Two Distinct Regions of Loss on Chromosome Arm 4q in Primary Head and Neck Squamous Cell Carcinoma

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Objective: To more clearly define the frequency and the regions of chromosome arm 4q loss in head and neck squamous cell carcinoma.

Design: A retrospective microsatellite analysis of DNA from previously microdissected primary tumor samples.

Setting: Academic medical center.

Patients and Methods: One hundred primary tumor samples from patients with head and neck squamous cell carcinoma were analyzed for loss of heterozygosity on the long arm of chromosome 4. The Kaplan-Meier method was used to estimate survival for 97 patients for whom clinical data were available. The Cox proportional hazards model was used to compare survival, and logistic regression was used to search for associations between clinical tumor characteristics and 4q status.

Results: Analysis of 33 polymorphic microsatellite markers identified 51 samples (51%) exhibiting loss of heterozygosity of 4q in at least 1 locus. Eighteen tumors revealed loss at all informative markers, indicating monosomy or complete deletion of 4q. Thirty-three tumors displayed partial loss of heterozygosity and delineated 2 minimal areas of loss at 4q23 and 4q28. Eleven tumors displayed loss solely at the 4q23 region, 13 tumors displayed deletions confined to the 4q28 region, and 9 tumors displayed selective loss at both regions. A separate analysis in a subset of 94 primary head and neck tumors was done to further delineate the minimal area of chromosomal loss at 4q23. Analysis of 8 markers in this region allowed us to identify the smallest region of loss between markers D4S2986 and D4S1564 (a distance of 2 centimorgans). Review of the clinical records of 97 patients revealed no statistically significant association between 4q status and any clinical variable, including survival.

Conclusion: These results confirm a high frequency of chromosome arm 4q loss in primary head and neck squamous cell carcinoma and might demarcate 2 novel putative suppressor loci involved in progression of this carcinoma.

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PATIENTS, MATERIALS, AND METHODS

PATIENT POPULATION

The study population comprised 100 patients with HNSCC. Clinical information was available from medical records for 97 patients. All clinical statistical analyses were performed on this subset. All patients had been treated with aggressive curative intent and had been followed up for at least 18 months at the time of data analysis.

SAMPLE COLLECTION AND DNA EXTRACTION

Primary HNSCC tumors were obtained fresh at the time of surgical resection with prior consent from patients at the Johns Hopkins Hospital, Baltimore, Md, as described previously. Samples were fresh frozen in liquid nitrogen or at 0°C and carefully microdissected on a cryostat to separate out nonneoplastic cells. Samples with greater than 70% tumor tissue were digested in sodium dodecyl sulfate/proteinase K at 60°C for 6 hours, followed by phenol-chloroform extraction and ethanol precipitation. Blood samples were obtained by venipuncture from these patients with prior consent, and DNA samples from lymphocytes were obtained as described previously.

POLYMERASE CHAIN REACTION AMPLIFICATION AND DATA ANALYSIS

Normal and tumor DNA samples were analyzed for LOH after polymerase chain reaction (PCR) amplification of polymorphic dinucleotide repeat sequences. Oligonucleotide primers for microsatellite PCR analysis were obtained from Research Genetics (Huntsville, Ala). The primers were labeled with γ[32P]adenosine triphosphate using T4 polynucleotide kinase (New England Biolabs, Beverly, Mass). Fifty nanograms of genomic DNA was subjected to 3035 cycles of PCR amplification, as described previously. Products from PCR analysis were separated by electrophoresis in denaturing 7% urea-polyacrylamide-formamide gels followed by autoradiography. For informative cases, allelic loss was scored and confirmed by 2 independent observers (S.I.S. and D.S.). Loss was scored if the intensity of 1 allele was at least 50% reduced in the tumor compared with normal DNA.

The medical records of 97 patients were reviewed to tabulate clinical variables, including age at diagnosis, sex, site and stage of disease, treatment, and clinical outcome. Follow-up for surviving patients ranged from 20 to 84 months (mean, 48 months). Disease-free survival and overall survival were calculated from the date of initial diagnosis. Stage was recorded as that at initial presentation, although some patients were entered into the study (biopsy specimen obtained) at the time of local recurrence after initial therapy. Survival was then calculated using the Kaplan-Meier method, censoring for death due to unrelated cause and loss to follow-up. Survival of patients with and without loss of any marker on 4q was compared using the Cox proportional hazards model. Associations between 4q status and patient age, tumor site, stage, sex, and cervical nodal status were sought using logistic regression.

RESULTS

We selected 33 well-spaced markers from informative microsatellite loci previously identified on chromosome arm 4q. We then amplified these microsatellite markers by PCR from primary HNSCC tumor and matched control DNA to screen for allelic loss. Fifty-one (51%) of the 100 tumors displayed loss of at least 1 marker on 4q. Eighteen of these samples demonstrated loss at all informative markers, indicating the probable presence of monosity. The 33 remaining samples displayed only partial loss and helped define the 2 minimal regions of loss on 4q. We further analyzed the proximal region with 8 additional markers in a subset of 94 tumors to define the smallest region of loss.

Figure 1 denotes representative tumors defining the minimal areas of deletion on 4q. A small area of loss confined to 4q2324, between markers D4S2986 and D4S1364, is seen in tumor sample 5. Another small region of loss confined to 4q2829, between markers D4S247 and D4S2998, is seen in tumor sample 1072. A scarcity of markers in this region did not allow further mapping. These regions span physical distances of 2 and 11 centimorgans (cM), respectively. Figure 2 shows the pattern of chromosome arm 4q loss for 7 of 9 HNSCC tumors in which both regions were lost. These samples add evidence for the presence of 2 distinct regions of loss and potentially 2 novel tumor suppressor loci.

