Molecular evidence for putative tumour suppressor genes on chromosome 13q specific to BRCA1 related ovarian and fallopian tube cancer


Background/Aims: Loss of heterozygosity (LOH) on chromosome 13q has been reported to occur frequently in human ovarian cancer, and indications have been found that chromosome 13 may also play a specific role in the inherited form of ovarian cancer. The aim of this study was to define regions on chromosome 13 that may harbour additional tumour suppressor genes involved in the tumorigenesis of BRCA1 related ovarian and fallopian tube cancer.

Materials/methods: DNA extracted from paraffin wax blocks of 36 BRCA1 associated ovarian and fallopian tube carcinomas was analysed by LOH polymerase chain reaction using seven highly polymorphic microsatellite markers spanning chromosome 13q.

Results: High LOH frequencies were found on loci 13q11, 13q14, 13q21, 13q22–31, 13q32, and 13q32–4, suggesting the presence of putative tumour suppressor genes on the long arm of chromosome 13 that may play a role in the pathogenesis of BRCA1 related ovarian and fallopian tube cancer. LOH patterns appeared to be independent of the type of BRCA1 mutation, stage, and grade. Although in some cases there were indications for loss of larger parts of chromosome 13, in most cases losses were fairly randomly distributed over chromosome 13 with retained parts in between lost parts. Microsatellite instability was found in six cases.

Conclusion: Several loci on chromosome 13q show high frequencies of LOH in BRCA1 related ovarian and fallopian tube cancer, and may therefore harbour putative tumour suppressor genes involved in the carcinogenesis of this particular type of hereditary cancer.

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were collected from three institutes (London, Toronto, and Amsterdam). BRCA1 mutations had been established before by various strategies including the protein truncation test and direct sequencing. FIGO stage distribution was: stage I, one case; stage II, two cases; stage III, 19 cases; and stage IV, four cases; the FIGO stage of 10 tumours was unknown. The isolated tissues from archival, formalin fixed, paraffin wax embedded histological specimens were reviewed. Histopathological review confirmed serous cystadenocarcinoma in all cases. The grade distribution was as follows: two cases of grade I, 21 of grade II, 13 of grade III. Table 1 summarises the data of the individual subjects.

DNA isolation

DNA was isolated as described previously. Briefly, normal and tumour tissue were isolated from areas of 3–6 mm² in 10 µm thick paraffin wax sections, guided by haematoxylin and eosin stained sections in which the tumour and the normal areas had been marked by the pathologist (PvD). A laser microdissection microscope was used when necessary (Leica, Rijswijk, the Netherlands). The isolated DNA was amplified by PCR with primers for each subject were pooled and DNA was extracted in 50 µl of lysis buffer (100mM Tris/HCl (pH 8.8), 2mM EDTA, and 400 µg/ml proteinase K (Boehringer Mannheim, Mannheim, Germany). The samples were incubated overnight at 56°C, boiled for eight minutes to inactivate proteinase K, and stored at 4°C.

DNA amplification

The isolated DNA was amplified by PCR with primers for seven microsatellite markers on chromosome 13: D13S263 (13q11–q12), D13S175 (13q11), D13S260 (13q12.3), D13S312 (13q21.1–3), D13S271 (13q22–31), D13S71 (13q32), and D13S173 (13q32–4). These markers were chosen because of more than 70% heterozygosity in the population. Moreover, the choice of the markers was restricted to amplification products of at most 200 bp because DNA isolated from paraffin wax blocks can be fragmented.

DNA was amplified in a final volume of 15 µl of PCR mix including dNTPs (dATP, dTTP, and dGTP, each at 200 µM), dCTP-CY5 (Amersham Pharmacia Biotech, Buckinghamshire, UK) at 1 µM of each primer, and 0.1 U of Taq polymerase (Life Technologies). PCR was carried out in a thermal cycler PTC-100 (MJ Research, Watertown, Massachusetts, Canada). The gels were loaded with CY5 labelled PCR products of at most 200 bp because DNA isolated from paraffin wax blocks can be fragmented.

The amplified PCR products were analysed using the LongRaid Toversystem V3.1 (Visible Genetics Inc, Toronto, Canada). The gels were loaded with CY5 labelled PCR products and run in accordance with the suppliers protocol. As a control, CEPH DNA was used to validate the expected length.
of the amplified products, which appeared, in all cases, to be within the expected size ranges.

As a control for baseline LOH in BRCA1 related carcinomas, LOH frequency on chromosome 15 was determined in the same subset of tumours as described above with markers D15S1364, D15S118, D15S117, and D15S87, and the 99% confidence interval for this proportion was calculated.

