Lifetime Cancer Risks in Individuals with Germline PTEN Mutations

Min-Han Tan1, Jessica L. Mester1,3, Joanne Ngeow1, Lisa A. Rybicki2,3, Mohammed S. Orloff1,3, and Charis Eng1,3,4,5

Abstract

Purpose: Age-adjusted cancer incidence and age-related penetrance studies have helped guide cancer risk assessment and management. PTEN hamartoma tumor syndrome (PHTS) is a term encompassing subsets of several clinical syndromes with germline mutations in the PTEN tumor suppressor gene. We conducted the first prospective study to clarify corresponding cancer risks to shed biologic insights on human germline PTEN mutations, and to better inform current surveillance recommendations on the basis of expert opinion.

Experimental Design: A series of 3,399 individuals meeting relaxed International Cowden Consortium PHTS criteria were prospectively recruited; 368 individuals were found to have deleterious germline PTEN mutations. Age-adjusted standardized incidence ratio (SIR) calculations and genotype–phenotype analyses were carried out.

Results: Elevated SIRs were found for carcinomas of the breast [25.4, 95% confidence interval (CI), 19.8–32.0], thyroid (51.1, 38.1–67.1), endometrium (42.9, 28.1–62.8), colorectum (10.3, 5.6–17.4), kidney (30.6, 17.8–49.4), and melanoma (8.5, 4.1–15.6). Estimated lifetime risks were, respectively, 85.2% (95% CI, 71.4%–99.1%), 35.2% (19.7%–50.7%), 28.2% (17.1%–39.3%), 9.0% (3.8%–14.1%), 33.6% (10.4%–56.9%), and 6% (1.6%–9.4%). Promoter mutations were associated with breast cancer, whereas colorectal cancer was associated with nonsense mutations.

Conclusion: Lifetime risks for a variety of cancers, now extending to colorectal cancer, kidney cancer, and melanoma, are increased in patients with PTEN mutations. The genotype–phenotype associations here may provide new insights on PTEN structure and function. We propose a comprehensive approach to surveillance of patients with PTEN mutations. Clin Cancer Res; 18(2): 400–7. ©2012 AACR.

Introduction

Individuals with germline mutations of the PTEN (MIM 601728) tumor suppressor gene on 10q23.3 have diverse phenotypic features affecting multiple systems, with the primary clinical concern of high lifetime risks of cancer of the breast, endometrium, and thyroid. The PTEN tumor suppressor gene, located on 10q23.3, encodes a dual-specificity phosphatase that can dephosphorylate both protein (1) and phospholipid substrates (2). Somatic PTEN alterations are common and well-recognized in a variety of cancers, such as endometrial, prostate, breast, thyroid, and kidney cancers. Germline PTEN mutations underpin the PTEN hamartoma tumor syndrome (PHTS), an umbrella term that includes a range of autosomal-dominant clinical syndromes mainly including Cowden syndrome (MIM 158350), presenting in adulthood, and Bannayan–Riley–Ruvalcaba syndrome [BRRS (MIM 153480; ref. 3)] in children. Inheritance of PHTS is autosomal dominant and age-related penetrance is believed to be high, around 80% (4). A primary clinical concern for affected individuals is the high lifetime risk of cancer, including cancers of the breast, endometrium, thyroid, colon, and kidney. Consequently, clear evidence-based surveillance strategies for these individuals are required. To date, however, our understanding of cancer risks for these individuals has been gleaned from limited reports of retrospectively identified patients from single centers and on expert opinion. To address this, since 2000, the International Cowden Consortium (ICC; ref. 5) has prospectively recruited patients from international centers (mainly North America and Europe) for the purpose of studying PHTS, corresponding risks for cancer and other associated disorders, and genotype–phenotype correlation. Over this period, this study identified additional key features of PHTS, particularly polyposis (6) and autism (7, 8), which were eventually included in the operational criteria. We have recently developed a new diagnostic scoring...
Translational Relevance

