Genetic variation in AKT1, PTEN and the 8q24 locus, and the risk of testicular germ cell tumor


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STUDY QUESTION: Is there an association between testicular germ cell tumor (TGCT) and genetic polymorphisms in AKT1, PTEN and the 8q24 locus?

SUMMARY ANSWER: Our findings suggest that genetic variation in PTEN may influence the risk of TGCT.

WHAT IS KNOWN ALREADY: There is strong evidence that genetic variation influences the risk of TGCT. The oncogene, AKT1, the tumor suppressor gene, PTEN and the chromosome 8q24 locus play important roles in cancer development in general.

STUDY DESIGN, SIZE, DURATION: We have conducted a population-based Norwegian-Swedish case–parent study, based on cases diagnosed in 1990–2008, including 831 triads (TGCT case and both parents), 474 dyads (TGCT case and one parent) and 712 singletons (only the TGCT case). In addition we expanded the study to include 3922 unrelated male controls from the TwinGene project.

PARTICIPANTS/MATERIALS, SETTING, METHODS: We genotyped 26 single nucleotide polymorphisms (SNPs) in AKT1, PTEN and the 8q24 locus. First, triads and dyads were included in a likelihood-based association test. To increase the statistical power, case singletons and controls from the TwinGene project were included in a single test for association. We examined if the allelic effect on TGCT risk differed by histological subgroup, country of origin or parent of origin. Odds ratios (ORs) and 95% confidence intervals (CI) were calculated with Bonferroni correction ($P_{\text{bonf}}$) for multiple testing.

MAIN RESULTS AND THE ROLE OF CHANCE: In the case–parent analyses, none of the 26 SNPs were significantly associated with TGCT. Of the 23 SNPs investigated in the combined study, one SNP in PTEN (rs11202586) remained associated with TGCT risk after adjusting for multiple testing (OR = 1.16, 95% CI = 1.06–1.28, $P_{\text{bonf}} = 0.040$). We found no difference in risk according to histological subgroup, country of origin or parent of origin.

LIMITATIONS, REASONS FOR CAUTION: Our study is strengthened by the population-based design and large sample size, which gives high power to detect risk alleles. The reported association was not highly significant, and although it was based on an a priori hypothesis of this tumor suppressor gene being implicated in the etiology of TGCT, replication studies, as well as functional studies of this polymorphism, are warranted.

WIDER IMPLICATIONS OF THE FINDINGS: We report, to our knowledge, a novel association between TGCT and a marker in the tumor suppressor gene PTEN. Previous studies have linked PTEN to TGCT etiology, and there is also a link between PTEN and KITLG, which contains TGCT susceptibility loci revealed through recent genome-wide studies.
Introduction

Testicular germ cell tumors (TGCTs) are believed to originate from transformed primordial germ cells (PGCs) during early embryonic development (Hoei-Hansen et al., 2005; Rajpert-De Meyts and Hoei-Hansen, 2007). These tumors are relatively rare, but the incidence has increased several folds during the last decades in most western countries (Huyghe et al., 2003; Huyghe et al., 2007; Chia et al., 2010). This rapid increase in incidence suggests an important role of environmental factors in the development of TGCT. However, the increased risk of TGCT among brothers and sons of affected men (Heimdal et al., 1996; Hemminki and Li, 2004) and especially among men with an affected monozygotic twin-brother (Swerdlow et al., 1997), points towards a strong genetic component. Several recent studies have explored the impact of single nucleotide polymorphisms (SNPs) on TGCT susceptibility. Three genome-wide association studies (GWASs) have revealed six genes associated with TGCT risk (Kenetsky et al., 2009; Rapley et al., 2009; Turnbull et al., 2010): KIT ligand (KITLG), sprouty-4 (SPRY4), BCL-2 antagonist/killer 1 (BAK1), telomerase reverse transcriptase (TERT), activating transcription factor 7 interacting protein (ATF7IP) and double sex and mab-3-related transcription factor 1 (DMRT1). Because these genes are involved in the regulation of PGC development, telomerase activity and sex-determination, a causal role in the development of TGCT is biologically plausible.

