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Human Cancer Biology

Lifetime Cancer Risks in Individuals with Germline *PTEN* Mutations

Min-Han Tan[1], Jessica L. Mester[1,3], Joanne Ngeow[1], Lisa A. Rybicki[2,3], Mohammed S. Orloff[1,3], and Charis Eng[1,3,4,5]

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

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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 × l; ref. 12). Deletion analysis using the multiplex ligation-dependent probe amplification (MLPA) assay (13) was carried out with the P158 MLPA Kit (MRC-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 1. Cohort baseline data for 368 research participants with germline deleterious *PTEN* mutations

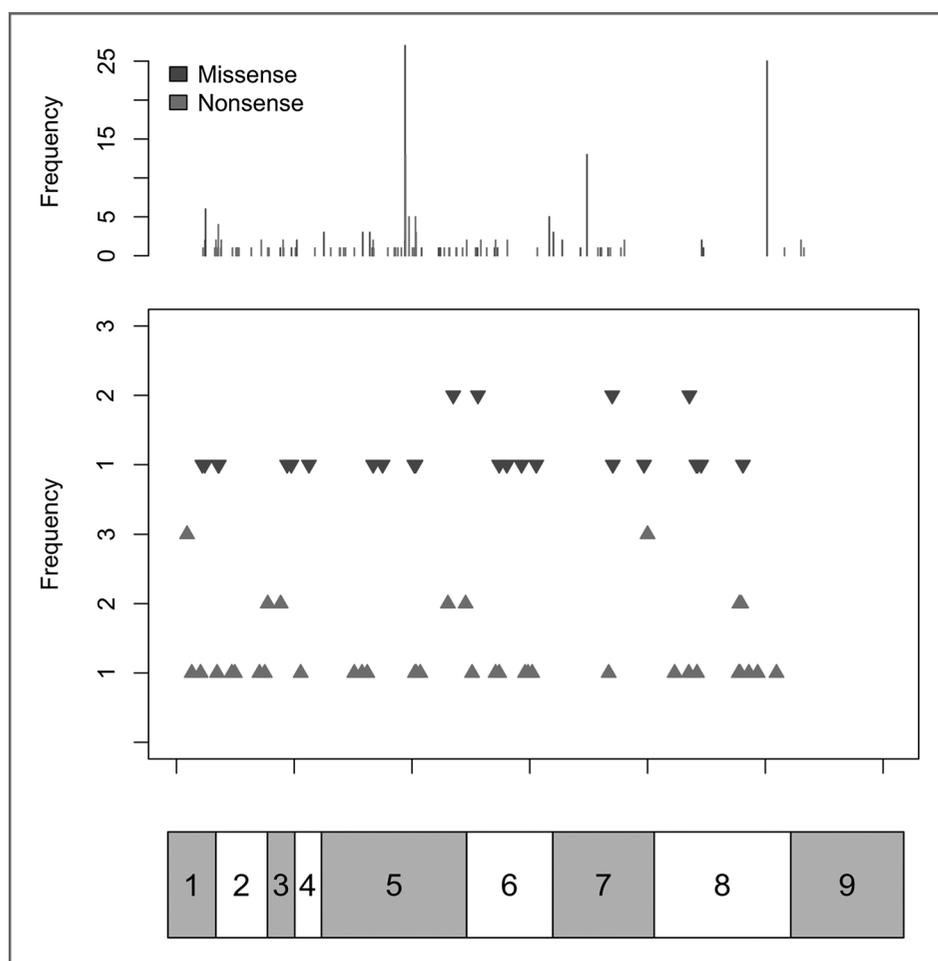| Variable	Frequency counts
Gender (%)	
Male	163 (44)
Female	205 (56)
Age, y	
Median	39
Range	0.4–83
Pediatric subjects (%)	
<18	98 (27)
Proband status (%)	295 (80)
Mutation type (%)	
Missense	102 (28)
Nonsense	109 (30)
Small insertion	33 (9)
Small deletion	47 (13)
Small indel	5 (1)
Splice junction	35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

