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Patterns of chromosomal imbalances in benign solitary fibrous tumours of the pleura

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Abstract Solitary fibrous tumours (SFTs) of the pleura, in contrast to malignant mesothelioma, occur independently of previous asbestos exposure. They are benign tumours, but may recur if the stalk to the adjacent pleural or lung tissue remains in situ during surgical removal. The molecular pathology of SFTs is largely unknown. We used comparative genomic hybridisation (CGH) to characterise 12 localised SFTs and 12 predominantly sarcomatoid mesotheliomas. Fifty-eight percent of the investigated SFTs did not show any chromosomal imbalances. The most frequent defects were losses on chromosome arms 13q (33%), 4q and 21q (17% each). Significant gains were seen at chromosome 8 and at 15q in two cases each. There was no correlation between tumour size and molecular pathology findings. In contrast, 75% of the mesotheliomas carried chromosomal defects. On average, the mesotheliomas showed over three times as many defects per tumour as the SFTs. Localisation of several frequent losses and gains were similar to those of the SFTs. Therefore, in individual cases, a clear distinction between SFTs and sarcomatoid mesotheliomas is not possible based on CGH analysis alone. Further molecular characterisation of this rare tumour entity will be necessary to elucidate possible genes involved in early tumorigenesis.

Keywords Fibrous pleural tumour · Solitary fibrous tumour · Sarcomatoid mesothelioma · Comparative genomic hybridisation · Paraffin material

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Introduction

Solitary fibrous tumours (SFTs) may occur in the pleura, pericardium, mediastinum and retroperitoneum, but sometimes also in tissues far away from serous membranes, such as the pancreas [14], nasal and paranasal sinuses [7, 8, 9, 10] or in soft tissues [21]. Gastrointestinal stromal tumours also belong to this group of immunohistochemically CD34-positive tumours. Fibrous tumours of the pleura show a benign clinical course in most cases. In contrast to malignant mesotheliomas, 80% arise from the visceral pleura and are not associated with previous asbestos exposure. The size may range from 1 cm to 36 cm. In resected specimens, it is always important to look for the stalk of the tumour carrying the vessels. If this stalk can be completely resected, the probability of a recurrent tumour is low. Indications of a possible unfavourable course are elevated mitotic figures (more than 4 per 10 high-power fields), high cellularity, haemorrhage and cytological pleomorphism [2]. The histogenetic origin has been a controversial subject. It is supposed that fibrous tumours arise from pluripotent mesenchymal connective tissue cells rather than from submesothelial cells. However, Doucet et al. presented electron microscopic evidence in support of a mesothelial origin of fibrous pleural tumours (FPTs) [6], although this view has not lasted until today. El-Naggar et al. found proof of a mesenchymal–fibroblastic origin in their electron microscopic analysis 3 years later [7]. In the current World Health Organization (WHO) classification, fibrous tumours are listed as soft tissue tumours (ICD-O 8815/0) and not as mesothelial tumours [19]. Attempts of histological subclassification of FPTs into three types (rich in fibres, highly cellular and hyaline) [4] have had no direct influence on daily diagnostic work.

Malignant sarcomatoid mesotheliomas are in most cases asbestos-associated tumours of submesothelial origin. Many well-known but obsolete synonyms of fibrous pleural tumours, e.g. solitary/localised mesothelioma, pleural fibroma, submesothelial fibroma or localised fibrous mesothelioma, reflect the uncertainty of classifica-

tion and even nowadays sometimes result in misinterpretation and confusion with malignant mesotheliomas. This may have disastrous consequences for the patient as far as prognosis and medicolegal aspects are concerned.

There are two reports on cytogenetic alterations detected using classical cytogenetics in FPTs, one case of a translocation (2;3)(p21;p26) and one trisomy 21, indicating that there may be different types of genetic changes in FPTs [5, 15].

We have investigated 12 FPTs using comparative genomic hybridisation (CGH) in order to look for recurrent chromosomal aberrations and possible early arising defects. In addition, we have tested 12 sarcomatoid mesotheliomas in search of a possible clear distinction from the FPTs.