Analysis of data

Results were read on computer print outs by at least two observers (AJ/JKG/RPZ/JMJP) until consensus was reached. In some cases, PCR and reading of the amplified products were repeated to improve the quality of the results. The area under the curve was calculated for both alleles in normal and tumour tissue, ignoring stutter bands. PCR products were classified into five categories, namely: retention (R), LOH, non-informative (X), microsatellite instability (MSI), and non-evaluable (−). Retention was defined as when the PCR products of both alleles recognised in the normal tissue were equally amplified, or differed by less than 50% (fig 1). A difference of at least a factor of two between the amount of DNA of such heterozygous alleles was designated as LOH, because even microdissected tumour material will be contaminated to some extent with normal cells. MSI represented a shift of the pattern, resulting from the loss or insertion of base pairs. If only one PCR product could be recognised in the normal tissue, because the individual was homozygous for the amplified sequence, the chosen marker was non-informative. Finally, cases were assigned non-evaluable when no PCR product from either tumour or normal tissue could be obtained. PCR amplification with poor results, obtained in a subset of the preparations, might be the result of suboptimal fixation and/or storage conditions. For some of the markers reliable results were obtained after repeated attempts. Lack of sufficient normal tissue in these sections hampered further investigations. MSI might be involved in tumorigenesis but because MSI provides no indication for the presence of a tumour suppressor gene, cases with MSI were excluded from the estimation of LOH frequencies.

RESULTS

Table 1 shows the LOH patterns over chromosome 13, the detected BRCA1 mutation, and grade (GOG) and FIGO stage if known for the 36 cases studied. In 10 cases, LOH patterns could be evaluated for at least five loci. Some of these patterns point to a deletion of the entire long arm of chromosome 13 (cases 10, 14, and 143) because LOH is present for all informative markers spread over the chromosome. In four cases (3, 9, 12, and 19) a variable number of q terminal adjacent markers are lost, pointing to a partial deletion of the long arm of chromosome 13, because at least one of the proximal markers showed retention. In only one case was retention of all informative markers seen (case 13). However, in many cases, the LOH pattern seemed to be fairly random, with retained parts in between lost parts and vice versa, which can be explained only by multiple complex chromosomal breaks and rearrangements (for example, 23 and 109f), a pattern which is also seen in cases where less than five markers were informative (1, 2, 11, 143, and 154).

Six PCR products in five cases showed MSI, two for 13q14 and 13q32, and one each for 13q11 and 13q12.

Table 2 summarises the LOH data of the seven markers on chromosome 13. Overall, LOH frequencies for the markers investigated were high at 59%. LOH was most frequent (69%) at 13q22−31, closely followed by 13q14 and 13q21 (67%), 13q32, and 13q32−4 (60%). The frequencies of LOH were lowest at 13q11 (50%) and 13q12 (47%). Figure 1 shows a computer representation of 13q22−31 PCR fragment analyses of tumours showing retention in one case and LOH in the other. We found no differences in LOH frequencies between tumours of different stages or grades, or associations between LOH frequencies and type of BRCA mutations (data not shown). LOH for the four markers on chromosome 15 was on average 20% (99% confidence interval, 4.6% to 47%).
**Table 2** Frequency of loss of heterozygosity (LOH), retention (R), microsatellite instability (MSI), and non-informative results because of homozygosity (X) or non-evaluable PCR (-) for seven microsatellites spanning chromosome 13q in 36 BRCA1 related ovarian and fallopian tube carcinomas

<table>
<thead>
<tr>
<th>Marker locus</th>
<th>D13S175 13q11</th>
<th>D13S260 13q12.3</th>
<th>D13S263 13q14</th>
<th>D13S312 13q21</th>
<th>D13S271 13q22–31</th>
<th>D13S71 13q32</th>
<th>D13S173 13q32–4</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>LOH</td>
<td>8</td>
<td>9</td>
<td>14</td>
<td>8</td>
<td>9</td>
<td>12</td>
<td>9</td>
<td>69</td>
</tr>
<tr>
<td>R</td>
<td>8</td>
<td>10</td>
<td>7</td>
<td>4</td>
<td>4</td>
<td>8</td>
<td>6</td>
<td>47</td>
</tr>
<tr>
<td>MSI</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>6</td>
</tr>
<tr>
<td>X</td>
<td>15</td>
<td>4</td>
<td>6</td>
<td>7</td>
<td>11</td>
<td>6</td>
<td>11</td>
<td>60</td>
</tr>
<tr>
<td>% LOH</td>
<td>50%</td>
<td>47%</td>
<td>67%</td>
<td>67%</td>
<td>69%</td>
<td>60%</td>
<td>60%</td>
<td>59%</td>
</tr>
</tbody>
</table>

**DISCUSSION**

In the 36 BRCA1 related adnexal carcinomas studied we found high (≥ 50%) LOH frequencies on chromosome 13 for the markers D13S175, D13S263, D13S312, D13S271, D13S71, and D13S173. This implies the presence of putative tumour suppressor genes at the loci 13q11, 13q14.1–2, 13q21.1–3, 13q22–31, 13q32, and 13q32–4, which may be involved in the pathogenesis of the hereditary form of adnexal adenocarcinoma.

