Clinical problems of colorectal cancer and endometrial cancer cases with unknown cause of tumor mismatch repair deficiency (suspected Lynch syndrome)

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Abstract: Carriers of a germline mutation in one of the DNA mismatch repair (MMR) genes have a high risk of developing numerous different cancers, predominantly colorectal cancer and endometrial cancer (known as Lynch syndrome). MMR gene mutation carriers develop tumors with MMR deficiency identified by tumor microsatellite instability or immunohistochemical loss of MMR protein expression. Tumor MMR deficiency is used to identify individuals most likely to carry an MMR gene mutation. However, MMR deficiency can also result from somatic inactivation, most commonly methylation of the MLH1 gene promoter. As tumor MMR testing of all incident colorectal and endometrial cancers (universal screening) is becoming increasingly adopted, a growing clinical problem is emerging for individuals who have tumors that show MMR deficiency who are subsequently found not to carry an MMR gene mutation after genetic testing using the current diagnostic approaches (Sanger sequencing and multiplex ligation-dependent probe amplification) and who also show no evidence of MLH1 methylation. The inability to determine the underlying cause of tumor MMR deficiency in these “Lynch-like” or “suspected Lynch syndrome” cases has significant implications on the clinical management of these individuals and their relatives. When the data from published studies are combined, 59% (95% confidence interval [CI]: 55% to 64%) of colorectal cancers and 52% (95% CI: 41% to 62%) of endometrial cancers with MMR deficiency were identified as suspected Lynch syndrome. Recent studies estimated that colorectal cancer risk for relatives of suspected Lynch syndrome cases is lower than for relatives of those with MMR gene mutations, but higher than for relatives of those with tumor MMR deficiency resulting from methylation of the MLH1 gene promoter. The cause of tumor MMR deficiency in suspected Lynch syndrome cases is likely due to either unidentified germline MMR gene mutations, somatic cell mosaicism, or biallelic somatic inactivation. Determining the underlying cause of tumor MMR deficiency in suspected Lynch syndrome cases is likely to reshape the current triaging schemes used to identify germline MMR gene mutations in cancer-affected individuals and their relatives.

Keywords: Lynch syndrome, cancer risk, screening, somatic mutation, germline mutation

Introduction

Lynch syndrome is the most common form of hereditary colorectal cancer and hereditary endometrial cancer, accounting for up to 6% of all colorectal and endometrial cancer cases.1,2 Lynch syndrome is an autosomal dominantly inherited disorder caused by germline mutations in one of the DNA mismatch repair (MMR) genes (MLH1, MSH2, MSH6, and PMS2). Additionally, mutations in the gene upstream of MSH2
The proportion of suspected Lynch syndrome cases in colorectal cancer cohorts varies among different studies.

The magnitude of the clinical problem of suspected Lynch syndrome cases

Across studies of differing design, up to 72% of colorectal cancer and 64% of endometrial cancer cases with tumor MMR deficiency do not have an MMR gene mutation identified by standard MMR gene testing approaches, nor do they show somatic MLH1 promoter methylation, depending on the gene and the population studied. Two recent studies have indicated that while MMR deficiency and the presence of the BRAF V600E mutation are both common in colorectal tumors, the presence of MMR deficiency and the BRAF V600E mutation are not independent events. This suggests that MMR deficiency is a common mechanism for the development of BRAF V600E-mutant colorectal tumors, and that this mechanism is likely to be present in a significant proportion of tumors with BRAF V600E mutations. Therefore, the identification of MMR gene mutation carriers is critical to the development of targeted colonoscopic screening programs, and to the development of targeted early intervention strategies for individuals at high risk of developing colorectal cancer.
Suspected Lynch syndrome: a clinical problem (Table 1). In a large population-based study of the Colon Cancer Family Registry, 3.8% (186/4,853) of all the colorectal cancer cases were confirmed MMR gene mutation carriers, whereas 5.6% (271/4,853) of all colorectal cancer cases were classified as suspected Lynch syndrome. Of the identified MMR-deficient colorectal cancers from this study (as evident by the loss of MMR protein expression in IHC) not related to MLH1 promoter methylation or the BRAF V600E somatic mutation, 56% (95% CI: 51% to 62%) were considered suspected Lynch syndrome. Similar proportions of suspected Lynch syndrome cases were reported in studies by Hampel et al at 69% (95% CI: 67% to 71%).

