Amplification of the c-myc Gene in Human Medulloblastoma Cell Lines and Xenografts

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ABSTRACT

Cultured cell lines and xenografts derived from 7 human medulloblastomas were evaluated for amplification of the c-myc, N-myc, epidermal growth factor receptor, and gli genes by Southern blot analysis. Karyotypes of the original biopsies and early passaged cell lines demonstrated double minute chromosomes in 4 of the 7 cases. All 7 samples (3 cell lines and 4 xenografts) from the 4 tumors with double minute chromosomes contained amplification of the c-myc gene. Cell lines and xenografts derived from the 3 biopsies without double minute chromosomes failed to demonstrate amplification of the 4 genes which were tested, but a rearrangement of the c-myc gene occurred in 1 of the 3 tumors. These observations demonstrate that the c-myc gene is often amplified and/or rearranged in human medulloblastomas and suggest that amplification of this gene provides a growth advantage for medulloblastoma cells in vitro and in vivo.

INTRODUCTION

The incidence of gene amplification and the spectrum of genes which are amplified varies markedly among human tumor types. Tumors of neurogenic origin, in particular, have a relatively high incidence of gene amplification. For example, 30–40% of malignant human gliomas contain amplification of the EGFR 

AMplification of the N-myc gene is amplified in approximately 40% of neuroblastomas (1–3). Gliomas often lose EGFR gene amplification during their establishment in culture (4). Glioma xenografts, however, maintain amplification of the EGFR gene during passage in athymic mice (5). Neuroblastomas present a different situation in that the majority of cultured neuroblastoma-derived cell lines contain amplification of the N-myc gene suggesting that N-myc gene amplification increases the probability that a neuroblastoma can be established in vitro (6).

In addition to providing insight into the pathogenesis of human tumors, the presence of gene amplification sometimes has useful clinical correlates. For example, patients whose neuroblastomas contain amplification of the N-myc gene tend to have a more advanced stage of tumor at diagnosis and more rapid clinical course than patients without this characteristic (3, 7); amplification of the EGFR gene in human gliomas is almost exclusively in high grade tumors (8); similarly neu gene amplification appears to preferentially occur in more aggressive forms of breast tumors (9).

Approximately 10–20% of human medulloblastomas contain DMs, thus providing cytogenetic evidence for gene amplification (10). Identification of the amplified gene, however, has been limited to one example of amplification of the c-myc gene in the D-341 Med medulloblastoma cell line and 2 cases of amplification of the N-myc gene in biopsied cerebellar medulloblastomas, one of which contained gangliocytic differentiation (11, 12). In the present study, cultured cell lines and xenografts derived from 7 medulloblastomas were evaluated for amplification of the EGFR, N-myc, c-myc and gli genes. All xenografts and cell lines from the 4 tumors with DMs contained amplification of the c-myc gene; specimens without DMs failed to demonstrate amplification of the 4 genes which were tested. These observations suggest that amplification of the c-myc gene imparts a growth advantage to medulloblastoma cells in vitro and in vivo.

MATERIALS AND METHODS

Medulloblastoma Biopsies. Freshly resected biopsies from 7 human medulloblastomas which were established in vitro or which grew progressively in athymic mice were subjected to chromosome and molecular analyses. These tumors originated in 5 boys and 2 girls ranging from 17 months to 12 years of age (Table 1). D-283 Med-bx was obtained from a peritoneal metastasis of a cerebellar medulloblastoma while the remaining biopsies were from the initial resections of cerebellar medulloblastomas.

Xenograft Establishment and Transplantation. Male or female athymic BALB/c- nu/nu mice, 3–4 weeks of age, were given single cell suspensions of tumor cells prepared from the resected tumor tissue as above into the right cerebral hemisphere (1–3 × 10'6 cells/mouse) or s.c. into the right flank (1–5 × 10'4 cells/mouse). Resulting xenografts were serially transplanted into additional mice as described previously (13).

Cell Lines. Permanent cultured cell lines D-283 Med-C, D-341 Med-C, D-384 Med-C, and D-425 Med-C were derived at Duke Medical Center by mechanical dissociation of resected tumor tissue and plating into Richter's (14) improved minimal essential zinc supplementation medium containing 10% fetal calf serum. Permanent cell lines were serially transplanted into additional mice as described previously (13).

