A Multicenter Study of Cancer Incidence in CHEK2 1100delC Mutation Carriers

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Abstract

The CHEK2 1100delC protein-truncating mutation has a carrier frequency of ~0.7% in Northern and Western European populations and confers an ~2-fold increased risk of breast cancer. It has also been suggested to increase risks of colorectal and prostate cancer, but its involvement with these or other types of cancer has not been confirmed. The incidence of cancer other than breast cancer in 11,116 individuals from 734 non-BRCA1/2 breast cancer families from the United Kingdom, Germany, Netherlands, and the United States was compared with that predicted by population rates. Relative risks (RR) to carriers and noncarriers were estimated by maximum likelihood, via the expectation-maximization algorithm to allow for unknown genotypes. Sixty-seven families contained at least one tested CHEK2 1100delC mutation carrier. There was evidence of underreporting of cancers in male relatives (422 cancers observed, 860 expected) but not in females (322 observed, 335 expected); hence, we focused on cancer risks in female carriers. The risk of cancers other than breast cancer in female carriers was not significantly elevated, although a modest increase in risk could not be excluded (RR, 1.18; 95% confidence interval, 0.64-2.17). The carrier risk was not significantly raised for any individual cancer site, including colorectal cancer (RR, 1.60; 95% confidence interval, 0.54-4.71). However, between ages 20 to 50 years, the risks of colorectal and lung cancer were both higher in female carriers than noncarriers (P = 0.041 and 0.0001, respectively). There was no evidence of a higher prostate cancer risk in carriers than noncarriers (P = 0.26), although under-reporting of male cancers limited our power to detect such a difference. Our results suggest that the risk of cancer associated with CHEK2 1100delC mutations is restricted to breast cancer, although we cannot rule out a small increase in overall cancer risk.

Introduction

CHEK2 is a G2 checkpoint kinase that plays a critical role in DNA repair. In mammalian cells, it is activated in response to ionizing radiation through phosphorylation by ATM, and its activation phosphorylates other key cell cycle proteins, including BRCA1 and p53 (reviewed in ref. 1). The role of CHEK2 in breast cancer susceptibility was first suggested by the identification of a truncating mutation in exon 10 that abolishes CHEK2 kinase activity (1100delC) in three members of a family with Li-Fraumeni syndrome (2). Although this mutation is no longer thought to be involved in the Li-Fraumeni syndrome (3), it has since been shown to have a population carrier frequency of ~0.7% in Northern and Western European populations (with substantial heterogeneity) and to confer an ~2-fold increased risk of breast cancer to female heterozygous carriers (4-6). The highest frequencies have been reported in Finland and the Netherlands (1.3% and 0.99%, respectively), whereas only five carriers were seen among 1,665 healthy New Yorkers (4, 7). Reports of an association between CHEK2 1100delC mutations and prostate or colorectal cancer have not been confirmed, although there is some evidence that other variants within CHEK2 may increase risk (8-12). In this study, we estimate the risks of all cancers other than breast cancer in carriers of the CHEK2 1100delC mutation using cancer incidence data from a cohort of 11,116 individuals from 734 breast cancer families, in which at least one person had been genotyped for this mutation.

Materials and Methods

Subjects. Seven hundred thirty-four families were ascertained through centers in the United Kingdom (236 families), the Netherlands (233 families), Germany (17 families), and the United States (248 families) based on breast cancer occurrence via clinical genetics clinics. Five hundred eighty-seven (80%) families had three or more members with breast cancer and...
Among the cohort of 11,116 individuals, 442 cancers were reported in males [860 expected; standardized incidence ratio (SIR), 0.51; 95% confidence interval (CI), 0.47-0.56] and 322 in females (335 expected; standardized incidence ratio, 0.96; 95% CI, 0.86-1.07), excluding breast, ovarian, bone, liver, and nonmelanoma skin cancers. In view of the apparent under-reporting of cancer among male family members, this report will focus on cancer risk in females, except where otherwise specified.

For the female ‘all cancers’, 4 were in known carriers (3.4 expected), 43 in noncarriers (30.9 expected), and 275 in untested women (301.1 expected). The estimated RR was 1.22 (95% CI, 0.66-2.26) in carriers and 0.95 (95% CI, 0.85-1.06) in noncarriers. Because the estimated risk in female noncarriers was close to that expected in the general population, the RRs presented in Table 1 are those estimated assuming the noncarrier RR is fixed at one (overall carrier RR, 1.18; 95% CI, 0.64-2.17). Although there was no
Table 1. Observed and expected numbers of cancers in female members of the cohort, with estimated carrier RR

