Risk of Colorectal Cancer for Carriers of Mutations in MUTYH, with and without a Family History of Cancer

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Running Title
Cancer risks for MUTYH mutation carriers

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**FUNDING**
This work was supported by the National Cancer Institute, National Institutes of Health under RFA #CA-95-011 and through cooperative agreements with members of the Colon Cancer Family Registry and Principal Investigators. Collaborating centers include Australasian Colorectal Cancer Family Registry (U01 CA097735), Familial Colorectal Neoplasia Collaborative Group (U01 CA074799) [USC], Mayo Clinic Cooperative Family Registry for Colon Cancer Studies (U01 CA074800), Ontario Registry for Studies of Familial Colorectal Cancer (U01 CA074783), Seattle Colorectal Cancer Family Registry (U01 CA074794), and University of Hawaii Colorectal Cancer Family Registry (U01 CA074806). This work was also supported by a grant from the National Cancer Institute, USA (R01CA170122) and a Centre for Research Excellence grant from the National Health and Medical Research Council (NHMRC), Australia (APP1042021). AKW is supported by the Picchi Brothers Foundation Cancer Council Victoria Cancer Research Scholarship, Australia. MAJ is an NHMRC Senior Research Fellow. JLH is a NHMRC Senior Principal Research Fellow. CR is a Jass Pathology Fellow.

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**DISCLOSURE**
The authors have no conflict of interest to declare with respect to this manuscript.

**ACKNOWLEDGEMENTS**
The authors thank all study participants of the Colon Cancer Family Registry and staff for their contributions to this project.
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Mark A. Jenkins: study concept and design; acquisition of data; interpretation of data; critical review of the manuscript for important intellectual content; approval of the final version of the manuscript
ABSTRACT

We studied 2332 individuals with monoallelic mutations in MUTYH among 9504 relatives of 264 colorectal cancer (CRC) cases with a MUTYH mutation. We estimated CRC risks, through 70 y of age, of 7.2% for male carriers of monoallelic mutations (95% confidence interval [CI], 4.6%–11.3%) and 5.6% for female carriers of monoallelic mutations (95% CI, 3.6%–8.8%), irrespective of family history. For monoallelic MUTYH mutation carriers with a first-degree relative with CRC, diagnosed by 50 y of age who does not have the MUTYH mutation, risks of CRC were 12.5% for men and (95% CI, 8.6%–17.7%) and 10% for women (95% CI, 6.7%–14.4%). Risks of CRC for carriers of monoallelic mutations in MUTYH with a first-degree relative with CRC are sufficiently high to warrant more intensive screening than for the general population.

KEYWORDS: colon cancer, genetics, base excision repair gene, DNA damage response
MUTYH is a base excision repair gene that detects and protects against oxidative DNA damage. Individuals with germline mutations in both alleles (biallelic mutation carriers), whether they are homozygotes or compound heterozygotes, develop MUTYH-associated polyposis, an autosomal recessive disorder with substantially increased risk of CRC. Individuals with germline mutations in one allele (monoallelic mutation carriers) have a small increased risk of CRC. Due to the rarity of these mutations, previous studies have had limited ability to provide precise estimates of age- and sex-specific CRC risks for MUTYH mutation carriers. Further, the variability in CRC risk between carriers has not been quantified. Modelling of this variability can indicate a potential role for modifiers of risk.

RESULTS

We identified 9504 relatives (4613 females) from the families of the 264 (236 population-based and 28 clinic-based) probands with a monoallelic or biallelic MUTYH mutation from the Colon Cancer Family Registry; 138 (52%) from USA, 81 (31%) from Canada, and 45 (17%) from Australia and New Zealand. In the relatives, we observed 261 CRCs (114 females) whose ages at diagnosis had a median of 65 (range 26-98) years. MUTYH mutation status was known for 340 relatives (13 biallelic mutation carriers, 142 monoallelic mutation carriers, and 185 non-carriers). We estimated an additional 43 biallelic and 2190 monoallelic mutation carriers among non-genotyped relatives, giving a total estimated number of 56 biallelic and 2332 monoallelic mutation-carrying relatives in our sample.