Figure 1 Classic molecular testing approach for triaging colorectal cancer cases for germline mismatch repair (MMR) gene mutation testing.

Figure 2 The three groups of tumor mismatch repair (MMR) deficiency.

Notes: The types of MMR deficiency are denoted as: 1) “inherited” MMR deficiency resulting from germline MMR gene mutations where individuals and their carrier relatives are at a high risk of colorectal cancer (CRC) and endometrial cancer (EC), and established screening guidelines are used to clinically manage and counsel mutation-positive families; 2) “sporadic” MMR deficiency resulting from somatic inactivation, predominantly MLH1 hypermethylation in the tumor. These individuals are at low risk of metachronous CRC or EC and their relatives are at low risk of cancer i.e., their risks are similar to cancer risks for those with MMR proficient tumor. Receive management established for low-risk cases and individuals; and 3) MMR deficiency of “unknown molecular cause”, therefore cases have suspected Lynch syndrome. There is no established clinical management guideline for cases and their relatives.
51% to 83%) and Rodriguez-Soler et al at 71% (95% CI: 58% to 83%). When data from these three studies are combined, the prevalence of suspected Lynch syndrome in MMR-deficient colorectal cancer cases with no MLH1 promoter methylation was estimated to be 59% (95% CI: 55% to 64%). Further, in a recent study of 102 early-onset colorectal cancer cases (diagnosed before age 50 years), Antelo et al identified that 13 of the 18 MMR-deficient colorectal cancer cases not related to MLH1 promoter methylation (72%; 95% CI: 47% to 90%) were considered suspected Lynch syndrome cases.

Similar proportions of suspected Lynch syndrome cases are observed in endometrial cancer cohorts (Table 2). In a population-based endometrial cancer cohort from Australia, Buchanan et al tested 686 endometrial cancer cases for tumor MMR protein expression using IHC, tumor MLH1 promoter methylation, and germline MMR gene mutations. They found that, of the 55 endometrial cancer cases with MMR deficiency, only 45% (25/55) exhibited germline MMR gene mutations and 55% (95% CI: 41% to 68%) were identified as suspected Lynch syndrome. Of the 30 suspected Lynch syndrome–endometrial cancer cases, only one (3%) fulfilled the Amsterdam II criteria and 14 (47%) fulfilled the revised Bethesda Guidelines. Therefore, half of the suspected Lynch syndrome cases from this Australian endometrial cancer cohort had either no family history of cancer or a family history that did not meet criteria used for the identification of Lynch syndrome.

Moline et al found a higher proportion of suspected Lynch syndrome cases at 64% (95% CI: 41% to 83%), while two other studies reported that around one-third of the MMR-deficient endometrial cancer cases were identified as suspected Lynch syndrome: 30% (95% CI: 7% to 65%) in Leenen et al and 36% (95% CI: 13% to 65%) in Hampel et al. When we combined the data from these four studies, suspected Lynch syndrome was identified in 52% (95% CI: 41% to 62%) of MMR-deficient endometrial cancer cases.