Figure 1. Consolidated *PTEN* mutation spectrum. Distribution and number of substitutions (missense and/or nonsense), small insertion mutations, and small deletion mutations across the gene. Top, blue bars represent missense mutations and red bars represent nonsense mutations. Middle, the blue arrowheads represent small insertions and the red arrowheads represent small deletions along the gene. Complex mutations (indels, splice-site mutations, and large deletions) and promoter mutations are not depicted. For both, frequencies of both the substitution mutations and the insertion/deletion mutations are shown on the left. Bottom, the bar corresponds to the multiple exons of the PTEN cDNA molecule, with exon 1 on the left to exon 9 on the right, allowing for matching of mutation to exon.

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

| Cancer | Number of cancers | | SIR | 95% CI | *P* |
	Observed	Expected			
Breast[a]	67	2.64	25.4	19.8–32.0	<0.001
Thyroid	48	0.94	51.1	38.1–67.1	<0.001
Endometrium[a]	24	0.56	42.9	28.1–62.8	<0.001
Colorectal	12	1.17	10.3	5.6–17.4	<0.001
Kidney	15	0.49	30.6	17.8–49.4	<0.001
Melanoma	9	1.06	8.5	4.1–15.6	<0.001

[a]Female subjects only.

Figure 2. Age-related penetrance curves for (A) female breast cancer; (B) thyroid cancer; (C) endometrial cancer; (D) colorectal cancer; (E) kidney cancer (renal cell carcinoma); and (F) melanoma. The highest age-related penetrance is observed in female breast cancer, with an estimated 85% lifetime risk.
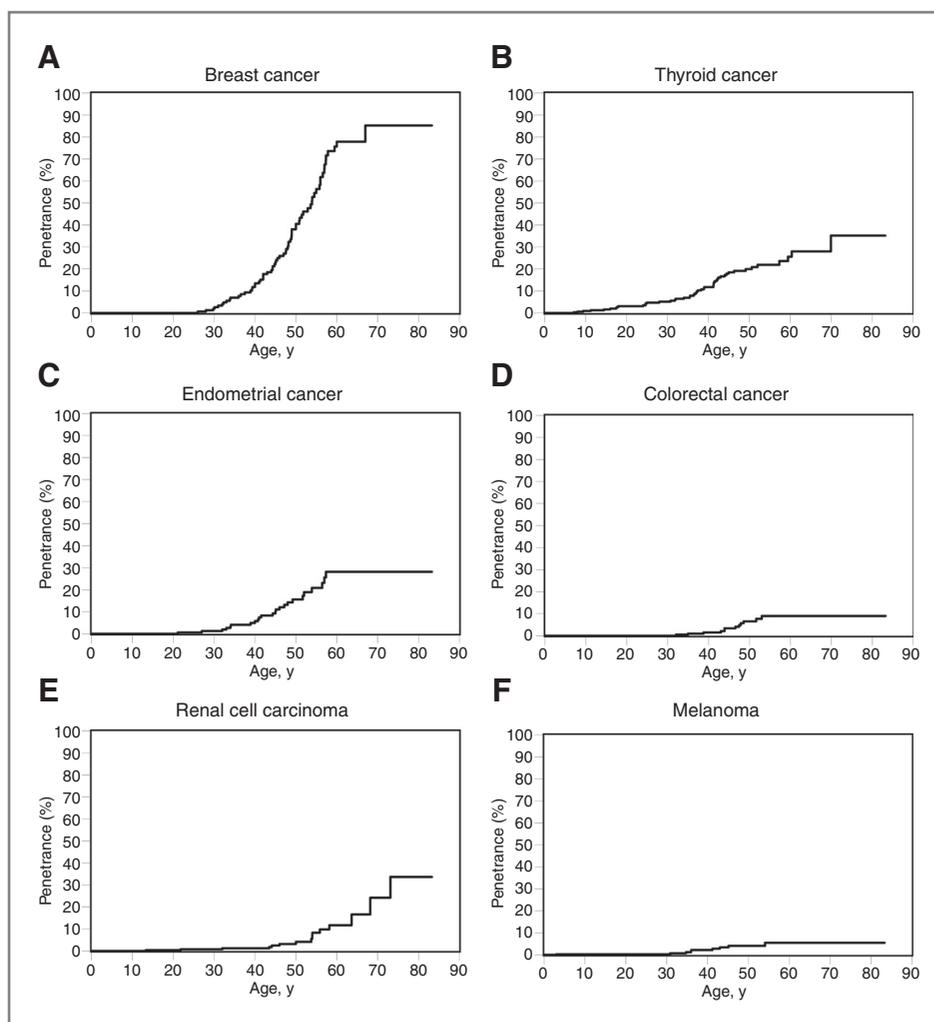
Genotype–phenotype correlation was carried out using logistic regression, evaluating the association between mutation status/type and the corresponding clinical phenotypes. For evaluation of correlation between conservation and clinical phenotypes, conservation of bases was determined using phylogenetic *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,