Our methods allowed for CRC risk estimation in mutation families to be due to the MUTYH mutation as well as polygenic factors (combination of a large number of CRC-associated genetic susceptibility loci). We estimated CRC risks, through 70y of
age, for male and female to be: 75.4% (95%CI, 41.2%–96.6%) and 71.7% (95%CI, 44.5%–92.1%), respectively, for biallelic mutation carriers, and 7.2% (95%CI, 4.6%–11.3%) and 5.6% (95%CI, 3.6%–8.8%), respectively, for monoallelic mutation carriers (Figure 1). The estimated CRC risks, through 70y of age, for monoallelic mutation carriers with a first-degree relative with CRC were similar whether the relative was untested or a non-carrier or a monoallelic mutation carrier: approximately 12% (95%CI, 9%–18%) and 10% (95%CI, 7%–14%) respectively for males and females in comparison with males and females from the general population (2.9% and 2.1% respectively). However, if their affected first-degree relative was a biallelic mutation carrier then risks of CRC, through 70y of age, for monoallelic mutation carriers was estimated to be 10.4% (95%CI, 7.0%–15.0%) and 8.2% (95%CI, 5.4%–12.0%) respectively for males and females (Table 1). In addition, we estimated CRC risks for six other scenarios (Supplementary Figure 1). The highest risk of CRC for a monoallelic mutation carrier corresponded to having two affected first-degree relatives: one is a biallelic mutation carrier and one is a non-carrier (Supplementary Figure 1C).

We found no evidence for a difference in hazard ratios of CRC for biallelic mutation carriers between males and females (108 (95%CI, 25.9–454) vs 129 (95%CI, 43.7–380); p=0.85), nor for monoallelic mutation carriers between males and females (2.46 (95%CI, 1.54–3.93) vs 2.67 (95%CI, 1.67–4.26); p=0.81). Hazard ratio of CRC for Y179C monoallelic carriers was higher than for G396D monoallelic carriers (4.81 (95%CI, 3.00–7.71) vs 2.42 (95%CI, 1.48–3.98); p=0.05), but there was no difference between biallelic carriers of Y179C and G396D (p=0.84) (Supplementary Table 1).
The standard deviation of the polygenic component was estimated to be 1.11 (0.74–1.49, p<0.001); see the Materials and Methods for a general formula relating this standard deviation to the hazard ratio. At ages less than 50y this formula reduces to Pharoah’s formula for early-onset disease\textsuperscript{7} and says that monoallelic \textit{MUTYH} mutation carriers with an affected first-degree relative have CRC incidences approximately 4.58 (for males) or 4.97 (for females) times the population incidences. However, Supplementary Figure 2 gives precise hazard ratios for all ages and shows that by age 70y, Pharoah’s formula over-estimates relative risks by roughly 30%.

\textbf{DISCUSSION}

Our finding of almost complete penetrance for biallelic \textit{MUTYH} mutation carriers is consistent with previous studies.\textsuperscript{8-10} There is some evidence that biallelic mutation carriers move rapidly along a mutator phenotype progression to cancer.\textsuperscript{11} These findings support the recommendation that biallelic mutation carriers should consider prophylactic total colectomy with ileorectal anastomosis depending on the individual, age of presentation and number and size of polyps present.\textsuperscript{12}

We estimated monoallelic mutation carriers had on average, an approximately 2.5-fold increased risk of CRC compared with the general population, consistent with one previous study.\textsuperscript{13} This level of increased risk for monoallelic mutation carriers is similar to that for people with a first-degree relative with CRC, who are recommended 5-yearly colonoscopy starting 10y younger than the youngest case in the family and before age 50y.\textsuperscript{13} However, monoallelic mutation carriers who have an affected first-degree relative were at approximately 5-fold increased risk. For these carriers, colonoscopy beginning at age 40y, with follow-up at intervals
dependent on the presence or absence of polyps but no less often than every 5 years, may be reasonable.

We observed strong evidence that CRC risks for carriers are highly heterogeneous. The observed heterogeneity in risk could also be caused by environmental factors shared between family members or by differences in risk between mutations. To our knowledge, thus far the only study investigating modifiers of CRC risks for MUTYH mutation carriers was on the relationship with hormone replacement therapy, which reported no evidence of interaction between hormone replacement therapy and MUTYH mutations.3

In this study of 12 variants of MUTYH mutations, 93% of the MUTYH mutations were Y179C and G396D (Supplementary Table 2); consistent with a previous study of Caucasians.14 We found CRC risk was higher for monoallelic carriers of Y179C than for G396D; consistent with previous studies.3,15 However, given our approach of genotyping for 12 mutations by MS and WAVE followed by confirmatory Sanger sequencing of MUTYH in carriers (Materials and Methods), there is the possibility that we missed other pathogenic mutations in MUTYH that were not one of the 12 mutations genotyped. Although we identified additional variants from Sanger sequencing, their pathogenicity was considered inconclusive (unclassified variants) and therefore not included in this analysis. Additional MUTYH mutations may reside in different ethnic groups however this cohort was predominantly Caucasian.

