Assessment of Esophageal Adenocarcinoma Risk Using Somatic Chromosome Alterations in Longitudinal Samples in Barrett’s Esophagus

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Abstract

Cancers detected at a late stage are often refractory to treatments and ultimately lethal. Early detection can significantly increase survival probability, but attempts to reduce mortality by early detection have frequently increased overdiagnosis of indolent conditions that do not progress over a lifetime. Study designs that incorporate biomarker trajectories in time and space are needed to distinguish patients who progress to an early cancer from those who follow an indolent course. Esophageal adenocarcinoma is characterized by evolution of punctuated and catastrophic somatic chromosomal alterations and high levels of overall mutations but few recurrently mutated genes aside from TP53. Endoscopic surveillance of Barrett’s esophagus for early cancer detection provides an opportunity for assessment of alterations for cancer risk in patients who progress to esophageal adenocarcinoma compared with nonprogressors. We investigated 1,272 longitudinally collected esophageal biopsies in a 248 Barrett’s patient case-cohort study with 20,425 person-months of follow-up, including 79 who progressed to early-stage esophageal adenocarcinoma. Cancer progression risk was assessed for total chromosomal alterations, diversity, and chromosomal region-specific alterations measured with single-nucleotide polymorphism arrays in biopsies obtained over esophageal space and time. A model using 29 chromosomal features was developed for cancer risk prediction (area under receiver operator curve, 0.94). The model prediction performance was robust in two independent esophageal adenocarcinoma sets and outperformed TP53 mutation, flow cytometric DNA content, and histopathologic diagnosis of dysplasia. This study offers a strategy to reduce overdiagnosis in Barrett’s esophagus and improve early detection of esophageal adenocarcinoma and potentially other cancers characterized by punctuated and catastrophic chromosomal evolution. Cancer Prev Res; 8(9); 845–56. ©2015 AACR.

Introduction

Vast amounts of time and resources are spent on reducing the burden cancer has on individuals and society. One approach to cancer control is to identify individuals at highest risk of progressing to cancer and interrupt the process with currently available interventions such as resection. Unfortunately, many attempts to reduce cancer-related mortality through early detection tend to selectively identify individuals with slowly progressing or indolent conditions such as nonprogressing lesions of the esophagus, breast, prostate, thyroid, lung, and skin (1), resulting in overdiagnosis and overtreatment, and concomitantly fail to detect rapidly progressing disease (2).

Overdiagnosis and overtreatment are particularly relevant for persons with Barrett’s esophagus. Barrett’s esophagus develops in an estimated 2% to 10% of patients who have chronic heartburn (3). In response to an acid and bile reflux environment, Barrett’s esophagus appears to be a protective adaptation in which the normal, stratified squamous epithelium of the esophagus is replaced by a specialized intestinal metaplastic columnar epithelium (4) with properties that protect the esophagus from reflux injury (3, 5). Although Barrett’s esophagus is the only known precursor to esophageal adenocarcinoma, the absolute lifetime risk of a Barrett’s esophagus patient developing esophageal adenocarcinoma appears to be low, with the estimated annual incidence of cancer in large population-based studies ranging from 0.12% to 0.43% (3, 6–8). The vast majority of patients (90%–95%) in endoscopic biopsy surveillance programs for early cancer detection will neither be diagnosed with nor die of esophageal adenocarcinoma during their lifetime, resulting in overdiagnosis and overtreatment (3, 7). However, if esophageal adenocarcinoma is not detected until it is symptomatic, it is usually advanced and incurable with a 5-year survival rate of less than 15% (9).

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The inherently dynamic, stochastic evolutionary processes that lead to cancer and the diversity of somatic genomic mutations and chromosome alterations in cancer make it difficult to identify specific alterations that may be used to predict risk of progression to cancer (10–12). The ideal study to identify robust markers of cancer risk would include a study design with sufficient sample size, spatial and temporal tissue sampling with prospective follow-up, a nonprogressing control population with the same precursor condition, and a cancer outcome rather than nonvalid surrogate endpoints. Cancer-only studies in esophageal adenocarcinoma have provided information about possible targets for treatment of advanced cancers (13–20), but lack nonprogressing control populations required for early detection research. Cross-sectional studies have been frequently conducted, in which tissue samples are compared across different patients that represent different stages of progression, but these may not be representative of steps in progression in an individual patient given the diversity of genomic alterations present in different esophageal adenocarcinomas (21–24).

