Risk of urothelial bladder cancer in Lynch syndrome is increased, in particular among MSH2 mutation carriers

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ABSTRACT

Background Colorectal, endometrial and upper urinary tract tumours are characteristic for Lynch syndrome (hereditary non-polyposis colon carcinoma, HNPCC). The aim of the present study was to establish whether carriers of mutations in mismatch repair genes MLH1, MSH2 or MSH6 are at increased risk of urinary bladder cancer.

Methods Carriers and first degree relatives of 95 families with a germline mutation in the MLH1 (n=26), MSH2 (n=43), or MSH6 (n=26) gene were systematically questioned about the occurrence of carcinoma. The cumulative risk of cancer occurring before the age of 70 years (CR70) was compared to the CR70 of the general Dutch population. Microsatellite instability (MSI) testing and/or immunohistochemistry (IHC) for mismatch repair proteins was performed on bladder tumour tissue.

Results Bladder cancer was diagnosed in 21 patients (90% men) from 19 Lynch syndrome families (2 MLH1, 15 MSH2, and 4 MSH6). CR70 for bladder cancer was 7.5% (95% CI 3.1% to 11.9%) for men and 1.0% (95% CI 0% to 2.4%) for women, resulting in relative risks for mutation carriers and first degree relatives of 4.2 (95% CI 2.2 to 7.2) for men and 2.2 (95% CI 0.3 to 8.0) for women. Men carrying an MSH2 mutation and their first degree relatives were at highest risks: CR70 for bladder cancer of 11.9% (95% CI 3.1% to 20.3%) for men and 1.1% (95% CI 0.7% to 1.7%) for women. Bladder cancer tissue was MSI positive in 6/7 tumours and loss of IHC staining was found in 14/17 tumours, indicating Lynch syndrome aetiology.

Conclusion Patients with Lynch syndrome carrying an MSH2 mutation are at increased risk of urinary tract cancer including bladder cancer. In these cases surveillance should be considered.

INTRODUCTION

Lynch syndrome, previously called hereditary non-polyposis colon carcinoma (HNPCC), is caused by a germline mutation in one of the mismatch repair (MMR) genes MLH1, MSH2, MSH6 and PMS2. It results in a large increase in spontaneous mutations and thus has a direct oncogenic effect. Besides the high risk of developing colorectal carcinomas of 10–80%, Lynch syndrome family members are at increased risk of developing several extra-colonic cancers and tumours at a relatively young age: endometrial cancer, ovarian cancer, small bowel and biliary tract cancer, seba-

ceous gland tumours and urothelial carcinomas (UC) of the upper urinary tract.1–10 The lifetime risk of upper urinary tract cancer in Lynch syndrome varies in different studies from 0.4–20%.11–13 Microsatellite instability (MSI) is present in these urothelial carcinomas of the upper urinary tract.14–16

A study based on the Swedish family cancer database, quantifying the occurrence of UC in families with at least four generations, showed that families fulfilling the Bethesda criteria21 have an increased risk of cancers in the ureter, but not in the urinary bladder.16 It was concluded that in families at risk for Lynch syndrome, UC of the bladder occurs at a frequency comparable to that in the general population. The study did not report results which were stratified by type of mutation. On the contrary, in a study by Geary et al, bladder cancer was more common in MSH2 mutation families than expected in the general population, the relative risk (RR) being 5.6 (p=0.001).16 Cumulative risks were not presented. In their study every case of bladder cancer was accompanied by cancer of the ureter in the family. For that reason, the authors concluded that the risk of bladder cancer was increased only in families with ureter cancer.

In addition to morphologic resemblance, sporadic urothelial cell cancers of the renal pelvis, ureter and bladder share the most important risk factors and molecular genetic aberrations; it is therefore remarkable that the risk of bladder cancer does not appear to have increased in Lynch syndrome families, while the risk of upper urinary tract cancer has. The aim of the present study was to establish whether patients with Lynch syndrome are at increased risk of cancer of the urinary bladder.

PATIENTS AND METHODS

Patient population

From 95 Lynch syndrome families, we selected all carriers of a germline mutation in the MSH2, MLH1 or MSH6 gene, who had been seen and registered at the Department of Human Genetics of the Radboud University Nijmegen Medical Centre between 1996 and November 2008, and all their first degree relatives—a total of 627 men and 617 women. Information on mutation carriers and their first degree relatives was systematically collected by postal questionnaires and telephone calls with contact persons when data were outdated for more than 1 year. In each family, one to six such persons
were contacted in order to obtain up-to-date information on the occurrence of carcinoma in mutation carriers and their first degree relatives. First degree relatives with MMR gene mutation negative tests were excluded. All diagnoses of UC carcinoma were verified and confirmed by review of pathology reports or medical reports.

