Molecular cytogenetic investigations of synchronous bilateral breast cancer

K Agelopoulos, N Tidow, E Korschning, R Voss, B Hinrichs, B Brandt, W Boecker, H Buerger

Background: Bilaterality in breast cancer is a rare event and together with an early onset of disease points towards inheritance of the disease. However, most cases seem to occur sporadically, either in a synchronous or metachronous manner.

Methods: Thirty two invasive carcinomas and one in situ carcinoma from 16 patients with synchronous, bilateral breast cancer were investigated by means of comparative genomic hybridisation (CGH) and polymerase chain reaction based multiplex microsatellite analysis. The results were analysed conventionally and were also subjected to a biomathematical cluster analysis.

Results: On average, bilateral breast cancer cases showed a low number of genetic alterations, a low frequency of genetic amplifications, and a high rate of chromosomal 16q losses. A distinct, characteristic genetic alteration associated with bilateral breast disease could not be found. Although two tumour pairs appeared to be related using biomathematical processing for microsatellite analysis, this result was reproduced by CGH data processing in one patient only.

Conclusions: Most synchronous, bilateral breast cancer cases seem to represent independent tumours rather than metastatic events. Nevertheless, the possibility of a specific susceptibility remains.

ORIGINAL ARTICLE

Theoretically, from a tumour biological point of view, the coincidental occurrence of two independent malignant tumours within one organ or an organ system, such as the human breast, is a rather improbable event. In clinical practice, 5–10% of patients with breast cancer will suffer from bilateral tumours, predominantly metachronous disease, associated with a higher frequency of multicentricity, whereas only 1% of patients with breast cancer present with synchronous bilateral breast cancer. The roles of a positive family history or histological differentiation in the likelihood of acquiring bilateral breast cancer disease are controversial. Nevertheless, a young age of onset of disease points to an inherited, familial background, and patients with breast cancer who have BRCA 1 and BRCA2 germ line mutations are 5–10% of all breast cancers, defined as when both tumours were diagnosed within a time period of six months. All patients were diagnosed between 1997 and 2001. The average age was 68.5 years (range, 41–89; median, 68). Staging was performed according to established protocols.

Our study comprised 16 patients with synchronous bilateral breast cancers, defined as when both tumours were diagnosed within a time period of six months. All patients were diagnosed between 1997 and 2001. The average age was 68.5 years (range, 41–89; median, 68). Staging was performed according to established protocols.

Eight invasive carcinomas were graded as grade 1, 17 as grade 2, and seven as grade 3. Fifteen carcinomas were lymph node positive.

RESULTS

The roles of a positive family history or histological differentiation in the likelihood of acquiring bilateral breast cancer disease are controversial.

Results of immunohistochemical and genetic investigations have provided evidence to support the two different hypotheses concerning the evolution of synchronous bilateral breast cancer. Whereas conventional cytogenetic investigations showed the presence of identical balanced chromosomal alterations in bilateral breast cancer, indicating that these tumours result from a metastatic event, other investigators provided evidence for the independent pathogenesis of these tumours.

We aim to provide evidence that most synchronous bilateral breast cancer cases result from two tumours arising independently. Comparative genomic hybridisation (CGH), as a method to gain an overview of all unbalanced chromosomal alterations within a tumour, in combination with polymerase chain reaction (PCR) based multiplex microsatellite analysis and biomathematical cluster analysis, are an ideal combination of techniques to determine the degree of clonal association between synchronous bilateral breast cancer cases.

METHODS AND MATERIALS

Materials

Our study comprised 16 patients with synchronous bilateral breast cancers, defined as when both tumours were diagnosed within a time period of six months. All patients were diagnosed between 1997 and 2001. The average age was 68.5 years (range, 41–89; median, 68). Staging was performed according to established protocols.

