K-ras mutations appear in the premalignant phase of both microsatellite stable and unstable endometrial carcinogenesis

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Abstract

Aims—Sequential events of endometrial tumorigenesis can be studied by comparison of genetic lesions seen in normal, premalignant, and malignant tissues. The distribution of K-ras mutations in microsatellite stable and unstable premalignant lesions was studied to determine whether this gene is implicated in both tumorigenic pathways.

Methods—K-ras mutations were analysed by polymerase chain reaction–single strand conformation polymorphism (PCR–SSCP) and direct sequencing in matched endometrial normal, premalignant (atypical hyperplasias), and adenocarcinoma tissues from individual patients. Identification of precancers solely by their appearance as atypical endometrial hyperplasias is very subjective; therefore, in addition to histopathological assessment, we performed molecular testing (non-random X inactivation or clonal altered microsatellites) for an expected feature of precancers—that is, monoclonality.

Results—Equivalent K-ras mutation frequencies were seen in microsatellite stable (six of 33) and unstable (three of 23) cancers. In both types, K-ras mutation in monoclonal precancers usually corresponded to a change from normal to an equivocal (two of 12) or hyperplastic (10 of 12) histology. Divergent K-ras genotypes among multiple neoplastic tissues of individual patients (two of six patients) are exceptions explained either by multicentric premalignant disease, or acquisition of K-ras mutation late in neoplastic progression.

Conclusions—K-ras mutation occurs in both premalignant microsatellite stable and unstable endometrial neoplasia, sometimes before acquisition of features readily diagnostic as atypical endometrial hyperplasia.

Keywords: endometrial carcinoma; K-ras; endometrial hyperplasia

Endometrial carcinogenesis is a multistep process, the intermediate stages of which can be discerned as physically distinctive precursor lesions. These intervening stages, if accessible for genetic analysis, can provide insights into the sequence of events leading to endometrial adenocarcinoma: especially if normal, premalignant, and malignant tissues are studied in individual patients. Many of the common genetic changes seen in endometrial cancers, such as K-ras mutation and microsatellite instability, have been observed in endometrial hyperplasias, often equated with putative endometrial precancers. However, the pathological diagnosis of atypical endometrial hyperplasia is notoriously hard to reproduce, and despite efforts to standardise criteria and nomenclature, complicates attempts to understand the genetics of premalignant endometrial disease. The recent demonstration that some atypical endometrial hyperplasias are monoclonal suggests that premalignant hyperplasias are neoplasms that differ from their malignant sequelae in the ability to invade adjacent tissues. As might be anticipated, some monoclonal endometrial putative precancers have contentious histologies, but their role as precancers is reinforced by the demonstration that they are progenitors of malignant tissues. For these reasons, we and others have developed and extensively...
endometrioid-type endometrial adenocarcinoma was present in the hysterectomy; (2) areas of histologically non-malignant endometrium were present in the hysterectomy; and (3) paraffin wax blocks were available. Cases suitable for clonal analysis were identified by testing normal (myometrial) tissues for a heterozygous genotype at the X-linked marker used for X inactivation studies (human androgen receptor gene; HUMARA) and malignant (carcinoma) tissues for presence of MI. Thirty three MS cases and all 23 MI cases were accepted for complete analysis as follows.

### DNA ISOLATION AND CLONAL ANALYSIS
DNA was isolated from 7 µm thick paraffin wax embedded sections by selective ultraviolet irradiation, proteinase digestion, organic extraction, and ethanol precipitation, as described previously. Paired tumour/normal DNAs from each case were screened with primers for two tetranucleotide repeat (T3.1 and T5.2) loci found previously to contain novel alleles in most (100%). MI endometrial adenocarcinomas.

Those tumours with at least one novel allele in the screen underwent an expanded testing with a panel of 10 microsatellites. Tumours with novel alleles in two or more of 10 studied microsatellites were scored as MI, and the full 10 loci studied in a similar manner in DNAs isolated from non-malignant areas of the endometrium. Non-malignant areas were scored as monoclonal if at least one novel allele was clonally present relative to normal reference myometrium. The 10 sets of PCR primers and their loci listed below by locus/primer/laboratory identifier were amplified and resolved under conditions described previously:

- D1S518/GATA7C01/T1.2
- D2S1384/GATA52A04/T2.4
- D2S1399/GGA2A20G04/T2.3
- D3S2387/GATA22G12/T3.1
- D3S2459/GATA68D03/T3.4
- D4S1627/GATA7D01/T4.1
- D5S510/GATA62A04/T5.2
- D5S2459/GATA68D03/T3.4
- D5S384/GATA52A04/T2.4
- D5S8384/GATA52A04/T2.4
- D6S2459/GATA68D03/T3.4
- D7S510/GATA62A04/T5.2
- D7S8384/GATA52A04/T2.4
- D8S1132/GATA26E03/T8.2
- D12S1435/GATA49E01/T2.1
- D17S1132/GATA26E03/T8.2