Most esophageal adenocarcinomas have extensive chromosomal instability, high levels of chromosome copy-number alterations, and frequent catastrophic chromosomal events, including whole-genome doublings (13, 15–21, 23, 24). In addition, esophageal adenocarcinoma has a high overall mutation frequency and a distinct mutation spectrum, yet with the exception of TP53, no recurrently mutated genes have been identified at high frequency in high-risk Barrett’s esophagus or esophageal adenocarcinoma to be useful as predictors of esophageal adenocarcinoma risk (13, 14, 22, 23). Barrett’s esophagus is an excellent model in which to study the somatic genomic evolutionary process at a stage before the widespread genomic instability that characterizes advanced esophageal adenocarcinoma. The clinical practice of periodic endoscopic biopsy surveillance for early cancer detection has allowed the systematic collection of mapped surveillance biopsies sampled over space and time from Barrett’s and normal control tissue in patients who did or did not progress to esophageal adenocarcinoma (25, 26). We have recently reported that patients with Barrett’s esophagus who do not progress to esophageal adenocarcinoma typically have low levels of somatic chromosomal alterations (SCA) that remain stable over prolonged periods of time, whereas those who progress to esophageal adenocarcinoma develop high levels of SCA, increased diversity, and evolve punctuated chromosome instability and catastrophic whole-genome doublings within 4 years of esophageal adenocarcinoma detection (26).

We hypothesized that an esophageal adenocarcinoma risk prediction model based on SCA will improve risk stratification of Barrett’s esophagus patients. We developed cancer risk prediction models using genome-wide SCA assessed over time and space in a large study with longitudinal follow-up and tested whether the risk models improved cancer prediction relative to current risk stratification approaches. These models were derived from a 248 person case-cohort study designed with a cancer endpoint and used longitudinal SCA data from 1,272 biopsies obtained by unbiased sampling at 2-cm intervals throughout the Barrett’s esophagus segment measured at two time points. The resulting SCA-based risk models were compared with histopathologic assessment of dysplasia, DNA content flow cytometry, and TP53 mutations for cancer risk prediction. We show how the model can be applied in practice to deal with stochastic chromosome evolutionary processes during neoplastic progression. These results provide a path forward to identifying Barrett’s esophagus patients at highest risk for progression to esophageal adenocarcinoma who will benefit most from intervention.

Materials and Methods

Detailed methods are presented in Supplementary Methods. The cohort study has been approved by the University of Washington Human Subjects Review Committee since 1983. A case–cohort study design (27, 28) was adopted and patients were drawn from a cohort of 516 research participants with histopathologically documented Barrett’s esophagus at baseline and were followed on the basis of a standard protocol (25). The case–cohort study included 248 individuals followed for 20,425 person-months, including all (n = 79) individuals in the cohort who progressed to an endpoint of esophageal adenocarcinoma (progressors) and 169 who did not progress to esophageal adenocarcinoma during follow-up (nonprogressors; Supplementary Table S1). Human Omni1-Quad v1.0 SNP arrays were used to assess genome-wide SCA in epithelial isolated cell populations every 2 cm in the Barrett’s esophagus segment at two time points (T1 = baseline, T2 = penultimate) per individual (26). Genomes were divided into 3,064 1-Mb segments and the frequencies of five SCA types in each 1-Mb segment (genome build hg19) and their risk relative [hazard ratio (HR)] for future cancer were quantified. Three methods were applied independently to identify SCA features for esophageal adenocarcinoma risk prediction, including bootstrap and ranking, a combination of bootstrap and ranking with Lasso, and Lasso only. Eighty-six regions were selected for esophageal adenocarcinoma risk prediction. A 29-feature model (27 specific 1-Mb regions representing the 86 regions, and two summation features from these 86 specific 1-Mb segments) was built for risk prediction. The 29 features were trained either with T1 data only or T1–T2 data and cross-validated to obtain two esophageal adenocarcinoma risk prediction models. The 29 SCA features were also measured using SNP array data from six independent esophageal adenocarcinoma surgical specimens and from an independent set of 47 esophageal cancers from TCGA Research Network (29). The performance of the SCA-based risk prediction models was compared with TP53 mutations and with dysplasia and DNA content flow cytometry using receiver operating characteristic (ROC) prediction performance.

Results

Total SCA and SCA diversity

We have shown previously that total SCA and diversity increase in Barrett’s esophagus progressors at times closer to esophageal adenocarcinoma diagnosis (26). Therefore, we assessed the amount of five types of SCA (chromosome copy loss, copy gain, copy neutral loss of heterozygosity “cnLOH,” copy gain with balanced allele ratio “balanced gain,” and homozygous deletion) and SCA diversity throughout the genome as predictors of esophageal adenocarcinoma progression in Barrett’s esophagus at baseline (T1) and at the last endoscopy just prior to or at esophageal adenocarcinoma diagnosis in progressors or the penultimate endoscopy in nonprogressors (T2). Increasing amount of total SCA at T1 was associated with increased risk of progression (Fig. 1A). ROC curves were used to assess total SCA performance
for esophageal adenocarcinoma prediction using biopsies from T1 (area under ROC curve (AUC) = 0.78) or T1 combined with T2 (T1+T2; AUC = 0.80; Fig. 1B). Increasing genome-wide SCA diversity between T1 biopsies in an individual was also associated with increased risk of progression (Fig. 1C) and had similar ROC curves to total SCA (T1 AUC = 0.79; T1+T2 AUC = 0.80; Fig. 1D).

Thus, total SCA and SCA diversity are overall measures of chromosomal instability that confer an increased risk of progression to esophageal adenocarcinoma.

