Microsatellite Instability, Immunohistochemistry, and Additional PMS2 Staining in Suspected Hereditary Nonpolyposis Colorectal Cancer

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ABSTRACT

Purpose: Immunohistochemistry (IHC) and microsatellite instability (MSI) analysis can be used to identify patients with a possible DNA mismatch repair defect [hereditary nonpolyposis colorectal carcinoma (HNPPC)]. The Bethesda criteria have been proposed to select families for determination of MSI. The aims of this study were to assess the yield of MSI analysis in families suspected for HNPCC, to compare the results of immunohistochemical staining and MSI analysis, and to assess the additional value of PMS2 staining.

Experimental Design: Clinical data and tumors were collected from 725 individuals from 631 families with suspected HNPCC. MSI analysis was performed using eight markers including the 5 National Cancer Institute markers. Four immunohistochemical staining antibodies were used (MLH1, MSH2, MSH6 and PMS2).

Results: A MSI-H (tumors with instability for >30% of the markers) phenotype in colorectal cancers (CRCs) was observed in 21–49% of families that met the various Bethesda criteria. In families with three cases of CRC diagnosed at age >50 years, families with a solitary case of CRC diagnosed between ages 45 and 50 years, and families with one CRC case and a first-degree relative with a HNPCC-related cancer, one diagnosed between ages 45 and 50 years (all Bethesda-negative families), the yield of MSI-H was 10–26%. Immunohistochemical staining confirmed the MSI results in 93% of the cases. With IHC, adding PMS2 staining led to the identification of an additional 23% of subjects with an hMLH1 germ-line mutation (35 carriers were tested).

Conclusions: The Bethesda guidelines for MSI analysis should include families with three or more cases of CRC diagnosed at age >50 years. The age at diagnosis of CRC in the original guidelines should be raised to 50 years. Routine IHC diagnostics for HNPCC should include PMS2 staining.

INTRODUCTION

Colorectal cancer (CRC) is the second most common cause of death due to malignancy in the Western world. The cause of CRC is multifactorial, involving genetic and environmental factors (1). The most common hereditary colorectal carcinoma syndrome is hereditary nonpolyposis colorectal carcinoma (HNPCC), which accounts for 1–6% of all CRC cases (2). HNPCC is an autosomal dominant disease characterized by an increased risk of early-onset CRC and other cancers, including tumors of the endometrium, stomach, small intestine, hepatobiliary system, kidney, ureter, brain, and ovary (3–6). In up to 15–25% of all cases of CRC, clustering of this type of tumor is observed in the family (7). The role of environmental or genetic factors in these cases is largely unknown.

The increased risk for malignancy in HNPCC is caused by a mutation in one of the following DNA mismatch repair (MMR) genes: MLH1; MSH2; MSH6; PMS1; and PMS2 (8–10). Germ-line mutations of MLH1 and MSH2 account for >90% of all known MMR mutations in HNPCC (11), and germ-line mutations of MSH6 account for 5–10% of all known MMR mutations in HNPCC, whereas mutations of other genes are rare (10, 12).

Mutations in DNA MMR genes result in a failure to repair errors in repetitive sequences that occur during DNA replication. This failure leads to microsatellite instability (MSI) of the tumor, which is the hallmark of HNPCC (13–16).

Due to the heterogeneity of the mutation spectrum of the MMR genes, screening for mutations is both time-consuming and expensive. In addition to family history, MSI analysis and immunohistochemistry (IHC) can both be used to identify families eligible for mutation analysis of the MMR genes (2, 17). In 1997, the Bethesda criteria were proposed to select families for MSI testing. In the present study, we evaluated the yield of MSI analysis in families categorized according to these criteria. We also evaluated MSI in other subsets of families that do not meet these criteria.

Previous studies from numerous groups, including ours...
DNA was isolated from three punches, resuspended in 96 basis of a HE-stained slide. Using the Chelex extraction method, tissue was isolated from the paraffin-embedded material by abrogation of the total protein complex (20). In the present study, we compared the results of immunohistochemical staining with the outcome of MSI analysis and evaluated the additional value of IHC using PMS2 staining.