Chromosomal Analysis. Biopsies and xenografts were aseptically dissected free of necrosis and normal tissue, were finely minced, and plated into Richter's (14) improved minimal essential medium supplemented with 10% heat-inactivated fetal calf serum, 10 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid buffer, and 584 µg glutamine/liter and incubated at 37°C in a 5% CO2 atmosphere (11, 14). D-283 Med-C and D-341 Med-C have been described in earlier communications (11, 15); the remaining 2 lines have not been reported previously. All 4 lines grow in suspension. The cell lines were tested (negative results) every 10th passage for mycoplasma contamination by testing the ability of the conditioned medium to convert deoxyadenosine to adenine (in the presence of an inhibitor of adenosine deaminase) and thymidine to thymine (16).

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was cleaved with EcoRI, separated by electrophoresis through a 1% agarose gel, blotted onto a nylon membrane, and hybridized with a c-myc probe labeled with [\textsuperscript{32}P]dCTP via the random primer method. Washing of filters and autoradiography was as described before (18).

The c-myc probe was a 1.6-kilobase Si/I fragment of pHSR-1 containing the second exon of c-myc (19). Filters were rehybridized sequentially with 3 other probes: a 1.0-kilobase EcoRl/BamH\textsubscript{I} fragment of pNB-1 containing part of the second exon of the N-myc gene (20), a 1.6-kilobase EcoRI fragment of pE7, a complementary DNA clone of EGFR mRNA generously provided by Drs. G. Merlino and I. Pastan (21), and a 1.55-kilobase Psl\textsubscript{I} insert of pKK 36P1, containing gli sequences (22). Greater than 4-fold increase in gene copy number was considered to represent gene amplification.

**RESULTS**

Chromosomal Analyses. Karyotypes were obtained on short-term cultured preparations of original biopsies D-283 Med-Bx, D-306 Med-Bx, D-286 Med-Bx, and D-425 Med-Bx and on early passage cultured cells from D-341 Med-Bx, D-382 Med-Bx, and D-384 Med-Bx. All 7 samples had abnormal stemlines including 5 near-diploid and 2 hyperdiploid (greater than 50 chromosomes) tumors (Table 1). The most frequent structural abnormalities were i(17q) in 5 tumors and DMs in 4 cases. D-382 Med and D425 Med contained 10-20 tiny DMs in 10 and 20-30% of cells, respectively. D-384 Med and D-341 Med showed numerous DMs in all cells.

Xenografts were established from tumors both with and without DMs. All xenografts were similar histologically, composed of sheets of small anaplastic cells similar to those seen in the original biopsies. In each case, a stemline karyotype closely related or identical to the one seen originally was maintained through in\textit{vivo} passage. Serially transplantable D-283 Med-X, D-306 Med-X, D-341 Med-X, D-384 Med-X, and D-425 Med-X xenografts have been maintained. D-382 Med-X and D-386 Med-X are presently in the second in\textit{vivo} passage.

D-283 Med-C, D-341 Med-C, D-384 Med-C, and D-425 Med-C were established in\textit{vitro} from the corresponding biopsies. All 4 lines maintained the same karyotype as seen originally including the presence of numerous DMs in 3 of the 4 lines.

**Gene Amplification.** Biopsies D-341 Med-Bx and D-384 Med-Bx contained a 4-5-fold increase in c-myc gene copy number while the remaining biopsies including D-382 Med-Bx and D-425 Med-Bx did not show increased gene copy number (Fig. 1). A 15-kilobase fragment in addition to the normal 13-kilobase form was present in D-283 Med-Bx, suggesting that the gene was rearranged but not amplified (see below).