We used sophisticated statistical techniques to adjust for ascertainment, to account for residual familial aggregation of disease and therefore avoid bias, and to
use data for all family members, whether genotyped or not, and therefore maximized statistical power and avoided survival bias.

In conclusion, using the largest international study to date we have produced unbiased estimates of CRC risks for \textit{MUTYH} mutation carriers which are the most precise and reliable currently available. In addition to the confirmed very high risk of CRC to biallelic \textit{MUTYH} mutation carriers, CRC risk for monoallelic mutation carriers depends on family history and can be sufficiently high to warrant consideration of more intensive CRC screening than for the general population.

Figure 1 Cumulative risk of colorectal cancer for (A) male and (B) female \textit{MUTYH} mutation carriers. Note that the risks for a monoallelic carrier with an affected first-degree relative (FDR) who is either untested, a noncarrier or a monoallelic carrier are virtually identical (see Table 1) so the unbroken, darker grey lines cannot be distinguished in the figure.
REFERENCES


Author names in bold designate shared co-first authors.
Table 1 Cumulative risks (95% confidence intervals) of colorectal cancer for biallelic and monoallelic *MUTYH* mutation carriers

<table>
<thead>
<tr>
<th>Age (years)</th>
<th>General population</th>
<th>Biallelic mutation carriers irrespective of family history</th>
<th>Monoallelic mutation carriers</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>with untested FDR diagnosed at 50 years</td>
<td>with non-carrier FDR diagnosed at 50 years</td>
</tr>
<tr>
<td>Male</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>30</td>
<td>0.01</td>
<td>1.8 (0.4-6.8)</td>
<td>0 (0-0.1)</td>
</tr>
<tr>
<td>40</td>
<td>0.07</td>
<td>8.1 (2.1-25.2)</td>
<td>0.2 (0.1-0.3)</td>
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<tr>
<td>50</td>
<td>0.3</td>
<td>24.8 (7.7-57.1)</td>
<td>0.8 (0.5-1.3)</td>
</tr>
<tr>
<td>60</td>
<td>1.1</td>
<td>52.3 (21.8-85.4)</td>
<td>2.8 (1.8-4.5)</td>
</tr>
<tr>
<td>70</td>
<td>2.9</td>
<td>75.4 (41.2-96.6)</td>
<td>7.2 (4.6-11.3)</td>
</tr>
<tr>
<td>80</td>
<td>6.2</td>
<td>88.2 (58.4-99.3)</td>
<td>13.6 (8.8-21.1)</td>
</tr>
<tr>
<td>Female</td>
<td></td>
<td></td>
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<tr>
<td>30</td>
<td>0.01</td>
<td>2 (0.7-5.5)</td>
<td>0 (0-0.1)</td>
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<tr>
<td>40</td>
<td>0.06</td>
<td>8.7 (3.1-20.7)</td>
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<td>71.7 (44.5-92.1)</td>
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<tr>
<td>80</td>
<td>4.4</td>
<td>85.7 (61.8-97.8)</td>
<td>10.9 (7-16.8)</td>
</tr>
</tbody>
</table>

FDR, first-degree relative; CRC, colorectal cancer.
MATERIALS AND METHODS

Study Sample

Subjects were from families for which at least one family member had been identified as carrying a germline monoallelic or biallelic mutation in MUTYH. These families were recruited by the Colon Cancer Family Registry via probands between 1997 and 2007. Population-based probands were recently diagnosed colorectal cancer cases from state or regional population cancer registries in the USA (Washington, California, Arizona, Minnesota, Colorado, New Hampshire, North Carolina, and Hawaii), Australia (Victoria) and Canada (Ontario). Clinic-based probands were enrolled from multiple-case families referred to family cancer clinics in the USA (Mayo Clinic, Rochester, Minnesota, and Cleveland Clinic, Cleveland, Ohio), Australia (Melbourne, Adelaide, Perth, Brisbane, Sydney) and New Zealand (Auckland). No cases were ascertained because of having polyps alone. All cases with familial adenomatous polyposis were excluded.