**Statistical analysis**

We calculated follow-up time for each family member with the date of birth as starting point until the dates of last contact, death, or diagnosis of cancer, whichever came first. Kaplan–Meier (KM) survival analyses were used to calculate the cumulative risk (plus SE) of cancer until specified ages. We chose being at risk after that age is small. SPSS version 16.0 was used for KM analyses. For reference, we used life table cancer risk demographics in 2003.22 The life table risks of urinary tract cancers of the bladder, ureter or renal pelvis were collected. After written informed consent, histology reports and tissue blocks of UC of the bladder, ureter or renal pelvis were collected.

**Histology and molecular analysis**

After written informed consent, histology reports and tissue blocks of UC of the bladder, ureter or renal pelvis were collected. Clinicopathological features of the urothelial cell cancers were reviewed by two experienced pathologists using haematoxylin and eosin (H&E) slides. The following parameters were scored: (1) tumour differentiation according to the World Health Organization 2004 grading system; (2) T stage (TNM 2002); (3) growth pattern: papillary or solid; (4) presence of tumour infiltrating lymphocytes (TILs): absent, moderate or dense.

For MSI analysis, areas of the formalin fixed and paraffin embedded tissues containing either tumour cells (at least 50%) or normal cells were marked and material from these areas was isolated separately using a lysis buffer and a protein precipitation solution (Purogene, Gentra systems, Minneapolis, Minnesota, USA). PCR of the markers D2S123, D5S346, D17S250, G70220). Staining patterns of MMR proteins were evaluated using normal epithelial, stromal and inflammatory cells as internal control; or (3) not assessable

**RESULTS**

Members of 95 Lynch syndrome families diagnosed by a germline mutation in MLH1 (n = 26), MSH2 (n = 43) or MSH6 (n = 26) were questioned by contact persons for occurrence of cancer such as UC of the bladder, ureter or renal pelvis. The total cohort of 1244
Table 2  Clinico-histopathological features of all patients with urothelial carcinomas of the urinary bladder