PATIENTS AND METHODS

Patients. We used the database of colorectal tumors from the unit molecular diagnostics of the pathology department from the Leiden University Medical Center, the Netherlands. This database contains colorectal tumors (n = 771) sent to our department for MSI analysis from different medical genetic centers and laboratories in the Netherlands between November 1999 and December 2002. For 46 patients, it was impossible to perform MSI analysis because the obtained formalin-fixed, paraffin-embedded material was not sufficient, or MSI analysis was redundant due to the fact that the segregating mutation was already known in the family. This resulted in MSI analysis of 725 tumors from individuals with CRC of 631 families with clustering of CRC or with a solitary patient with CRC at a young age. Retrospectively, we scored the available complete pedigrees (528 pedigrees were enclosed with the request for MSI analysis from the medical genetic centers; from 103 subjects, only a fragmentary pedigree was sent) according to the Bethesda and additional criteria (Table 1), and we performed immunohistochemical staining (MLH1, MSH2, and, subsequently, MSH6 and PMS2). Finally, we had 528 tumors with complete information from the pedigree and MSI analysis, 330 tumors with results on MLH1 and PMS2 staining (including 35 tumors from patients with a hMLH1 mutation), and 284 tumors with interpretable results on both MSI and IHC (four proteins). The reason for the major decrease in the number of patients was that in this retrospective series, not all samples were still available for additional staining. From 84 families, we had tumor material of at least two relatives.

DNA Isolation. Genomic DNA of normal and tumor tissue was isolated from the paraffin-embedded material by taking tissue punches (diameter, 0.6 mm) with a tissue microarrayer (Beecher) from tumor and normal areas selected on the basis of a HE-stained slide. Using the Chelex extraction method, DNA was isolated from three punches, resuspended in 96 µl of PK-1 lysis buffer [50 mM KCl, 10 mM Tris (pH 8.3), 2.5 mM MgCl2, 0.45% NP40, 0.45% Tween 20, and 0.1 mg/ml gelatin] containing 5% Chelex beads (Bio-Rad, Hercules, CA) and 5 µl of proteinase K (10 mg/ml), and incubated for 12 h at 56°C. The suspension was incubated at 100°C for 10 min and centrifuged at 13,000 rpm for 10 min, and the supernatant containing the DNA was carefully transferred to a new tube.

MSI Analysis. Eight microsatellite markers were evaluated [two mononucleotide repeats (BAT25 and BAT26) and three dinucleotide repeats (D2S123, D5S346, and D17S250) recommended by the National Cancer Institute Workshop on MSI for Cancer Detection and Familial Predisposition (13), supplemented by three mononucleotide repeat markers (BAT40, MSH3, and MSH6)]. BAT40 is a very informative marker. The choice for MSH3 and MSH6 was initially for research purposes. Tumors were classified as (a) tumors with instability for >30% of the markers (MSI-H), (b) tumors with instability for <30% of the markers (MSI-L), and (c) tumors with no instability [microrosatellite stability (MSS)]. We distinguished between MSI-L with instability of only a dinucleotide marker (MSI-Ld) and instability of only a mononucleotide marker (MSI-Lm).

IHC. Staining of MMR proteins was performed with anti-MLH1 (initially with clone 14; 1:75; Calbiogen, Cambridge USA, later supplemented and substituted by clone G168-728; 1:50; BD Biosciences, NJ), anti-MSH2 (clone A16-4; 1:50; BD Biosciences), anti-MSH6 (clone GB-12; 1:100; Oncogene Research Products, San Diego, CA), and anti-PMS2 (clone 44; 1:400; BD Biosciences). Immunohistochemical staining was performed on 4-µm-thick, formalin-fixed, paraffin-embedded tissue sections that were prepared on DAKO slides and dried overnight at 37°C. Next, tissue sections were deparaffinized three times in xylene for a total of 15 min and subsequently rehydrated. Antigen retrieval was done by boiling in 10 mM citrate buffer [pH 6.0 (MSH6 and MLH1), clone G168-728] or in 1 mM EDTA (MLH1, clone 14, PMS2 and MSH2) for 10 min using a microwave oven, after which the sections were cooled in this buffer for at least 1 h at room temperature. After rinsing in demiwater, the tissue sections were stained in a DAKO Detection Kit Peroxidase/DAK K5011 (DAKO, Glostrup, Denmark). Briefly, in this system, slides were incubated with the primary antibody diluted in ChemMate Antibody diluent (DakoCytomation, Glostrup, Denmark) for 8 h at room temperature. Sections were automatically washed and incubated with ready-to-use biotinylated secondary antibody for 30 min and washed. Endogenous peroxidase was then blocked in peroxidase