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CGH analysis

CGH analysis and the evaluation of genetic alterations were performed as described previously. Only metaphase spreads showing an even, high intensity hybridisation with low granularity were taken into account. Corresponding ratio profiles were evaluated only if the 95% confidence limits did not exceed 0.15. The 50% thresholds (upper threshold, 1.25; lower threshold, 0.75) were applied to define the chromosomal regions of DNA sequence losses or gains. Independent confirmation of chromosomal aberrations has shown that these thresholds are reliable and eliminate the possibility of false positive results. The consistency of these aberrations has been confirmed by previous reverse CGH experiments (tumour DNA labelled with digoxigenin; reference DNA labelled with biotin). Each CGH experiment included a control hybridisation of fluorescein isothiocyanate and rhodamine labelled normal DNA to each other.

Abbreviations: CGH, comparative genomic hybridisation; DCIS, ductal carcinoma in situ; EGF, epidermal growth factor receptor; LOH, loss of heterozygosity; PCR, polymerase chain reaction
DNA was isolated from paraffin wax embedded material. If necessary, at least 25 sections of 10 µm thickness were manually microdissected under microscopic control.

**PCR based multiplex microsatellite analysis**

All breast lesions were analysed by means of PCR based multiplex microsatellite analysis using a panel of 11 polymorphic markers and using the same DNA as for CGH. Reference DNA was isolated from paraffin wax embedded, tumour free axillary lymph nodes of each patient.

PCR assays of epidermal growth factor receptor (EGFR) (forward primer, 5'-GTG TTA GTA ATT TGA GCC AAC A C-3'; reverse primer, 5'-TTT TCT TGC ACA ATT GGC AC-3') and p53 (forward primer, 5'-AAG AAA TTC GTG CTT AAC ACA TAG GG-3'; reverse primer, 5'-GTG TAA GCC CTC GAG TTG-3') were performed in 10 µl reactions containing 1X PCR buffer II (Perkin Elmer, Foster City, California, USA), 2 mM MgCl2, 50 µM of each GeneAmp® dNTP (Perkin Elmer), 1 µM of forward and reverse primer, 30 ng template DNA, and 0.5 U AmpliTaq Gold (Perkin Elmer). The other nine markers were grouped in three multiplex PCRs of three markers each with the following variations of the primer concentration: multiplex 1 (D7S522 forward primer, 5'-GGT GTG CAT GG A TTA GG TGA-3'; D7S522 reverse primer, 5'-GTG ATG CCA CTT CCT GCC AC-3'; D8S258 forward primer, 5'-AGG AAA TTC TCA CCT CCA CTG-3') and multiplex 2 (NEFL forward primer, 5'-GAT GCC CAT ACA ATA AAG GAG GGA GG-3'; D16S540 forward primer, 5'-GGT GGT TCA CAA TTG GAC AGT AT-3'; D16S540 reverse primer, 5'-GAA CCC TCC ATG CTG ACA T5-3') and multiplex 2 (NEFL forward primer, 5'-GAT GCC CAT ACA ATA AAG GAG GGA GG-3'; D16S540 forward primer, 5'-GGT GGT TCA CAA TTG GAC AGT AT-3'; D16S540 reverse primer, 5'-GAA CCC TCC ATG CTG ACA T5-3') and multiplex 2 (NEFL forward primer, 5'-GAT GCC CAT ACA ATA AAG GAG GGA GG-3'; D16S540 forward primer, 5'-GGT GGT TCA CAA TTG GAC AGT AT-3'; D16S540 reverse primer, 5'-GAA CCC TCC ATG CTG ACA T5-3').

Samples (1–2 µl) of the amplified PCR products were diluted in 20 µl water (high performance liquid chromatography grade) containing 0.5 µl GENESCAN® 400 HD [ROX] fluorescent size standard (ABI; Foster City, California, USA). The mix was denatured at 95°C for two minutes and cooled for at least 10 minutes at 4°C.