The strongest reported GWAS associations for TGCT to date were those in KITLG, encoding the ligand to the receptor tyrosine kinase KIT, with reported allelic odds ratios (ORs) > 2 (Kenetsky et al., 2009; Rapley et al., 2009). KIT signaling activates the downstream phosphoinositide-3-kinase (PI3K)-AKT pathway, which is important in cell proliferation and apoptosis (Osaki et al., 2004). PTEN is a tumor-suppressor gene that through its protein product, phosphatase, negatively regulates the PI3K-AKT pathway (Rottapel et al., 1991; Osaki et al., 2004). PTEN is among the most commonly mutated genes in human cancer, and somatic mutations in this gene have been identified in several tumor forms, such as glioblastoma, endometrial carcinoma and prostate cancer (Cairns et al., 1996; Hemminki et al., 2000). There have also been a few case reports of TGCTs in patients with Cowden disease. In 2004, Mazereeuw-Hautier et al. (2004) reported a case of testicular seminoma in a 42-year-old man with Cowden disease. In 2007, Devi et al. reported a mixed germ cell tumor in a 17-year-old man with Cowden disease. Previous studies have investigated changes in the expression of PTEN and the oncogene AKTI in TGCT (Kimura et al., 2003; Di Vizio et al., 2005; Nakai et al., 2005; Hennekens et al., 2005), but to our knowledge, no candidate-gene studies have addressed the association between inherited genetic polymorphisms in these genes and TGCT risk.

The chromosome 8q24 locus has been linked particularly to cancer of the prostate, colon and breast (Ghoussaini et al., 2008; Wokolorczyk et al., 2008). In 2008, Cook et al. examined 15 specific SNPs in the 8q24 locus; they found no association with TGCT, but noted that an association might have been missed.

Our aim was to examine the association between TGCT and genetic polymorphisms in AKTI, PTEN and in the 8q24 locus. We also wanted to compare the results according to histology (seminoma/non-seminoma) and country of origin (Norway and Sweden). In addition, our study design allowed us to examine whether any allelic effect was modified by the gender of the parent from whom the allele was transmitted (parent of origin effect). In order to address these aims, we conducted a combined nation-wide case–parent/case–control study in Norway and Sweden.

Materials and Methods

Norwegian TGCT patients

All patients diagnosed with a histologically verified TGCT (patients with spermatocytic seminoma were excluded) in the period 1990–2008 and registered to the Cancer Registry of Norway were identified. Of these 4354 men, 4222 (97%) were alive and eligible for the study. From the group of eligible patients, 1855 men were randomly selected and invited to participate in the study; of these, 974 (53%) consented (Table I). There was no difference in tumor stage when comparing those identified in the Cancer Registry with those invited to participate in the study (23 versus 22.4% had metastatic disease). The diagnosis was verified and the invitation was approved by the treating physician at the regional oncology division.

Swedish TGCT patients

Patients diagnosed with TGCT (patients with spermatocytic seminoma were excluded) between 1995 and 2006 and registered in the Swedish National Cancer Registry were identified. The diagnosis was verified by record linkage with the Swedish National Inpatient Register. In total, 2443 men were identified and 2373 (97%) of them were alive and eligible for the study. From the group of eligible patients, 2327 were randomly selected and invited to participate in the study, out of whom 1188 (51%) consented (Table I).

Men consenting to the study were slightly older at time of diagnosis compared with those who did not consent (32.4 versus 31.1 years). There was no difference in tumor stage (22.4 versus 22.3% with metastatic disease) or lag time between diagnosis and study recruitment (8.5 years for both groups) between those consenting and those not consenting.

Enrollment

During the period September 2008 through September 2010, all eligible cases received an invitation to participate in the study. The mailing included an information letter, an informed consent form and an Oragene DNA-self collection kit. If they consented, the participants were asked to provide saliva into the container (2 ml) according to the manufacturer’s instruction and return it to the Cancer Registry of Norway (for Norwegian participants) and to the Karolinska Institutet (for Swedish participants) along with the signed consent form. In the information letter, the participants were asked for approval to contact their parents and, if they gave their consent, to write down contact information. The parents were then invited to participate in the study and asked to provide a saliva sample as described above.

STUDY FUNDING/COMPETING INTEREST(S): This work was financially supported by the Norwegian Cancer Society (418975) and the Nordic Cancer Union (S-12/07). No competing interests are declared.

Key words: testicular cancer / single nucleotide polymorphism / PTEN / AKT1 / 8q24
Table I Characteristics of cases and controls.