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<tr>
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<tbody>
<tr>
<td>Immunohistochemistry/microsatellite instability tested, n</td>
<td>4,853</td>
<td>1,066</td>
<td>1,689</td>
<td>7,608</td>
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<td>MMR-deficient and germline tested, n (%)</td>
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<td>85 (8)</td>
<td>135 (8)</td>
<td>812 (11)</td>
</tr>
<tr>
<td>MLH1 and PMS2 loss</td>
<td>403</td>
<td>69</td>
<td>104</td>
<td>576</td>
</tr>
<tr>
<td>MLH1 mutation-negative, n</td>
<td>250</td>
<td>50</td>
<td>79</td>
<td>379</td>
</tr>
<tr>
<td>MLH1 methylated, n</td>
<td>49</td>
<td>4</td>
<td>4</td>
<td>57</td>
</tr>
<tr>
<td>MLH1 mutation-positive, n</td>
<td>104</td>
<td>15</td>
<td>21</td>
<td>140</td>
</tr>
<tr>
<td>MLH1 suspected Lynch syndrome proportion (%)</td>
<td>104/153 (68)</td>
<td>15/19 (79)</td>
<td>21/25 (84)</td>
<td>140/197 (71)</td>
</tr>
<tr>
<td>MSH2 and MSH6 loss</td>
<td>104</td>
<td>13</td>
<td>22</td>
<td>139</td>
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<td>MSH2 mutation-negative, n</td>
<td>45</td>
<td>8</td>
<td>14</td>
<td>67</td>
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<td>MSH2 suspected Lynch syndrome proportion (%)</td>
<td>45/104 (43)</td>
<td>8/13 (62)</td>
<td>14/22 (64)</td>
<td>67/139 (48)</td>
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<td>MSH6 solitary loss</td>
<td>41</td>
<td>1</td>
<td>6</td>
<td>48</td>
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<td>1</td>
<td>3</td>
<td>18</td>
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<td>MSH6 mutation-negative, n</td>
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<td>0</td>
<td>3</td>
<td>30</td>
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<td>MSH6 suspected Lynch syndrome proportion (%)</td>
<td>27/41 (66)</td>
<td>0/1 (0)</td>
<td>3/6 (50)</td>
<td>30/48 (63)</td>
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<td>PMS2 solitary loss</td>
<td>44</td>
<td>2</td>
<td>3</td>
<td>49</td>
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<tr>
<td>PMS2 mutation-positive, n</td>
<td>27</td>
<td>1</td>
<td>1</td>
<td>29</td>
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<td>PMS2 mutation-negative, n</td>
<td>17</td>
<td>1</td>
<td>2</td>
<td>20</td>
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<td>PMS2 suspected Lynch syndrome proportion (%)</td>
<td>17/44 (39)</td>
<td>1/2 (50)</td>
<td>2/3 (67)</td>
<td>20/49 (41)</td>
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<tr>
<td>Total suspected Lynch syndrome cases/number tested, % (95% confidence interval)</td>
<td>193/342, 56 (51%–62%)</td>
<td>24/35, 69 (51%–83%)</td>
<td>40/56, 71 (58%–83%)</td>
<td>257/433, 59 (55%–64%)</td>
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</table>

Abbreviation: MMR, mismatch repair.
Table 2 Summary of suspected Lynch syndrome cases from endometrial cancer cohorts