SCA frequency and HR
We hypothesized that prediction accuracy could be further improved by identifying only those SCA features that are selected during development of esophageal adenocarcinoma. The case-cohort study was designed to determine the temporal relationship between SCA and patient outcomes while preserving the characteristics of the entire cohort, allowing a cost-effective approach for genomic investigations (26–28). This study design allowed quantification of genome-wide SCA HRs for risk of progression to esophageal adenocarcinoma to distinguish genomic alterations that occurred primarily during progression to cancer from those detected at similar frequencies in nonprogressors (Fig. 2). After SCA calls were made throughout the genome for each biopsy (Supplementary Methods), the genome of each sample was divided into 3,064 one megabase (1-Mb) segments and each of the five SCA types were called as a binary variable, either present or

Figure 1. Total SCA, SCA diversity and esophageal adenocarcinoma risk. A, the Kaplan–Meier survival curves showing cumulative probability to develop esophageal adenocarcinoma over time per risk group stratified by total SCA at T1. SCA amount per biopsy was calculated as the sum of all base pairs of SCA from start to end of each alteration. For each patient, the T1 biopsy with the maximum SCA was used. B, ROC curves showing performance of maximum SCA for esophageal adenocarcinoma risk prediction using T1 data only (gray line, AUC = 0.78) and T1+T2 combined data (black line, AUC = 0.80). C, the Kaplan–Meier survival curves showing cumulative probability to develop esophageal adenocarcinoma over time per risk group stratified by maximum SCA diversity across 3,064 1-Mb genomic segments at T1. D, ROC curves showing performance of maximum SCA diversity for esophageal adenocarcinoma risk prediction using T1 data only (gray line, AUC = 0.79), and T1+T2 combined data (black line, AUC = 0.80). The Kaplan-Meier plots were adjusted for case-cohort study (see Supplementary Methods).
absent. HRs were calculated for all five SCA types independently at each 1-Mb segment. Some high-frequency SCA such as frequent loss and homozygous deletion spanning CDKN2A, FHIT, and WWOX had a similar frequency in both nonprogressors and progressors and therefore conferred no or low risk (low HR) of progression to esophageal adenocarcinoma (Fig. 2A). In contrast, progressors were characterized by many low to moderate frequency SCA segments with high HRs that were infrequent in nonprogressors such as loss and cnLOH on chromosome 17p linked to TP53 and amplification spanning ERBB2 (Fig. 2B). Large-scale chromosome alterations, coupled with intra- or inter-individual heterogeneity, resulted in a large portion of the genome having significant HRs for one or multiple SCA types in the same chromosomal regions (Fig. 2C and 2D).

Figure 2.
SCA frequency and HR for esophageal adenocarcinoma risk. SCA types are colored for cnLOH (blue), loss (green), balanced gain (yellow), allele-specific copy gain (orange). SCA data were combined from baseline (T1) and last endoscopy before esophageal adenocarcinoma diagnosis or final endoscopy (T2) for HR estimation. Each data point in the scatter plots represents a 1-Mb segment SCA HR for esophageal adenocarcinoma (x-axis) versus its SCA frequency (y-axis) in nonprogressors (A) and progressors (B). The plots show all 1-Mb segments in which the frequency in nonprogressors and/or progressors is significantly larger than zero (statistical significance adjusted for multiple comparisons). Many of the 1-Mb segments with SCA were correlated because of whole chromosome arm alterations or large chromosomal events spanning many Mb. SCA HR (x-axis) and genomic location (y-axis) are shown in C and D. Regions of significant homozygous deletions with significant HR were small and few in number and therefore not plotted.
SCA feature selection for esophageal adenocarcinoma risk prediction

A stepwise feature selection was performed within each of the five SCA types using univariate HRs to identify 1-Mb genome segments that were significantly associated ($P < 0.1$) with development of esophageal adenocarcinoma. Out of 15,320 possible 1-Mb segments representing all five types of SCA throughout the 3,064 Mb genomic segments, 9,391 were significantly associated with progression to esophageal adenocarcinoma (Fig. 3). Further feature selection to reduce correlated events resulted in 86 SCA regions for cancer risk prediction (Supplementary Table S2 and Supplementary Methods). To reduce the number of variables for esophageal adenocarcinoma prediction and minimize overtraining, bootstrapping and feature construction and ranking were used to identify a smaller set of predictors from the 86 SCA regions, resulting in 29 SCA features (Table 1; Fig. 3; Supplementary Methods). These 29 SCA features capture regions indicative of an overall process of genomic instability and take into account large genomic regions that are correlated (co-occur). Thus, any one of the 86 1-Mb segments may involve many megabases and may not in and of itself be causative for progression. The robustness of this feature selection approach was supported by two independent feature selection methods (Supplementary Fig. S1; Supplementary Methods; ref. 30).

Genomic segmentation and SCA calls by biopsy. Using 248 patient data, the genomes of each biopsy (average 2.6 biopsies/time point/patient) were divided into 3,064 1Mb segments. For each segment, five classes of somatic chromosome alteration (SCA) were measured using Illumina 1M SNP arrays, on average resulting in 79,664 potential predictors per subject (3,064 genomic segments × 5 SCA types × ~2.6 biopsies/time point × 2 time points/subject).