Probands were asked for permission to contact their relatives to seek their enrollment in the Cancer Family Registry. For population-based families, first-degree relatives of probands were recruited at all centers and recruitment was extended to more distant relatives at some centres. For clinic-based families, recruitment was based on availability but attempts were made to recruit up to second-degree relatives of affected individuals (detail in Newcomb et al.¹). Written informed consent was obtained from all study participants, and the study protocol was approved by the institutional research ethics review board at each centre.
Data Collection

Standardized questionnaires were used to collect information on demographics, personal characteristics, personal and family history of cancer, cancer screening history, history of polyps, polypectomy and other surgeries were obtained by questionnaires from all probands and participating relatives. Reported cancer diagnoses and age at diagnosis were confirmed, where possible using pathology reports, medical records, cancer registry reports and/or death certificates. Standardized protocols were used to collect and prepare blood samples and tumour tissues for genetic testing and laboratory analyses.

MUTYH Mutation Testing

We tested all probands for mutations in the MUTYH gene, and also relatives of those with mutations who provided a DNA sample. As described in detail by Cleary et al., \(^2\) genomic DNA extracted from each participant was sent to a central testing facility (Analytic Genetics Technology Centre, Toronto, Canada). DNA was screened for 12 previously identified MUTYH mutations: Y179C, G396D, Y104X, R274Q, E480X, Q391X, c.1145delC, c.933+3A>C, c.1437_1439delGGA, R241W, c.1228_1229insGG, c.1187-2A→G using the MassArray MALDI-TOF Mass Spectrometry (MS) system (Sequenom, San Diego, CA). Screening for R241W, c.1228_1229insGG and c.1187-2A→G was discontinued when testing of 6000 samples failed to identify any carriers of these three variants. All samples with MS mobility shifts underwent screening of the entire MUTYH coding region, promoter, and splice sites regions by denaturing high-performance liquid chromatography (Transgenomic Wave 3500HT System; Transgenomic, Omaha, NE), to confirm the mutation and to identify additional mutations. All MS-detected variants and WAVE
mobility shifts were submitted for sequencing for mutation confirmation (ABI PRISM 3130XL Genetic Analyser).

From the Colon Cancer Family Registry, we identified 273 probands who were known to carry germline mutations in MUTYH. We excluded 9 probands who were also known to carry pathogenic mismatch repair germline mutations in a mismatch repair gene (Lynch syndrome). Of the remaining 264 probands, 41 were biallelic mutation carriers and 223 were monoallelic mutation carriers. The variants of MUTYH mutations of the probands are shown in Supplementary Table 3. The average age at diagnosis of colorectal cancer was 47.7 (standard deviation [SD] 10.0) years in probands with biallelic mutations and 52.0 (SD 11.9) years in probands with monoallelic mutations.

**Statistical Analysis**

The median, range, mean and standard deviation of the age at colorectal cancer diagnosis were calculated using Stata 12.1. Hazard ratios (HRs), i.e. the age- and sex-specific cancer incidence for carriers divided by that for the general population, were estimated using modified segregation analysis. Models were fit by maximum likelihood with the statistical package MENDEL version 3.2. Estimates were appropriately adjusted for the clinic- and population-based ascertainment of families using a combination of retrospective likelihood and ascertainment-corrected joint likelihood, in which each pedigree’s data was conditioned on the proband’s genotype, cancer status and age of onset (for population-based families) or on the proband’s genotype and the affected statuses and ages of onset of all family members at the time the proband was found to be a MUTYH mutation carrier (for clinic-based families).
To model any residual familial aggregation of colorectal cancer risk, a mixed model that incorporated an unmeasured polygene in addition to the major gene\(^8,\ 12\), was used in the modified segregation analyses (see detail methods in a previous report \(^13\)). This mixed model was used since major gene models (which attribute all familial aggregation to the major gene being studied alone) are often biased\(^10\). The polygenic part of this mixed model, which models the cumulative effect of a large number of biallelic genes that individually have small effects on cancer susceptibility, was implemented as a hypergeometric polygenic model with four loci\(^8,\ 12\). Under this model, the number of disease alleles for each person is approximately normally distributed and is correlated within families with correlation coefficients equal to the kinship coefficients\(^14\).