DNA from normal myometrium of all patients was amplified at the HUMARA trinucleotide repeat locus using primers

### Methods

#### CASE SELECTION
One hundred and fifty eight archival paraffin wax embedded hysterecomy specimens were identified from the division of women’s and perinatal pathology at Brigham and Women’s Hospital, Boston, MA, after meeting the following criteria: (1) histologically confirmed endometrioid-type endometrial adenocarcinoma was present in the hysterectomy; (2) areas of histologically non-malignant endometrium were present in the hysterectomy; and (3) paraffin wax blocks were available. Cases suitable for clonal analysis were identified by testing normal (myometrial) tissues for a heterozygous genotype at the X-linked marker used for X inactivation studies (human androgen receptor gene; HUMARA) and malignant (carcinoma) tissues for presence of MI. Thirty three MS cases and all 23 MI cases were accepted for complete analysis as follows.

### Table 1 Distribution of mutations in 56 endometrial adenocarcinomas

<table>
<thead>
<tr>
<th>Tumour feature</th>
<th>K-ras mutations</th>
<th>p53 mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Histological grade</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Grade I</td>
<td>39</td>
<td>6</td>
</tr>
<tr>
<td>Grade II</td>
<td>6</td>
<td>1</td>
</tr>
<tr>
<td>Grade III</td>
<td>11</td>
<td>2</td>
</tr>
<tr>
<td>MI</td>
<td>23</td>
<td>3</td>
</tr>
<tr>
<td>MS</td>
<td>33</td>
<td>6</td>
</tr>
</tbody>
</table>

### Table 2 DNA from non-malignant endometrium (non-CA) of patients with K-ras mutated tumours

<table>
<thead>
<tr>
<th>Case number</th>
<th>MS/MI</th>
<th>K-ras mutation</th>
<th>Non-CA mutation</th>
<th>Non-CA tissue</th>
<th>Non-CA diagnosis</th>
<th>Non-CA clonality</th>
</tr>
</thead>
<tbody>
<tr>
<td>94-154</td>
<td>MS</td>
<td>12 GGT→GTT</td>
<td>+</td>
<td>a</td>
<td>Atypical hyperplasia</td>
<td>Monoclonal</td>
</tr>
<tr>
<td>94-04</td>
<td>MS</td>
<td>12 GGT→GAT</td>
<td>+</td>
<td>E1</td>
<td>Atypical hyperplasia</td>
<td>Polyclonal</td>
</tr>
<tr>
<td>96-06</td>
<td>MS</td>
<td>12 GGT→GTT</td>
<td>+</td>
<td>E2</td>
<td>Normal</td>
<td>Polyclonal</td>
</tr>
<tr>
<td>96-12</td>
<td>MI</td>
<td>12 GGT→GTT</td>
<td>+</td>
<td>E3</td>
<td>Atypical hyperplasia</td>
<td>Monoclonal</td>
</tr>
<tr>
<td>96-41</td>
<td>MS</td>
<td>12 GGT→GTT</td>
<td>+</td>
<td>E3 (prior)</td>
<td>Insufficient tissue</td>
<td>Monoclonal</td>
</tr>
<tr>
<td>96-51</td>
<td>MS</td>
<td>12 GGT→GAT</td>
<td>+</td>
<td>E3 (prior)</td>
<td>Atypical hyperplasia</td>
<td>Monoclonal</td>
</tr>
<tr>
<td>96-67</td>
<td>MS</td>
<td>12 GGT→GTT</td>
<td>+</td>
<td>E3</td>
<td>Unclassified</td>
<td>Monoclonal</td>
</tr>
<tr>
<td>96-100</td>
<td>MI</td>
<td>12 GGT→GTT</td>
<td>+</td>
<td>E1</td>
<td>Normal</td>
<td>Polyclonal</td>
</tr>
<tr>
<td>96-150</td>
<td>MI</td>
<td>12 GGT→TGT</td>
<td>+</td>
<td>E2</td>
<td>Atypical hyperplasia</td>
<td>Monoclonal</td>
</tr>
</tbody>
</table>