<table>
<thead>
<tr>
<th>Bethesda Criteria</th>
<th>Positive</th>
<th>Negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fulfiling the Amsterdam II criteria</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Solitary patient with CRC and a HNPCC-related cancer</td>
<td>2</td>
<td>5</td>
</tr>
<tr>
<td>Patient with CRC and a FDR with a HNPCC-related cancer, one of the cancers diagnosed age &lt; 45 yrs</td>
<td>3</td>
<td>6</td>
</tr>
<tr>
<td>Solitary patient with CRC diagnosed at age &lt; 45 yrs</td>
<td>4</td>
<td>7</td>
</tr>
<tr>
<td>Solitary patient with CRC diagnosed at age 45–50 yrs</td>
<td>5</td>
<td>8</td>
</tr>
<tr>
<td>Patient with CRC and a FDR with a HNPCC-related cancer, one of the cancers diagnosed age &gt; 45–50 yrs</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td>Late-onset family: patient with CRC and two FDRs with a HNPCC-related cancer, both cancers diagnosed at age &gt; 50 yrs</td>
<td>7</td>
<td></td>
</tr>
<tr>
<td>Patient with CRC and a FDR with a HNPCC-related cancer, both cancers diagnosed at age &gt; 50 yrs</td>
<td>8</td>
<td></td>
</tr>
</tbody>
</table>

Note: CRC, colorectal cancer; HNPCC, hereditary nonpolyposis colorectal carcinoma; FDR, first-degree relative.
blocking solution for 7.5 min and washed and incubated with ready-to-use streptavidin-conjugated with peroxidase for 30 min. Sections were washed and developed with two-component hydrogen peroxide/diaminobenzidine for 15 min. The sections were then counterstained with hematoxylin for TechMate, dehydrated, cleared in xylene, and mounted with micromount. Microscopic analysis was done by a pathologist (H. M.). Tissue stroma and normal epithelium or lymph follicles served as positive internal controls when analyzing MLH1, PMS2, MSH2, and MSH6 expression. Expression of MLH1, PMS2, MSH2, and MSH6 was scored as positive (+/H11), negative with a positive internal control (0/H11), and doubtfully negative [when both tumor and internal control stain negative (0/0)], and when the internal control was stronger than the positive tumor cells, it was scored as +/-/H11.

**RESULTS**

**Yield of MSI in Subjects from Bethesda-Positive and -Negative Families.** In the families that met the Bethesda criteria (Bethesda-positive group; \(n = 272\)), 84 tumors (31%) were MSI-H, 23 tumors (8%) were MSI-L, and 165 tumors (61%) showed MSS (Table 1; Fig. 1). In tumors from subjects from an Amsterdam-positive family (\(n = 74\)), the yield of MSI-H was 49%; for Bethesda 2 (\(n = 45\)), it was 40%; for Bethesda 3 (\(n = 90\)), the yield was 19%; and for Bethesda 4 (\(n = 63\)), it was 21%. The proportion of MSI-L tumors in these four groups was 11%, 4%, 9%, and 8%, respectively.

In the families that did not meet the criteria (Bethesda-negative group; \(n = 256\)), 32 colorectal tumors (12.5%) were MSI-H, 32 tumors (12.5%) were MSI-L, and 165 tumors (61%) showed MSS. We subdivided the Bethesda-negative families into four subgroups (Table 1, criteria 5–8). In Fig. 1, the yield of MSI for the different subgroups is shown.

**IHC and MSI.** Data on MSI analysis as well as immunohistochemical staining (four proteins) were available for 284 tumors. Among these 284 tumors (Table 2), 91 tumors showed MSI-H as well as abnormal staining, and 136 tumors showed MSS and normal protein expression, leading to concordant results in 93% (227 of 245) of the MSI-H and microsatellite stable tumors. In view of the remarks by Perucho (21) on the marker sets used for MSI, we subdivided MSI-L in MSI-Lm (instability of only a mononucleotide marker) and MSI-Ld (instability of only a dinucleotide marker). Although the number of tumors is small, we found a difference between both groups: 35% of tumors in the MSI-Lm group and 13% of tumors in the MSI-Ld group showed absence of at least one MMR protein (Table 2).

Subsequently, we evaluated the results of IHC in the Bethesda-negative groups (Table 3).

