**Costs and outcomes of Lynch syndrome screening in the Australian colorectal cancer population**

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**Abstract**

**Background and Aim:** Individuals with Lynch syndrome (LS) are at increased risk of LS-related cancers including colorectal cancer (CRC). CRC tumor screening for mismatch repair (MMR) deficiency is recommended in Australia to identify LS, although its cost-effectiveness has not been assessed. We aim to determine the cost-effectiveness of screening individuals with CRC for LS at different age-at-diagnosis thresholds.

**Methods:** We developed a decision analysis model to estimate yield and costs of LS screening. Age-specific probabilities of LS diagnosis were based on Australian data. Two CRC tumor screening pathways were assessed (MMR immunohistochemistry followed by MLH1 methylation (MLH1-Pathway) or BRAF V600E testing (BRAF-Pathway) if MLH1 expression was lost) for four age-at-diagnosis thresholds—screening < 50, screening 50–60, screening < 70, and universal screening.

**Results:** Per 1000 CRC cases, screening < 50 identified 5.2 LS cases and cost $A7041 per case detected in the MLH1-Pathway. Screening < 60 increased detection by 1.5 cases for an incremental cost of $A25 177 per additional case detected. Screening < 70 detected 1.6 additional cases at an incremental cost of $A40 278 per additional case detected. Compared with screening < 70, universal screening detected no additional LS cases but cost $A158 724 extra. The BRAF-Pathway identified the same number of LS cases for higher costs.

**Conclusions:** The MLH1-Pathway is more cost-effective than BRAF-Pathway for all age-at-diagnosis thresholds. MMR immunohistochemistry tumor screening in individuals diagnosed with CRC aged < 70 years resulted in higher LS case detection at a reasonable cost. Further research into the yield of LS screening in CRC patients ≥ 70 years is needed to determine if universal screening is justified.

**Introduction**

Colorectal cancer (CRC) is a leading cause of cancer incidence and mortality in Australia. 1 While diagnoses are predominantly made in those at older ages, certain groups are at increased risk of early-onset CRC, largely as a result of inherited genetic mutations. 2 Lynch syndrome (LS), an autosomal dominant condition, is a well-known genetic syndrome that increases risk of early-
onset CRC (average age at diagnosis is 42 years for men and 47 years for women). Caused by a germline mutation in one of the DNA mismatch repair (MMR) genes (MLH1, MSH2, MSH6, or PMS2), LS is characterized by tumors that develop with high levels of microsatellite instability (MSI) and loss of expression of one or more of the MMR proteins, collectively referred to as tumor MMR deficiency.

Lynch syndrome is estimated to cause 1–3% of all CRC cases with carriers experiencing accelerated carcinogenesis and an increased lifetime risk for CRC (10–47% by age 70 years compared with 4–5% in the general population) as well as predisposing individuals to other cancers. A diagnosis of LS aids clinical decision-making, including more extensive surgery and highly intensive long-term surveillance, which impacts patient outcomes. Furthermore, a diagnosis permits cascade testing of at-risk family members to determine LS carrier status, thus enabling the commencement of intensive surveillance, which has been shown to lead to a reduction in LS-related cancer incidence and mortality.

Historically, LS testing has been guided using the Amsterdam or revised Bethesda criteria, both of which rely on obtaining an accurate family history but have limited sensitivity and specificity for LS detection and are poorly implemented in routine clinical practice. More recently, screening for LS has begun with tumor testing for MMR deficiency, prior to proceeding to germline MMR gene testing. However, as MMR deficiency can also be caused by sporadic somatic hypermethylation of the MLH1 gene promoter, tumors showing loss of MLH1/PMS2 protein expression require further testing (with either somatic MLH1 methylation testing or BRAF V600E somatic mutation testing). If LS is still suspected after these tumor tests, genetic testing is offered in association with genetic counseling.

Within Australia, there is no national policy for LS screening; however, the National Health and Medical Research Council recently recommended universal screening, as a means of increasing identification of carriers and their at-risk relatives. While this recommendation is in line with other jurisdictions, no cost-effectiveness analyses have been conducted in the Australian setting and therefore the optimal screening strategy remains unclear.