<table>
<thead>
<tr>
<th>Family number</th>
<th>Sex</th>
<th>Mutated MMR gene</th>
<th>Mutation</th>
<th>Age bladder cancer</th>
<th>Other malignancies (age at diagnosis)</th>
<th>Immunohistochemistry</th>
<th>Analysed samples of the urinary bladder</th>
<th>T stage</th>
<th>Grading</th>
<th>Morphology</th>
</tr>
</thead>
<tbody>
<tr>
<td>77</td>
<td>M</td>
<td>MLH1</td>
<td>c.588+588+6del</td>
<td>64</td>
<td>RP(63)</td>
<td>+        -        +        -</td>
<td>ND</td>
<td>B</td>
<td>Ta</td>
<td>HG 1</td>
</tr>
<tr>
<td>73</td>
<td>M</td>
<td>MLH1</td>
<td>c.1852_1854del (p.Lys618del)</td>
<td>66</td>
<td>ES(73)</td>
<td>-        +        -        -</td>
<td>ND</td>
<td>B</td>
<td>T1</td>
<td>HG 1</td>
</tr>
<tr>
<td>12</td>
<td>M</td>
<td>MSH2</td>
<td>c.1387_1510del (Del exon 9)</td>
<td>41</td>
<td>C(49)</td>
<td>+        -        -        +</td>
<td>MSI</td>
<td>TUR</td>
<td>T1</td>
<td>HG 1</td>
</tr>
<tr>
<td></td>
<td>F</td>
<td>MSH2</td>
<td>(sister)</td>
<td>42</td>
<td>UR(50), RP(51), E(45), Cx2(52)</td>
<td>+        -        -        +</td>
<td>MSI</td>
<td>TUR</td>
<td>T1</td>
<td>HG 1</td>
</tr>
<tr>
<td>13</td>
<td>M</td>
<td>MSH2</td>
<td>c.1_1076+del (Del exon 1-6)</td>
<td>43</td>
<td>RP(51), C(41)</td>
<td>+        -        -        +</td>
<td>MSI</td>
<td>TUR</td>
<td>Ta</td>
<td>LG 1</td>
</tr>
<tr>
<td>12</td>
<td>M</td>
<td>MHS2 50%</td>
<td>(father)</td>
<td>68</td>
<td>Cx3(52, 59, 66)</td>
<td>ND       ND       ND       ND</td>
<td>ND</td>
<td>NA</td>
<td>≥T1</td>
<td>HG 1</td>
</tr>
<tr>
<td>7</td>
<td>M</td>
<td>MSH2</td>
<td>c.1_211+del (Del exon 1)</td>
<td>44</td>
<td>+        -        -        +</td>
<td>ND</td>
<td>B</td>
<td>≥T1</td>
<td>HG 1</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>M</td>
<td>MSH2</td>
<td>c.1_211+del (Del exon 1)</td>
<td>49</td>
<td>C(58), PR(49)</td>
<td>+        -        -        +</td>
<td>MSI</td>
<td>CP</td>
<td>T2a</td>
<td>HG 1</td>
</tr>
<tr>
<td>17</td>
<td>M</td>
<td>MSH2</td>
<td>c.1386_1G→T</td>
<td>52</td>
<td>Cx2(42, 47)</td>
<td>+        -        tws      +</td>
<td>MSI</td>
<td>B</td>
<td>T1</td>
<td>HG 1</td>
</tr>
<tr>
<td>10</td>
<td>M</td>
<td>MSH2</td>
<td>c.1_1076+del (Del exon 1-6)</td>
<td>57</td>
<td>C(42)</td>
<td>+        -        -        +</td>
<td>MSI</td>
<td>TUR</td>
<td>Ta</td>
<td>LG 1</td>
</tr>
<tr>
<td>6</td>
<td>M</td>
<td>MSH2</td>
<td>c.1203dup (p.Gln402fs)</td>
<td>51</td>
<td>C(58)</td>
<td>ND       ND       ND       ND</td>
<td>ND</td>
<td>NA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>M</td>
<td>MSH2</td>
<td>c.1216C→T (p.Arg406X)</td>
<td>58</td>
<td>UR(58), Cx3(33,34)</td>
<td>ND       ND       ND       ND</td>
<td>ND</td>
<td>NA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>M</td>
<td>MSH2</td>
<td>EPCAM 3rd deletion</td>
<td>66</td>
<td>+        +        +        +</td>
<td>ND</td>
<td>B</td>
<td>Ta</td>
<td>HG 1</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>M</td>
<td>MSH2</td>
<td>c.642_845del (p.Gln215X)</td>
<td>66</td>
<td>C(46)</td>
<td>ND       ND       ND       ND</td>
<td>ND</td>
<td>NA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>MSH2</td>
<td>c.793_1_1076+del (Del exon 5-6)</td>
<td>63</td>
<td>UR(67), C(50), BR(72)</td>
<td>+        -        tws      +</td>
<td>MSI</td>
<td>TUR</td>
<td>T1</td>
<td>HG 1</td>
</tr>
<tr>
<td>1</td>
<td>M</td>
<td>MSH6 50% carrier risk</td>
<td>c.212_1G→A</td>
<td>70</td>
<td>+        +        +        +</td>
<td>ND</td>
<td>B</td>
<td>T2a</td>
<td>HG 2</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>M</td>
<td>MSH2</td>
<td>c.942_2Z→G</td>
<td>74</td>
<td>C(55)</td>
<td>+        -        tws      +</td>
<td>ND</td>
<td>B</td>
<td>Ta</td>
<td>HG 1</td>
</tr>
<tr>
<td>49</td>
<td>M</td>
<td>MSH6</td>
<td>c.1_467+del (Del exon 1-2)</td>
<td>56</td>
<td>UR(56), RP(57), ME(58), PR(57)</td>
<td>+        -        +        +</td>
<td>ND, RP</td>
<td>CP</td>
<td>T1</td>
<td>HG 1</td>
</tr>
<tr>
<td>67</td>
<td>M</td>
<td>MSH6</td>
<td>c.3514dup (p.Arg1172fs)</td>
<td>71</td>
<td>UR(70), C(70)</td>
<td>+        +        +        +</td>
<td>ND</td>
<td>B</td>
<td>Ta</td>
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</tr>
<tr>
<td>60</td>
<td>M</td>
<td>MSH6</td>
<td>c.651dup (p.Lys218X)</td>
<td>73</td>
<td>UR(73), PR(67), C(61)</td>
<td>+        +        +        +</td>
<td>ND</td>
<td>TUR</td>
<td>Ta</td>
<td>LG 1</td>
</tr>
<tr>
<td>48</td>
<td>M</td>
<td>MSH6</td>
<td>c.3261del (p.Phe1088fs)</td>
<td>84</td>
<td>URx2(84), C(63)</td>
<td>+        +        +        +</td>
<td>ND</td>
<td>TUR</td>
<td>Ta</td>
<td>LG 1</td>
</tr>
</tbody>
</table>