**PMS2 Staining.** To evaluate the additional value of PMS2 staining, we compared the results of MLH1 and PMS2 staining in 330 tumors (see “Patients and Methods”). Among these, 35 tumors were from \(hMLH1\) mutation carriers (25 tumors had been described previously, without staining for PMS2; Ref. 18). Thirty tumors were from subjects in whom a \(hMLH1\) mutation could not be detected, and 265 tumors were from subjects with an unknown mutation status of \(hMLH1\) (from these 265 tumors, 7 tumors were from carriers of a \(hMSH2\) germ-line mutation, and 10 were from subjects with a \(hMSH6\) germ-line mutation; Table 4). In Fig. 2, three staining examples are shown. In 292 tumors (88%), both stainings gave the same results. If MLH1 stained negative with a positive internal con-
control (0/+), PMS2 also stained 0/+ in 39 cases (93%). If MLH1 stained positive, PMS2 stained positive in 252 (92%) cases. Among these 252 cases is 1 carrier of a hMLH1 mutation (unclassified variant; Table 5, case 8). In 19 tumors 7% (all MSI-H tumors), there was 0/+ staining of PMS2, whereas staining of MLH1 was positive (+, 16 tumors; +/+ +, 3 tumors). In the latter scoring (+/+ +), the internal control clearly stained more positive than the tumor nuclei (Fig. 2). Among these 19 patients were 8 hMLH1 germ-line mutation carriers. In the whole database, there were 31 cases with remarkable absence of proteins. Then we noticed a group of patients (cases 15 and 21–25) without a microsatellite stable tumor and the absence of one or more proteins. The last group is patients with microsatellite stable tumors and families with one microsatellite stable and one MSI-H or MSI-L tumor. Overall, in the 69 families in which we assessed MSI in tumors from at least two relatives, 23 tumors showed absence of at least MLH1. In only 17 tumors (49%) was an MLH1-negative staining accompanied by normal MSH2 and MSH6 staining patterns. Eight of the 35 tumors showed absence of only PMS2 (all other three proteins showed positive expression). Therefore, an additional 23% of the subjects with an hMLH1 germ-line mutation were identified solely with IHC.

**Table 3** MSI and IHC results of the Bethesda-negative groups

<table>
<thead>
<tr>
<th>Intact expression of all 4 proteins</th>
<th>Absent expression ≥ 1 protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group 5</td>
<td>Group 6</td>
</tr>
<tr>
<td>Total no. of cases</td>
<td>25</td>
</tr>
<tr>
<td>No. of MSS</td>
<td></td>
</tr>
<tr>
<td>No. of MSI-L</td>
<td>3</td>
</tr>
<tr>
<td>No. of MSI-H</td>
<td>0</td>
</tr>
</tbody>
</table>

<sup>a</sup> MSI, microsatellite instability; IHC, immunohistochemistry; MSS, microsatellite stability.

<sup>b</sup> Abrogation of MSH6.

<sup>c</sup> Abrogation of MSH6.

<sup>d</sup> Abrogation of MLH1/PMS2, or MLH1/MSH6 (2 cases), or MSH2/MSH6.

<sup>e</sup> Abrogation of MLH1/MSH6, PMS2, or MSH2/MSH6, or MSH6 (4 cases).

<sup>f</sup> Abrogation of MLH1/MSH6 (2 cases), or PMS2, or MSH2 (2 cases), or MSH2/MSH6/MSH2.

<sup>g</sup> Abrogation of MLH1/PMS2.

When only evaluating the 35 tumors of hMLH1 mutation carriers, 23 tumors showed absence of at least MLH1. In only 17 tumors (49%) was an MLH1-negative staining accompanied by normal MSH2 and MSH6 staining patterns. Eight of the 35 tumors showed absence of only PMS2 (all other three proteins showed positive expression). Therefore, an additional 23% of the subjects with an hMLH1 germ-line mutation were identified solely with IHC.

**Table 4** PMS2 and MLH1 staining

<table>
<thead>
<tr>
<th>hMLH1 mutation</th>
<th>0/+&lt;sup&gt;a&lt;/sup&gt;</th>
<th>+</th>
<th>0/0</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>0/+#&lt;sup&gt;a&lt;/sup&gt;</td>
<td>21</td>
<td>1</td>
<td>1</td>
<td>23</td>
</tr>
<tr>
<td>+</td>
<td>5</td>
<td>1</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td>+/++</td>
<td>3</td>
<td>3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0/0</td>
<td>3</td>
<td>3</td>
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<td></td>
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</table>

