Malignant fibrous histiocytomas and H-ras-1 oncogene point mutations

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Abstract

Aims—To investigate the types and the frequencies of H-ras-1 gene mutations in malignant fibrous histiocytomas.

Methods—Thirty five samples of malignant fibrous histiocytoma tissue were searched for point mutations within “hot spot” codons 12 and 13 of the H-ras-1 oncogene by the specific “nested” polymerase chain reaction followed by restriction fragment length polymorphism (PCR-RFLP) and a direct cycle sequencing procedure.

Results—In contrast to previous reports, none of the tumours contained a point mutation or any other changes within or around the hot spot gene sequences.

Conclusions—These data indicate that H-ras-1 oncogenic activation is not required in the molecular pathway of malignant fibrous histiocytoma formation and cannot be used as a discriminating factor for diagnostic sarcoma typing.

Keywords: malignant fibrous histiocytoma; restriction fragments length polymorphism; H-ras-1 oncogene

Cytogenetic and molecular studies have greatly improved our understanding of the role of different chromosomal translocations specific for soft tissue sarcomas and have given clues to the functions of many genes involved in their tumorigenesis. The role of certain oncogenes and tumour suppressor genes in the evolution and progress of soft tissue sarcomas has also been determined.1–4 Soft tissue tumour research has included the determination of structural and functional changes seen in well known families of proto-oncogenes—for example, the ras gene family.6–7 The ras proto-oncogene family (H-ras-1, K-ras-2, and N-ras genes) encodes a specific class of highly conserved G proteins (21 kDa in size), which exhibit GTPase and GTP/GDP binding activities. These proteins are involved in the transduction of external signals from the cell surface to the nucleus. Wild-type Ras protein (p21) is activated by GTP binding; it becomes inactive after conversion of GTP to GDP. Structurally altered p21 cannot become inactivated; such conformational changes are caused by point mutations in H-ras, K-ras, and N-ras, which have been identified in a wide variety of human cancers.8–10 How these mutations produce their effect remains unclear, but it is noteworthy that the sites for mutations within ras genes are limited to codons 12, 13, and 61, which are located within the regions coding for GTP/GDP binding.11 The frequency of ras mutations within different types of neoplasm is estimated, on average, to be 15–30%,11 but varies greatly between tumours of different types, being < 5% in Hodgkin’s disease or neuroblastoma,12,13 37% in endometrial carcinoma,14 and almost 90% in pancreatic cancer.15 However, although ras proto-oncogene mutations are involved in tumorigenesis, they do not seem to be sufficient or specific for any type of neoplastic process; their appearance has been connected with poor prognosis in some tumours, mainly lung and colonic cancers.16–18 The accumulation of additional DNA defects, detected in all types of tumours, is mandatory for malignant transformation.19,20

The data concerning ras oncogene mutations in soft tissue and bone sarcomas are limited to a few reports.21–23 Bohle et al have demonstrated a single somatic H-ras-1 gene point mutation in a high fraction of malignant fibrous histiocytomas, particularly in the myxoid subtype (30% of tumours).23 Codon 12 of the H-ras-1 gene was the only one affected and contained the GGC→GTC (Gly→Val) transversion in all mutated cases. Most of these mutations were homozygous and affected more than 80% of the tumour cells. The authors suggested that the presence of a single and often homozygous point mutation within the H-ras-1 gene was a specific feature of myxoid malignant fibrous histiocytomas, and could be used as a further genomic marker and discrimination factor of sarcomas.

The aim of our work was to investigate further the types and the frequencies of H-ras-1 gene mutations in malignant fibrous histiocytomas using a simple and sensitive polymerase chain reaction restriction fragment length polymorphism (PCR-RFLP) technique and direct sequencing method.