**Prior** designations refer to pre-hysterectomy curettings, whereas remaining non-malignant tissues were harvested from the hysterectomy specimen. Non-CA mutation refers to the genotype of the non-malignant tissue and is shown as as either wild-type (wt) or with the mutation seen in the corresponding cancer (+).
Alleles resolved by a minimum of 3 mm on non-denaturing polyacrylamide gel electrophoresis (PAGE) were judged to be informative for X inactivation analysis. Informative cases underwent full X inactivation analysis of DNAs selectively isolated from the tumour and representative areas of other endometrial types present. HUMARA PCR (primers AR-a/b5) of HhaI predigested and undigested matched myometrial/endometrial DNAs was performed in the presence of 32P-TTP, substituting 7-deaza-2'-dGTP for dGTP during amplification, and products resolved by non-denaturing 8% PAGE followed by autoradiography. Scoring of paired normal/tumour results was based on visual assessment of band patterns validated previously in a study comparing results of quantitative and visual analysis of HUMARA data.27

K-ras AND p53 MUTATION ANALYSIS
Tumour DNA was screened for p53 and K-ras mutations by non-radioactive single strand conformation polymorphism (cold SSCP), followed by confirmatory direct sequencing. Exons 5, 6, 7, and 8 of the p53 gene and exon 1 of the K-ras gene were amplified individually by PCR using published primer sequences.20 21 Cold SSCP was performed as described previously.22 A mixture consisting of 5 µl of PCR product (equivalent to 20–200 ng of DNA), 0.2 µl 1 M methylmercury hydroxide, 3 µl of loading buffer (15% ficoll of Mr 40 000, 0.25% bromophenol blue, and 0.25% xylene cyanol), and 13.6 µl of 1× TBE (Tris/borate/EDTA) buffer was prepared to yield a total volume of 20 µl. This mixture was heated to 90°C for four minutes to denature double stranded DNA and then plunged into ice before loading. The entire 20 µl was loaded on to 18% polyacrylamide TBE gels and run at 25°C for exon 8 of p53 and exon 1 of K-ras, at 35°C for exons 5 and 6 of p53. The gels were stained with ethidium bromide. Samples that showed one or more band migrated apart from the wild-type bands by cold SSCP analysis were analysed further by direct sequencing. The variant bands were selected from the gels and reamplified. PCR products were gel purified by electrophoresis on 10% polyacrylamide TBE gels and sequences were determined by direct sequencing using the dye terminator cycle sequencing ready reaction kit (Perkin-Elmer, Foster City, California, USA) and a model 310 genetic analyser (Perkin-Elmer). DNA isolated from non-cancerous endometrial tissues in those 11 patients with confirmed mutations was then isolated, and tested for the presence of mutations by cold SSCP analysis and subsequently confirmed by direct sequencing. Mutation results were correlated with histopathology and the clonal growth pattern of the sampled area.

Results
The distribution of K-ras mutations (fig 1) was similar among all grades of endometrial adenocarcinomas (table 1), with an overall rate of 16% (nine of 56) comparable to the 12–25%
reported by others. K-ras mutation rates did not change with the appearance of MI (table 1). Nine patients with K-ras mutant cancers had non-malignant areas of endometrioid tissue available as discrete foci (n = 15) within the cancer bearing hysterectomies or biopsy samples (n = 4) obtained in a two month window preceding hysterectomy. Table 2 shows the clonal composition, K-ras mutation status, and histopathological appearance of these tissues. p53 mutations were seen in only three of 56 cancers studied, neither of which had coexisting K-ras mutations. These three patients were not informative in evaluating premalignant lesions, because the only non-malignant endometrium present was polyclonal, histologically normal endometrium with a wild-type p53 genotype.

**Discussion**

Microsatellite instability had no influence on the rates of K-ras mutation in cancers (table 1), and appeared in the premalignant phases of both MI and MS pathways (table 2). These findings are similar to those of most other groups, although isolated reports have suggested enrichment for K-ras mutations in MI endometrial adenocarcinomas. K-ras mutation might play a similar role in the premalignant phases of endometrial carcinoma, irrespective of the presence or absence of MI.

After exclusion of contentious or subdiagnostic histologies, acquisition of K-ras mutation usually corresponds to a change in morphology from a non-hyperplastic to a hyperplastic type (fig 2). In patients with K-ras mutant cancers, all six associated polyclonal areas with non-hyperplastic morphologies had wild-type K-ras. In contrast, all 10 regions with mutant K-ras genotypes had a histopathology that was either hyperplastic or non-diagnostic. Aggregated data from three independent studies support the idea that K-ras mutant tissues (E2 and T2–5) shared multiple novel microsatellites not seen in the one area of tumour with a wild-type K-ras genotype (T1). Either tumour T1 is an independent clone, or it diverged from other neoplastic tissues very early in neoplastic progression.
K-ras mutation in endometrial precancers