<table>
<thead>
<tr>
<th>Study</th>
<th>Immunohistochemistry/microsatellite instability tested, n</th>
<th>MMR-deficient and germline tested, n (%)</th>
<th>MLH1 and PMS2 loss</th>
<th>MSH2 and MSH6 loss</th>
<th>MSH6 solitary loss</th>
<th>PMS2 solitary loss</th>
<th>Total suspected Lynch syndrome proportion (%)</th>
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<tbody>
<tr>
<td>Buchanan et al,2014</td>
<td>686</td>
<td>154 (22)</td>
<td>113</td>
<td>20</td>
<td>20</td>
<td>1 (0)</td>
<td>12/14 (86)</td>
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<tr>
<td>Moline et al,2013</td>
<td>227</td>
<td>32 (14)</td>
<td>35</td>
<td>5</td>
<td>2</td>
<td>0/0 (0)</td>
<td>11/13 (85)</td>
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<tr>
<td>Leenen et al,2012</td>
<td>179</td>
<td>42 (23)</td>
<td>31</td>
<td>2</td>
<td>6</td>
<td>2/2 (100)</td>
<td>0/0 (0)</td>
</tr>
<tr>
<td>Hampel et al,2006</td>
<td>543</td>
<td>127 (23)</td>
<td>84</td>
<td>3</td>
<td>6</td>
<td>0/3 (0)</td>
<td>4/5 (80)</td>
</tr>
<tr>
<td>Combined</td>
<td>1,635</td>
<td>355 (22)</td>
<td>263</td>
<td>27</td>
<td>34</td>
<td>17/30 (57)</td>
<td>27/32 (84)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Study</th>
<th>MLH1 mutation-negative, n (%)</th>
<th>MLH1 methylated, n (%)</th>
<th>MLH1 mutation-positive, n (%)</th>
<th>MLH1 unmethylated, n (%)</th>
<th>MLH1 suspected Lynch syndrome proportion (%)</th>
<th>MSH2 mutation-positive, n (%)</th>
<th>MSH2 mutation-negative, n (%)</th>
<th>MSH2 suspected Lynch syndrome proportion (%)</th>
<th>MSH6 mutation-positive, n (%)</th>
<th>MSH6 mutation-negative, n (%)</th>
<th>MSH6 suspected Lynch syndrome proportion (%)</th>
<th>PMS2 mutation-positive, n (%)</th>
<th>PMS2 mutation-negative, n (%)</th>
<th>PMS2 suspected Lynch syndrome proportion (%)</th>
<th>Total suspected Lynch syndrome proportion (%)</th>
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<tr>
<td>Buchanan et al,2014</td>
<td>99 (22)</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>12/14 (86)</td>
<td>8</td>
<td>12</td>
<td>6/20 (30)</td>
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<td>6/20 (30)</td>
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<td>6/20 (30)</td>
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<td>30/55, (41%–68%)</td>
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<tr>
<td>Moline et al,2013</td>
<td>22 (31)</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>11/13 (85)</td>
<td>2</td>
<td>12</td>
<td>0/2 (0)</td>
<td>1</td>
<td>0/2 (0)</td>
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<td>Leenen et al,2012</td>
<td>79 (31)</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0/0 (0)</td>
<td>0</td>
<td>0</td>
<td>0/0 (0)</td>
<td>3</td>
<td>3/10 (30%)</td>
<td>1/2 (50)</td>
<td>3/10 (30%)</td>
<td>1/2 (50)</td>
<td>3/10, (7%–65%)</td>
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<td>Hampel et al,2006</td>
<td>79 (31)</td>
<td>1</td>
<td>0</td>
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<td>4/5 (80)</td>
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<td>12</td>
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<td>0/3 (0)</td>
<td>5/14, (36%–65%)</td>
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<tr>
<td>Combined</td>
<td>79 (31)</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>4/5 (80)</td>
<td>3</td>
<td>12</td>
<td>0/3 (0)</td>
<td>5</td>
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<td>0/3 (0)</td>
<td>0/3 (0)</td>
<td>5/14, (36%–65%)</td>
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Abbreviation: MMR, mismatch repair.

These studies highlight a large proportion of colorectal and endometrial cancer cases that have no explanation for their tumor MMR deficiency. The move from MMR deficiency testing defined by age and/or family history criteria to universal screening is likely to increase the number of suspected Lynch syndrome cases identified.

Cancer risks in suspected Lynch syndrome

Little is known about the cancer risks for individuals with suspected Lynch syndrome. Only three studies have investigated cancer risks for suspected Lynch syndrome cases and their relatives (Table 3). Overbeek et al observed that 66% (50/75) of Lynch syndrome families from a Netherlands cohort fulfilled the Amsterdam II criteria; however, only 11% (2/18) of families with suspected Lynch syndrome fulfilled Amsterdam II (P<0.001). Rodriguez-Soler et al first quantified the risk of colorectal cancer for first-degree relatives of colorectal cancer cases with suspected Lynch syndrome and found the highest risk of colorectal cancer for first-degree relatives of MMR gene mutation carriers, an intermediate risk for those of individuals with suspected Lynch syndrome, and the lowest risk for those of MLH1-methylated MSI-H cases. A larger study confirmed the finding that first-degree relatives of colorectal cancer cases with suspected Lynch syndrome have an intermediate risk of colorectal cancer (between Lynch syndrome and sporadic MMR-deficient cases). The mean age at diagnosis of colorectal cancer of suspected Lynch syndrome was either similar to Lynch syndrome cases, or intermediate between Lynch syndrome and sporadic MMR-deficient cases. Currently, no studies have investigated the risk of cancers other than colorectal cancer for relatives of colorectal cancer cases with suspected Lynch syndrome. Further, no information is known about the risk of cancers for relatives of endometrial cancer cases with suspected Lynch syndrome.
Table 3 Estimates of cancer risks in SLS from previously published studies