Material and methods

There were 104 patients with different types of soft tissue sarcomas treated in the Regional Center of Oncology in Lodz from 1991 to 1997. The 115 formalin fixed, paraffin wax embedded samples from all analysed tumour lesions were diagnosed in the department of
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et al to Bohle samples. Templates were sequenced directly for all 35 tumour sequencing kit (Epicentre Technologies, Madison, Wisconsin, USA) for all 35 tumour amplification of H-ras codons 12/13 control for further analysis. gene (GGC homozygous mutation of codon 12 of the H-ras phenol/chloroform extraction procedure. DNA by a routine proteinase K digestion and milne normal tissue as possible. We isolated DNA according to the predominant pattern. Ten tumours were of the myxoid subtype and the remaining tumours were of the storiform-pleomorphic subtype (25 specimens).

Tumour tissue was selected to contain as little normal tissue as possible. We isolated DNA by a routine proteinase K digestion and phenol/chloroform extraction procedure. DNA isolated from the T24 cell line, which has a homozygous mutation of codon 12 of the H-ras gene (GGC→GTC) was used as a positive control for further analysis.

A “nested” PCR was performed for the amplification of H-ras codons 12/13, according to Bohle et al. The procedure was carried out in a final volume of 20 µl in a Perkin Elmer 2400 thermocycler. DNA template (50 ng) was added to the reaction mixture containing 0.5 U Taq DNA polymerase, 12.5 mM of each dNTPs, 1.5 mM MgCl2, and 0.25 µM specific external primers (upstream: 5'-GGAGACCCCTGTTAGGAAGAC-3' and downstream: 5'-TCTATAGTGGGGTGAGAGCCCC-3'; located at nucleotide positions 1751–1733, and 1779–1756, respectively). The PCR comprised an initial denaturation step at 94°C for five minutes, followed by 35 cycles of denaturation at 94°C for one minute, annealing at 58°C for one minute, and extension at 72°C for one minute, with the final extension at 72°C for 10 minutes. Aliquots of the first PCR products (5 µl) were used for nested reactions. In this case, the specific internal primers were added (upstream: 5'-GAAGAGGTCCCTGAGGAGCTG-3' and downstream: 5'-AAATATGCTCTGGATCA-GCTGGATG-3'; located at nucleotide position 1652–1672 and 1753–1729, respectively). The amplification programme included 25 cycles with annealing at 60°C. The other components of the reaction mixture and parameters of the thermal profile were the same as above. PCR products were analysed electro- phoretically on a 2% agarose gel, stained with ethidium bromide.

The nucleotide sequences of the H-ras-1 gene amplified samples were determined by the modified dyeoxy chain termination method using the SequiTern EXCEL™ DNA sequencing kit (Epicentre Technologies, Madison, Wisconsin, USA) for all 35 tumour samples. Templates were sequenced directly (25 cycles), according to the manufacturer’s instructions. The specific sequencing primer H 12/13 (5'-ATGTGCTCTGGATCA-GCTGGATG-3'; located at nucleotide positions 1751–1733, with an annealing temperature of 60°C) allowed us to establish the primary structure of analysed products in the reverse direction. It prevented the compression effect during se- quencing of CG rich fragments. The reaction products were labelled internally by 32P (700 Ci/mmol; Amersham, Amersham, Buckinghamshire, UK), and they were visualised by autoradiography after standard electro- phoresis on sequencing gels. For detection of point mutations, we screened the autoradio- graphic patterns for coexisting bands. The intensity of bands was analysed with molecular analyst software using the Gel Doc 1000 Bio-Rad system. Signals were considered to represent a mutation only if the intensity of the ratio of the new to normal band was &gt; 0.25.

In addition, the possible point mutations in codons 12/13 of H-ras-1 gene were detected in all 35 malignant fibrous histiocytoma specimens by the specific PCR-RFLP method, based on the procedure published previously. Briefly, a 102 bp long product of the nested PCR was digested with the NaeI restriction nucleace, and the digestion product was electrophoresed using a 2% agarose gel. Only samples with the wild-type sequence within the investigated codons were cleaved, to produce two fragments, 48 and 54 bp long.