- 80,000 features per subject

I. By endoscopy data reduction. For each SCA type, the maximum SCA call was made across all biopsies from the same endoscopy for a given 1Mb segment, resulting in 15,320 features per endoscopy (3,064 segments × 5 SCA types) for each of the two time points.

15,320 features per endoscopy

II. Case–cohort data analysis and feature reduction using HR for EA: 15,320 potential candidate features from both time points were analyzed using a case–cohort analysis to select features with a hazard ratio for EA greater than significance level $P < 0.1$, resulting in 9,381 significant SCA features.

9,381 significant SCA features

III. Cox regression within each SCA type across 9,381 significant features. Within each of the five SCA types, stepwise Cox regression selection ($P < 0.01$) was performed using the 9,381 features, resulting in 219 1Mb selected genomic segments of various SCA types.

219 selected SCA features

IV. Cox regression across all 219 selected features. Across all SCA types, stepwise Cox regression selection was performed ($P < 0.01$) using the 219 selected features, resulting in 86 1Mb selected genomic segments.

86 selected SCA features

Generation of prediction model. Six summation features were constructed by counting the number of SCA within the 86 regions for each SCA type, plus total SCA across all 86 regions. Bootstrap sampling was used for feature selection. In each iteration, logistic regression based on the 86 features, plus the six constructed features, was used to select a set of prediction features and record the order in which features were selected. After 1,000 iterations, features that were consistently selected with $P < 0.5$ significance level were ranked. As measured by AUC, 27 1Mb genomic segments plus two constructed features (summation of copy loss within the 86 regions and summation of all SCA in the 86 regions) provided the smallest number of features with maximum predictive power, resulting in 29 selected SCA features.

29 selected SCA features

29 selected SCA features were used for risk prediction models using multiple datasets.
The performance of these 29 features for esophageal adenocarcinoma risk prediction in Barrett’s esophagus was evaluated by multiple model training and cross-validation methods (Supplementary Fig. S2 and Supplementary Methods). First, the 29 SCA features from T1 were used with one individual patient’s SCA data omitted during each round to train the prediction models. Parameters of the models were averaged to obtain the T1 risk prediction model (T1 model), and the model then was tested for predicting esophageal adenocarcinoma outcome using SCA data from T1 (AUC = 0.94; Fig. 4A). The performance of predictions using the leave-one-out-sample approach (the jackknife cross-validation of T1 SCA) showed similar results with slightly lower AUC (AUC = 0.86; Supplementary Fig. S3). Next, the 29 SCA features from T2 were used to test the T1 model. T2 biopsies were collected from independent locations in the esophagus on average 64.7 months after T1 biopsies. The T1 model was robust for esophageal adenocarcinoma risk prediction when it was tested using 29 SCA features from T2 (AUC = 0.84; Fig. 4B).

Application of longitudinal SCA data for esophageal adenocarcinoma risk prediction

We sought to develop a risk model that could be applied to SCA data for risk prediction regardless of whether it was collected from one or multiple time points from an individual patient. The same 29 features used in the T1 model were used to train a model with SCA data from both endoscopic time points (T1 and T2) treated independently to test whether this combined dataset, with roughly twice the number of endoscopies, would improve the accuracy and robustness of esophageal adenocarcinoma risk prediction in Barrett’s esophagus (Supplementary Fig. S2 and Supplementary Methods). To minimize over-training, a random set of two third of the combined T1 and T2 data were used for model training and the remaining one third were used as a set to test prediction performance (AUC = 0.86; Supplementary Fig. S4; Supplementary Methods). This procedure was repeated 10,000 times, and the model parameters from these iterations were averaged, resulting in a single “T1T2 model.” This model was applied to a composite (maximum by patient T1 + T2) SCA call at each of the 29 SCA features for esophageal adenocarcinoma risk prediction (AUC = 0.94; Fig. 4C; Supplementary Fig. S2; Supplementary Methods). A bootstrap method showed that the T1T2 model had consistently higher AUC than the T1 model (bootstrap ranking test $P = 0.0136$; see Supplementary Methods). The T1T2 model was trained with data from two time points treated independently and therefore provides flexibility to be used for data collected from either one or multiple time points. The T1T2 model, which generates an

Table 1. Selected SCA features for esophageal adenocarcinoma risk prediction models