<table>
<thead>
<tr>
<th></th>
<th>Norwegian</th>
<th>Swedish</th>
<th>Total</th>
<th>Included in the final analysis*</th>
</tr>
</thead>
<tbody>
<tr>
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<td>974</td>
<td>1188</td>
<td>2162</td>
<td>2017</td>
</tr>
<tr>
<td>Triads</td>
<td>483</td>
<td>521</td>
<td>1004</td>
<td>831</td>
</tr>
<tr>
<td>Dyads (mothers/fathers)</td>
<td>192 (150/42)</td>
<td>248 (178/70)</td>
<td>440 (328/112)</td>
<td>474 (340/134)</td>
</tr>
<tr>
<td>Singletons</td>
<td>299</td>
<td>419</td>
<td>718</td>
<td>712</td>
</tr>
<tr>
<td>Seminoma</td>
<td>499</td>
<td>672</td>
<td>1171</td>
<td>1103</td>
</tr>
<tr>
<td>Non-seminoma</td>
<td>467</td>
<td>503</td>
<td>970</td>
<td>900</td>
</tr>
<tr>
<td>Age at diagnosis (mean)</td>
<td>15–65 (33)</td>
<td>18–45 (32)</td>
<td>15–65 (32)</td>
<td>15–65 (32)</td>
</tr>
<tr>
<td>Unrelated controls</td>
<td>3922</td>
<td>3922</td>
<td>3922</td>
<td>3922</td>
</tr>
</tbody>
</table>

*After excluding samples with low DNA yield or not approved in the quality control.

Ethical approval
The study was approved by the Regional Committee for Medical Research Ethics, Southern Norway, the Norwegian Social Science Data Services and the Regional Research Ethics Committee in Stockholm, Sweden. The dedicated research biobank in Oslo was approved by the Ministry of Health and Care Services, Norway.

Control group
A population-based Swedish study conducted in 2004–2008 (TwinGene project), included blood samples and questionnaires from 12,591 twins born in the period 1911–1958. All participants had given informed consent, and the study was approved by the local ethics committee at Karolinska Institute (Rahman et al., 2009). From this population, 3,922 unrelated men were randomly selected as a control group for the present study. For these individuals, DNA was already extracted and genome-wide genotyping with Illumina OmniExpress bead chip had been performed.

Selection of SNPs
Regarding AKT1, SNPs were selected for genotyping if the minor allele frequency (MAF) was >5% and had at least 90% genotyping success rate in HapMap2 CEU individuals. Haplotype block structure, based on confidence bounds of D’ prime values, was inferred using data from the catalog of common genetic variants generated from the International HapMap Project (The International HapMap Consortium, 2003). Within each haplotype block, haplotype tagging SNPs (htSNPs) were selected using the Tagger software (de Bakker et al., 2005), applying aggressive tagging and a minimal coefficient of determination equal to 0.95 in order to capture the common genetic variation across the gene.

For PTEN and the 8q24 locus, SNPs were selected based on previously published evidence of an association with TGCT or other relevant cancers. In total, 31 SNPs were selected, and 26 of those were successfully genotyped and passed quality control.

Genotyping
Saliva was collected using the Oragene® DNA sample collection kit (DNA Genotek, Inc., Kanata, ON, Canada). Isolation of DNA was performed according to the manufacturer’s protocol in ‘Laboratory Protocol for Manual Purification of DNA from 4.0 ml of Oragene® DNA/saliva’ (http://www.dnagenotek.com/DNA_Genetek_Industry_CGT_SCA_P.html). Cases with a DNA yield <25 μg were excluded from the study (35 Norwegian and 79 Swedish cases). Genotyping was performed using the Sequenom MassARRAY® iPLEX Gold platform (Sequenom, Inc., San Diego, CA, USA) at the Center for Integrative Genetics (CIGENE), Norwegian University of Life Sciences, Ås, Norway. Imputation and quality control of TwinGene control samples
In the TwinGene controls, we used full-genome imputed data to increase the number of SNPs available. Imputation was performed using IMPUTE2 (Howie et al., 2009), and CEU reference haplotypes from the HapMap project, release 22. We extracted TwinGene genotypes for all SNPs that passed quality control in the case–parent sample, and were either directly genotyped or imputed in the TwinGene dataset. The same SNP quality control measures as for the cases were then applied to the control genotypes.

Statistical analysis
The statistical methods used in this study have been described in detail previously (Kristiansen et al., 2012), and an abridged version is presented here.