<table>
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<tr>
<th>Author</th>
<th>Year</th>
<th>Sample</th>
<th>Main findings</th>
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| Win et al13             | 2014 | 1,799 FDRs of 271 SLS CRC cases            | • FDRs of SLS CRC cases developed CRC at a mean age (57.9 years, SD 14.8 years) that was less than that of FDRs of MMR-proficient CRC cases (63.9 years, SD 13.1 years; \( P < 0.001 \)) and greater than that of FDRs of LS CRC cases (49.1 years, SD 13.1 years; \( P < 0.001 \)).  
• FDRs of SLS CRC cases have 3.45 times higher risk of CRC (95% CI: 2.62–4.57) compared with the general population.  
• FDRs of SLS CRC cases have 2.06 times higher risk of CRC (95% CI: 1.59–2.67) compared with FDRs of MMR-proficient CRC cases. |
| Rodríguez-Soler et al34 | 2013 | 177 FDRs of 25 SLS CRC cases               | • FDRs of SLS CRC cases developed CRC at a mean age (53.7 years, SD 16.8 years) that was less than that of FDRs of MMR-proficient CRC cases (68.8 years, SD 9.0 years; \( P = 0.004 \)) but similar to that of FDRs of LS CRC cases (48.5 years, SD 14.1 years; \( P = 0.23 \)).  
• FDRs of SLS CRC cases have 2.12 times higher risk of CRC (95% CI: 1.16–3.56) compared with the general population.  
• FDRs of SLS CRC cases have a significantly higher risk of CRC compared with FDRs of MMR-proficient CRC cases. |
| Overbeek et al40        | 2007 | 18 SLS CRC cases                           | • The mean age at diagnosis of SLS CRC cases and LS CRC cases are very similar, at 44 years.  
• SLS CRC cases had a lower risk of familial cancer than LS CRC cases, given that Amsterdam II criteria were fulfilled in 11% of SLS cases compared with 66% of the LS cases (\( P < 0.001 \)). |

Abbreviations: CI, confidence interval; CRC, colorectal cancer; FDRs, first-degree relatives; LS, Lynch syndrome; MMR, mismatch repair; SD, standard deviation; SLS, suspected Lynch syndrome.

Current clinical management recommendation for suspected Lynch syndrome

The clinical management of individuals with suspected Lynch syndrome and their relatives in current practice is challenging, as there is insufficient information for defining evidence-based screening and treatment guidelines for them. As a consequence, individuals with suspected Lynch syndrome and their relatives are likely to receive varying degrees of screening, ranging from guidelines recommended for MMR gene mutation carriers to those recommended for low-risk individuals. Therefore, some individuals and their relatives are likely to be unnecessarily over-screened while others are likely to be under-screened, despite relatives of suspected Lynch syndrome cases having an increased risk of developing colorectal cancer. Such uncertainty in management is a great burden to both clinicians and families, as well as to the health care system.

Given that risk of colorectal cancer for first-degree relatives of colorectal cancer cases with suspected Lynch syndrome is intermediate (between that for first-degree relatives of Lynch syndrome and sporadic MMR-deficient cases), an intermediate screening strategy has been proposed, ie, a longer interval of colonoscopic screening for those without a strong family history of colorectal cancer (rather than 1- to 2-yearly colonoscopy given to MMR gene mutation carriers). However, optimal screening (including the age of starting colonoscopies) and clinical management strategies are yet to be defined, given that this group is likely to be heterogeneous with regards to family history and to the mechanism of MMR inactivation, as described in the next section.

Potential causes of tumor MMR deficiency in suspected Lynch syndrome

The potential underlying causes of tumor MMR deficiency in suspected Lynch syndrome cases may include: 1) germline inactivation via unidentified MMR gene mutations or genetic mutations in other MMR-related genes not attributed to Lynch syndrome that indirectly result in tumor MMR deficiency; and 2) somatic inactivation resulting from DNA hypermethylation or somatic mutations. In this section, we review evidence for each of these two mechanisms.