Germline mutation of PTEN underlies the PTEN hamartoma tumor syndrome (PHTS), which is manifested by increased lifetime risks of a wide variety of cancers. As PTEN plays a role in suppressing tumor growth in multiple tissues, the extent and magnitude of these risks are of interest, particularly, as no prospective studies have been previously conducted. Here, we report estimated lifetime risks of patients with PHTS mutations for breast, colorectal, thyroid, endometrial, skin (melanoma), and kidney cancer from the only international prospective study accruing patients with PHTS mutations, noting that PTEN mutation is associated with an estimated lifetime breast cancer of 85%. In addition, genotype-phenotype analysis shows several associations, including an association between promoter mutation and breast cancer, allowing for potentially better understanding of PTEN structure and function. Our data here provide a basis for cancer risk assessment and counseling. We also suggest a comprehensive surveillance approach for these patients on the basis of this collective experience.

system, permitting more accurate identification of individuals with PTEN mutations and hence genetic counseling over conventional National Comprehensive Cancer Network (NCCN) criteria (9). We report here results from the first prospective international study conducted from 2000 to 2010. This study identified a consecutive series of adult and pediatric patients with PTEN mutation from North America, Europe (majority), and Asia, allowing us to investigate age-related cancer risks and genotype-phenotype correlations to gain biologic insights and to inform genetic counseling, cancer risk assessment, and surveillance recommendations.

Patients and Methods

Research participants

A total of 3,399 individuals meeting relaxed ICC criteria (pathognomonic criteria, or at least 2 criteria; either major or minor; refs. 10, 11) were accrued prospectively into protocols approved by the respective institutions’ Institutional Review Boards. These patients were recruited from both community and academic medical centers throughout North America, Europe (>85% originating from these 2 continents), and Asia using a standard protocol. Upon providing informed consent, checklists to document the presence or absence of specific features were completed by specialist genetic counselors or physicians concurrently with submission of samples. Specialist genetics staff reviewed all checklists and corresponded with the enrolling center; if necessary, further primary documentation of medical records, particularly pathology reports, were obtained for phenotype confirmation with patient consent (9). For each mutation-positive individual, the diagnosis of cancer was obtained through referring physicians, and confirmed through primary records wherever possible. Relatives of mutation-positive probands were offered mutation testing where appropriate.

PTEN mutation analysis

Genomic DNA was extracted from peripheral blood leukocytes using standard methods, and scanned for PTEN mutations using methods and primers previously reported (9). In brief, genomic DNA samples for PTEN mutations were carried out with a combination of denaturing gradient gel electrophoresis, high-resolution melting (HRM) curve analysis (Idaho Technology), and direct Sanger sequencing (ABI 3730 ×1; ref. 12). Deletion analysis using the multiplex ligation-dependent probe amplification (MLPA) assay (13) was carried out with the P158 MLPA Kit (MRD-Holland) according to manufacturer’s protocol. All patients underwent resequencing of the PTEN promoter region (14), and promoter mutations were defined as previously reported on the basis of individual characterization (9).

Statistical methods

We calculated standardized incidence ratios [a.k.a. standardized incidence rates (SIR)] using incidence data from the Surveillance Epidemiology and End Results (SEER) database. For age-adjusted analysis, the projected U.S. population (year 2000) was used (15): 84% of the 3,399 individuals were white, justifying the use of the U.S. SEER population. Age-adjusted SIRs and mid-P exact tests were