Sample and SNP quality control
Samples with >20% missing genotypes or a heterozygosity rate more than three standard deviations from the sample mean (indicating possible sample contamination) were excluded (n = 277). To confirm parent–offspring relations, pairwise genotype identity-by-state (IBS) was examined. If the standard deviation of the number of alleles per SNP shared IBS exceeded 0.55, indicating that the parent is not biological, the parent was excluded (n = 41). After these steps in the quality control, 21 remaining Mendelian errors were resolved by setting the offending genotypes to missing. Furthermore, 34 samples identified as duplicates were excluded. If the proband was lost to quality control, samples from the parents were excluded from the final analysis (n = 111). SNPs with >10% missing genotypes or an MAF of <0.01 were also excluded from further analysis (n = 3). Two more SNPs were removed because they were considered ‘problematic’ by CIGENE. After completing quality control, 831 triads, 474 dyads and 712 case singletons were included in the final analysis (Table I).

Imputation and quality control of TwinGene control samples
In the TwinGene controls, we used full-genome imputed data to increase the number of SNPs available. Imputation was performed using IMPUTE2 (Howie et al., 2009), and CEU reference haplotypes from the HapMap project, release 22. We extracted TwinGene genotypes for all SNPs that passed quality control in the case–parent sample, and were either directly genotyped or imputed in the TwinGene dataset. The same SNP quality control measures as for the cases were then applied to the control genotypes.
Association analysis for the case–parent population

We used a likelihood-based association test for nuclear families and unrelated subjects with missing data in the main analysis, using the software package UNPHASED (Dudbridge, 2008). This test is robust to population stratification. Initially, only complete case–parent triads and dyads were included in the analysis. The assumption of an allelic main effect led to a 1-df likelihood-ratio test. Further, we included interaction terms in the model to examine if the allelic effect on TGCT risk differed by histological subgroups (seminoma and non-seminoma), country of origin (Norway or Sweden) or parent of origin.

Association analysis for the combined case–parent/case–control population

To increase the power to detect associations, we included case singletons and controls from the TwinGene project in the analysis. A single test for association was performed, including triads, dyads and case–control samples. Both family-based controls and unrelated controls were included in an unmatched analysis.

To account for multiple comparisons, P-values were adjusted using the Bonferroni correction ($P_{\text{bonf}}$). P-values < 0.05 were considered statistically significant.

Results

All SNP positions in this section are reported in genomic build hg18 coordinates, and all alleles are reported relative to the positive (+) strand.

Case–parent study

In the case–parent part of the study, including 831 triads and 474 dyads, we studied a total of 26 SNPs in the three different genes. None of these SNPs were significantly associated with TGCT (Table II).

Combined case–parent/case–control study

Three of the AKT1 SNPs were not genotyped or successfully imputed in the TwinGene control group, and could not be included in the combined case–parent/case–control study. Therefore, in the expanded study that included 718 singletons and 3922 controls in addition to the case–parent study, we only investigated 23 SNPs. The principal finding was that for one SNP in PTEN, rs11202586, the T allele was associated with a 16% increased risk of developing TGCT. This association was not modified by the gender of the parent from whom the allele was transmitted, which might indicate that neither genomic imprinting nor any other epigenetic component, resulting from environment influences, is involved in the inheritance of this risk allele (Guilmare and Sharp, 2012). We found no significant association between AKT1 or 8q24 locus and TGCT risk.

Despite several studies indicating a role of AKT1 and PTEN in TGCT pathogenesis, no previous candidate-gene studies have, to our knowledge, investigated the association between common genetic variants in these genes and TGCT. As such, our finding is novel and suggests a possible role for PTEN in the pathogenesis of TGCT. Although the association was not highly significant, it was based on an a priori hypothesis of this tumor-suppressor gene being implicated in the etiology of this cancer form, but replication studies and functional analyses of this polymorphism are warranted.

In mice, estrogens increase the production of kitl and thereby stimulate growth of PGCs via the AKT1/PTEN pathway (Moe-Behrens et al., 2003). Further, it has been shown that knockout of Pten in male mice PGCs causes bilateral testicular teratomas (Kimura et al., 2003). In 2005, a study by Nakai et al. indicated an activation of the Kit-Pi3K-AKT1 pathway in seminomas. Another group found that PTEN was expressed in normal germ cells, whereas it was lost in more than half of all seminomas, 86% of embryonal carcinomas and almost all teratomas. PTEN was, however, abundantly expressed in intratubular germ cell neoplasia (ITGCN) suggesting a crucial role in the transition from ITGCN to invasive TGCT (DiVizio et al., 2005).