<table>
<thead>
<tr>
<th>Chromosome: (1-Mb segment) of SCA location selected in model</th>
<th>SCA type</th>
<th>Frequency of SCA by patient (T1 + T2) in progressors (%)</th>
<th>Frequency of SCA by patient (T1 + T2) in nonprogressors (%)</th>
<th>Average size contiguous SCA (Mb) spanning selected location in progressors (SD)</th>
<th>Average size contiguous SCA (Mb) spanning selected location in nonprogressors (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1: 36–37</td>
<td>Loss</td>
<td>&gt;30</td>
<td>2.5</td>
<td>6.0</td>
<td>25.5 (31.8)</td>
</tr>
<tr>
<td>2: 226–227</td>
<td>cnLOH</td>
<td>&gt;30</td>
<td>8.6</td>
<td>0.0</td>
<td>48.7 (46.7)</td>
</tr>
<tr>
<td>5: 93–94</td>
<td>cnLOH</td>
<td>7.9</td>
<td>11.9</td>
<td>0.6</td>
<td>102.7 (41.1)</td>
</tr>
<tr>
<td>6: 1–2</td>
<td>Gain</td>
<td>8.2</td>
<td>12.7</td>
<td>0.6</td>
<td>30.1 (26.0)</td>
</tr>
<tr>
<td>6: 5–6</td>
<td>Gain</td>
<td>5.9</td>
<td>15.2</td>
<td>0.6</td>
<td>35.3 (22.7)</td>
</tr>
<tr>
<td>6: 29–30</td>
<td>cnLOH</td>
<td>5.2</td>
<td>14.9</td>
<td>3.0</td>
<td>24.1 (19.3)</td>
</tr>
<tr>
<td>6: 146–147</td>
<td>cnLOH</td>
<td>8.5</td>
<td>6.5</td>
<td>0.6</td>
<td>91.8 (35.2)</td>
</tr>
<tr>
<td>7: 77–78</td>
<td>cnLOH</td>
<td>23.1</td>
<td>6.3</td>
<td>0.0</td>
<td>74.0 (45.5)</td>
</tr>
<tr>
<td>7: 78–79</td>
<td>cnLOH</td>
<td>&gt;30</td>
<td>6.5</td>
<td>0.0</td>
<td>67.6 (38)</td>
</tr>
<tr>
<td>8: 158–159</td>
<td>cnLOH</td>
<td>&gt;30</td>
<td>5.9</td>
<td>0.0</td>
<td>35.8 (40.1)</td>
</tr>
<tr>
<td>9: 0–1</td>
<td>Loss</td>
<td>2.0</td>
<td>59.5</td>
<td>33.1</td>
<td>25.8 (16.1)</td>
</tr>
<tr>
<td>9: 15–14</td>
<td>Loss</td>
<td>4.8</td>
<td>38.0</td>
<td>12.4</td>
<td>27.5 (18.3)</td>
</tr>
<tr>
<td>9: 65–66</td>
<td>Loss</td>
<td>2.6</td>
<td>12.7</td>
<td>3.6</td>
<td>23.9 (27.4)</td>
</tr>
<tr>
<td>11: 38–39</td>
<td>cnLOH</td>
<td>6.9</td>
<td>4.6</td>
<td>0.6</td>
<td>34.9 (17.8)</td>
</tr>
<tr>
<td>11: 50–51</td>
<td>cnLOH</td>
<td>3.8</td>
<td>3.3</td>
<td>1.2</td>
<td>39.2 (17.7)</td>
</tr>
<tr>
<td>11: 110–111</td>
<td>cnLOH</td>
<td>4.3</td>
<td>6.0</td>
<td>1.8</td>
<td>55.3 (20.4)</td>
</tr>
<tr>
<td>12: 45–46</td>
<td>Loss</td>
<td>4.0</td>
<td>11.4</td>
<td>2.4</td>
<td>39.9 (44.3)</td>
</tr>
<tr>
<td>13: 42–43</td>
<td>Loss</td>
<td>18.0</td>
<td>17.7</td>
<td>0.6</td>
<td>81.9 (27.2)</td>
</tr>
<tr>
<td>15: 70–71</td>
<td>Gain</td>
<td>14.4</td>
<td>40.5</td>
<td>1.8</td>
<td>58.6 (22.2)</td>
</tr>
<tr>
<td>17: 8–9</td>
<td>Loss</td>
<td>8.9</td>
<td>46.8</td>
<td>7.1</td>
<td>21.0 (3.5)</td>
</tr>
<tr>
<td>17: 9–10</td>
<td>cnLOH</td>
<td>8.5</td>
<td>24.2</td>
<td>2.4</td>
<td>20.7 (3.0)</td>
</tr>
<tr>
<td>17: 12–13</td>
<td>cnLOH</td>
<td>10.8</td>
<td>24.2</td>
<td>1.8</td>
<td>20.4 (4.0)</td>
</tr>
<tr>
<td>18: 57–58</td>
<td>Gain</td>
<td>12.3</td>
<td>34.2</td>
<td>2.4</td>
<td>23.2 (22.3)</td>
</tr>
<tr>
<td>18: 19–20</td>
<td>Gain</td>
<td>4.6</td>
<td>60.8</td>
<td>21.3</td>
<td>16.2 (19.9)</td>
</tr>
<tr>
<td>19: 48–49</td>
<td>cnLOH</td>
<td>&gt;30</td>
<td>5.8</td>
<td>0.0</td>
<td>25.0 (9.7)</td>
</tr>
<tr>
<td>20: 42–43</td>
<td>Loss</td>
<td>&gt;30</td>
<td>13.9</td>
<td>0.0</td>
<td>46.5 (19.2)</td>
</tr>
<tr>
<td>21: 15–14</td>
<td>Loss</td>
<td>4.6</td>
<td>54.4</td>
<td>16.6</td>
<td>15.3 (3.0)</td>
</tr>
</tbody>
</table>

Sum of copy loss events in the 86 regions
Sum of all SCA events in the 86 regions

NOTE: Loss = allele-specific copy loss; Gain = allele-specific copy gain.