<table>
<thead>
<tr>
<th>Cancer</th>
<th>Observed cancers</th>
<th>Expected cancers</th>
<th>Age 0-80 y Carrier RR*</th>
<th>Age 0-80 y Noncarrier RR</th>
<th>Age 20-50 y Carrier RR</th>
<th>Age 20-50 y Noncarrier RR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colorectal (153-154)</td>
<td>73</td>
<td>71.9</td>
<td>1.60 (0.54-4.71)</td>
<td>8.54 (2.12-34.4)</td>
<td>1.72 (0.89-3.31)</td>
<td></td>
</tr>
<tr>
<td>Lung (162)</td>
<td>34</td>
<td>43.8</td>
<td>1.62 (0.44-5.91)</td>
<td>20.8 (3.53-123)</td>
<td>0.46 (0.13-1.57)</td>
<td></td>
</tr>
<tr>
<td>Melanoma (172)</td>
<td>13</td>
<td>14.2</td>
<td>0.77 (0.016-38.0)</td>
<td>3.87 (0.066-228)</td>
<td>0.53 (0.17-1.64)</td>
<td></td>
</tr>
<tr>
<td>Uterus (180)</td>
<td>38</td>
<td>40.0</td>
<td>1.39 (0.24-8.09)</td>
<td>2.81 (0.47-16.9)</td>
<td>0.61 (0.37-1.00)</td>
<td></td>
</tr>
<tr>
<td>Kidney (189)</td>
<td>7</td>
<td>9.70</td>
<td>3.77 (0.28-51.6)</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Brain (191)</td>
<td>12</td>
<td>8.60</td>
<td>7.30 (0.70-75.8)</td>
<td>7.73 (0.14-439)</td>
<td>2.89 (1.29-6.50)</td>
<td></td>
</tr>
<tr>
<td>Thyroid (193)</td>
<td>8</td>
<td>14.71</td>
<td>3.83 (0.075-196)</td>
<td>9.55 (0.17-538)</td>
<td>1.95 (0.87-4.37)</td>
<td></td>
</tr>
<tr>
<td>Lymphoid and leukemia (200-209)</td>
<td>32</td>
<td>33.1</td>
<td>1.16 (0.14-9.77)</td>
<td>0</td>
<td>1.40 (0.50-3.97)</td>
<td></td>
</tr>
<tr>
<td>All excluding breast, ovarian, liver, bone, and nonmelanoma skin cancer</td>
<td>322</td>
<td>335</td>
<td>1.18 (0.64-2.17)</td>
<td>4.91 (2.11-11.4)</td>
<td>1.54 (1.22-1.94)</td>
<td></td>
</tr>
</tbody>
</table>

NOTE: Cancers shown are those for which the carrier RR estimate did not converge to zero.
*Estimated with noncarrier RR fixed at one.

Discussion

This cohort study has found no evidence for an overall increase in the risk of cancer other than breast cancer in female CHEK2 1100delC mutation carriers, although the 95% CI does not exclude a possible 2-fold increase in risk. Our findings support those of recent case-control studies that have also found no significant association between the CHEK2 1100delC mutation and non-breast cancers (8, 30-33). There was some evidence for an increase in the risk of cancer before the age of 50 years, although the only cancer sites for which this was statistically significant were lung and colorectal cancer. Eight of the 11 female cases and 6 of the 10 male cases of colorectal cancer before the age of 50 years came from the Netherlands center, including three cases from one family. This family has been published previously in the context of a possible association between CHEK2 1100delC and a combined hereditary breast and colorectal cancer phenotype, along with several of the other families analyzed here from the Netherlands (11). Reestimating the RR without the Dutch families showed that there was no other evidence of an association between colorectal cancer and CHEK2 1100delC (noncarrier RR, 0.92; 95% CI, 0.14-6.16; carrier RR tends to zero). Other studies have also failed to find an association between CHEK2 1100delC and colorectal cancer (8, 10, 34) or multiple colorectal adenomas (35).

One strength of this study was that the large majority of the families were included irrespective of their CHEK2 1100delC carrier status (the remaining 28 carrier families were ascertained in an identical fashion and added to improve the power). The simultaneous estimation of RRs for carriers and noncarriers in these families relative to the general population allowed us to distinguish between effects attributable to the CHEK2 1100delC mutation and those due to other factors present in multiple-case breast cancer families (whether genetic or environmental) or artifacts of the methods of family ascertainment. For example, the overall risk of cancer in 20- to 50-year-old noncarriers was modestly, but statistically significantly, increased over that expected in the general population, but the magnitude of the increase was a third of that estimated for carriers (P = 0.008).
The apparent excess of childhood cancers is of interest, given that CHEK2 1100delC was first detected in a Li-Fraumeni syndrome family that included a childhood sarcoma (2). However, the number of cancers is small and the carrier RR was not significant when compared with the estimated noncarrier risk \( P = 0.42 \). It is also possible that, influenced by that report, a few of the families in this study may have been tested for CHEK2 1100delC specifically because of the presence of a childhood cancer in a relative of a breast cancer patient; hence, these results should be viewed with caution. For example, the three childhood connective tissue cancers were all in mutation-negative families from the same center, each of which had only one breast cancer case (19 of the 734 families had just one breast cancer case). When the analysis was restricted to the 586 families with three or more breast cancer patients, the noncarrier risk under 20 years old was no longer significantly increased (noncarrier RR, 1.33; 95% CI, 0.69-2.59), but the point estimate of the carrier RR was higher (carrier RR, 9.97; 95% CI, 0.55-180; \( P = 0.16 \) for the difference between carrier and noncarrier RRs).

A limitation of this study was the reliance on family members’ reports of cancer in their relatives. This should not have introduced differential bias because the pedigrees were collected before mutation testing, although inaccuracies in the reporting of some cancers could lead to underestimates of the true effect. Noncarrier RR estimates for women suggest that underreporting was not a major problem for female relatives. However, the extent of the underreporting for male relatives was such that it was not possible to obtain meaningful estimates of the risks to male carriers. Families were primarily collected for breast cancer research projects, and family members or research staff involved in taking the family histories may have not given equal attention to male and female relatives. We were therefore unable to confirm or refute reports of a possible association between CHEK2 1100delC and prostate cancer (8, 9, 12, 36).

Although the limitations of the available data prevent us from assessing cancer risks in male CHEK2 1100delC mutation carriers, we conclude that the excess risk to female carriers is largely confined to breast cancer, although modest risks of other cancers cannot be excluded.

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References
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