Germline inactivation

It is possible that a proportion of suspected Lynch syndrome cases are due to the existence of complex or cryptic mutations in MMR genes that are not readily identified by current Sanger sequencing and multiplex ligation-dependent probe amplification (MLPA) techniques. It could also be argued that suspected Lynch syndrome–colorectal cancer cases carry...
undetected mutations associated with a more moderate penetration of cancer compared with that of exonic and splice site mutations that are more readily detected.\textsuperscript{43}

**Unidentified germline MMR gene mutations in suspected Lynch syndrome cases**

Unidentified mutations within regulatory/promoter regions of the MMR genes may also underlie suspected Lynch syndrome cases. The c.-93G→A single-nucleotide polymorphism (SNP) (rs1800734) within the MLH1 gene is associated with the risk of MSI-H colorectal cancer and endometrial cancer; however, the strength of the associations suggests the mutation is a low-penetrance variant.\textsuperscript{44,45} In contrast, a rare European haplotype containing the c.-27C→A variant in MLH1 has been shown to predispose individuals to dominantly inherited epimutation and silencing of the MLH1 gene.\textsuperscript{46} A deletion of the last exon of the EPCAM gene, which is located upstream of MSH2, results in a fusion transcript between EPCAM and MSH2 and promoter methylation-induced transcriptional silencing of MSH2.\textsuperscript{47} The 3′ untranslated region (UTR) of most genes contain regulatory sequences controlling all aspects of mRNA processing, including message stability, and these regions are typically A/U-rich elements or U repeats. Germline mutations within 3′ UTR repetitive regulatory sequences could suppress MMR gene expression,\textsuperscript{48} as has been described for the MLH1 gene.\textsuperscript{49} Similarly, altered regulation of MMR gene expression by miRNA binding in the 3′ UTR, in particular by miR-21 and miR-155, has been demonstrated.\textsuperscript{49,50} These examples suggest that more extensive screening of the 5′ and 3′ UTR sequence of the MMR genes for germline mutations within suspected Lynch syndrome cases is warranted and may account for a proportion of these cases.

More extensive MMR gene mutation testing to include deeper intronic sequence may yet yield further germline mutations. An example of germline MMR gene mutations that would be undetected by current mutation testing approaches involves a MSH2 mutation within intron 1 of the MSH2 gene (c.212-553_c.212-479) in a single family with multiple colorectal cancer-affected individuals that demonstrated loss of expression of MSH2 and MSH6 by IHC.\textsuperscript{41} RNA-based splicing detection revealed an intronic insertion of 75 nucleotides between exon 1 and 2. Germline sequencing revealed a T→G transversion at intronic position c.212-478, creating a canonical splice donor site at the 3′ end of the inserted sequence. The inserted sequence contains a stop codon at the 3′ end and is predicted to result in a truncated protein of just 94 amino acids. This newly identified mutation was not identified by standard Sanger sequencing due to its location deep within intron 1. Although next-generation sequencing could easily extend to capture intronic sequences, the high level of repetitive sequence within the introns of MMR genes means designing probes and aligning sequence to these regions will be difficult. For instance, 54% of the intronic regions for the MSH2 gene comprise interspersed repeats, where 33% of this sequence is Alu repeats (MLH1: 53% interspersed repeats with 20% Alu; MSH6: 48% interspersed repeats with 42% Alu; PMS2: 57% interspersed repeats with 45% Alu).

Complex structural variations involving MMR genes have been described, including: 1) an interstitial deletion on chromosome 3p21.3, which leads to an in-frame fusion of MLH1 (exons 1–11) with ITGA9 (integrin α9; exons 17–28),\textsuperscript{51} 2) a paracentric inversion on chromosome 3p22.2, creating two new stable fusion transcripts between the MLH1 and LRRFIP2 genes,\textsuperscript{42} and 3) an inversion involving MSH2 exon 1–7,\textsuperscript{52,53} which is known to be a disease-causing mechanism in Lynch syndrome and was present in six out of the ten MSH2 suspected Lynch syndrome cases tested.\textsuperscript{54}