Because there can be much “background” LOH in advanced tumours like adnexal cancers, especially in the case of defective DNA repair genes such as BRCA1 or BRCA2 as seen in breast cancer, one has to set a threshold to define a locus as harbouring a putative tumour suppressor gene. The baseline LOH value in BRCA1 related tumours can be read from the frequency of LOH on chromosome 15, which can be assumed to have a similar probability to be broken and (mis)repaired because it is similar in size to chromosome 13. Because this frequency is 20%, we decided to consider that an LOH frequency ≥ 50% indicates the presence of putative tumour suppressor genes because this threshold is outside the 99% confidence interval of this proportion, and is therefore expected to indicate non-random chromosomal deletions.

“Our results suggest that different genes on chromosome 13 can be involved in the early carcinogenesis of BRCA1 related adnexal cancer”

LOH on chromosome 13 was previously also suggested to play a role in the carcinogenesis of these tumours because it was found to be relatively common in advanced sporadic ovarian carcinomas (up to 50%). Three LOH studies have shown a common region on chromosome 13—13q33–4—with a high frequency of LOH in high grade tumours. Because we found a frequency of 60% LOH in this region, it seems plausible that the presumed role of chromosome 13 in the progression of sporadic ovarian cancer holds also for the hereditary form. Cytogenetic and CGH analyses have shown that aberrations in ovarian carcinomas mostly include partial deletions or monosomies, so we assumed that the observed LOH represents a real loss of loci on chromosome 13. Therefore, the LOH on chromosome 13 is indicative of the presence of tumour suppressor genes. There are several candidate genes at the loci that are suspected to harbour tumour suppressor genes. Locus 13q14 harbours the retinoblastoma gene (RB1), but different studies have shown that the expression of RB1 is retained in most primary ovarian carcinomas, indicating that another yet unknown tumour suppressor gene near to RB1 may be involved. In non-BRCA1/BRCA2 related breast cancer families, CGH and linkage analysis revealed strong evidence for the presence of a tumour suppressor gene on 13q21–2. Our observation of a high frequency of LOH at 13q21–1.3 in BRCA1 related adnexal cancer supports the presence of such a tumour suppressor gene on this narrowed chromosomal region, involved in both hereditary breast and adnexal cancer. Other candidate genes localised to 13q21–2 are protocadherin 9, the serine/threonine protein kinase EMK, the human homologue of the drosophila dachshund gene, and ubiquitin C-terminal esterase L3. No other genes in close relation with breast or ovarian cancer were found on 13q11, 13q21, or 13q22–3.

An interesting gene localised to 13q32–34 is involved in the excision repair system, which is impaired in xeroderma pigmentosum complementation group G (Cockayne syndrome) (www.gdb.org/gdbreports >2001).

Kerangueven and colleagues suggested that after impairment of BRCA1 function the next obligatory step in tumorigenesis is the inactivation of one of a limited repertoire of tumour suppressor genes, rather than one particular tumour suppressor gene that initiates a fixed cascade of events. This option has gained acceptance with respect to breast carcinomas and probably holds true for BRCA1 related adnexal carcinomas also, because we and other groups failed to find evidence of the involvement of one common tumour suppressor gene in hereditary ovarian carcinomas.

Indeed, our results suggest that different genes on chromosome 13 can be involved in the early carcinogenesis of BRCA1 related adnexal cancer. Additional chromosome 13 markers may narrow these regions to localise the genes of interest more precisely. However, because we also found a high frequency of breaks, particularly in chromosome 13, tiny deletions or small retained chromosome fragments may be missed by the technique used. Even an increased number of markers cannot exclude these possibilities in tumours with a high number of chromosomal breaks. In these cases, only the demonstration of the presence of genes themselves will be reliable. If one gene of several optional suppressor genes is required early in carcinogenesis, the subsequent hits may vary also, so that various gene expression profiles can be expected in BRCA1 related adnexal tumours. Hedenfalk et al showed different molecular pathways in BRCA1 related, BRCA2 related, and sporadic breast cancer using gene expression profiles. It would be interesting to see whether relatively small differences in gene expression, owing to the impairment of different tumour suppressor genes and subsequent genetic aberrations, can be noted from microarray data within the group of BRCA1 related adnexal tumours. In future studies, we plan to apply CGH-array to narrow down the chromosomal regions of loss, in addition to microarray expression analysis to study gene expression. In the future the analysis of microarrays may lead to the identification of candidate genes involved in the early pathogenesis of BRCA1 related adnexal cancer.

There were no correlations between LOH or MSI and grade or stage. However, these data need to be interpreted with some care, because there were few grade 1 cases, and stage was usually 3 or 4 and lacking in several cases.

In conclusion, there are several loci on chromosome 13 (13q11, 13q14.1–2, 13q21.1–3 13q22–31, 13q32, and 13q32–4)
that show high frequencies of LOH in BRCA1 related adnexal cancer, and may therefore harbour putative tumour suppressor genes involved in the carcinogenesis of this particular type of hereditary cancer.

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REFERENCES