*The frequency was calculated from all biopsies from both time points within each patient.

**The average of the sizes of SCA in a chromosome arm surrounding the SCA locations used in prediction models.

*Boundaries for each 1-Mb segment follow the standard as in chromosome 1: 36–37, which includes the nucleotides on chromosome 1 from 36,000,001 to 37,000,000 base pairs on human genome reference hg19.

*Only one sample with SCA in this region so no variance in average SCA size can be calculated.

*No samples had SCA spanning this region.
esophageal adenocarcinoma risk score (predicted probability of esophageal adenocarcinoma) ranging from low to high esophageal adenocarcinoma risk (0 to 1, Supplementary Methods), was used in subsequent analyses.

Validation of a prediction model would ideally be performed on a large, independent sample set from a separate prospective Barrett’s esophagus cohort. This is challenging due to the prolonged nature of the study, including some non-progressors followed for more than two decades, and the relative rarity of esophageal adenocarcinoma outcomes without use of surrogate endpoints. However, the T1 model and T1T2 models generated high esophageal adenocarcinoma risk scores of ≥0.96 in six advanced esophageal adenocarcinomas from esophagectomy specimens (Supplementary Table S2) and risk scores of >0.99 in 39 of 47 esophageal adenocarcinoma samples from TCGA (downloaded September, 2014; ref. 29) from individuals who were not part of the case–cohort study (Supplementary Methods).

Comparison of SCA with histopathology, DNA content flow cytometry, and TP53 mutation for esophageal adenocarcinoma risk prediction in Barrett’s esophagus

Histopathologic evaluation of surveillance biopsies is the current clinical standard to identify patients at high risk of developing esophageal adenocarcinoma. In this study, histopathology was assessed using a standard protocol of four biopsies every 2 cm, whereas SCA was assessed in one biopsy every 2 cm in the esophagus. To compare the performance of the T1T2 model with histopathologic diagnosis of dysplasia, the prediction

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**Figure 4.**

ROC curves of esophageal adenocarcinoma risk prediction models, histopathology, and DNA content flow cytometry. ROC curve of the T1 model applied to SCA data from T1 (A) or T2 (B) biopsies to predict esophageal adenocarcinoma risk. C, ROC curve using the T1T2 model to predict esophageal adenocarcinoma risk based on maximum SCA calls by patient (T1+T2 data), where the maximum SCA at each of the 29 SCA features was used from any biopsy, regardless of whether it came from T1 or T2. D–F, histopathology and DNA content flow abnormalities were treated as binary variables to generate ROC curves, with each curve consisting of three points: one with sensitivity equal to 0 (perfect specificity), one with specificity equal to 0 (perfect sensitivity), and the third being the sensitivity and specificity for esophageal adenocarcinoma risk prediction of the binary variable. D, ROC curves of histopathologic diagnosis of HGD alone (blue), and LGD and/or HGD (red) from 1, 2, 3, or 4 biopsies per 2 cm sampled in Barrett’s esophagus along the esophagus from T1 data. E, ROC curves of histopathologic diagnosis of HGD alone (blue), and LGD and/or HGD (red) from 1, 2, 3, or 4 biopsies per 2 cm sampled in Barrett’s esophagus along the esophagus from combined T1+T2 data. F, ROC curves of DNA content flow cytometric assessment of tetraploidy and/or aneuploidy from one biopsy per 2 cm in the esophagus from T1 (gray arrow) and from combined T1+T2 data (black arrow).
performance was evaluated for histopathology using 1, 2, 3, or 4 biopsies per 2-cm intervals for esophageal adenocarcinoma risk prediction using only T1 histopathology data (Fig. 4D), and combined T1 + T2 histopathology data (Fig. 4E). High-grade dysplasia (HGD) or any dysplasia (either HGD or low-grade dysplasia [LGD]) were separately evaluated for esophageal adenocarcinoma risk. The highest AUC was obtained using four biopsies every 2 cm (AUC = 0.79; Fig. 4F). The T1T2 model using only one biopsy every 2 cm (AUC = 0.94) outperformed both dysplasia and DNA content flow cytometry, even when evaluating the histopathology in up to four times the number of biopsies.