Materials and methods

Tissue samples

From a collection of 32 benign fibrous tumours, we were able to obtain 12 specimens with a DNA quality that was suitable for CGH analysis. All of the tumours were typical FPTs without necrosis or cellular pleomorphism, had mitotic counts of less than 4 per 10 high-power fields and were located in the pleura or mediastinum. For comparison, we analysed 12 cases of malignant sarcomatoid pleural mesotheliomas (categories A/B of the European mesothelioma panel – secure/probable, without essential doubt including all available information). All of the cases are recorded in the files of the Institute of Pathology and the German Mesothelioma Registry, both located at the University Clinic Bergmannsheil in Bochum. The samples were either submitted for consultation or sent directly by clinicians. Selection of the cases was based on prior conventional histological and immunohistochemical analysis. For all analyses, we used paraffin-embedded material. One sample of a sarcomatoid mesothelioma was gained during an autopsy; the other samples were surgically removed and immediately fixed in formalin. In all cases, light microscopical analysis was done using haematoxylin and eosin (H&E) and Elastica van Gieson (EvG) stained sections. Basic patient data, including tumour size and kind of tumour (primary or recurrent), are shown in Table 1 and Table 2. The mean patient age was 64.8 years in the fibrous tumour group (range 45–87 years) and 64.7 years in the mesothelioma group (range 49–77 years). All sarcomatoid mesotheliomas are asbestos associated. Only one of the sarcomatoid mesotheliomas occurred in a woman, whereas in fibrous tumours the ratio of females to males was 5:7.

Immunohistochemical staining

Both tumour groups were subjected to immunohistochemical analysis using the following two antibody panels. The first panel, in diagnostics applied to confirm fibrous tumours, consisted of CD34 (Immunotech, 1:50, microwave pretreatment, citrate buffer pH 6.0), CD99 [Dako, 1:50, microwave pretreatment, ethylene diamine tetraacetic acid (EDTA) buffer pH 8.0], vimentin (Dako, 1:4000, microwave pretreatment, citrate buffer pH 8.0), Ki67 (MiB1, Dianova, 1:800, microwave pretreatment, EDTA buffer pH 8.0) and keratin AE1/AE3 (Camon, 1:800, protease pretreatment). The second panel, established for identification of sarcomatoid mesotheliomas, consisted of keratin AE1/AE3, vimentin, calretinin (SWant, 1:3000, microwave pretreatment, citrate buffer pH 6.0), HEA (BerEP4, Dako) and Ki67. All immunohistochemi-

Table 1 Solitary fibrous tumours. Patient data and basic information on the tumours. All tumours were positive for CD34 antigen and negative for cytokeratin antibody AE1/AE3. *PT* primary tumour; *RT* recurrent tumour; *ND* not detectable

Case	Gender	Age (years)	PT/RT	Tumour size (cm)	MiB1	Localisation
F1	Male	77	RT	11×7×5	≈5%	Pleura
F2	Female	74	PT	10.5×2×5	≈5%	Pleura
F3	Female	73	RT	10×8×5	<1%	Mediastinum
F4	Male	67	PT	13×12×6	ND	Pleura
F5	Male	59	PT	6×4.5×3	<2%	Pleura
F6	Male	65	PT	4.5	ND	Pleura
F7	Female	65	PT	3	<5%	Pleura
F8	Female	45	PT	3×2×1	ND	Pleura
F9	Female	51	PT	10×6×4	ND	Pleura
F10	Male	47	PT	3.8×2×1.1	<5%	Pleura
F11	Male	68	RT	10.5×9×7	5–10%	Pleura
F12	Male	87	RT	27	≈1%	Pleura

Table 2 Sarcomatoid mesotheliomas. Patient data

Case	Gender	Age (years)	Asbestos exposure	Calretinin staining	MiB1	Special features
M1	F	64	Yes	Negative	≈35%	
M2	M	75	Yes	Positive	≈25%	900 asbestos bodies/cm^3 lung tissue
M3	M	77	Yes	Focally positive	≈20%	
M4	M	76	Yes	Strongly positive	≈15%	2300 asbestos bodies/cm^3 lung tissue
M5	M	56	Yes	Negative	<10%	
M6	M	54	Yes	Positive	≈25%	Lung infiltration, many mitoses
M7	M	63	Yes	Negative	<10%	Lung infiltration
M8	M	76	Yes	Negative	≈20%	
M9	M	59	Yes	Negative	≈30%	
M10	M	63	Yes	Positive	≈20%	
M11	M	64	Yes	Negative	≈20%	
M12	M	49	Yes	Negative	≈40%	

cal analyses were performed with a Techmate immunostainer (Dako) using the alkaline phosphatase-antialkaline phosphatase (APAAP) method.