<table>
<thead>
<tr>
<th>Variable</th>
<th>Frequency counts</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gender (%)</td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>163 (44)</td>
</tr>
<tr>
<td>Female</td>
<td>205 (56)</td>
</tr>
<tr>
<td>Age, y</td>
<td></td>
</tr>
<tr>
<td>Median</td>
<td>39</td>
</tr>
<tr>
<td>Range</td>
<td>0.4–83</td>
</tr>
<tr>
<td>Pediatric subjects (%)</td>
<td></td>
</tr>
<tr>
<td>&lt;18</td>
<td>98 (27)</td>
</tr>
<tr>
<td>Proband status (%)</td>
<td>295 (80)</td>
</tr>
<tr>
<td>Mutation type (%)</td>
<td></td>
</tr>
<tr>
<td>Missense</td>
<td>102 (28)</td>
</tr>
<tr>
<td>Nonsense</td>
<td>109 (30)</td>
</tr>
<tr>
<td>Small insertion</td>
<td>33 (9)</td>
</tr>
<tr>
<td>Small deletion</td>
<td>47 (13)</td>
</tr>
<tr>
<td>Small indel</td>
<td>5 (1)</td>
</tr>
<tr>
<td>Splice junction</td>
<td>35 (10)</td>
</tr>
<tr>
<td>Promoter</td>
<td>20 (5)</td>
</tr>
<tr>
<td>Large deletion</td>
<td>17 (5)</td>
</tr>
</tbody>
</table>

Table 1. Cohort baseline data for 368 research participants with germline deleterious PTEN mutations

www.aacrjournals.org  Clin Cancer Res; 18(2) January 15, 2012 401
calculated with OpenEpi using indirect standardization and age-specific SEER incidence rates (2003–2007). There were 38 categories on the basis of 2 genders and 19 age groups. Incidence was assumed to be 0 for categories where statistics were not provided. Person-years of observation (PYO) were calculated for each type of cancer from birth date to the date of cancer for subjects who developed cancer, or to the date of most recent information for subjects without cancer. The expected number of cancers was calculated by multiplying SEER incidence rates in each of the 38 categories by PYO in each category (indirect standardization). For female-specific cancers, calculations were done using 19 age categories among female subjects only. Prophylactic surgery was not considered in the analyses. Age-related penetrance of cancer was estimated using the Kaplan–Meier method. R 2.12.0 was used for additional analysis (16).

Table 2. Standardized incidence rates of cancer in the patient population

<table>
<thead>
<tr>
<th>Cancer</th>
<th>Observed</th>
<th>Expected</th>
<th>SIR</th>
<th>95% CI</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast&lt;sup&gt;a&lt;/sup&gt;</td>
<td>67</td>
<td>2.64</td>
<td>25.4</td>
<td>19.8–32.0</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Thyroid</td>
<td>48</td>
<td>0.94</td>
<td>51.1</td>
<td>38.1–67.1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Endometrium&lt;sup&gt;a&lt;/sup&gt;</td>
<td>24</td>
<td>0.56</td>
<td>42.9</td>
<td>28.1–62.8</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>colorectal</td>
<td>12</td>
<td>1.17</td>
<td>10.3</td>
<td>5.6–17.4</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Kidney</td>
<td>15</td>
<td>0.49</td>
<td>30.6</td>
<td>17.8–49.4</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Melanoma</td>
<td>9</td>
<td>1.06</td>
<td>8.5</td>
<td>4.1–15.6</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

<sup>a</sup>Female subjects only.
Genotype–phenotype correlation was carried out using logistic regression, evaluating the association between mutation status/type and the corresponding clinical phenotypes. For evaluation of correlation between conservation and clinical phenotypes, conservation of bases was determined using phylogenetic P-values (PHYLOPS). For each base pair, a dichotomous classification for conservation was set up through classification of mammalian conservation scores at the median threshold. A similar logistic regression procedure was conducted, where substitution mutations (higher versus lower conserved bases) were analyzed with corresponding patient phenotypes, to determine whether the phenotypic profiles of these patients differed.

All statistical tests were 2-sided, and P values less than 0.05 were deemed significant.

**Results**

**PTEN mutation spectra**

Of the 3,366 individuals tested, 295 probands (8.8%) were found to carry germline pathogenic PTEN mutations. An additional 73 individuals with germline PTEN mutations were identified following screening of the relatives of the probands. Baseline clinicopathologic information is presented in Table 1. The PTEN mutation spectra show clear hot-spots in exons 5, 7, and 8, corresponding to 3 truncation mutations R130X, R233X, and R335X (Fig. 1). All types of mutations, including insertions, deletions, indels, splice site mutations, and large deletions were represented.