We aimed to determine the cost-effectiveness of CRC tumor screening to identify LS at different age-at-diagnosis thresholds for two alternative tumor screening pathways using data from the Australian setting.

**Methods**

**Overview.** We developed a decision analysis model to simulate LS screening in individuals with CRC to estimate the annual yield and costs associated with identifying LS in this population. For tumors exhibiting loss of MLH1/PMS2 expression by MMR immunohistochemistry (IHC), we tested two alternative pathways based on the follow-up tumor test (MLH1 methylation test or a BRAF V600E mutation test). The primary focus was to determine how yield and cost would vary for each pathway by age-at-diagnosis and compare the incremental differences within and between the pathways.

**Data.** Model parameters were based on two Australian research studies, the Australasian Colorectal Cancer Family Registry and the Melbourne Collaborative Cohort Study, which have been systematically characterized for LS. Detailed information about the recruitment strategy and tumor testing for these studies has been previously reported. In brief, the Australasian Colorectal Cancer Family Registry recruited population-based incident CRC cases of individuals aged 18–59 years (eligible cases n = 813) between 1997 and 2007. The Melbourne Collaborative Cohort Study is an Australian cohort study of 41,513 Melbourne residents recruited during 1990–1994 with age range at recruitment of 27–80 years. Data from 826 CRC cases diagnosed from recruitment until 2010 and aged 41–86 years at diagnosis were used for this analysis.

Colorectal cancer tumor samples from both studies were tested for MMR protein expression using IHC. Tumors showing MMR deficiency underwent germline testing to identify a MMR gene mutation and confirm LS diagnosis. For tumors demonstrating loss of MLH1/PMS2 expression by IHC, testing for tumor MLH1 promoter hypermethylation and BRAF V600E somatic mutation were performed, and only those cases with no evidence of somatic MLH1 methylation or BRAF wild-type underwent germline testing of MLH1 gene.

**Decision analysis model.** Using TreeAge Pro 2016 (Williamstown, Massachusetts), we developed a decision analysis model to simulate LS screening. For tumors exhibiting loss of MLH1/PMS2 expression by MMR IHC, we assessed two screening pathways for identifying LS based on follow-up tumor testing. In the first model (MLH1–Pathway), IHC was followed by somatic MLH1 methylation testing (Fig. 1), while in the second model (BRAF–Pathway), IHC was followed by BRAF V600E mutation testing (Fig. 2). For each pathway, we simulated 1000 CRC cases and assumed 100% participation in tumor and genetic testing at all stages. Once a diagnosis of CRC has been made, eligible individuals entered the LS screening pathway and progressed based on age-specific probabilities (Figs 1, 2). Costs are applied at appropriate time points along the pathway, such as when a test is conducted or when genetic counseling would be initiated.

**Screening scenarios.** For this analysis, we used empirical data to assess four age-at-diagnosis scenarios: screening < 50, screening < 60, screening < 70, and universal screening. In the reference scenario, screening < 50, screening was restricted to CRC diagnoses occurring before the age of 50 years. Screening < 60 expanded tumor screening to include those aged 50–59 years, and screening < 70 is a further expansion to include cases aged 60–69 years. The universal scenario included screening of all incident CRC diagnoses regardless of age. The probability of meeting the LS screening eligibility criteria for the age-restricted scenarios was based on Australian CRC incidence data from 2008 to 2012.

**Cost assumptions.** The cost of MMR IHC was provided by The Royal College of Pathologists of Australasia Benchmarking in Pathology Quality Assurance Program (St. Leonards, NSW) (2013) results (Dr Tony Badrick, pers. comm.). For the MLH1 methylation testing, cost data were provided by PathWest Laboratory Medicine, Nedlands, the sole government pathology service for Western Australia (Dr Benhur Amanuel, pers. comm.). The
The cost of BRAF V600E testing was taken from MBS Online\(^2\) (Table 1). Germine testing costs were provided by the Department of Diagnostic Genomics, PathWest Laboratory Medicine, Nedlands, the primary laboratory for genetic testing in Western Australia (Dr Karen Carpenter, pers. comm.). The costs for genetic counseling were obtained from primary sources at Genetic Services of Western Australia (Subiaco, WA), including the Business Unit and genetic counselors (Anne Hawkins and Cassandra Nichols, pers. comm.). All costs are presented in 2016 Australian dollars, and as they are incurred in a single year, no discounting is required.