Large-scale intragenic insertions and deletions in the MMR genes are a relatively common cause of MMR deficiency, particularly in the case of MSH2. Complications arising due to the presence of a large set of highly homologous pseudogenes have made the detection of such mutations very difficult for the PMS2 gene. Recently, the development of a new method, which integrates the findings from long-range polymerase chain reaction (PCR)-based sequencing with a modified MLPA panel, allows for accurate detection and interpretation of large-scale rearrangements in the 3′ end of the gene.\textsuperscript{50} A single large cohort study, which had previously identified a mutation in 78% of suspected PMS2 cases, reanalyzed its mutation-negative samples and screened them using this new method.\textsuperscript{55} No additional mutations were identified in this subset of samples (n=16), suggesting that alternate mutational mechanisms also exist within the PMS2 locus. As such, other structural and complex mutations that disrupt MMR gene function through similar mechanisms are likely to exist and it is possible that the progression from Sanger sequencing and MLPA-based testing to targeted resequencing of the MMR genes will aid in the routine detection of such structural mutations. It should, however, be noted that current next-generation technologies are not compatible with the issues faced when screening the PMS2 gene and, as such, this gene is likely to be left in the shadows again when it comes to routine screening.

The mismatch repair pathway is comprised of genes other than MLH1, MSH2, MSH6, and PMS2, including the MSH3,
MLH3, PMS1, and EXO1 genes, among others. Although rare variants that are putatively associated with colorectal cancer risk have been identified within these additional MMR genes, the literature provides little to no evidence for the presence of germline mutations in these minor MMR binding partners in individuals with tumor MMR deficiency; Loukola et al found no germline mutations in MLH3 in 52 MSI-H colorectal cancers; Wu et al and Liu et al found no loss of MMR expression or MSI in colorectal cancers from carriers of germline MLH3 variants; and Taylor et al found no loss of MMR expression or MSI in endometrial cancers from two carriers of germline MLH3 variants. Similarly, Plaschke et al found no loss of MMR protein expression in colorectal cancers from carriers of germline variants in MSH3. While germline variants in these additional MMR genes may predispose individuals to colorectal cancer, none to date has been shown to be associated with tumor MMR deficiency.

A number of studies have identified mutations within the heterodimer binding partner of the MutLα and MutSα complexes. For example, a MSH2 gene mutation was identified in a colorectal cancer-affected individual, where the tumor demonstrated isolated loss of MSH6 expression, suggesting that mutation screening of the heterodimer binding partner should be a high priority in cases with suspected Lynch syndrome. The most commonly reported of these scenarios (although still rare) are those with MLH1 mutations identified in cases demonstrating loss of PMS2 protein expression with normal or weak MLH1 staining in their tumor and may represent the occurrence of immunostable MLH1 mutations. Conversely, in a study of 80 colorectal cancer cases with loss of MLH1 and PMS2 protein expression, in which germline MLH1 mutations and MLH1 DNA hypermethylation had been excluded, no mutations were identified within the PMS2 gene. The increasing use of gene panel resequencing of colorectal cancer-affected individuals, including blood-derived DNA as well as normal mucosa- and tumor tissue-derived DNA, would be necessary along with confirmation of the mutation in blood relatives.

Somatic inactivation

A recent meta-analysis has shown that somatic mutations in the MLH1 and MSH2 genes are more common in tumors from individuals carrying a germline mutation within the same MMR gene. This supports the concept that a somatic MMR gene mutation is the “second hit” that contributes to tumor MMR deficiency in Lynch syndrome. The prevalence of biallelic somatic mutations in MMR genes in colorectal cancers has been estimated to be around 10%. Biallelic mutations identified as “double somatic mutation” are likely in trans (one on each allele), and may explain the inactivation of the MMR gene involved and the MMR-deficient status of the tumor. In a study of 25 suspected Lynch syndrome cases, Mensenkamp et al found that 13 (52%; 8/18 in MLH1 and 5/7 in MSH2) had biallelic somatic mutations in the form of point mutations and loss of heterozygosity. Biallelic somatic inactivation for at least some of these suspected Lynch syndrome cases would explain why the risk of colorectal cancer for first-degree relatives of suspected Lynch syndrome cases is reduced compared with Lynch syndrome cases. Therefore, additional studies aimed at confirming the high proportion of biallelic somatic mutations as a cause of MMR deficiency in suspected Lynch syndrome is necessary.