Comparative genomic hybridisation

For CGH analyses, 20 sections of 10 µm each were cut from the paraffin blocks. Selected tissue areas were microdissected with a scalpel. After deparaffinisation, genomic DNA was extracted and purified using a commercially available kit (QIAamp Tissue Kit, Qiagen). Reference DNA was isolated from peripheral human blood using a QIAamp Blood Kit (Qiagen). The following steps represent a slightly modified version of a published CGH protocol [18]. DNA labelling was done using nick translation with digoxigenin-11-dUTP or biotin-16-dUTP (Roche). The probe length, checked using agarose gel electrophoresis, was between 300 bp and 3000 bp. Typically, 0.9 µg labelled reference DNA, 0.9 µg labelled tumour DNA, 30 µg human Cot-1 DNA (Roche) and 10 µg herring sperm DNA (Promega) were co-precipitated and then redissolved in 5 µl formamide. After addition of 10 µl 20% dextran sulfate/4× standard saline citrate (SSC), the DNA mix was denatured for 5 min at 77°C and prehybridised for 1 h at 37°C.

In parallel, commercially available metaphase preparations (Vysis) were denatured at 76°C in 70% formamide/2× SSC for 1–5 min (duration depended on the metaphase batch), washed with 70% ethanol, dehydrated in ascending concentrations of ethanol and finally air dried. After pipetting the DNA mix onto the slide carrying the metaphase spreads, hybridisation was performed for 3 days at 37°C. The hybridised metaphase chromosomes were washed three times for 3 min in 50% formamide/2× SSC at 37°C, three times for 3 min in 0.1× SSC at 60°C and then kept in 4× SSC/0.1% Tween 20 at 37°C until the next step. Blocking was done for 1 h with 5% blocking reagent (Roche)/3% bovine serum albumin (Sigma)/4× SSC/0.1% Tween 20 (125 µl/slide). After a brief washing step in 4× SSC/0.1% Tween 20 at 37°C, the staining (1 h, 37°C) was performed with 3.2 µg/ml anti-digoxigenin-rhodamine (Roche) and 16 µg/ml fluorescein-avidin (Vector Labs) in 125 µl blocking solution. Unbound antibodies were removed by washing three times (3 min, 45°C) in 4× SSC/0.1% Tween 20. 4'-6' Diamidino-2-phenylindole (DAPI, 40 ng/ml, Roche) served as counterstain for chromosome identification.

The DNA of each case was labelled, hybridised and stained at least twice. The fluorescence images were recorded with a cooled 12-bit charged coupled device (CCD) camera (SensiCam, PCO) on an Axiophot fluorescence microscope (Zeiss). Finally, the images were processed and evaluated with the CGH programme Quips (Vysis) on a Macintosh G3 PowerPC (Apple). For each case, at least ten metaphases were analysed and each was analysed twice. A 99% confidence interval was used for confirmation. The threshold values for losses and gains were set to 0.8 and 1.2, respectively. As controls, the samples were also labelled inversely and analysed. In addition, we used DNA from a tumour with known defects (MPE 600, Vysis) as a positive and DNA from normal tissue as a negative control. Besides telomeric and centromeric regions, certain chromosomes and chromosomal regions are prone to false-positive signals, especially over-representations [13]. Taking into account the results from the control experiments and the prevailing background stain visible in some hybridisations, the following known areas of error were interpreted with special care and, if necessary, excluded: 1p32-pter, 7q21, 9q34, 16, 17, 19, 20, 22.