Table 3. *PTEN* mutation spectra and corresponding cancers

Mutation type	Nonsense	Missense	Deletion	Indel	Insertion	Splice junction	Large deletion	Promoter
Female breast cancer								
Cases	21	19	7	0	5	3	3	9
% Case total	31.34	28.36	10.45	0	7.46	4.48	4.48	13.43
OR	1.11	1.05	0.76	0	0.78	0.39	0.95	4.04
P	0.77	0.88	0.69	0.59	0.81	0.17	1	<0.01
Endometrial cancer								
Cases	7	8	2	0	5	1	0	1
% Case total	29.17	33.33	8.33	0	20.83	4.17	0	4.17
OR	0.98	1.34	0.6	0	2.94	0.39	0	0.74
P	1		0.75	1	0.05	0.72	0.62	1
Thyroid cancer								
Cases	14	13	8	1	4	3	1	4
% Case total	29.17	27.08	16.67	2.08	8.33	6.25	2.08	8.33
OR	0.98	0.97	1.43	1.67	0.91	0.6	0.4	1.71
P	1	1	0.36	0.51	1	0.6	0.71	0.31
Kidney cancer								
Cases	5	3	3	0	1	1	1	1
% Case total	33.33	20	20	0	6.67	6.67	6.67	6.67
OR	1.2	0.65	1.74	0	0.71	0.67	1.49	1.25
P	0.77	0.77	0.42	1	1	1	0.52	0.58
Colorectal cancer								
Cases	6	1	1	0	0	1	0	0
% Case total	66.67	11.11	11.11	0	0	11.11	0	0
OR	4.97	0.32	0.85	0	0	1.19	0	0
P	0.02	0.45	1	1	1	0.6	1	1

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
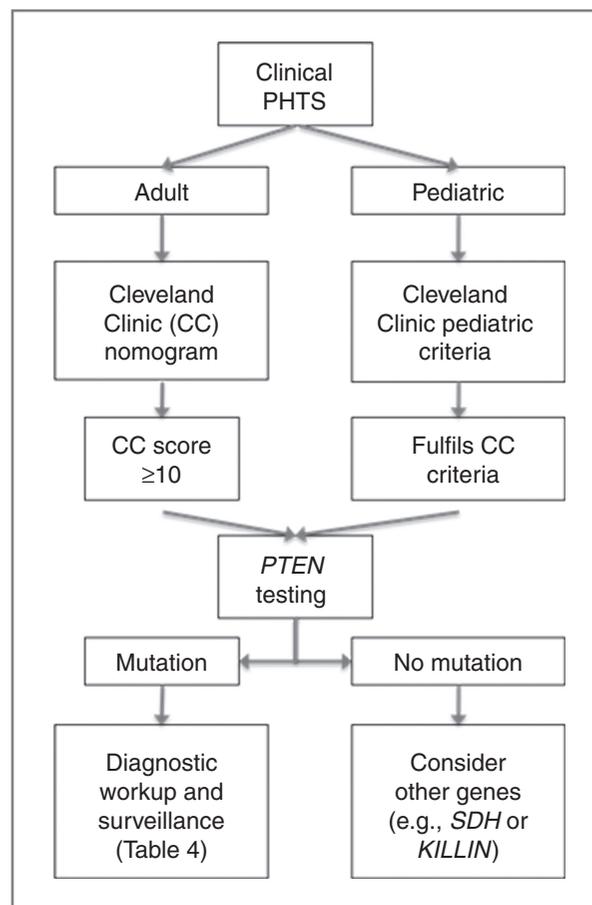

Figure 3. Schematic showing a flowchart of recommendations for the evaluation, workup, and screening for a patient with a potential *PTEN* mutation.