TP53 mutations status in exons 5–9 had been previously assessed in a longitudinal study in separate biopsies every 2 cm in the esophagus at a single time point before last endoscopy or esophageal adenocarcinoma diagnosis in 122 participants in this study, including 33 who subsequently progressed to esophageal adenocarcinoma (33). In these 122 patients, TP53 mutations had 42% sensitivity and 92% specificity for future progression to esophageal adenocarcinoma. In comparison, for these 122 patients, the 29-SCA feature model with a 0.6 risk score threshold (Supplementary Methods) resulted in 82% sensitivity and 92% specificity for future progression to esophageal adenocarcinoma using the T1 model, and 91% sensitivity and 90% specificity for future progression to esophageal adenocarcinoma using the T1T2 model.

Dynamic stratification of esophageal adenocarcinoma risk: illustration of risk management during stochastic evolution to cancer

The stochastic nature of the development of cancer means that a cancer risk assessment at a single point in time may be insufficient (34). To demonstrate how the prediction model might be used for dynamic esophageal adenocarcinoma risk stratification over time, the T1T2 model was applied to T1 SCA data to stratify patients into low-, intermediate-, and high-risk groups (Fig. 5A and Supplementary Methods). The patients with intermediate risk were then further stratified by using T2 SCA data (Fig. 5B). An additional 13 patients, 8 of whom ultimately developed cancer, were identified as high risk based on the T2 data. This demonstrated that applying this risk prediction model to SCA data from a second time point increased the number of Barrett’s esophagus patients who could be stratified into low- and high-risk groups.

Figure 5.
SCA-based risk stratification of Barrett’s esophagus patients over time. A, the Kaplan-Meier (KM) curves of Barrett’s esophagus patients at baseline stratified into three esophageal adenocarcinoma risk groups based on the T1T2 model SCA data from T1 biopsies only. Risk groups included 35 patients with low esophageal adenocarcinoma risk (green, progressors = 0, nonprogressors = 35), 147 patients with medium esophageal adenocarcinoma risk (red, progressors = 17, nonprogressors = 130) and 66 with high esophageal adenocarcinoma risk (black, progressors = 62, nonprogressors = 4). B, the Kaplan-Meier curve of the 147 medium risk patients identified at baseline were further stratified into low-, medium-, and high-risk group using the SCA data from T2 biopsies. This resulted in 13 patients changing to low esophageal adenocarcinoma risk (green, progressors = 1, nonprogressors = 12), 177 patients remaining at medium esophageal adenocarcinoma risk (red, progressors = 5, nonprogressors = 112), and 13 patients changing to high esophageal adenocarcinoma risk (black, progressors = 8, nonprogressors = 5). Four patients in the medium-risk group from panel A had T1 data only and are plotted in panel A but not plotted in panel B. The proportion of patients stratified in each risk group reflects the makeup of the case-cohort study design, which is enriched with progressors; different proportions would be expected when examining the entire cohort. The Kaplan-Meier plots were adjusted for case-cohort study (see Supplementary Methods).
Discussion

Although progress has been made in characterizing cancer genomes, other strategies beyond this catalog are needed to identify markers of future progression for early cancer detection. Our results provide an esophageal adenocarcinoma risk prediction model that achieved a 0.94 AUC using 29 SCA features representative of chromosomal instability from individuals who progress to esophageal adenocarcinoma compared with those who remain cancer free during follow-up. Comparing the somatic genomes of progressors before cancer to the genomes of non-progressors allowed us to identify SCA features that capture high-risk somatic genomic characteristics for accurate esophageal adenocarcinoma risk prediction. To our knowledge, this is the first cancer risk prediction model based on longitudinal investigation of genome-wide SCA with consideration of temporal and spatial heterogeneity to account for the dynamic, stochastic evolution in neoplastic progression.

There is a strong rationale for using the process of chromosome instability in Barrett’s esophagus as a biologically significant measure of risk for future progression to esophageal adenocarcinoma, rather than focusing on specific gene mutations. Esophageal adenocarcinoma has been shown to have a high overall frequency of point mutations, yet with the exception of TP53, few individual genes are recurrently mutated in more than 15% of esophageal adenocarcinomas (14, 20, 22). Most of the genes that are recurrently mutated in esophageal adenocarcinoma are also mutated at similar frequency in non-dysplastic Barrett’s esophagus, HGD, and esophageal adenocarcinoma (23). In contrast, the vast majority of esophageal adenocarcinomas have high levels of chromosomal instability (13, 18) and punctuated events in which large regions of the genome are altered and detectable by SNP arrays. Catastrophic events are also common with half of esophageal adenocarcinomas having evidence of genome doublings (19) and nearly a third developing chromothripsis (20). In our study, chromothripsis was detected using SNP arrays (see Supplementary Methods; refs. 20, 35) in 13 of 79 progressors (16.5% CI, 9.4%–26.9%) before detection of esophageal adenocarcinoma (data not shown). All 13 patients with chromothripsis had risk scores of 1, indicating the SNP array–based SCA features used in our risk models identify individuals who have undergone punctuated or catastrophic chromosomal events. Our study design allowed us to discount low-risk chromosomal lesions arising in nonprogressors and capture complex chromosomal alterations arising from punctuated and catastrophic events in cancer (19, 20, 36, 37). Therefore, measuring chromosome instability with SNP arrays provided a cost-effective tool for robust assessment of cancer progression risk in individuals with Barrett’s esophagus.