Results

The immunohistochemistry resulted in a clear differentiation between fibrous tumours and sarcomatoid mesotheliomas. Benign fibrous tumours showed a uniformly positive reaction for CD34 (Fig. 1a) and vimentin and a negative reaction with the keratin antibody AE1/AE3. With the exception of case F11, which was positive in 5–10% of the cells, less than 5% of the cells in fibrous tumours stained MiB1 positive (Fig. 1b, Table 1). On the contrary, all malignant sarcomatoid mesotheliomas were at least focally positive for keratin and vimentin. Calretinin, which has proven to be one of the best indicators for mesothelial origin in the last few years [17], was focally positive in five cases (42%, Fig. 1c). The proliferation index was higher in malignant sarcomatoid mesotheliomas: eight cases with 20–40% and only two cases with less than 10% MiB1 immunoreactivity. As controls, we found that all mesotheliomas stained negative for CD34 and all FPTs stained negative for calretinin, whereas the overlying mesothelium stained positive.

The CGH results for the fibrous tumours are presented in Table 3. There are seven cases (58%) with no significant defects detectable using CGH analysis. Losses of DNA material are more frequent than gains. Loss of chromosome 13q occurs in 33% of all cases and in 80% of the cases that have any detectable defects. Noteworthy are the losses of 13q and 21q in case F11. This is the only case, in which the fluorescence ratio is exactly 0.5, which indicates a high tumour homogeneity with all of the cells missing exactly one copy each of the respective chromosome arms. Other losses are localised on chromosomes 4q, 6, 9p, 10, 15q, 21q and Xq. Two cases show a gain of chromosome 8 and another two cases a gain at 15q22. Other gains occur only in single cases on chromosomes 5, 12 and 21. No high-level amplifications are seen. The results are depicted in more detail in Fig. 2a.

Table 3 Comparative genomic hybridisation results. Chromosomal defects in solitary fibrous tumours

Case	Losses	Gains	Σ Losses	Σ Gains	Σ Defects
F1	4q, 9p, 10, 13q, 15q	5, 8, 12p, 12q, 21	5	5	10
F2	–	–	–	–	–
F3	–	–	–	–	–
F4	–	–	–	–	–
F5	–	–	–	–	–
F6	–	–	–	–	–
F7	4q, 13q, 21q, Xq	15q	4	1	5
F8	13q	15q	1	1	2
F9	–	–	–	–	–
F10	–	–	–	–	–
F11	13q, 21q	–	2	0	2
F12	6	8	1	1	2

Table 4 Comparative genomic hybridisation results. Chromosomal defects in malignant sarcomatoid mesotheliomas

Case	Losses	Gains	Σ Losses	Σ Gains	Σ Defects
M1	2q, 4, 5q, 7p, 7q, 9, 13q, 14q, 15q, 18q	1p, 3q, 5p, 6, 8q, 10, 12p, 12q, 21q, 22q	10	10	20
M2	1p, 4, 10p, 11q, 13q, 15, 18p, 19q, 22q	1q, 3p, 3q	9	3	12
M3	18p, 22q	5p, 8q	2	2	4
M4	4, 6q, 13q, 14q	–	4	–	4
M5	19p	–	1	–	1
M6	–	–	–	–	–
M7	–	–	–	–	–
M8	4p, 13q	15q	2	1	3
M9	4q, 6q, 13q	3p, 5p, 10q	3	3	6
M10	–	–	–	–	–
M11	1p, 2q, 4q, 6q, 9p, 14, 19p, 22q	1q,15q	8	2	10
M12	7p, 8p, 9p, 11q, 12p, 13q, 14q, 21	1q, 2p, 2q, 10q, 11q, 20q	8	6	14