M, male; F, female; C, colon; UR, ureter; RP, renal pelvis; E, endometrial; PR, prostate; BR, breast; ES, esophageal; ME, melanoma; tws, tumor weaker than stroma; +, MMR protein immunohistochemical staining present; -, MMR protein immunohistochemical staining absent; MSS, microsatellite stable; MSI, microsatellite unstable; TUR, transurethral resection; CP, cystoprostatectomy; B, biopsy; NA, not accessible; HG, high grade; LG, low grade; 1, papillary; 2, solid growth pattern.
persons consisted of 406 proven mutation carriers (individuals with a pathogenic mutation on germline mutation analysis) and 838 first degree relatives. The latter group consisted of 111 obligate mutation carriers (concluded because of their position in the pedigree in relation to relatives tested positive for a mutation) and 727 persons at 50% risk to be mutation carriers. In 22 families, at least one (n=27) confirmed mutation carrier or first degree relative of a mutation carrier was diagnosed with UC of the urinary bladder, ureter or renal pelvis. In two additional families, the patient with UC of the bladder was not a first but a second degree relative of the mutation carrier diagnosed. Second degree relatives were not included in the KM risk analysis but the two second degree relatives with UC were included in the histopathology study. UC of the bladder was diagnosed in 21 patients from 19 Lynch syndrome families, the majority (71%) coming from MSH2 families (15 MSH2, two MLH1, and four MSH6); 19 out of 21 (90%) were men. Two patients with bladder cancer were at 50% risk of being an MSH2 mutation carrier, but could not be tested. Bladder cancer was diagnosed at an average age of 60±12 years (range 41–84 years), which is approximately 10 years younger than the average age of sporadic bladder cancer in the Netherlands.

The cumulative risk of bladder cancer until the age of 70 (CR70) in all MMR mutation carriers and their first degree relatives was 7.5% (95% CI 5.1% to 11.9%) for men and 1.0% (95% CI 0% to 2.4%) for women (table 1). The corresponding CR70 for the Dutch population is 1.2% for men and 0.5% for women. The RR for carriers of any MMR mutation, as compared to the general Dutch population, was 7.0 (95% CI 3.4 to 15.0, p<0.001) for men and 5.8 (95% CI 0.5 to 16.1, p=0.15) for women. The overall CR70 risk for urinary tract cancer, including the bladder, in MSH2 mutation carriers and first degree relatives was 18.2% (95% CI 5.0% to 31.4%) in men and 8.4% (95% CI 0% to 15.4%) in women (table 1).

Two or more primary urinary tract cancers, of which one was in the bladder, were diagnosed in nine of all 21 patients with bladder cancer; in six patients these two cancers were diagnosed synchronously or within 1 year. The remaining three patients, with a metachronous combination of bladder and upper urinary tract cancer, had their bladder cancer diagnosed earlier in life than the upper urinary tract cancer. Exclusive upper urinary tract cancer was diagnosed in eight patients from seven Lynch syndrome families, with 68% caused by MSH2 (five MSH2, two MLH1, and one MSH6). The CR70 of colorectal cancer for confirmed MMR mutation carriers was 68.2% (95% CI 56.6% to 69.8%) and the CR70 of endometrial cancer was 35.4% (95% CI 26.8% to 44.0%) (table 1).

Bladder cancers from germline MSH2 mutation carriers were tested for mismatch repair deficiency: MSI was present in bladder tumour DNA from six out of seven cases, and IHC staining of MSH2 protein was absent in nine out of 11 cases, indicating mismatch repair deficiency (figure 2, table 2). Additionally, IHC staining of MLH1 or MSH6 proteins was absent in five out of six bladder carcinomas from MLH1 or MSH6 germline mutation carriers, respectively (figure 1, table 2). Three bladder tumours were identified having normal IHC staining and one tumour was MSS. As a control, IHC of five sporadic bladder carcinomas showed normal staining of all four MMR system proteins. No typical histological characteristics were observed in the bladder carcinomas when compared with sporadic bladder carcinomas (table 2).
DISCUSSION
This study indicates an increased risk of urothelial cancer of both the urinary bladder and the upper urinary tract (ureter and renal pelvis) in patients with Lynch syndrome carrying a germline MSH2 mutation. Furthermore, this study indicates that cancer of the urinary bladder, ureter and renal pelvis is also, though rarely, associated with MSH6 or MLH1 mutations. A causal relation between MSH2 deficiency and bladder cancer is likely: in the first place, because bladder cancers in these families often show MSI and/or absence of IHC staining of the MSH2 protein, just like upper urothelial tract cancer and colorectal cancer; in the second place, because of the presence of two MSH2 mutation families, each of which contained two first degree family members with bladder cancer, and with three of the bladder cancers diagnosed under the age of 50 (as illustrated in figure 3).