One study has reported on a small number of cases where reduced or absent MSH6 protein expression can be attributed to somatic frameshift mutations within the (C) tract in exon 5 of the MSH6 gene, secondary to the loss of mismatch repair function in MLH1/PMS2-deficient colorectal cancers. The same study also reported on non-genetic mechanisms as a further cause of MMR deficiency. Preoperative chemotherapy or chemoradiation therapy was shown to be associated with reduced MSH6 protein expression in the absence of germline somatic mutations in otherwise MMR-proficient colorectal cancers, presumably as a result of hypoxia or cytotoxic stress secondary to treatment.

Epigenetic mechanisms of MMR gene inactivation

MMR gene inactivation as a result of promoter hypermethylation has been previously demonstrated in both the germline (epimutations) and tumor tissue (somatic mutations) for the MLH1 gene. For MSH2, MSH6, and PMS2 genes,
however, much less is known regarding their inactivation by DNA hypermethylation. Rare cases of germline MSH2 methylation have been reported,\textsuperscript{3,76} the majority of which were attributable to 3′ EPCAM (TACSTD1) deletions. One study found somatic MSH2 hypermethylation in 24% (11/46) of MSH2-deficient tumors without a germline MSH2 mutation, and no MSH2 hypermethylation in sporadic colorectal cancers with normal expression of the MMR genes.\textsuperscript{77} For seven of the eleven cases with somatic MSH2 hypermethylation, a germline mutation in the MSH2 gene was present, suggesting methylation of the wild-type allele acted as the second hit in these MSH2-deficient colorectal cancers. However, nothing is known about somatic MSH2 or MSH6 hypermethylation in endometrial cancers with suspected Lynch syndrome. Furthermore, somatic PMS2 hypermethylation has not been previously investigated in colorectal or endometrial cancer cases.

**Future directions**

It is clear from the few studies of suspected Lynch syndrome cases conducted to date that the underlying cause of MMR deficiency is likely to be heterogeneous, comprising both cases with inherited MMR deficiency due to unidentified mutations in the MMR genes and cases with sporadic MMR deficiency resulting from biallelic somatic mutations or MMR gene promoter hypermethylation. More comprehensive studies will be needed to determine: 1) the full spectrum of genetic mutations in the MMR genes; and 2) the proportion of cases attributable to genetic, epigenetic, or somatic inactivation mechanisms. Strategies exploiting the power of massively parallel sequencing are likely to aid in the identification of germline noncoding and structural variation mutations that were beyond previous testing feasibility. The recently reported biallelic somatic mutation frequency of 50% in suspected Lynch syndrome cases, if confirmed by others, suggests triaging strategies designed to identify germline MMR gene mutation carriers within colorectal- and endometrial cancer-affected populations will need to be revised to accommodate additional tumor testing steps prior to germline MMR gene testing. Similarly, as suspected Lynch syndrome cases are apportioned into inherited or sporadic MMR deficiency groups, the cancer risks for first-degree relatives will need to be reevaluated. Translation of new knowledge regarding MMR gene somatic inactivation into clinical practice is essential for a large number of families who have previously tested negative for MMR gene mutations but exhibited tumor MMR deficiency. Findings will be instrumental for partitioning these individuals and their relatives as low-risk or high-risk, and then more intensive screening and surveillance can be targeted to those individuals at high risk. To provide optimal care, the underlying causes of tumor MMR deficiency in suspected Lynch syndrome cases will need to be identified in order to provide effective and targeted clinical management for the affected individuals and their relatives, thereby reducing the burden on the health system.

**Acknowledgments**

AKW is an Australian National Health and Medical Research Council (NHMRC) Early Career Fellow. ABS is an NHMRC Senior Research Fellow. CR is the Jass Pathology Fellow. DDB is a Senior Research Fellow funded by Research at Melbourne University Accelerator Program (R@MAP).

**Disclosure**

The authors report no conflicts of interest in this work.

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