Separation of the PCR generated alleles was performed by the ABI PRISM® 3700 DNA analyser (ABI) using the Polymer 3700 POP-6® and 1× 3700 running buffer + EDTA (ABI). The data were analysed by means of the GeneScan analysis software.3.5 To standardise the analysis, the loss of heterozygosity (LOH) score was calculated according to Canzian et al.8

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**Table 1** Overview of all unbalanced chromosomal alterations in bilateral breast cancer determined by comparative genomic hybridisation

<table>
<thead>
<tr>
<th>Case</th>
<th>Chromosomal gains</th>
<th>Chromosomal losses</th>
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<tr>
<td>4598A</td>
<td>1q</td>
<td>22</td>
</tr>
<tr>
<td>4598B</td>
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<td>16q</td>
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<td>16</td>
<td>3pter-13; 13q11-31</td>
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<td>1q, 8q</td>
<td>6q24-ter; 8pter-21</td>
</tr>
<tr>
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<td>1q</td>
<td>2q23-ter; 6q18</td>
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<tr>
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<td></td>
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<td>16q12.2-ter</td>
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<td>1q21-ter</td>
<td>16q12.2-ter</td>
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<td>16q12.2-ter</td>
</tr>
<tr>
<td>4603A</td>
<td></td>
<td>11q21-ter; 16q22-ter; 22q11.2-ter</td>
</tr>
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<td>8q</td>
<td>2q22-32; 7q; 16q12.2-ter; 22q12-ter</td>
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<tr>
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<td>8pter-22; 12q11-ter; 12q23-ter; 16q21-ter</td>
<td>8pter-22; 10q11.1-23; 11q14-ter; 12q23-ter; 16q21-ter</td>
</tr>
</tbody>
</table>
Biomathematical analysis of the results was performed by producing an Euclidean distance metric of the result vectors and ordering the results by agglomerative hierarchical clustering (complete linkage). The results were assembled in vectors, representing an ordered view of observations from chromosome 1 arm q to chromosome X (for example, chromosome1q+, chromosome1q−, chromosome1p+, etc) or from processed microsatellites (for example, BB1/2, D7S522, etc). LOH was counted as one event, irrespective of the allele affected.

Distance matrices of these vectors give a measure of the relatedness of feature vectors, consisting of the observable features of one case/patient. Cluster analysis was used to produce similarity groups out of the distance matrices. This approach was used because of the good agglomerative coefficient, which is an indicator of the amount of clustering structure found, and the comparability with other result sets. The methods used are part of the mathematical system SPlus6.

RESULTS

CGH analysis
On average, 4.9 alterations/case (range, 0–13) were found in the invasive breast cancer cases.

Chromosomal gains were most commonly seen on 1q (58%), 8q (30%), 17q (16%), and 20q (14%). Chromosomal regions commonly involved in chromosomal losses were 2q (19%), 6q (3%), 8p (22%), 11q (25%), 16q (52%), and 17p (22%). In the patient with associated ductal carcinoma in situ (DCIS; patient 4602), identical CGH ratio profiles (1q+ and 16q−) were obtained from all three tumours (two tubular invasive carcinomas, ductal carcinoma grade 1; fig 1). All other tumour pairs revealed dissimilar CGH ratio profiles.

LOH analysis
DNAs originating from 16 patients with bilateral breast cancer were analysed. Frequencies of LOH varied from 15% (EGFR) to 95% (D16S400), with a median frequency of 43%. In detail: EGFR, 15% (three cases with LOH and 20 heterozygous); caveolin 1+2, 43% (six cases with LOH and 14 heterozygous); D8S258, 46% (11 cases with LOH and 24 heterozygous); NEFL, 67% (four cases with LOH and six heterozygous); PTEN, 20% (four cases with LOH and 20 heterozygous); Rb1, 35% (nine cases with LOH and 26 heterozygous); D16S400, 95% (19 cases with LOH and 20 heterozygous); D16S422, 77% (20 cases with LOH and 26 heterozygous); D16S422, 77% (20 cases with LOH and 26 heterozygous); p53, 23% (six cases with LOH and 26 heterozygous); and BRCA1, 18% (four cases with LOH and 22 heterozygous) (fig 2). The LOH pattern was identical for all microsatellite markers in one patient only.