**Outcomes.** For each screening pathway, our decision analysis model estimated the annual yield and costs of identifying LS in the four age-restricted scenarios per 1000 CRC cases.

**Sensitivity analyses.** To evaluate the robustness of our model outcomes, we conducted a number of univariate analyses. Firstly, we assessed the uncertainty of the diagnostic accuracy by calculating the 95% confidence intervals around the probability of being diagnosed with LS after demonstrating MMR deficiency using the Wilson confidence interval. This provided lower and upper confidence limits of yield and costs of LS screening in the CRC population.

Furthermore, as no cases of LS were diagnosed in CRC patients aged \(\geq 70\) years in our data set, we performed an analysis of the MLH1-Pathway using age-specific probabilities derived from Buchanan et al.\(^18\) These probabilities differ slightly as we considered LS cases that did not show MMR deficiency with IHC to be missed cases (three cases in screening < 60 and screening < 70 and four cases in universal). In addition, one LS case was excluded from the probabilities in our analysis because although the case showed PMS2 loss, genetic testing identified an MLH1 mutation, and this could not be factored into the model. Using screening < 50 as the example, 7.6% of all CRC cases were eligible for testing with IHC to determine MMR deficiency status and 13.5% were MMR deficient. Of these, 52.8% had loss of MLH1/PMS2, 18.1% had loss of MSH2/MSH6, 12.5% had loss of MSH6 only, and 16.7% had loss of PMS2 only. Of the tumors with or MLH1/PMS2, 92.1% were unmethylated and went on for germline testing. LS was confirmed in 66.7% of CRC cases demonstrating MLH1/PMS2 loss (excluding MLH1-methylated CRCs), 61.5% of the cases demonstrating MSH2/MSH6 loss, 77.8% of the cases demonstrating MSH6 loss, and 66.7% of the cases demonstrating PMS2 only. CRC, colorectal cancer; IHC, immunohistochemistry; LS, Lynch syndrome; MMR, mismatch repair; < 60, age-specific probabilities for CRC cases aged under 60 years; 60–69, age-specific probabilities for CRC cases aged between 60 and 69 years; 70+, age-specific probabilities for CRC cases aged over 70 years.
increase of all costs (Table 1 and tables in the Supporting Information). This provided lower and upper bound cost estimates for each age cohort in the analyses.

Results

**MLH1-Pathway.** By restricting testing to CRC cases diagnosed < 50 years, 76 (7.6%) of the 1000 CRC cases would be tested with IHC, leading to the identification of 5.2 LS cases. Total costs for this pathway were $36 864 per 1000 CRC cases, equating to $7041 per LS case diagnosed.

By expanding screening to include those aged between 50 and 59 years (screening < 60), an extra 142 individuals (totaling 21.8% of total CRC patient population) would be tested with IHC to identify 1.5 additional LS cases (6.7 LS cases in total). This would cost an additional $36 794 or $25 177 per additional LS case diagnosed. Cost per case detected increased to $10 999.

With further expansion to also screen CRC cases aged between 60 and 69 years (screening < 70), an additional 255 individuals (totaling 47.3% of total CRC patient population) would be tested by IHC. This identified 1.6 additional LS cases (8.3 LS cases in total), annual program cost increased to $138 663, and the cost per additional case detected was $40 278. Cost per case detected increased to $16 685.

Based on our data, universal screening would not identify any additional LS cases; however, annual program cost would increase by $158 724 to $297 387 per 1000 CRC cases. Cost per LS case detected increased to $35 784.