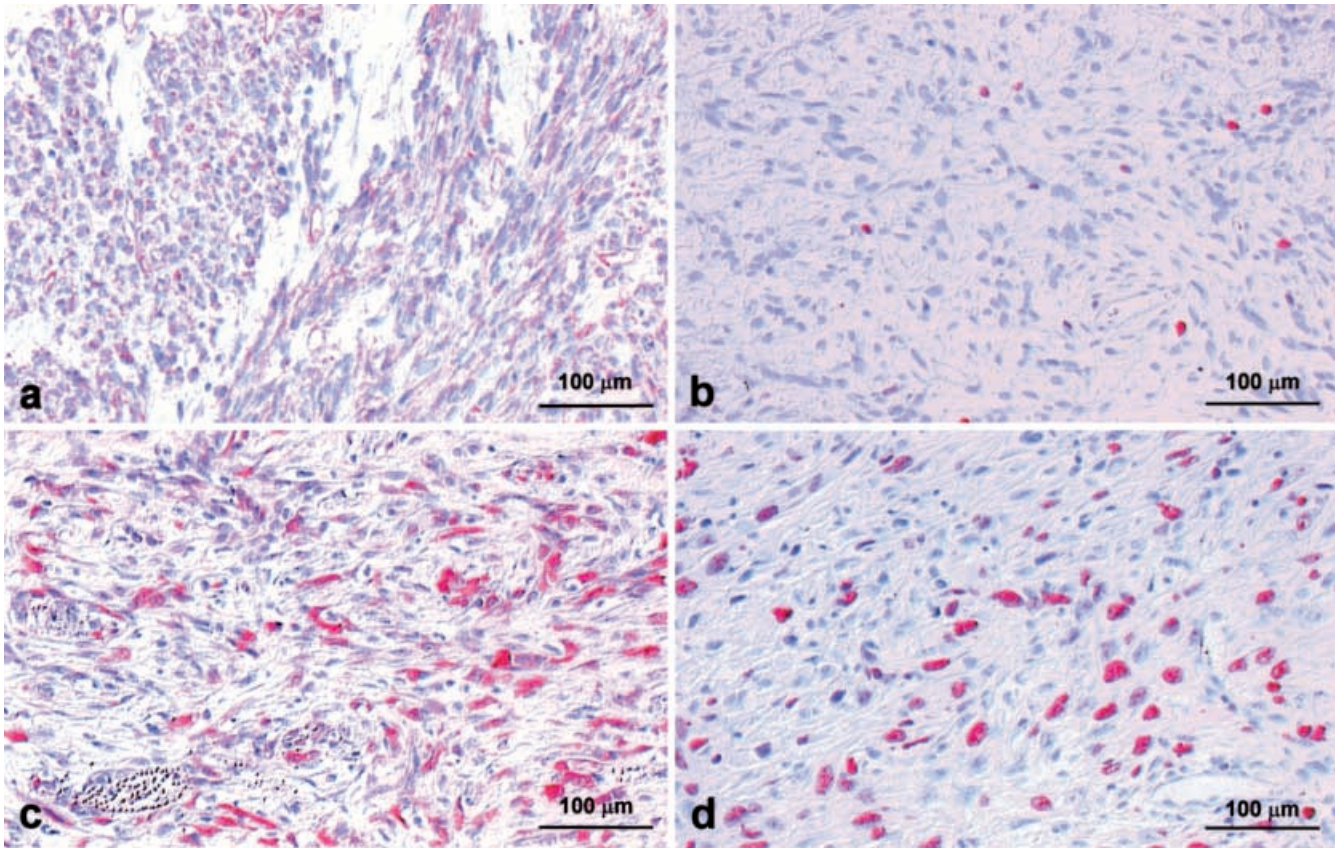

Fig. 1 Immunohistochemical findings in fibrous tumours and sarcomatoid mesotheliomas. **a** Fibrous pleural tumour (FPT; case F1), CD34. **b** FPT (case F2), MiB1. **c** Sarcomatoid mesothelioma (case M6), calretinin. **d** Sarcomatoid mesothelioma (case M12), MiB1

The CGH analysis of the sarcomatoid mesotheliomas is presented in Table 4. In contrast to the fibrous tumours, only three cases (25%) have no significant defects. We observed more than three times as many chromosomal defects in mesotheliomas as in fibrous tumours. On average, mesotheliomas show a higher number of losses as well as gains per case (Table 5). Frequent losses are located at 4p, 4q, 6q, 9p, 13q, 14q and 22q. The highest frequency of defects affects chromosome 13q (50%). Recurring gains of DNA material are less pronounced, with chromosomes 1q, 5p and 10q being affected most (25% each). A detailed summary of all defects can be seen in Fig. 2b. Comparison of the results of fibrous tumours and mesotheliomas surprisingly reveals recurrent common losses of chromosomal material at 4q and 13q, and gains at 8q and 15q (Table 6). In single cases, common defects can also be seen on 6q, 9p, 10p, 12p and 21q. However, chromosomes 1, 2, 3, 7, 11, 14, 18, 19, 20 and 22 carry defects that cannot be seen in the group of SFTs.