In all 32 invasive breast cancer cases, simultaneous LOH affecting the same genetic locus was seen. The same allele was affected in 23 cases only.

Cluster analysis for LOH and CGH data
Cluster analysis of both the CGH and microsatellite analysis data revealed tree-like structures. Two tumour pairs were found to be almost identical or related (cases 4602 and 4797) in LOH analysis. Clustering analysis of the CGH data showed close cytogenetic similarity in only one patient (case 4602; fig 3A, B).

The two tumours found to be similar by CGH clustering were both staged as lymph node negative. Morphologically, the two tumours from patient 4797 were classified as ductal invasive and lobular invasive carcinomas. In patient 4602, both invasive tumours were classified as tubular invasive carcinomas, whereas the DCIS component was highly differentiated. CGH analysis showed that all three tumours had an identical combination of 16q loss and 1q gain. Microsatellite analysis
for 16q markers in this patient revealed loss of the same allele in both invasive tumours, in contrast to the associated DCIS, which showed loss of the other allele.

**DISCUSSION**

Bilateral breast cancer accounts for 3–4% of all breast cancer cases, and might be interpreted as the extreme form of multifocal breast cancer disease. Only a few reports have dealt with genetic findings in sporadic, synchronous breast cancer, concentrating on different aspects and factors in breast carcinogenesis.

The clinical history of our patients provided no evidence to suggest that our series might include cases of familial breast cancer, and the high mean age of our patients supports this assumption. It was also interesting that the average number of genetic alterations seen in each case was lower than that reported in unilateral, sporadic breast cancer. In addition, the rate of 16q losses as another indicator of tumour grade, and the low number of tumours with high level chromosomal...
gains revealed a high degree of homology with well differenti-  
ed ductal invasive tumours, such as well and intermediate-  
differentiated DCIS. Nevertheless, because these cytogenetic  
differences were not significant (data not shown), it is not  
possible to distinguish between unilateral and bilateral breast  
cancer cases on a cytogenetic basis alone.

“Comparative genomic hybridisation offers the opportu-  
nity to gain an overview of all unbalanced chromo-  
osomal alterations within a given tumour, thereby provid- 
ing a single tumour specific cytogenetic fingerprint”

Distinguishing between bilateral and unilateral breast can- 
cer is also not possible using a “higher resolution” technique,  
such as microsatellite analysis, because chromosomal regions  
harbouring the responsible genes were not affected at an  
increased frequency, as in unilateral breast cancers. The  
frequencies of LOH in the respective alleles in our tumour  
series were comparable to those described in the literature.  
It is still not clear whether bilateral breast cancers have an  
independent origin or are the result of a breast to breast  
metastasis sequence. CGH offers the opportunity to gain an  
overview of all unbalanced chromosomal alterations within a  
given tumour, thereby providing a single tumour specific  
“cytogenetic fingerprint” with a high, but limited, number of  
parameters investigated. A major drawback of this technique  
is that balanced translocations within breast cancer cannot  
be detected, and that bilateral breast cancer cases resulting  
from a putative breast to breast metastasis sequence based on  
such translocations will be missed. Identical CGH ratio pro- 
files were found in the in situ and invasive tumour parts on  
both sides in only one patient. Nevertheless, these results are  
usually interpreted subjectively and biomathematical pro- 
ducts provide the possibility for a more objective evaluation  
of the genetic data. Various algorithms to solve such tasks  
have been described. The above mentioned algorithm has  
been chosen after a careful review of our results and com- 
parison with the results of similar algorithms. Using  

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doi: 10.1136/jcp.56.9.660

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