**Cancer risks**

Elevated risks of breast [age-adjusted SIR 25.4, 95% confidence interval (CI), 19.8–32.0], thyroid (SIR 51.1, 95% CI, 38.1–67.1), endometrial (SIR 42.9, 95% CI, 28.1–62.8), colorectal (SIR 10.3, 95% CI, 5.6–17.4), kidney cancers (SIR 30.6, 95% CI, 17.8–49.4), and melanoma (SIR 8.5, 95% CI, 4.1–15.6) were found (Table 2). Age-related penetrance estimates (Fig. 2) reveal 85.2% (95% CI, 71.4%–99.1%) lifetime risk for invasive female breast cancer, 35.2% (19.7%–50.7%) for epithelial thyroid cancer, 28.2% (17.1%–39.3%) for endometrial cancer, 9.0% (3.8%–14.1%) for colorectal cancer, etc.
33.6% (10.4%–56.9%) for kidney cancer, and 6% (1.6%–9.4%) for melanoma. The particularly elevated penetrance of breast cancer in females with PTEN mutations is noted, beginning around age 30 and rising to an estimated 85% lifetime risk. PTEN-related endometrial cancer-risk begins at age 25 rising to 30% by age 60, whereas for thyroid cancer, risk begins at birth and continues lifelong (Fig. 2). Risks of colorectal and kidney cancers begin around age 40, with a lifetime risk of 9% and 34%, respectively. For melanoma, the earliest reported age of onset was 3 years.

**Genotype–phenotype correlation**

We analyzed genotype–phenotype associations, finding significant correlations between promoter mutations and breast cancer and between nonsense mutations and colorectal cancer (Table 3). No correlation between any cancer risk and mutations within the catalytic core motif of the N-terminal phosphatase domain (aa 123–131) were noted (data not shown), nor was any correlation between mutations upstream and within the phosphatase core motif and involvement of all major organ systems (central nervous system, thyroid, breast, skin, and gastrointestinal tract) found. Analysis by conservation of bases (more versus less conserved bases) did not yield any correlation with cancer incidence.

**Discussion**

We have reported elevated risks of a protein variety of solid tumors in patients with germline PTEN mutations, testimony to the key role of the PTEN tumor suppressor in regulating cell proliferation in a wide range of tissues (4). Multiple mechanisms have been identified to underpin this effect, chief among which is the concept of reduced PTEN protein dose (17). The effect of reduced PTEN protein dose on cancer susceptibility has been shown both in animal models (18) and recently, in humans (9).

**Cancer risks**

Our study highlights that 3 additional cancers (colorectal, kidney, and melanoma) should be considered as members of the cancer spectra arising from germline mutations of PTEN. Our results also yield new insights on the classic features of breast, endometrial, and thyroid cancers, where a much higher estimated lifetime risk of female breast cancer (85%) is reported relative to the traditional estimates of 25% to 50% that were previously used for clinical risk discussion and counseling (4). Individuals with promoter mutations are at particular risk. Strikingly, this risk is even higher than the best estimates for individuals with BRCA1 or BRCA2 mutations (19). Previously, endometrial cancer was noted...
while conducting a genotype–phenotype analysis (20) and expert opinion believed that risk was only mildly elevated over that of the population (4% lifetime risk). Here, we show that endometrial cancer follows a similar age-of-onset as breast cancer with 28% lifetime risk. For thyroid cancer, the early onset of elevated risk from birth, which is sustained throughout life, is of key clinical interest especially for pediatric surveillance. The onset of colorectal cancer and renal cell carcinoma occurs at about age 40, with a lifetime risk of 9% and 34%, respectively. In terms of the new additions of melanoma and kidney cancer to the cancer spectrum, several individual case reports have previously noted melanoma in patients with Cowden syndrome (21). This is of particular interest, given that there has been conflicting evidence in the somatic setting (as compared with the germline setting here) of the involvement of the PTEN signaling pathway in melanoma (22, 23). While the penetrance of melanoma is relatively low, ease in detection should mean that regular dermatologic surveillance is helpful for patients with PTEN mutations. For kidney cancer, whereas somatic PTEN mutations are relatively rare (24), reduced PTEN expression has been associated with renal carcinogenesis (25) and poorer prognosis (24, 26). The very high lifetime risk of kidney cancer (34%) in these PTEN mutation carriers, however, strongly supports the inclusion of PHTS as a hereditary RCC syndrome as well.