Results
All 35 tumours were diagnosed as malignant fibrous histiocytomas and subclassified as storiform (n = 15), pleomorphic (n = 10), or myxoid (n = 10) according to the predominate pattern. We are aware of the great heterogen- city of malignant fibrous histiocytomas, the diagnostic criteria of which are still discussed, and our pathologists were very cautious with their classification. The analysed tumours expressed CD 68 and vimentin. There was very little expression of desmin, endothelium, S-100 protein, and CD34. Twenty one cases were classified as high grade sarcomas (G3), whereas 14 were considered to be low grade tumours (G1 or G2).

Codon 12 was not mutated and there were no other changes of the H-ras-1 exon 1 in any of the malignant fibrous histiocytoma specimens. In addition, no tumours diagnosed as the myxoid subtype (10 of 35 tumours) had mutations of codon 12 of the H-ras-1 gene, whereas Bohle et al found the typical transversion of G→T in codon 12 as the most characteristic change (with a frequency of ~ 45%) in the myxoid subtype of malignant fibrous histiocytoma. None of 32 malignant fibrous histiocytoma cases were described as myxoid subtype in their report, and the overall number of cases investigated and the proportion of myxoid malignant fibrous histiocytomas were exactly the same as in our studies.

Our results indicated that the second hot spot within the H-ras-1 gene, codon 13, and its flanking regions were also normal. Figure 1
DNA the direct sequencing test allowed the detection of abnormal nucleotides in tumour samples containing 50% transformed cells.

The technique of direct sequencing of PCR products has the advantage of giving detailed information about the codons of interest and their surrounding sequences. When mutational events are limited to known codons (mainly codons 12 or 13 in the ras gene) RFLP analysis of PCR products is faster, less expensive, and more sensitive. The results of PCR-RFLP analysis performed using the series of reciprocally diluted normal and mutated DNA amplification products is shown in fig 2A.

It should be noted that this test was two to three times more sensitive than the direct sequencing technique for the detection of mutated template (we should be able to detect a codon 12 mutation in an admixture of tumour cells and normal cells containing 12% tumour cells). Nevertheless, this test did not detect mutations within exon 1 of H-ras-1 in any examined malignant fibrous histiocyteoma samples (fig 2B).

Discussion

Models of neoplastic transformation assume that the accumulation of abnormalities of genes whose protein products are involved in cell cycle regulation (such as ras genes), or play an important role in signal transduction into the cell (such as ras genes), are mainly responsible for uncontrolled tumour growth. Reports showing that impaired function of the p53 protein is often accompanied by specific mutation in ras family genes support this presumption. Because the mutations in ras genes are widely recognised in many types of tumours, the search for their presence in sarcoma cells was justified.

Thirty five tumour specimens were reviewed diagnostically before molecular analysis. As described, all selected tumour samples were unequivocally diagnosed as malignant fibrous histiocyteomas, excluding other soft tissue sarcomas with a similar phenotype. In addition, their subclassification was performed according to all contemporary criteria. Therefore, we can expect that the tissues used in our study and that of Bohle et al were comparable. In our search for the mutation “specific” for malignant fibrous histiocyteomas, we used two separate methods—direct cycle sequencing and PCR-RFLP. The PCR methods were based on the procedure of Bohle et al with special attention to the nested PCR, to avoid the amplification of ras pseudogenes. This PCR-RFLP technique was more sensitive and we introduced it to confirm data from sequencing tests. All control experiments, especially those with the dilution series of DNA from the homozygously mutated cell line, T24, and normal donor unmutated DNA, indicated that we were able to detect the presence of 10–15% of changed template. In such a system, heterozygously mutated tumour cells would have to constitute 20–30% of the analysed sarcoma samples (for homozygously mutated tumour cells, the fraction ∼10–15% is sufficient for detection). Our previous immunohistochemi-

![Figure 1 Cycle sequencing data for exon 1 of the H-ras-1 oncogene.](Image)

![Figure 2 PCR-RFLP analysis of exon 1 of H-ras-1 oncogene.](Image)
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