<table>
<thead>
<tr>
<th>No hMLH1 mutation</th>
<th>0/+</th>
<th>-</th>
<th>0/0</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>0/+</td>
<td>5</td>
<td>-</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>+</td>
<td>3</td>
<td>18</td>
<td>22</td>
<td></td>
</tr>
<tr>
<td>0/0</td>
<td>3</td>
<td>3</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Mutation status unknown</th>
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<th>+</th>
<th>0/0</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>0/+</td>
<td>13</td>
<td>1</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td>+</td>
<td>8</td>
<td>233</td>
<td>2</td>
<td>243</td>
</tr>
<tr>
<td>0/0</td>
<td>2</td>
<td>5</td>
<td>1</td>
<td>8</td>
</tr>
<tr>
<td>Total</td>
<td>63</td>
<td>262</td>
<td>5</td>
<td>330</td>
</tr>
</tbody>
</table>

<sup>a</sup> Staining results: +, nuclear staining; +/++, internal control is stronger than the positive tumor cells; 0/++, negative with a positive internal control; 0/0, tumor and internal control stain negative.

**DISCUSSION**

Identification of families with HNPCC is extremely important because it makes it possible to target effective preventive measures that lead to a substantial reduction in CRC-related
mortality (22). In the present study, we evaluated the value of MSI analysis and immunohistochemical staining for the identification of HNPCC in a large series of families. A significant proportion of MSI-H tumors were detected not only in families that complied with the Bethesda criteria but also in families that met other specific criteria. In addition, we found that immunohistochemical staining (including staining for PMS2) and MSI analysis gave concordant results in 93% of the cases. IHC alone, including PMS2 staining, led to the identification of an additional 23% of subjects with an hMLH1 germ-line mutation.

Several years ago, the Bethesda guidelines were developed for selection of families whose tumors should be tested for MSI. In the present study, we examined the validity of these criteria in relation to MSI status. Another important aim was to assess
whether other criteria should be added to identify more families with MSI-positive tumors.

The yield of MSI-H in our series of families that met the different Bethesda criteria varied from 19% to 49%. This is in agreement with the results of previous studies on the yield of MSI in such families (23, 24).

The families in our series who did not meet the Bethesda criteria comprised families with one CRC diagnosed between age 45 and 50 years (category 5); families with one case of CRC and a first-degree relative with an HNPPC-related cancer, one diagnosed between age 45 and 50 years (category 7); and families with one CRC and a first-degree relative with a HNPPC-related cancer, both diagnosed at age > 50 years (category 8). In categories 5, 7, and 8, the yield of MSI-H tumors was relatively low. In categories 5 and 7, all MSI-H tumors showed absence of at least one protein (see earlier). It is remarkable that only 4 of 13 tumors in these two categories might be explained by MLH1 abrogation due to promoter methylation. Theoretically, hypermethylation of the other MMR genes is possible, but not yet known. In the families of category 6, the yield of MSI-H tumors was 26%, which is higher than the percentage of MSI-H tumors (~10%) reported for sporadic CRC (25), often due to MLH1 promoter methylation (16, 26). Based on these results, we suggest the extension of the Bethesda criteria with criteria that can identify these types of families (groups 5–7).

A few studies have shown that immunohistochemical staining of tumors using antibodies against the MMR proteins is a sensitive method to identify families eligible for mutation analysis (27–30). Most studies reported so far used antibodies against MLH1, MSH2, and MSH6. Rigau et al. (19) also included PMS2 antibodies. Because the PMS2 protein forms a heterodimer with the MLH1 protein, absence of the MLH1 protein due to a mutation also leads to loss of the PMS2 protein caused by abrogation of the total protein complex (20). Absence of PMS2 staining might therefore suggest the presence of hMLH1 or PMS2 germline mutation or somatic abrogation of hMLH1.

When we compare the results of MLH1 and PMS2 staining, concordant results were observed in 88% of the cases. In the 35 tumors associated with a known hMLH1 mutation, absence
of both MLH1 and PMS2 staining was observed in 21 tumors. In eight other tumors, staining for PMS2 was negative, whereas staining for MLH1 was positive. This finding means that by using staining for PMS2, significantly more hMLH1 mutation carriers would have been identified. Rigau et al. (19) observed four cases with isolated loss of PMS2, and all were microsatellite-stable. Rigau et al. (19) concluded that there is no need to include PMS2 in the panel of antibodies to be used when looking for MMR-deficient cases by IHC. The majority of their MSI-H tumors, however, most likely consisted of tumors with sporadic abrogation of MLH1, in which PMS2 staining is indeed not necessary. In our studied cases, the type of underlying mutation (missense mutation, in-frame deletion, or unclassified variant) may explain why the MLH1 protein was still intact in the nucleus, whereas the binding of PMS2 was abrogated (e.g., due to conformational changes). Another possibility is that, in the case of an unclassified MLH1 variant, an unidentified pathogenic mutation in PMS2 is responsible. We also do not know what exactly happened with the second MLH1 allele in these tumors, which potentially might influence the staining results. Finally, technical problems with the MLH1 staining in individual cases and perhaps also the type of the MLH1 antibody used might play a role (31, 32). An illustration of the arguments above follows: seven cases in our database with an identical MLH1 mutation (K618del) were tested (18). Only one of these (case 27, Table 5) was concluded to have retained nuclear MLH1 staining in tumor cells, but with loss of PMS2 staining. We identified three tumors (Table 5), all from hMLH1 carriers, that stained +/+ + for MLH1. In the literature, it is known that in individual cases, abnormally high sensitivity of the IHC can account for false positive interpretation (31). Whatever the explanation, the latter three cases illustrate the additional value of adding the +/+ + score to the traditional scoring scheme.