Figure 4  K-ras mutations in histologically ambiguous endometria. Two (96-06E2 and 96-51E2) endometrial tissues subdiagnostic for atypical endometrial hyperplasias (photomicrographs, lower panels) are identified as precancers based upon a monoclonal growth pattern on HUMARA assay (upper panel) and appearance of K-ras mutations identical to those seen in matching carcinomas. The non-uniform histological appearance of growth pattern on HUMARA assay (upper panel) and appearance of K-ras mutations (photomicrographs, lower panels) are identified as precancers based upon a monoclonal growth pattern and presence of K-ras mutation. Only through use of matched tissues from single patients is it possible to discern this pattern. Two patients showed K-ras mutation discordance among multiple precancers (cases 96-06 and 96-51; table 2), whereas one had divergent mutant and wild-type K-ras genotypes among subregions of adenocarcinoma (case 96-150). The latter has been noted previously in detailed mapping of K-ras mutations in microdissected tumours, but our use of tetranucleotide repeats as loci for scoring of MI provided additional genetic markers to distinguish between multicentric disease and late onset mutation. In case 96-150, the K-ras mutation seen in the precancer was conserved in only four of five sampled areas of associated cancer. We mapped the constellation of altered microsatellites seen in each tissue area and found that premalignant and malignant tissues sharing K-ras mutations also shared novel marker alleles not seen in the area of cancer devoid of K-ras mutation (fig 3). The finding that these K-ras mutant and non-mutant tissues are genetically divergent at loci other than K-ras favours a multicentric process, or very early divergence of premalignant lineages into multiple subgroups.

Because of the lack of monoclonal precancers in the three patients with p53 mutant cancers, we are unable to comment on K-ras mutations in precancers. This is unfortunate, because there has been some controversy about whether p53 mutation is or is not a feature of premalignant endometrium. Two of three endometrial cancers with a mutant p53 were MS, whereas the remaining one was MI. The 5% rate of p53 mutation in endometrial cancer is somewhat lower than the 13–23% reported previously. In part, this could be because all the cases studied were endometrioid adenocarcinomas, thereby excluding papillary serous and clear cell subtypes, which are particularly associated with high p53 mutation rates. All three p53 mutant cancers were poorly differentiated (grade III), as would be expected. The molecular basis of precancer initiation is increasingly being resolved as additional genes are found to have aberrant function in these tissues compared with their normal counterparts. For example, mutation of the tumour suppressor gene PTEN also occurs in the premalignant phases of MS and MI endometrial tumorigenesis. A mechanistic basis for MI in endometrial neoplasia, transcriptional silencing of the hMLH1 gene through de novo CpG island methylation, suggests that modifications of gene expression are not all explained by primary structural mutations within the coding regions of genes.

Morphological diagnosis occasionally fails to recognise precancers that are apparent either through clonality or mutational analysis. Indeed, it is the unreliability of histopathological diagnosis that prompted us to define potential precancers by their monoclonal growth patterns. Tissue E2 from case 96-06 (fig 4) is a scrap of mucinous epithelium in a previous curetting that was interpreted as inadequate for diagnosis of the endometrium. This patient had an endometrial adenocarcinoma with focal mucinous differentiation, and the non-endometrioid character of the fragment was misinterpreted as endocervical in origin. Similarly, a consistent diagnostic label was not rendered for area E2 from case 96-51 (fig 4) after review by several pathologists, yet it can be identified as a precancer because of its monoclonal growth pattern and presence of K-ras mutation.

K-ras mutation in colonic mucosa might also precede the acquisition of histological stigmata
of neoplasia,35 confirming in that model that K-ras changes are among the earliest detectable features of neoplastic transformation, and that they may play a role in the early clinical detection of cancer risk. In addition to early acquisition, the colonic and endometrial carcinoma models both have K-ras mutations in equivalent frequencies in MS and MI tumours.36

PCR-SSCP can detect K-ras mutations characteristic of some precancers at a level of sensitivity that exceeds that of the HUMARA assay. This is because polyclonal stromal or epithelial cells contaminate most DNA isolates intended to sample a focal epithelial lesion. PCR-SSCP can detect a mutant K-ras allele if only 5% of all alleles are mutant (T. Enomoto et al, 1998, unpublished observation), whereas the HUMARA assay requires 50–75% of tested cells to be derived from the neoplastic clone.2 3 7

Area E1 from case 96-04 (fig 2) is an atypical area of neoplasia,26 27 reduces a highly specific association between K-ras mutation in normal polyclonal tissues and carcinoma. Absence of K-ras mutant, on average pathological, but vary in the extent to which they yield the criteria for atypical endometrial hyperplasia. Absence of K-ras mutation in normal polyclonal tissues produces a highly specific association between K-ras mutation and the onset of neoplasia, which might be useful in the recognition of the earliest stages of precancer initiation.

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