotypes; four additional craniopharyngiomas showed no mutations of the TP53 tumour suppressor gene. In view of the association of naevoid basal cell carcinoma or Gorlin syndrome with the occurrence of craniopharyngiomas, a recent study was carried out on 22 adamantinomatous craniopharyngiomas. This found no mutations in the Gorlin syndrome gene PTCH, localised on chromosome 9q22.3, while the putative proto-oncogenes encoding the α subunits of the stimulatory (Gsα) or the inhibitory (Gi2α) GTP binding proteins on respective chromosome subunits 20q13.2 and 3p21 were also found not to be mutated. Interestingly, a subset of these adamantinomatous craniopharyngiomas turned out to be monooclonal in origin. While it has to be borne in mind that CGH is only sensitive for detecting deletions that are of the order of several megabases in size, and that smaller deletions or balanced alterations may thus be missed, the lack of DNA copy number changes in any of our adamantinomatous and papillary craniopharyngiomas is also in accordance with previously published CGH data on low grade cerebral neoplasms: pineocytomas, subependymal giant cell astrocytomas, and pilocytic astrocytomas were reported to show 0.0, 0.23, and 0.31 imbalances per tumour, respectively. In view of our data, and most other molecular data on craniopharyngiomas, one has to assume that chromosomal aberrations do not play a major role in their tumorigenesis, and the only two cytogenetically abnormal cases may have represented tissue culture artefacts.

In conclusion, our CGH data suggest that chromosomal imbalances are a rare event in primary adamantinomatous and papillary craniopharyngiomas.
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