Discussion

The uniformly positive reaction for CD 34 in solitary fibrous tumours is well known [20]. All of our tested fi-

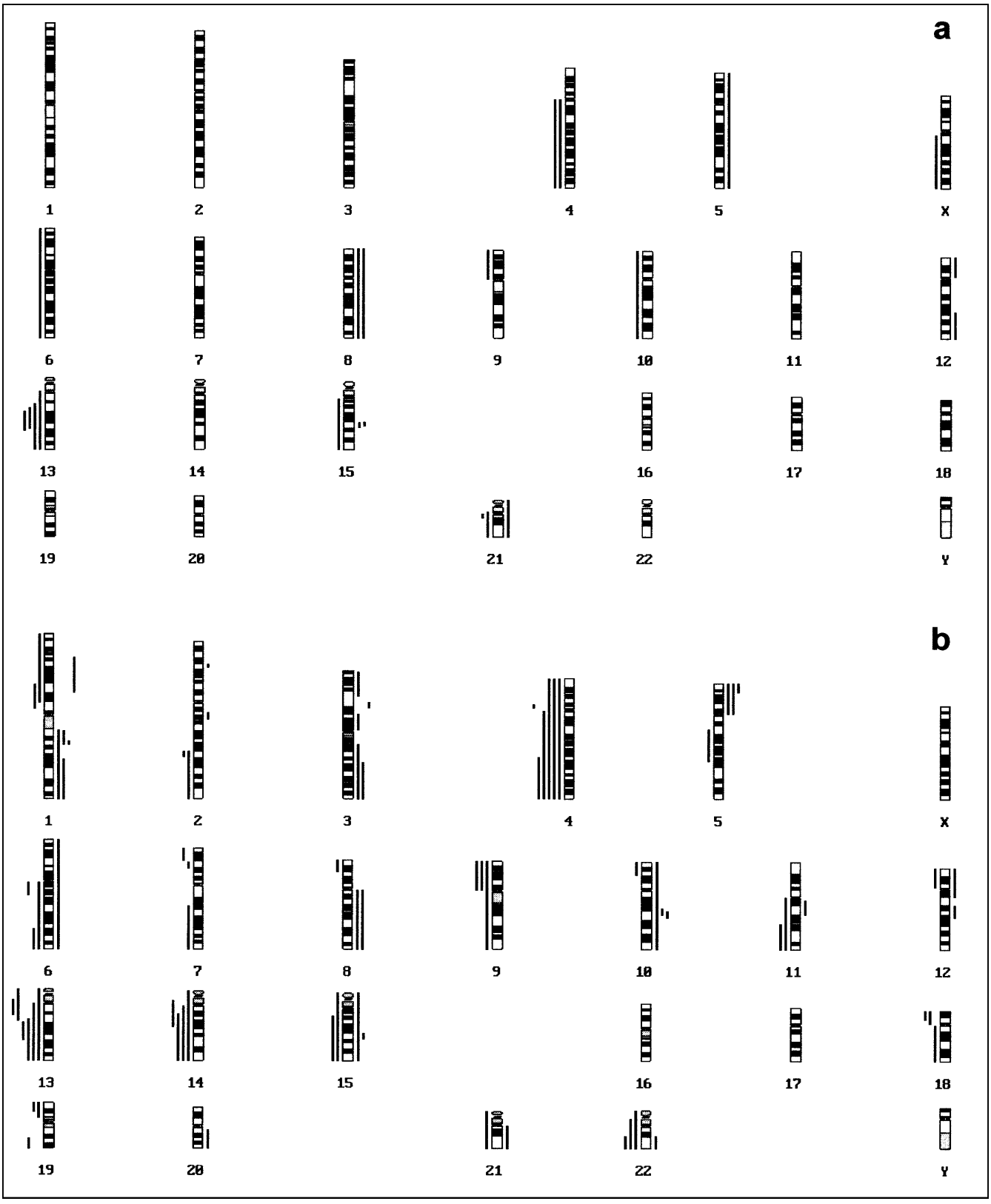

Fig. 2 Compilation of chromosomal aberrations from the 12 investigated fibrous pleural tumours (FPTs) (**a**) and 12 malignant sarcomatoid mesotheliomas (**b**) in so-called superkaryograms. Losses are depicted as *bars* on the *left* side of each chromosome ideogram; gains are depicted on the *right* side