Recently, Hennenlotter et al. (2011) investigated PTEN expression in non-seminoma TGCTs. They found that PTEN expression was reduced in all non-seminoma subgroups with no altered expression or negative regulation of AKT1. This result was in contrast to the previously mentioned findings (Nakai et al., 2005), and might reflect a difference in tumor biology between seminoma and non-seminoma TGCTs. Some evidence suggest that genetic variation in CYP1A1/CYP1A2 or androgen receptor CAG repeat length is associated with histological subtype of TGCT, but the results are inconsistent (Figueroa et al., 2008; Davis-Dao et al., 2011; Kristiansen et al., 2011). In a previous study among the same group of individuals as in the present one, the association of TGCT with polymorphisms in the sex hormone pathway genes did not differ significantly between histological subtypes of TGCT (Kristiansen et al., 2012).

Our observed lack of association between histological subtypes for genetic variation in AKT1, PTEN and the 8q24 locus is thus in accordance with the null results most often reported in genetic association studies on histological subtype of TGCT.

The gene-poor region 8q24 has been linked particularly to breast cancer, prostate cancer and colorectal cancer (Yeager et al., 2009; He et al., 2011; Li et al., 2011). Several recent studies suggest that enhancers involved in tissue-specific MYC regulation are located in this region (Jia et al., 2009; Ahmadieh et al., 2010; Wasserman et al., 2010). Since MYC is a well-known proto-oncogene located immediately downstream

Discussion

In this large case–parent study, the association between risk of TGCT and 26 SNPs in AKT1, PTEN and the 8q24 locus was investigated. In addition, we conducted an expanded case–parent/case–control analysis that included 23 of these SNPs. The principal finding was that for one SNP in PTEN, rs11202586, the T allele was associated with a 16% increased risk of developing TGCT. This association was not modified by the gender of the parent from whom the allele was transmitted, which might indicate that neither genomic imprinting nor any other epigenetic component, resulting from environment influences, is involved in the inheritance of this risk allele (Guilmare and Sharp, 2012). We found no significant association between AKT1 or 8q24 locus and TGCT risk.
Table II  ORs for associations between polymorphisms in *AKT1*, *PTEN* and 8q24 locus and TGCT risk in the case–parent and the combined case–parent/case–control study (includes all triads and dyads from the case–parent study).

<table>
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<th>Gene (CHR)</th>
<th>SNP</th>
<th>Genomic position</th>
<th>A1</th>
<th>A2</th>
<th>MAF</th>
<th>Genotype</th>
<th>Case–parent OR (95% CI)</th>
<th>P</th>
<th>Combined OR (95% CI)</th>
<th>P</th>
<th>Pconf&lt;sup&gt;b&lt;/sup&gt;</th>
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<tbody>
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<td><strong>AKT1 (14)</strong></td>
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<td>104308725</td>
<td>C</td>
<td>G</td>
<td>0.34</td>
<td>0.91 (0.80–1.03)</td>
<td>0.128</td>
<td>0.93 (0.86–1.01)</td>
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<tr>
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<td>rs2498794</td>
<td>104316296</td>
<td>A</td>
<td>G</td>
<td>0.48</td>
<td>1.03 (0.91–1.15)</td>
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<td>0.92 (0.73–1.16)</td>
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<td>0.96 (0.83–1.11)</td>
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<td>G</td>
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<td>1.02 (0.83–1.24)</td>
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<td>1.14 (0.89–1.45)</td>
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<td>0.95 (0.77–1.16)</td>
<td>0.585</td>
<td>1.07 (0.95–1.22)</td>
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<td>rs6983561</td>
<td>128176062</td>
<td>A</td>
<td>C</td>
<td>0.37</td>
<td>0.94 (0.69–1.28)</td>
<td>0.676</td>
<td>0.98 (0.80–1.19)</td>
<td>0.815</td>
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<td>rs13571797</td>
<td>128194098</td>
<td>A</td>
<td>C</td>
<td>0.04</td>
<td>1.02 (0.75–1.39)</td>
<td>0.906</td>
<td>0.94 (0.78–1.15)</td>
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<tr>
<td></td>
<td>rs6983267</td>
<td>128482487</td>
<td>G</td>
<td>T</td>
<td>0.47</td>
<td>0.97 (0.86–1.09)</td>
<td>0.556</td>
<td>0.98 (0.91–1.05)</td>
<td>0.548</td>
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<td></td>
<td>rs7000448</td>
<td>128510352</td>
<td>C</td>
<td>T</td>
<td>0.39</td>
<td>1.08 (0.96–1.22)</td>
<td>0.190</td>
<td>0.97 (0.90–1.05)</td>
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<td>rs10541255</td>
<td>128554220</td>
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<td>C</td>
<td>0.12</td>
<td>1.08 (0.90–1.30)</td>
<td>0.411</td>
<td>0.99 (0.88–1.11)</td>
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<td>rs4242382</td>
<td>128586755</td>
<td>A</td>
<td>G</td>
<td>0.11</td>
<td>1.11 (0.92–1.34)</td>
<td>0.277</td>
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<td>A</td>
<td>C</td>
<td>0.15</td>
<td>0.92 (0.77–1.08)</td>
<td>0.301</td>
<td>0.94 (0.85–1.05)</td>
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<td>rs7837688</td>
<td>128605842</td>
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<td>T</td>
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<td>1.06 (0.94–1.19)</td>
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</table>