Estimated cumulative risks (penetrance) of cancers to age \(t\) years for carriers living in the USA were calculated by from the relevant population incidences \(\lambda_0(\tau)\) at age \(\tau\) years multiplied and the estimated HR \(\theta\) with the formula:

\[
1 - \exp\left(-\int_0^t \theta \lambda_0(\tau) \, d\tau\right)
\]

We estimated the total number of carriers in the study using the same method in previous studies\(^15,\ 16\): by summing \(MUTYH\) carrier probabilities for all individuals, as calculated from Mendel's laws of inheritance, the known genetic relationship of each individual to his or her genotyped relatives (but not affected status) and a population allele frequency of 0.0085.\(^15\) These calculations were performed using R 2.15.0\(^17\) and a modified version of Mendel 3.2.\(^7\)

Observation time for each subject started at birth and ended at first diagnosis of colorectal cancer or other cancer, first polypectomy, last follow-up or death,
whichever occurred first. Where age at diagnosis of cancer was not reported (n=43; 16% of all cancer cases), we assumed the age of diagnosis to be one year prior to the last known age or, if last known age was not available, the median age at diagnosis of colorectal cancer for the general population obtained from SEER Cancer Statistics Review (1975–2007)\textsuperscript{18}.

**Effect of family history on disease risks for major gene mutation carriers**

In the following section, we describe statistical methods used to derive the age-dependent cumulative risks and HRs for a carrier of a major gene mutation who has an affected first-degree relative, under the genetic mixed model used in this paper. The cumulative risks and HRs are given in equations (2) and (3), respectively, and equation (4) gives approximate HRs for rare diseases or for early-onset forms of common diseases.

Consider two individuals who are indexed by \(i = 1\) and \(2\) and let \(T_i, G_i\) and \(H_i\) be random variables representing (respectively) the age at disease onset, major gene genotype and polygenotype of individual \(i\). We assume the two individuals are first-degree relatives, so that \((H_1, H_2)\) is a bivariate, normally-distributed random variable, with the correlation coefficient of \(H_1\) and \(H_2\) being \(\frac{1}{2}\) and each \(H_i\) having mean \(\mu\) and variance \(\sigma^2\). We assume that mutations in the major gene are rare, so that we can ignore biallelic carriers and we can assume \(P(G_2 = 1|G_1 = 1) = \frac{1}{2}\) where \(G_i = 0\) if \(i\) is a non-carrier and \(G_i = 1\) if \(i\) is a carrier, though the derivation below can easily be changed to incorporate common alleles (and general modes of inheritance). We also assume \(T_1\) and \(T_2\) are conditionally independent given all
genotypes and polygenotypes, that \( T_1 \) only depends on \( G_1 \) and \( H_1 \) (and similarly for \( T_2 \)) and that \( G_1 \) and \( G_2 \) are independent of \( H_1 \) and \( H_2 \).

Let \( \lambda_0(t) \) be the average incidence of disease at age \( t \) years for non-carriers (the average being over the polygene) and recall that the hazard function \( \lambda(x) \) of any continuous random variable \( X \) is defined to be

\[
\lambda(x) = -\frac{d}{dx} \log(1 - P(X \leq x)).
\]  

Then, as in the rest of this paper, we assume that the hazard of \( T_i \) (i.e. the incidence of disease for individual \( i \)) at age \( t_i \) years, conditioned on \( G_i = g_i \) and \( H_i = h_i \), is equal to \( \theta_{g_i} r_i \lambda_0(t_i) \), where \( \theta_{g_i} \) is the HR associated with major gene genotype \( g_i \) and \( r_i = e^{h_i} \) is the HR associated with polygenotype \( h_i \). Using the shorthand \( t_i, g_i \) and \( h_i \) for the events \( T_i \leq t_i, G_i = g_i \) and \( H_i = h_i \) (respectively) in all probability statements below, it therefore follows from (1) that

\[
P(t_i | g_i, h_i) = 1 - s_i^{\theta_{g_i} r_i},
\]

where \( s_i = \exp(-\int_0^{t_i} \lambda_0(\tau) \, d\tau) \) is the survival function to age \( t_i \) years for non-carriers. We assume the HR \( \theta_0 \) for non-carriers is 1, so in order that the average incidence of disease for non-carriers at age \( t \) years will equal \( \lambda_0(t) \), we need each log-normal random variable \( e^{h_i} \) to have an expected value of 1, i.e. we need \( \mu = -\sigma^2 / 2 \).