In terms of genotype–phenotype analysis, we showed interesting genotype–phenotype associations between truncating mutations and colorectal cancer, as well as between promoter mutations and breast cancer. Given that these associations do not have absolute predictive value one way or the other, these should not directly inform counseling, at this time. Nonetheless, these associations would be of biologic interest. In an early study over 10 years ago, we reported an exploratory association between mutations upstream and within the phosphatase core motif, and the involvement of 5 major organ systems (central nervous system, thyroid, breast, skin, and gastrointestinal tract) versus 4 or fewer (20), recommending that this finding be validated in a larger number of patients. Following the prospective accrual of a much larger number of patients over 10 years for this study, this association was no longer shown, most likely because of the increasing number of organs and phenotypes that have been formally associated with PHTS in the intervening 12 years. For example, we found that more than 90% of mutation carriers have polyps (6) and 94% have macrocephaly (27), then it is almost certain that we would not find such an association.

Ascertainment bias is always a potential limitation when evaluating patients with rare syndromes. We have sought to minimize this through inclusion of asymptomatic family members with pathogenic PTEN mutations identified through screening.

**Surveillance**

We aim to improve existing recommendations for surveillance on the basis of our prospective study. The NCCN recommendations for cancer surveillance are largely on the basis of retrospective data accrued by the International ICC (5), which we started 14 years ago. We present recommendations for management of patients with PTEN mutations (Fig. 3, Table 4) supported by our analyses and extensive clinical experience from this prospective series of patients, by far the largest in the literature, all of whom have been clinically reviewed by a single author (C. Eng). Our recommendations deviate from the current NCCN guidelines in several ways: (i) biannual renal imaging is proposed on the basis of the relatively high incidence of RCC; (ii) endometrial sampling as a routine surveillance procedure in our patients on the basis of the high incidence of endometrial cancer; (iii) we are able to pinpoint a starting age for breast and endometrial screening; (iv) surveillance for colorectal cancers is now included on the basis of accrued data showing an increase of colorectal cancers (6). It is true that none of these procedures have been shown in randomized trials to prolong survival; it is however impractical, and some would consider unethical, to conduct such a procedure in patients with PTEN mutations. It

![Figure 3. Schematic showing a flowchart of recommendations for the evaluation, workup, and screening for a patient with a potential PTEN mutation.](image-url)
should be noted that conclusive randomized data showing the benefits of surveillance and prophylactic surgery in patients with BRCA1 and BRCA2 mutations took more than a decade to accrue (28). It should be noted that we are not recommending the use of specific mutation types to guide surveillance; whereas the genotype–phenotype analysis is very interesting, and may shed light on biologic correlations, its use to directly inform surveillance recommendations currently may be premature because of the relatively low specificity. Our current data will prove critical for informing new comprehensive surveillance recommendations, which should also take into account clinically significant but nonmalignant features of PHTS, such as arteriovenous malformations and autism.