Table 5 Comparative genomic hybridisation results in summary. In general, mesotheliomas are characterised by more complex alterations than solitary fibrous tumours (SFTs), but do not differ significantly in the ratio of losses to gains

	SFT		Sarcomatoid mesothelioma	
	Range	Mean value	Range	Mean value
Defects/case	0–10	1.8	0–20	6.2
Losses/case	0–5	1.1	0–10	3.9
Gains/case	0–5	0.7	0–10	2.3

Table 6 Comparative genomic hybridisation results. Comparison of the frequency of chromosomal defects in solitary fibrous tumours (SFTs) and sarcomatoid mesothelioma. Only those defects that occur in at least two cases are listed

Defect	SFT		Sarcomatoid mesothelioma	
Losses	13q[a]	(33%)	13q[a]	(50%)
	4q[a], 21	(17%)	4q[a]	(42%)
			4p, 14q	(33%)
			6q, 9p, 22q	(25%)
			1p, 2q, 11q, 15q, 18p, 19p	(17%)
Gains	8[a], 15q[a]	(17%)	1q, 5p, 10q	(25%)
			3pq, 8q[a], 15q[a]	(17%)

[a]Defects that are common in both tumour entities

brous tumours were positive. In cases of typical histological appearance, this marker in combination with an absence of cytokeratin staining is confirmatory for the diagnosis. The proliferation rate was low in all of the cases we investigated, usually with less than 5% MiB1-positive cells. On the contrary, malignant sarcomatoid mesotheliomas show a mean proliferation index of about 20%. As a consequence, in cases of histological doubt in highly cellular FPTs, it is useful to test MiB1. The calretinin antibody has become a powerful immunohistochemical tool in mesothelioma diagnosis because of its good discrimination between pleurally disseminated adenocarcinomas and predominantly epithelioid and biphasic mesotheliomas [17, 22], being positive in up to 100% of biphasic mesotheliomas and only focally positive in up to 15% of tumour cells in adenocarcinomas [22]. Nevertheless, in predominantly sarcomatoid mesotheliomas, calretinin expression has been demonstrated in about 20% of a larger group of mesotheliomas [22]. A calretinin expression was detectable in 42% of the investigated mesotheliomas in this study, whereas no FPTs stained positive for calretinin.

Our results demonstrate that CGH is an appropriate diagnostic tool for investigation of fibrous tumours. We have documented a genomic disorder with a number of significant defects. So far, there is only one published study describing a CGH-based analysis of fibrous tumours [16]. Miettinen et al. compared 15 FPTs with 11 hemangiopericytomas. The authors found a relationship between tumour size of the FPTs and frequency of genetic disorders. Tumours smaller than 10 cm in diameter showed no or only minimal chromosomal aberrations. About 50% of the cases were without any detectable defects. The average number of chromosomal defects per case was 1.6, with losses (0.6 per case) less frequent than gains (1.0 per case). The most frequent defect (4 cases, 27%) was a trisomy 8, the most frequent losses were at chromosomes 13 and 20.

Our study shows similar results regarding the average number of chromosomal defects (1.8 per case) and the number of cases without a single defect (58%). However, we saw more losses than gains. An average of 1.1 chromosomal localisations per case were affected by a loss, the average gain was 0.7 per case. A gain of chromosome 8 corresponding to a trisomy 8 was also seen, but only in two cases (17%). Similarly, losses on chromosome 13 were detected, representing the most frequent of all defects in our study. These losses appeared in 80% of the tumours that carried detectable defects. Interestingly, we found a single loss at 13q in a SFT of the thigh (unpublished results). According to Miettinen et al., a single loss of chromosome 13 might suggest an early involvement of this chromosome in the development of the SFTs. A relationship between tumour size and severity of genetic alterations was not evident in our series. There were only three of five tumours smaller than 10 cm without detectable defects, whereas four of seven tumours larger than 10 cm were without defects. Since all of our SFTs were of the typical variant, a correlation between degree of chromosomal changes and transformation into the atypical variant was not possible with the present collective. In contrast, four of the cases of Miettinen et al. showed a mitotic activity exceeding 4 mitoses per 10 high-power fields. This might account for most of the differences seen between the two studies.