We are interested in the cumulative risk of disease for individual 1 by age \( t_1 \) given that he or she is a carrier and that his or her first-degree relative, individual 2, was affected by age \( t_2 \). In other words, we want to calculate \( P(t_1 | g_1, t_2) \) when \( g_1 = 1 \). But \( P(t_1 | g_1, t_2) = P(t_1, t_2 | g_1) / P(t_2 | g_1) \) and
\[
P(t_1, t_2 | g_1) = \sum_{g_2 h_1 h_2} P(t_1, t_2, g_2, h_1, h_2 | g_1) = \sum_{g_2 h_1 h_2} P(t_1, t_2 | g_1, g_2, h_1, h_2) P(g_2, h_1, h_2 | g_1)
\]
\[
= \sum_{g_2 h_1 h_2} P(t_1 | g_1, h_1) P(t_2 | g_2, h_2) P(g_2 | g_1) P(h_1, h_2)
\]
\[
= \frac{1}{2} \sum_{h_1 h_2} P(h_1, h_2) \left( (1 - s_1^{\theta_1})(1 - s_2^{R_2}) + (1 - s_1^{\theta_2})(1 - s_2^{\theta_R}) \right)
\]
\[
= \frac{1}{2} \mathbb{E}\left[ (1 - s_1^{\theta_1})(2 - s_2^{R_2} - s_2^{\theta_R}) \right],
\]

where \( R_i = e^{\theta_i} \), \( \mathbb{E} \) is the expectation functional, and \( \theta = \theta_1 \) is the HR for carriers of major gene mutations compared to non-carriers. Similarly, \( P(t_2 | g_1) = \frac{1}{2} \mathbb{E}[2 - s_2^{R_2} - s_2^{\theta_R}] \), so the cumulative risk is

\[
P(t_1 | g_1, t_2) = \frac{\mathbb{E}\left[ (1 - s_1^{\theta_1})(2 - s_2^{R_2} - s_2^{\theta_R}) \right]}{\mathbb{E}[2 - s_2^{R_2} - s_2^{\theta_R}]} = 1 - \frac{\mathbb{E}\left[ s_1^{\theta_1}(2 - s_2^{R_2} - s_2^{\theta_R}) \right]}{\mathbb{E}[2 - s_2^{R_2} - s_2^{\theta_R}]}.
\] (2)

By (1), the hazard \( \lambda(t_1 | g_1, t_2) \) of \( T_1 \) at \( t_1 \) given \( G_1 = 1 \) and \( T_2 \leq t_2 \) is therefore
\[ \lambda(t_1|g_1, t_2) = -\frac{d}{dt_1} \log(1 - P(t_1|g_1, t_2)) = -\frac{d}{dt_1} \log \mathbb{E}[s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})] \]

\[ = -\frac{\mathbb{E}\left[\frac{d}{dt_1} (e^{\theta R_1 \log s_1})(2 - s_2^{R_2} - s_2^{\theta R_2})\right]}{\mathbb{E}[s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})]} \]

\[ = \frac{\mathbb{E}\left[-\frac{d}{dt_1} (\log s_1) \theta R_1 s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})\right]}{\mathbb{E}[s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})]} \]

\[ = \theta \lambda_0(t_1) \frac{\mathbb{E}[R_1 s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})]}{\mathbb{E}[s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})]} \]

So the hazard ratio \( HR(t_1|g_1, t_2) \) for \( T_1 \) given \( G_1 = 1 \) and \( T_2 \leq t_2 \) (i.e. the relative risk of disease at age \( t_1 \) for carriers with an affected first-degree relative) is

\[ HR(t_1|g_1, t_2) = \theta \frac{\mathbb{E}[R_1 s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})]}{\mathbb{E}[s_1^{\theta R_1}(2 - s_2^{R_2} - s_2^{\theta R_2})]} \] (3)

It is unlikely that a simple formula can be given for these expectations because, for instance, \( \mathbb{E}[s_1^{\theta R_1}] = M_{R_1}(\theta \log s_1) \) where \( M_{R_1} \) is the moment-generating function of the log-normal random variable \( R_1 \), and no closed-form expression for \( M_{R_1} \) is known. However, the expectations can be readily evaluated by simulating draws of \((H_1, H_2)\) from the multivariate normal distribution described above.