D-341 Med-C, D-341 Med-X, D-382 Med-X, D-384 Med-C, D-384 Med-X, D-425 Med-C and D-425 Med-X contained 10-30 copies of the c-myc gene (Fig. 2a). Additional and usually lower molecular weight bands were seen in all samples with gene amplification. Additional bands were also seen when Hind\textit{III} or PstI was used to digest the samples. No bands were seen when the blots were rehybridized with vector sequences alone (data not shown). D-283 Med-C did not show an increased gene copy number. D-283 Med-X, however, showed a slightly elevated copy number of the c-myc gene in comparison to the other genes tested. We did not consider this to be definitive evidence for gene amplification. For both D-283 Med-C and D-283 Med-X there was a more slowly migrating band.
Amplification of c-myc gene was demonstrated in 2 of the 4 biopsies from which the cell lines and xenografts with amplification of this gene were derived. In the remaining 2 cases (D-382 Med-Bx and D-425 Med-Bx) increased copy numbers of the c-myc gene were not seen. There are several potential explanations for this observation. The possibility that DNA samples from these 2 tumors contained nonneoplastic tissue rather than representing solid tumor tissue was largely excluded by histologic examination of the same blocks. The demonstration of unique karyotypes for the cell lines and xenografts derived from the individual biopsies excluded cross-contamination. Thus, the most likely explanations are that (a) only a small proportion of cells in the D-382 Med-Bx and D-425 Med-Bx samples contained amplification of the c-myc gene, and the cells had a selective growth advantage in vitro; (b) gene amplification occurred in the majority of neoplastic cells within the biopsy tissue but at a relatively low level; in vitro culture selected for gradually increasing levels of c-myc gene amplification, just as methotrexate can select for cells with gradually increasing levels of DHFR gene amplification (28); and (c) amplification did not exist at all in the biopsy tissue but was an in vitro phenomenon. We believe that the first of these three explanations is more likely, since DMs were observed in the earliest karyotypes made from both D-382 Med-Bx and D-425 Med-Bx and the proportion of metaphase spreads with DMs was much lower in these initial karyotypes than in those generated from the cell lines. Application of in situ hybridization or immunohistochemical assays with myc-specific probes or antibodies could possibly answer this question in the future. In either case, our observations suggest that the amplification of the c-myc gene provides a selective advantage for medulloblastoma cells when propagated in vitro or through serial transplantation in athymic mice.

Another difference between the behavior of the c-myc gene in medulloblastoma biopsies and cells propagated in vitro and in vivo from the corresponding tumors is that abnormally migrating amplified bands were seen in D-341 Med C and X and D-384 Med-C and X while the corresponding biopsies in vivo from the corresponding tumors is that abnormally migrating amplified bands were seen in D-341 Med C and X and D-384 Med-C and X while the corresponding biopsies contained c-myc gene amplification without rearrangement. The possibility that the abnormal bands were due to cleavage at EcoRI* sites was excluded by the demonstration of abnormally migrating bands following HindIII and PstI digestion. One explanation for this observation is that cells with rearrangements of the amplified c-myc gene may represent only a minor proportion of cells in the original tumors but these populations may be selected through propagation in vitro and in athymic mice. Alternatively, the gene alterations may have been acquired during progressive rounds of amplification in their new environments.

Other neurogenic tumors which often contain amplified genes include malignant adult gliomas, in which approximately 1 of 3 of the tumors contain amplification of the EGFR gene, and neuroblastomas, in which about 40% of primary tumors contain amplification of the N-myc gene (1–3). It is interesting that the only reported case of c-myc gene amplification in a glioma occurred in a child, raising the possibility that amplification of this gene may be associated with childhood malignant brain tumors in general rather than being associated with medulloblastoma alone (27).

All medulloblastoma-derived cell lines established in our laboratory grow in suspension as do the majority of neuroblastoma cell lines. Three of the 4 medulloblastoma lines contain amplification of the c-myc gene and this gene is rearranged, although not amplified, in the remaining cell line. These find-

Fig. 2. In a, 5 μg of DNA from the 7 original medulloblastoma biopsies was hybridized with the c-myc probe as described in Fig. 1a. D-341 Med-Bx (Lane 5) and D-384 Med-Bx (Lane 8) contained amplification of the c-myc gene, while D-283 Med-Bx (Lanes 1 and 2), D-306 Med-Bx (Lanes 3 and 4), D-382 Med-Bx (Lanes 6 and 7), D-386 Med-Bx (Lanes 9 and 10), D-425 Med-Bx (Lane 11), and normal human lymphocyte DNA (Lane 12) showed equivalent gene copy numbers. A slowly migrating band similar to the one seen in D-283 Med-C and D-283 Med-X (Fig. 1a) was also seen in the D-283 Med-Bx. In b, the filter shown in a was hybridized with the N-myc probe showing equivalent gene copy numbers in all samples.
ings suggest that alterations in this gene may be necessary for medulloblastomas to establish in culture, just as N-myc gene amplification appears to increase the efficiency of neuroblastoma growth in vitro.

This demonstration that patients whose neuroblastomas contain amplification of the N-myc gene have later stage and more rapidly progressive tumors than patients without this characteristic (3,17) suggests that amplification of the myc genes can alter the growth properties of neuroectodermal cells in vivo as well as in vitro. Examination of a large series of patients with medulloblastoma for the presence of c-myc or N-myc gene amplification will be necessary to determine whether a similar relationship exists for this tumor type.

REFERENCES


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