**BRAF-Pathway.** The BRAF-Pathway identified the same number of LS cases as the MLH1-Pathway at higher costs (Table 2). For example, screening < 50 identified 5.2 LS cases per 1000 CRC cases and cost $36 462 for the MLH1-Pathway and $37 177 in the BRAF-Pathway. Therefore, LS screening based on IHC followed by BRAF V600E is more expensive than the alternative, and the BRAF-Pathway is subsequently dominated in terms of cost-effectiveness.
Sensitivity analyses. When the probability of a diagnosis of LS was altered, our results changed significantly (Table S1). Although overall costs remained similar to the original analysis, in the lower bound analysis, the number of LS cases diagnosed reduced to between 3.2 and 3.8, while the cost per LS case diagnosed increased from $11 521 to $79 091. The reverse was true for the upper bound analysis where the number of LS cases diagnosed increased to between 7.0 and 23.7 and cost per LS case diagnosed ranged from $5350 to $13 731. A similar pattern was seen when the age-specific probabilities derived from Hampel et al.23 were applied to the MLH1-Pathway. Using these data, the number of LS cases diagnosed in each age restricted scenario was higher, and the cost per LS case diagnosed was lower. However, program costs remained similar to our original analysis (Table S2).

Lowering adherence to genetic counseling and germline testing reduced diagnostic yield by up to 25%. This resulted in a slight reduction in total costs (5–15% for MLH1-Pathway and 7–15% for BRAF-Pathway), while the cost per LS case detected increased (8–24% for MLH1-Pathway and 8–21% for BRAF-Pathway) (Table S3). Similar results were found when both costs and acceptance of genetic counseling and germline testing were altered.

Changes to the cost parameters affected the costs proportionally (Table 2 and tables in the Supporting Information).

Discussion

We developed a decision analysis model and used empirical data²⁸ to determine the cost and yield of screening for LS per 1000 CRC cases. Based on our results, screening for LS using the MLH1-Pathway is more cost-effective than the BRAF-Pathway. Limiting screening to CRC cases aged under 50 years in the MLH1-Pathway would identify 5.2 LS cases per 1000 CRC cases for the overall lowest cost, with a cost per LS case detected of $7041. Expanding this pathway to also screen individuals aged 50–59 years (screening < 60) increased diagnostic yield by 28% (1.5 cases). This was associated with a doubling of program costs, an increase in cost per LS case detected (to $10 999) and an incremental cost of $25 177 to detect one additional case. Screening < 70 further increased diagnostic yield of screening with program costs increasing by 88%. Cost per case detected in this scenario increased to $16 685, equating to an incremental cost per additional case detected of $40 278. Universal screening more than doubled program costs compared with screening < 70 for no additional yield; however, this was because no LS cases were identified in this age group in our dataset. Cost per LS case detected increased to $35 784. The BRAF-Pathway identified the same number of LS cases; however, costs were higher for all age-at-diagnosis thresholds.

There remains ongoing discussion about the optimal age to stop screening for LS in the CRC-affected population,⁴,²¹ and our model, like others,²⁴–²⁷ demonstrates that applying age restrictions to screening criteria results in fewer LS cases being identified. This impacts patient care and has downstream effects for at-risk relatives who would not be identified, thereby diminishing the opportunity to commence interventions to reduce mortality and morbidity in this cohort. However, concerns have been raised about the feasibility of expanded screening for LS, particularly in relation to the associated costs.²⁴ While individuals with LS are at higher risk of LS-related cancers compared with the general population, the likelihood of developing such a cancer diminishes with age.¹⁴ This suggests that, while expanding screening to include older individuals will identify more cases, the increased...
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**Table 2**

| Costs and outcomes of Lynch syndrome | Number of CRC cases undergoing IHC testing | Number of MMR-deficient cases detected by IHC | Number of MMR-deficient cases diagnosed | Probability of meeting inclusion criteria in the age restricted scenarios is based on the age distribution of CRC cases.30 We have previously noted that implementation of clinical guidelines in routine practice is poor.4,16,17 this would likely impact the effectiveness of this strategy, leading to missed opportunities to diagnose LS and reduced cost-effectiveness. While universal screening using Braf-Pathway has also been shown to...
be cost-effective, two studies indicated that this strategy was not as effective as alternative strategies that included predictive modeling as a first step and the inclusion of both BRAF V600E and MLH1 methylation testing. When we assessed the BRAF-Pathway, we found it to be as effective but more expensive than the MLH1-Pathway at all age thresholds. This was due to the increased number of individuals undergoing germline testing in the BRAF-Pathway as BRAF V600E only achieves ~75% efficiency as a surrogate marker for MLH1-methylated sporadic CRC showing loss of MLH1/PM2. Only one other study has made a direct comparison between the two pathways we investigated, and although the authors determined that the BRAF-Pathway was more cost-effective than the MLH1-Pathway, the differences were small.