We can also derive approximations to these expectations if we restrict our attention to rare diseases or to early-onset forms of common diseases. For in these cases, each \( s_i \approx 1 \) so \( |\log s_i| \ll 1 \) and we can evaluate approximations to the above expectations to a first order in \( \log s_i \). Using \( s_i^{\theta R_i} = e^{\theta R_i \log s_i} \approx 1 + \theta R_i \log s_i \) we have
\[ E[s_1^{θR_1}(2 - s_2^{R_2} - s_2^{θR_2})] \]
\[ \approx E[2(1 + θR_1 \log s_1) - (1 + θR_1 \log s_1 + R_2 \log s_2) - (1 + θR_1 \log s_1 + θR_2 \log s_2)] = -(θ + 1) \log s_2 \ E[R_2] \]
\[ = -(θ + 1) \log s_2. \]

Similarly, \( E[R_1s_1^{θR_1}(2 - s_2^{R_2} - s_2^{θR_2})] \approx -(θ + 1) \log s_2 \ E[R_1R_2]. \) But \( R_1R_2 = e^{H_1+H_2} \) is log-normally distributed and \( H_1 + H_2 \) has mean \( 2μ = -σ^2 \) and variance \( 3σ^2 \), so
\[ E[R_1R_2] = e^{σ^2/2}. \] Therefore
\[ HR(t_1 | s_1, t_2) \approx θe^{σ^2/2} \] 
(4)
to first order in \( \log s_1 \) and \( \log s_2 \). Setting \( θ \), the major gene HR, equal to 1 then gives the formula derived in the appendix of Pharoah et al.\(^{19} \)
REFERENCES


SUPPLEMENTARY MATERIALS

Supplementary 1: Materials and Methods

Supplementary 2: Supplementary Table 1

Hazard ratios (95% confidence intervals) of colorectal cancer for biallelic and monoallelic MUTYH mutation carriers

Supplementary 3: Supplementary Table 2

Variants of MUTYH mutations in probands

Supplementary 4: Supplementary Figure 1

Cumulative risk of colorectal cancer (CRC) to age 70y for counselees in six different scenerios. We assumed that CRC to be diagnosed at or before age 70y for affected persons, and last known age to be age 70y for unaffected persons.

Legend: +/-, biallelic MUTYH mutation carrier; +/-, monoallelic MUTYH mutation carrier; -/-, no MUTYH mutation; ?, ungenotyped for MUTYH; filled in symbol, CRC; <70, age of CRC diagnosis (years); arrow, counselee.

Supplementary 5: Supplementary Figure 2

Age-specific hazard ratios for monoallelic mutation carriers with affected first-degree relatives (FDRs) diagnosed by certain ages (grey lines) as well as the HRs given in equation 4 of the Materials and Methods and derived under an early-onset approximation (black lines).
Supplementary Table 1 Hazard ratios (95% confidence intervals) of colorectal cancer for biallelic and monoallelic \textit{MUTYH} mutation carriers

<table>
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<tr>
<th></th>
<th>Biallelic mutation carriers</th>
<th>Monoallelic mutation carriers</th>
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<tr>
<td><strong>Sex</strong></td>
<td></td>
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<tr>
<td>Male</td>
<td>108 (25.9–454)</td>
<td>2.46 (1.54–3.93)</td>
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<tr>
<td>Female</td>
<td>129 (43.7–380)</td>
<td>2.67 (1.67–4.26)</td>
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<tr>
<td><strong>Variants</strong></td>
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<tr>
<td>Y179C</td>
<td>115 (23.3–569)</td>
<td>4.81 (3.00–7.71)</td>
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<tr>
<td>G396D</td>
<td>94.2 (29.2–304)</td>
<td>2.42 (1.48–3.98)</td>
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Supplementary Table 2 Variants of \textit{MUTYH} mutations in probands

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<td>536A&gt;G, TAC&gt;TGC, Y179C</td>
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Author/s:
Win, AK; Dowty, JG; Cleary, SP; Kim, H; Buchanan, DD; Young, JP; Clendenning, M; Rosty, C; MacInnis, RJ; Giles, GG; Boussioutas, A; Macrae, FA; Parry, S; Goldblatt, J; Baron, JA; Burnett, T; Le Marchand, L; Newcomb, PA; Haile, RW; Hopper, JL; Cotterchio, M; Gallinger, S; Lindor, NM; Tucker, KM; Winship, IM; Jenkins, MA

Title:
Risk of Colorectal Cancer for Carriers of Mutations in MUTYH, With and Without a Family History of Cancer

Date:
2014-05-01

Citation:

Persistent Link:
http://hdl.handle.net/11343/43899