The methodology applied in both studies differs in several points: DNA purification, labelling, data acquisition and evaluation. Miettinen et al. used direct labelling of DNA, whereas our group preferred the indirect method, which is more sensitive but also produces a higher background. The hybridisation conditions were similar, with some minor differences. The denaturation of metaphase chromosomes is known to be critical, but depends on the metaphase batch used. Therefore, conditions might vary from batch to batch and a comparison is difficult. We detected some decrease in hybridisation quality when reducing the duration from 3 days to 2 days, as in the protocol by Miettinen et al. Other steps we found to be more tolerant to variations. The different biochemical protocols that are well established and used by many other groups should yield basically the same results if the known regions of artefacts that are adherent to some labelling methods are interpreted with care. However, we found some variation when evaluating the data with two different computer programmes, mainly affecting borderline defects [Pathologe

(2000), in press]. These differences presumably were caused by the different default settings (e.g. the threshold levels) of the programmes. However, with the controls applied in both studies, none of the different methods should have caused major artefacts. Other factors that can influence the CGH analysis are the quality of metaphase preparations and the possible degradation of DNA from formalin-fixed tissues. Therefore, we have critically selected metaphases and DNA from the available material. Finally, the difference in the geographic origin of the tumour specimens might have had some influence.

In summary, the two available studies on SFTs using CGH show somewhat different results, which may rather be attributable to the selected collective of tumours (e.g. number of atypical variants) than the different methods applied. It seems to be essential to study a larger number of SFTs in order to determine whether there is indeed such a wide range of possible genetic changes in SFTs. The number of investigated cases in both studies and the number of cases that actually have chromosomal aberrations is too low to draw conclusions regarding a possible typical defect for SFTs of the pleura. Combining the results from both studies, locations on chromosomes 8, 13 and 20 remain candidates for harbouring genes involved in early tumour development. Further CGH studies of this rare tumour entity should either confirm or supplement these initial chromosomal defects, unless balanced translocations or small copy number changes that cannot be detected using CGH are the cause of tumour development.

CGH studies on chromosomal aberrations in malignant mesotheliomas have been published before [11]. Most recurrent defects were losses. Their locations and frequencies are 1p21-p22 (12%), 4cen-p15.3 (11%), 4cen-q24 (17%), 4q33-qter (18%), 6q16-q22 (24%), 9p21-p22 (24%), 10q23 (11%), 13q21-q22 (17%) and 14q21-q24 (24%). However, sarcomatoid mesotheliomas, as a distinct subgroup, have not been characterised using CGH in representative numbers so far. Our results are compiled in Fig. 2b and Table 6. Qualitatively, all of the published losses in the general group of mesotheliomas can also be found in our collective of sarcomatoid mesotheliomas. Differences exist in the frequencies of the losses and the detection of recurrent gains [1, 3, 12].

An interesting finding is the similarity of CGH results from SFTs and malignant sarcomatoid mesotheliomas. There is no comparable study in the literature. We found four common aberrations, located at chromosome arms 4q, 8q, 13q and 15q. The gain at 15q22 appeared to be the only defect with a more restricted minimal overlapping area that is identical in both groups. Loss of 13q is the most frequent defect in both tumour entities, being detectable in 33% of the SFTs and 50% of the tested sarcomatoid mesotheliomas. The minimal overlapping area in the SFTs is 13q21–22, whereas in the mesotheliomas the area additionally includes 13q11–14. However, the more benign SFTs show markedly fewer chromosomal defects than the mesotheliomas. Despite a different origin, growth pattern, histological appearance and immunohistochemical findings, there seems to be a common genetic disorder in these tumours. However, only five SFTs and nine mesotheliomas show any defects at all. Therefore, the results derived from these small numbers have to be interpreted very carefully, especially in view of the other existing SFT study that only shows matching results for the loss on chromosome 13q and the gain on 8q. For diagnostic purposes, CGH has only limited suitability to differentiate SFTs from malignant sarcomatoid mesotheliomas. A genome with no or minor defects would favour the diagnosis of a SFT. Immunohistochemistry appears to be a more preferable method to support the diagnosis. The CGH, however, remains a valuable tool to elucidate the molecular bases of SFT tumorigenesis.

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