Table 4. Recommendations for diagnostic workup and cancer surveillance in patients with PTEN mutations

<table>
<thead>
<tr>
<th></th>
<th>Pediatric (&lt;18 y)</th>
<th>Adult male</th>
<th>Adult female</th>
</tr>
</thead>
<tbody>
<tr>
<td>Baseline workup</td>
<td>Targeted history and physical examination</td>
<td>Targeted history and physical examination</td>
<td>Targeted history and physical examination</td>
</tr>
<tr>
<td></td>
<td>Baseline thyroid ultrasound</td>
<td>Baseline thyroid ultrasound</td>
<td>Baseline thyroid ultrasound</td>
</tr>
<tr>
<td></td>
<td>Dermatologic examination</td>
<td>Dermatologic examination</td>
<td>Dermatologic examination</td>
</tr>
<tr>
<td></td>
<td>Formal neurologic and psychologic testing</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cancer surveillance</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>From diagnosis</td>
<td>Annual thyroid ultrasound and skin examination</td>
<td>Annual thyroid ultrasound and skin examination</td>
<td>Annual thyroid ultrasound and skin examination</td>
</tr>
<tr>
<td>From age 30a</td>
<td>As per adult recommendations</td>
<td>As per adult recommendations</td>
<td></td>
</tr>
<tr>
<td>From age 40a</td>
<td>As per adult recommendations</td>
<td>Biannual colonoscopyb</td>
<td>Biannual colonoscopyb</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Biannual renal ultrasound/MRI</td>
<td>Biannual renal ultrasound/MRI</td>
</tr>
<tr>
<td>Prophylactic surgery</td>
<td>Nil</td>
<td>Nil</td>
<td>Individual discussion of prophylactic mastectomy or hysterectomy.</td>
</tr>
</tbody>
</table>

aSurveillance may begin 5 years before the earliest onset of a specific cancer in the family, but not later than the recommended age cutoff point.
bThe presence of multiple nonmalignant polyps in patients with PTEN mutations may complicate noninvasive methods of colon evaluation. More frequent colonoscopy should be considered for patients with a heavy polyp burden.

Disclosure of Potential Conflicts of Interest

M.-H. Tan is the Lee Foundation (Singapore) Fellow and an Ambrose Monell Foundation Cancer Genomic Medicine Clinical fellow at the Cleveland Clinic Genomic Medicine Institute. J. Ngeow is a SingHealth (Singapore) fellow and an Ambrose Monell Foundation Cancer Genomic Medicine Clinical fellow at the Cleveland Clinic Genomic Medicine Institute. C. Eng is the Sondra J. and Stephen R. Hardis Chair of Cancer Genomic Medicine at the Cleveland Clinic and is the recipient of an American Cancer Society Clinical Research Professorship, generously funded, in part, by the F.M. Kirby Foundation. The authors assume full responsibility for analyses and interpretation of these data. No funders of the study had any involvement in the design of the study; the collection, analysis, or interpretation of the data; the writing of the manuscript; or the decision to submit the manuscript for publication. No potential conflicts of interest were disclosed by other authors.

Acknowledgments

The authors thank the Genomic Medicine Biorepository of the Cleveland Clinic Genomic Medicine Institute, as well as members of the Eng laboratory, genetic counselor and research coordinators, and database managers over the last 14 years who have contributed technical assistance, technical advice, and helpful discussions and also like to express their gratitude to all the patients and clinical collaborators from all the centers around the world who have contributed their time and specimens over the last 10 years.

Grant Support

The study was supported by National Cancer Institute, Bethesda, MD (P01CA124570 and R01CA118989 to C. Eng); American Cancer Society (RPG-02-151-01-CCE to C. Eng); William Randolph Hearst Foundations and Doris Duke Distinguished Clinical Scientist Award (to C. Eng).

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received September 3, 2011; revised October 23, 2011; accepted October 28, 2011; published online January 17, 2012.
References


Lifetime Cancer Risks in Individuals with Germline PTEN Mutations

Min-Han Tan, Jessica L. Mester, Joanne Ngeow, et al.


Updated version
Access the most recent version of this article at:
http://clincancerres.aacrjournals.org/content/18/2/400

Cited articles
This article cites 27 articles, 8 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/18/2/400.full.html#ref-list-1

Citing articles
This article has been cited by 41 HighWire-hosted articles. Access the articles at:
/content/18/2/400.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.