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

	Pediatric (<18 y)	Adult male	Adult female
Baseline workup	Targeted history and physical examination Baseline thyroid ultrasound Dermatologic examination Formal neurologic and psychologic testing	Targeted history and physical examination Baseline thyroid ultrasound Dermatologic examination	Targeted history and physical examination Baseline thyroid ultrasound Dermatologic examination
Cancer surveillance			
From diagnosis	Annual thyroid ultrasound and skin examination	Annual thyroid ultrasound and skin examination	Annual thyroid ultrasound and skin examination
From age 30[a]	As per adult recommendations		Annual mammogram (for consideration of breast MRI instead of mammography if dense breasts) Annual endometrial sampling or transvaginal ultrasound (or from 5 years before age of earliest endometrial cancer)
From age 40[a]	As per adult recommendations	Biannual colonoscopy[b] Biannual renal ultrasound/ MRI	Biannual colonoscopy[b] Biannual renal ultrasound/MRI
Prophylactic surgery	Nil	Nil	Individual discussion of prophylactic mastectomy or hysterectomy.

[a]Surveillance may begin 5 years before the earliest onset of a specific cancer in the family, but not later than the recommended age cutoff point.
[b]The 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.

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.

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 inter-

pretation 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.

References

1. Li DM, Sun H. TEP1, encoded by a candidate tumor suppressor locus, is a novel protein tyrosine phosphatase regulated by transforming growth factor beta. Cancer Res 1997;57:2124–9.
2. Myers MP, Pass I, Batty IH, Van der Kaay J, Stolarov JP, Hemmings BA, et al. The lipid phosphatase activity of *PTEN* is critical for its tumor suppressor function. Proc Natl Acad Sci U S A 1998;95:13513–8.
3. Gorlin RJ, Cohen MM Jr, Condon LM, Burke BA. Bannayan–Riley–Ruvalcaba syndrome. Am J Med Genet 1992;44:307–14.
4. Hobert JA, Eng C. *PTEN* hamartoma tumor syndrome: an overview. Genet Med 2009;11:687–94.
5. Nelen MR, Padberg GW, Peeters EA, Lin AY, van den Helm B, Frants RR, et al. Localization of the gene for Cowden disease to chromosome 10q22-23. Nat Genet 1996;13:114–6.
6. Heald B, Mester J, Rybicki L, Orloff MS, Burke CA, Eng C. Frequent gastrointestinal polyps and colorectal adenocarcinomas in a prospective series of PTEN mutation carriers. Gastroenterology 2010;139:1927–33.
7. McBride KL, Varga EA, Pastore MT, Prior TW, Manickam K, Atkin JF, et al. Confirmation study of PTEN mutations among individuals with autism or developmental delays/mental retardation and macrocephaly. Autism Res 2010;3:137–41.
8. Butler MG, Dasouki MJ, Zhou XP, Talebizadeh Z, Brown M, Takahashi TN, et al. Subset of individuals with autism spectrum disorders and extreme macrocephaly associated with germline PTEN tumour suppressor gene mutations. J Med Genet 2005;42:318–21.
9. Tan MH, Mester J, Peterson C, Yang YR, Chen JL, Rybicki L, et al. A clinical scoring system for selection of patients for PTEN mutation testing is proposed on the basis of a prospective study of 3,042 probands. Am J Hum Genet 2011;88:42–56.
10. Eng C. Will the real Cowden syndrome please stand up: revised diagnostic criteria. J Med Genet 2000;37:828–30.