Whole-genome sequencing technology is rapidly becoming accessible for discovery research, but it is currently cost-prohibitive compared with using SNP array technology to assess chromosomal alterations for clinical cancer risk prediction. Our study required measuring SCA in 1,272 biopsies, and SNP arrays provided a relatively inexpensive tool to assess SCA, including cnLOH. Previous studies have used fluorescence in situ hybridization (FISH) to assess copy number alterations, but this technology does not scale-up sufficiently to encompass the 86 regions captured by the 29 SCA features. In addition, 39 of the 86 regions are cnLOH, which FISH cannot measure. We used a method to enrich for epithelial cells that do not require flow cytometric cell sorting and can readily be performed to reduce normal cell contamination. Our approach should be adaptable to SNP array platforms that have been validated for use in formalin-fixed paraffin-embedded (FFPE) samples routinely processed in clinical laboratories (38). The 29-feature model generates high-risk somatic genomic features representative of larger or correlated SCA events in somatic genome evolution, thus creating an opportunity for translating progression-associated chromosome instability measures to technology platforms applicable to clinical settings for screening for high-risk Barrett’s esophagus (23, 39).

Formal criteria for evaluating surrogate biomarkers for disease outcome were developed nearly two decades ago (40). Surrogate markers such as HGD do not meet these criteria (40, 41); they cannot be objectively and reproducibly measured, do not accurately represent the true endpoint (esophageal adenocarcinoma), and are variably predictive of cancer with misclassification relative to risk of esophageal adenocarcinoma in the published literature ranging from 42% to 84% (3). Despite the poor reproducibility of histopathologic evaluation of Barrett’s esophagus biopsies, histopathology has remained the standard for evaluating risk of progression to esophageal adenocarcinoma. Our SCA-based models improved esophageal adenocarcinoma risk prediction compared with traditional histopathologic assessment of dysplasia using a diagnosis of HGD or combined LGD or HGD as predictors of future esophageal adenocarcinoma, even when the histopathologic assessment was made in four times as many biopsies as the SCA assessment. TP53 is the most commonly mutated gene in esophageal adenocarcinoma with mutation frequency of 72% to 81% (13, 14, 20, 22, 23). TP53 mutations can be detected before development of esophageal adenocarcinoma in Barrett’s esophagus with TP53 mutations having 44.1% sensitivity and a 91.4% specificity for future progression to esophageal adenocarcinoma based on a previously published longitudinal study (33). Weaver and colleagues (23) sequenced commonly mutated genes in esophageal adenocarcinoma and reported that only TP53 mutations could discriminate HGD from non-dysplastic Barrett’s esophagus and non-Barrett’s esophagus controls in a cross-sectional study. A recent study found TP53 mutations in 81% of esophageal adenocarcinomas and an additional 9% of the remaining esophageal adenocarcinomas harbored structural alterations inactivating TP53 or amplifying MDM2 (20). We show that using specific features of SCA improves esophageal adenocarcinoma risk prediction over general measures of chromosomal instability such as total SCA and flow cytometry. Our results suggest assessing the outcome of disruptions of the TP53 signaling pathway and resultant high-risk chromosomal instability using measures of cancer risk–associated chromosomal alterations improves esophageal adenocarcinoma risk prediction over using TP53 mutation alone.

Spatial diversity among cell populations within an individual’s Barrett’s segment and stochastic temporal evolutionary dynamics during neoplastic progression are challenges for early detection (10, 26, 34, 42). The majority of progressors (62 of 79) in this study were categorized by the SCA prediction model as high risk for cancer based on results from their T1 endoscopy alone. However, using samples from a second time point identified additional patients whose high-risk SCA would have been missed if only a single time point were evaluated. For a new patient entering into the clinic, whether they will progress to esophageal adenocarcinoma and their actual time to cancer is unknown. In our study, measurements of SCA at follow-up time points improved assessment of esophageal adenocarcinoma risk in
OncoScan FFPE or Indication may be feasible using FFPE-optimized SNP arrays such as those treated, which may alter their disease trajectory. Future validation tools (3, 45). The importance of any single mutation depends on the underlying inherited genotype, the environment when the mutation arose, and the current tissue architecture (46). An extension of our study will be to develop a comprehensive esophageal adenocarcinoma risk management plan that includes esophageal adenocarcinoma risk prediction strategies, host and environmental factors (3, 45, 47–49), and esophageal adenocarcinoma risk assessment based on our SCA model, which could then be applied to at risk populations (50). This will be achieved by using either quantitative methods or computer simulations to optimize an objective function that considers risk and benefits of patients (10, 51) and cost at the population level to determine the optimal number of risk groups and the timing of follow-up endoscopies for each risk group, and ultimately translating a measure of chromosomal instability into esophageal adenocarcinoma risk management in clinical practice.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Assessment of Esophageal Adenocarcinoma Risk Using Somatic Chromosome Alterations in Longitudinal Samples in Barrett's Esophagus

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