Genomic positions refer to the UCSC hg18 version of the reference human genome. CHR, chromosome; SNP, single nucleotide polymorphism; A1, reference allele (allelic odds ratio = 1); MAF, minor allele frequency in founders; OR, odds ratio; CI, confidence interval. Bold denotes P < 0.05.

<sup>a</sup>Significant associations only.

<sup>b</sup>Bonferroni correction (P multiplied by the number of total SNP analyses, n = 23).
of the 8q24 locus, this notion is appealing; although the results are not conclusive. In 2008, Cook et al. investigated the association between TGCT and 15 SNPs in this region with no significant findings. However, since neither this study nor the present study investigated all SNPs in this region, we cannot exclude the possibility of an association between the 8q24 locus and TGCT.

For many years, the incidence rate of TGCT in Sweden has for unknown reasons been only about half of that in Norway. The present study was not able to demonstrate any interaction in the associations between the investigated SNPs and the risk of TGCT related to country, implying that the genetic susceptibility to TGCT concerning our investigated SNPs does not seem to be heterogeneous between the countries. Hence, our results thus do not shed any light on the difference in the incidence rate between these two neighboring countries. The same applies for the previously mentioned study on sex hormone pathway genes in the same study population (Kristiansen et al., 2012).

Our study is strengthened by the population-based design and large sample size, which give high power to detect risk alleles. In this study we performed the analyses in two stages, where the first stage only considered case–parent triads and dyads. This analysis is robust to bias from population stratification, since the non-transmitted parental alleles act as ‘controls’ within each family unit, and the analysis is thus implicitly stratified by country. Adding the unrelated cases and population controls to the second stage analysis increases the power to detect SNP-disease associations, but is exposed to potential population stratification issues due to the control sample consisting of Swedes only. Since the effect estimate (OR, 1.16) for the most strongly associated marker rs11202586 barely changed from the population-robust Stage 1 to the less robust but higher powered Stage 2, we believe this association, though minute in effect, to be a true finding. Finally, in tests for effect modification of alleles by country, we detected no significant effect modifications. Although the absence of evidence should not be taken as evidence for absence, this is in agreement with the previous paragraph, and with our assumption that the Swedish and Norwegian populations are genetically similar.

Regarding the 8q24 locus and PTEN, the SNPs were selected based on results from previously published reports. Regarding these non-tagged genes, we have not captured all common variation, and thus, some unknown risk alleles cannot be excluded.

In conclusion, we report an association between a genetic polymorphism in the tumor-suppressor gene PTEN and risk of TGCT. Exploring the functional role of the SNPs associated with TGCT will further clarify the biological mechanisms involved. Further, our results show that common variants in AKT1 probably do not substantially influence risk of TGCT, although we might have missed an association in the combined case–parent/case–control study because three of the htSNPs were not genotyped in the control group. Regarding the 8q24 locus more studies are needed to elucidate any possible association with TGCT risk.

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**Authors’ roles**


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**Conflict of interest**

None declared.

**References**