11. Pilarski R, Eng C. Will the real Cowden syndrome please stand up (again)? Expanding mutational and clinical spectra of the PTEN hamartoma tumour syndrome. J Med Genet 2004;41:323–6.
12. van der Stoep N, van Paridon CD, Janssens T, Krenkova P, Stambergova A, Macek M, et al. Diagnostic guidelines for high-resolution melting curve (HRM) analysis: an interlaboratory validation of BRCA1 mutation scanning using the 96-well LightScanner. Hum Mutat 2009;30:899–909.
13. Schouten JP, McElgunn CJ, Waaijer R, Zwijnenburg D, Diepvens F, Pals G. Relative quantification of 40 nucleic acid sequences by multiplex ligation-dependent probe amplification. Nucleic Acids Res 2002;30:e57.
14. Teresi RE, Zbuk KM, Pezzolesi MG, Waite KA, Eng C. Cowden syndrome-affected patients with PTEN promoter mutations demonstrate abnormal protein translation. Am J Hum Genet 2007;81:756–67.
15. Klein RJ, Schoenborn CA. Age adjustment using the 2000 projected U.S. population. Healthy People 2000 Stat Notes 2001;1–9.
16. Ihaka R, Gentleman R. R: a language for data analysis and graphics. J Comput Graph Stat 1996;5:299–314.
17. Trotman LC, Niki M, Dotan ZA, Koutcher JA, Di Cristofano A, Xiao A, et al. PTEN dose dictates cancer progression in the prostate. PLoS Biol 2003;1:E59.
18. Alimonti A, Carracedo A, Clohessy JG, Trotman LC, Nardella C, Egia A, et al. Subtle variations in Pten dose determine cancer susceptibility. Nat Genet 2010;42:454–8.
19. Metcalfe K, Lubinski J, Lynch HT, Ghadirian P, Foulkes WD, Kim-Sing C, et al. Family history of cancer and cancer risks in women with BRCA1 or BRCA2 mutations. J Natl Cancer Inst 2010;102:1874–8.
20. Marsh DJ, Coulon V, Lunetta KL, Rocca-Serra P, Dahia PL, Zheng Z, et al. Mutation spectrum and genotype–phenotype analyses in Cowden disease and Bannayan–Zonana syndrome, two hamartoma syndromes with germline PTEN mutation. Hum Mol Genet 1998;7:507–15.
21. Greene SL, Thomas JR III, Doyle JA. Cowden's disease with associated malignant melanoma. Int J Dermatol 1984;23:466–7.
22. Dankort D, Curley DP, Cartlidge RA, Nelson B, Karnezis AN, Damsky WE Jr, et al. Braf(V600E) cooperates with Pten loss to induce metastatic melanoma. Nat Genet 2009;41:544–52.
23. Nogueira C, Kim KH, Sung H, Paraiso KH, Dannenberg JH, Bosenberg M, et al. Cooperative interactions of PTEN deficiency and RAS activation in melanoma metastasis. Oncogene 2010;29:6222–32.
24. Velickovic M, Delahunt B, McIver B, Grebe SK. Intragenic PTEN/MMAC1 loss of heterozygosity in conventional (clear-cell) renal cell carcinoma is associated with poor patient prognosis. Mod Pathol 2002;15:479–85.
25. Brenner W, Farber G, Herget T, Lehr HA, Hengstler JG, Thuroff JW. Loss of tumor suppressor protein PTEN during renal carcinogenesis. Int J Cancer 2002;99:53–7.
26. Shin Lee J, Seok Kim H, Bok Kim Y, Cheol Lee M, Soo Park C. Expression of PTEN in renal cell carcinoma and its relation to tumor behavior and growth. J Surg Oncol 2003;84:166–72.
27. Mester JL, Tilot AK, Rybicki LA, Frazier TW II, Eng C. Analysis of prevalence and degree of macrocephaly in patients with germline PTEN mutations and of brain weight in Pten knock-in murine model. Eur J Hum Genet 2011;19:763–8.
28. Domchek SM, Friebel TM, Singer CF, Evans DG, Lynch HT, Isaacs C, et al. Association of risk-reducing surgery in *BRCA1* or *BRCA2* mutation carriers with cancer risk and mortality. JAMA 2010;304:967–75.