Benefits of an LS screening program are dependent on ensuring all eligible CRC cases are screened and that those detected with MMR-deficiency receive genetic counseling and germline testing. In our analysis, we assumed all eligible cases would undergo appropriate testing; however, we recognize that this may not occur in practice, as individuals may not wish to participate in genetic testing because of, among other things, possible negative psychological impacts (such as anxiety and depression) and concerns over personal information. Reducing the proportion of MMR-deficient individuals who agree to genetic counseling and subsequently agree to germline testing decreases yield and total cost in all scenarios, while increasing cost per additional LS case detected. Importantly, such reductions lead to more undiagnosed cases of LS and missed opportunities to identify and monitor at-risk relatives. The greatest benefits of LS screening will only be achieved if screening is appropriately implemented and eligible cases have appropriate and informed access to genetic counseling and germline testing.

An important strength of this study is that the model parameters are derived from two large population-based studies for LS testing and our results align with previous estimates of LS in the CRC population. However, despite this, three limitations are of note. Firstly, this analysis only examined testing incident CRC cases with IHC. However, while we acknowledge that MSI testing, either with or without IHC, is an alternative pathway for triaging CRC cases, our preliminary analyses indicated that this pathway was substantially more expensive, and therefore, we excluded it from further investigations.

Secondly, this analysis only considers costs to identify LS in CRC cases and does not take into account the subsequent costs and cost savings of cascade screening and surveillance of at-risk relatives. While predictive genetic testing of at-risk relatives has been shown to be cost saving in Australia, there is currently no research into the cost-effectiveness of surveillance in LS carriers. Research with similar cost per LS case detected to ours, which also assessed costs and benefits of surveillance in this group found screening for LS in those aged < 50 gained 43.6 life years ($7938/LYG). When screening was expanded to include those aged 51–60 years, a further 118 life years were gained ($6380 per additional LYG). An additional 44.3 life years were gained when those aged 61–70 years were screened ($10 648 per additional LYG). This suggests that with our cost per case detected, cascade screening and surveillance of at-risk individuals will be cost-effective at a willingness-to-pay threshold of $50 000. As much of the benefit in identifying LS relates to gains in life expectancy in this group, future research should incorporate analyses of these implications and costs.

Finally, data around the costs of laboratory testing for LS have been difficult to obtain, and our costs may not necessarily reflect the range of costs throughout Australia. To account for this, we conducted sensitivity analyses to provide the lower and upper cost estimates.

**Conclusions**

Based on our analysis, MLH1 methylation testing as a follow-up for CRCs showing loss of MLH1 protein expression is more cost-effective than BRAF V600E somatic mutation testing in identifying LS cases. An expanded screening program that includes screening CRC cases diagnosed <70 years will identify more LS cases at a reasonable cost. Future research into the yield of LS screening in CRC patients ≥ 70 years and the potential to offset additional costs by identifying at-risk relatives is needed to determine if universal screening is justified.

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**References**

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Supporting information

Additional Supporting Information may be found online in the supporting information tab for this article.

**Table S1.** Yield and costs for each pathway and age restricted scenario per 1,000 individuals diagnosed with colorectal cancer for the sensitivity analyses with a) the lower bound confidence boundary and b) upper bound confidence boundary.

**Table S2.** Yield and costs for each pathway and age restricted scenario per 1,000 individuals diagnosed with colorectal cancer for the sensitivity analyses using data from Hampel and colleagues.

**Table S3.** Yield and costs for each pathway and age restricted scenario per 1,000 individuals diagnosed with colorectal cancer for the sensitivity analyses a) when attendance at genetic counseling reduced to 92.5% and acceptance of genetic testing reduced to 81% and b) when attendance at genetic counselling reduced to 92.5% and acceptance of genetic testing reduced to 90%.