The Table provides data on the clinical characteristics of the patient population. The status of chromosome 4q was not found to correlate with any clinical variable, including patient sex, age at presentation, tumor stage, site, or the status of the cervical lymph nodes. Advanced age at presentation, the presence of cervical nodal metastases, and advanced tumor stage were each weakly associated with decreased overall survival. However, the status of chromosome arm 4q in the tumors had no impact on disease-free or overall survival. Chromosome arm 4q LOH conferred a hazard ratio of 1.3 for death by any cause, but P = .46 for the Cox proportional hazards survival analysis.

COMMENT

It has been established that cancer arises from a series of genetic changes. These alterations in DNA potentially lead to clonal outgrowth of cells, all of which will have a growth advantage initially provided by the parent cell. Discerning the timing and the nature of these alterations in HNSCC is crucial to biological and clinical comprehension of disease. Through analysis of the relative rate of molecular alterations in premalignant and invasive tu-
mors, it seems that deletion of chromosome arm 4q occurs late in HNSCC tumor progression.4

Initial allelotyping of HNSCC revealed LOH of 4q in many primary tumors tested at one microsatellite locus.3 We confirmed that 4q loss is a frequent genetic event in HNSCC, and our mapping with 33 dinucleotide markers reveals 2 minimal areas of loss on 4q. Although chromosome arm 4q loss has been described previously in other major tumor types, high-density mapping in primary HNSCC has allowed us to delineate 2 distinct loci at 4q23-24 and 4q28-29. These observations are consistent with the finding of more than 1 suppressor locus in many cases in which monosomy is present.12

Recently, investigators13 performed an allelotype of chromosome arm 4q, finding one large region of loss spanning 7 cM on 4q. Our study served to further extend their findings by defining a smaller minimal region of loss in the same region (2 cM) and identifying another distinct area of loss at 4q23-24 and 4q28-29. These observations are consistent with the finding of more than 1 suppressor locus in many cases in which monosomy is present.12

Figure 1. Loss of heterozygosity analysis on chromosome arm 4q for 2 selected samples of head and neck squamous cell carcinoma. Representative tumors (T) and corresponding normal tissue (N) are shown with microsatellite markers indicated on the bottom. Lost alleles are indicated by arrows. Sample 5 (left) demonstrates the first region of loss between markers D4S2986 and D4S1572. Sample 1072 (right) shows the second region of loss from markers D4S247 to D4S2998.

Figure 2. Schematic representation of chromosome arm 4q with approximate location of microsatellite markers depicted to the right for 7 head and neck squamous cell carcinoma tumors demonstrating partial losses in both minimal regions.

Clinical Characteristics of the Patient Population*

<table>
<thead>
<tr>
<th>4q Retained (n = 48)</th>
<th>4q Loss of Heterozygosity (n = 49)</th>
<th>Total (N = 97)</th>
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<tr>
<td>Age, mean (range), y</td>
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Survival at 48 mo,†

<table>
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<td>49 (30-65)</td>
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<td>55 (39-69)</td>
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</table>

*Data are given as number of patients except as noted otherwise. CI indicates confidence interval.
†Kaplan-Meier curves overlap.

the possibility that a putative tumor suppressor gene located at 4q22-23 plays a role in the progression of multiple forms of cancer.

It is now well established that tumor suppressor genes are a critical part of cancer progression. For example, it is known that TP53 and CDKN2A are 2 major tumor suppressor genes involved in HNSCC tumor progression.7,12 The study of these tumor suppressor genes has had a direct impact on patient treatment by augmenting diagnostic and prognostic tools.13 For patients with
HNSCC, clinical staging often fails to predict how an individual neoplasm will respond to therapy, and it cannot be relied on to elucidate the eventual outcome for a patient with HNSCC. Currently, these patients’ treatment options include radiation therapy, surgery, and/or chemotherapy, and the choice is usually based on the site and stage of disease. However, gross staging cannot predict which patients will fare well with which treatment modality.

Molecular markers have shown promise toward optimizing patient therapy and predicting patient response. TP53 suppresses the outgrowth of genetically damaged cells in 2 primary ways: by apoptosis or cell cycle arrest to allow for DNA repair. When TP53 function is lost, damaged cells can proliferate rather than be terminated by antineoplastic therapies. Koch et al found that patients with invasive HNSCC who had mutations of the TP53 gene had an increased risk of locoregional failure when treated with primary radiation given with curative intent. Because the tumor progression model places 4q LOH late in the process of malignant transformation, Koch et al had hoped that 4q status might be associated with clinical outcome. However, the results of the present study indicate no association of 4q status with more advanced clinical disease or decreased survival. These results might seem to be contradictory to earlier assertions of the position of 4q alteration in HNSCC tumor progression. However, for the purposes of the tumor progression model, all invasive carcinomas are regarded as advanced disease with a full spectrum of molecular changes. Molecular alterations that correlate with poor outcome or metastatic potential are actively being sought, but these results suggest that 4q status will not be a useful marker for aggressive disease.

Identification of the putative tumor suppressor genes that lie within these regions of minimal loss might allow us to develop better diagnostic and therapeutic targets for patients with HNSCC.

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REFERENCES