Overall, we found that immunohistochemical staining using four antibodies confirmed the results of MSI analysis in 93% of the cases. This is nearly identical to that reported in the recent literature in studies using only three antibodies [hMLH1, hMSH2, and hMSH6 (19)] or even two antibodies [hMLH1 and hMSH2 (30)]. This discordance might be explained by the consecutive case series used in the study of Rigau et al. (19). The majority of their MSI-H tumors (very few HNPCC cases) are most likely due to methylation of hMLH1. The concordance between MSI-H and loss of MLH1 expression in the sporadic cases will be 100%, as expected. In the study of Lindor et al. (30), the concordance in the consecutive case series was indeed 100%. In the other three series, included in the same study, all from centers from a Cooperative Family Registry for Colon Cancer Studies, the concordance varied widely, from 84% to 95%. The exact reason for the discordance is unknown (30).

We classified the MSI-L tumors in our series into two groups: tumors with instability of only a mononucleotide marker (MSI-Lm); or tumors with instability of only a dinucleotide marker (MSI-Ld). The MSI-Lm tumors seem more informative for a true MMR deficiency than the MSI-Ld tumors, which seems to be in line with the views of Perucho (21): “The alterations in di-, tri- or tetranucleotide repeats can be also due to spontaneous errors of replication of these highly unstable sequences.”

Ninety-five percent of all microsatellite stable tumors showed positive staining for the four MMR proteins, which implies that additional IHC in microsatellite stable tumors is often redundant. However, the value of MSH6 staining in microsatellite stable tumors might although not neglectable (33, 34). In our study, four of six microsatellite stable tumors with abnormal IHC showed an absence of MSH6 (Table 5, cases 2–5), although no mutation has been detected in this set of patients. On the basis of these results and the results of Wahlberg et al. (35), we recommend a possible decision scheme for (suspected) HNPCC as suggested previously (18). Rigau et al. (19) suggested that MSH6 (and possibly PMS2) can be considered as useful only in second line, when MLH1 and MSH2 show no abnormalities in MSI-H tumors or in suspected HNPCC. At our department, however, the costs for performing two or four stainings at the same time are almost equal, whereas performing them in two sessions is more labor intensive.

We recommend testing a second tumor from another relative in our decision scheme when MSI analysis of a tumor (from a family suspected of HNPCC) shows no evidence of instability because it is possible that we are dealing with a phenocopy within a HNPCC family. In the present series, we analyzed a second colon tumor in 69 families in which the first tumor showed MSS. MSI in the second tumor was found in 36% of the families. Furthermore, on basis of our results and those of others (36), we recommend, if possible, not to test a rectal tumor as first choice.

We noticed several cases in the whole database with discordant results (Table 5). The number of patients (8 patients) with a microsatellite stable tumor with a MMR mutation [five of eight were unclassified variants (in total, 11% of all subjects with a MMR mutation in our database)] falls within the range of about 10% published in the literature (12). In total, there were 70 cases (MSS, MSI-L, or MSI-H) in the whole database in which the search for a mutation in hMLH1, hMSH2, or hMSH6 was negative. Five of 70 cases had a MSI-H tumor with absence of one or more proteins. This number (7%) is comparable with that seen in the literature (25).

In sum, on the basis of the present study, we recommend the inclusion of PMS2 staining in the panel of antibodies to identify families eligible for mutation analysis. The addition of PMS2 staining will lead to a marked increase of detection of hMLH1 mutation carriers. Moreover, we suggest the following revisions to the Bethesda criteria: include late-onset families (three or more cases of CRC diagnosed at age > 50 years) and raise the age at diagnosis of CRC from 45 to 50 years in the original criteria.

REFERENCES


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