It is interesting that especially MSH2 mutation carriers are at increased risk of urothelial cancer, as observed in this cohort and in previous studies.2 12 16 The diversity in the function of the MSH2, MLH1 and MSH6 protein might be responsible for the variation in cancer risk. Environmental factors (eg, smoking status) may also affect the urologic tract cancer occurrence rates, but we do not have the necessary information to determine if this might contribute to the differences.

In eight out of 21 patients with bladder cancer, this was their first cancer diagnosis, whereas at this stage five of them developed another Lynch syndrome associated cancer at an older age. Therefore, early diagnosis of Lynch syndrome may prevent development of a second primary cancer, especially colorectal cancer (CRC) by regular colonoscopy with polypectomy.26 The diagnosis of Lynch syndrome in healthy relatives may lead to prevention or early detection of cancer, which improves the prognosis.26 Thus bladder cancer, just like upper urothelial tract cancer, can be added to the Bethesda criteria27 and the Amsterdam II criteria,27 and lead to the clinical suspicion of Lynch syndrome. The occurrence of bladder cancer can be used in family history taking and molecular diagnostics to identify the families that are at risk of Lynch syndrome.

Cumulative risks of colorectal and endometrial cancer are within the ranges published by other studies.2–5 8 13 28 29 Bladder cancer risk observed in our cohort was significantly higher than that observed in previous studies.6 9 12 16 18 These studies differed from our study by: (1) type of risk that was calculated; (2) by type of population; and (3) whether or not the type of mutation was distinguished. The data from these studies are given in table 3. Additionally the discrepancy in bladder cancer risk between our study and other studies may result from our systematic data collection approach (obtaining up-to-date information). This led to the discovery of nine new cases of bladder carcinoma, previously unrevealed with the standard procedure of a clinical geneticist taking the family history.

Considering the high risk of urothelial tract cancer in MSH2 mutation carriers, a surveillance programme needs to be developed. At present various recommendations have been published. The present European guidelines for families with an MMR mutation include ultrasound and urinalysis every 1–2 years with patients from the age of 30 or 35 only in cases where upper urinary tract cancer runs in the family (two or more cases of UC).11 The American guidelines include urinalysis with cytology every 1–2 years with patients from the age of 25 to 35 for all family members with Lynch syndrome.30 Watson et al proposed (unspecified) surveillance of patients starting with the age of 50, especially for families that carry mutations in MSH2.12 Although cytology is the superior marker in terms of specificity,31 Myrhoy et al showed that the sensitivity of urine cytology in diagnosing asymptomatic upper urinary tract cancer in Lynch syndrome is approximately 50%. Therefore, cytology only is not a proper method of surveillance.32 The most important biomarker of urothelial cancer is macro- or microscopically haematuria, which occurs in 85% of patients with bladder cancer.33 Consequently, Koornstra et al recommend annual surveillance for haematuria, by urinary dipstick, of all patients with Lynch syndrome, beginning at the age of 45 to 50.34 The recent use of sensitive transducers has improved imaging of the upper urinary tract and bladder by

Figure 3 Pedigree of a Lynch syndrome family with two MSH2 mutation carriers with urinary bladder cancer. CRC, colorectal cancer.
Table 3

<table>
<thead>
<tr>
<th>Source</th>
<th>Population</th>
<th>Data obtained from</th>
<th>Design and methods</th>
<th>Stratiﬁed by type of mutation</th>
<th>Risk of bladder cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Germain et al.13</td>
<td>All family members of 985 families fulﬁlling the Bethesda criteria</td>
<td>Retrospective; analysis of incidence of cancer, compared to the general population</td>
<td>Retrospective; analysis of incidence of cancer, compared to the general population</td>
<td>No</td>
<td>RR = 1.06 (95% CI 0.90 to 1.24)</td>
</tr>
<tr>
<td>Geary et al.14</td>
<td>All family members of 130 families with MSH2 or MSH6 mutations</td>
<td>Retrospective; analysis of incidence of cancer, compared to the general population</td>
<td>Retrospective; analysis of incidence of cancer, compared to the general population</td>
<td>No</td>
<td>RR = 1.52 (95% CI 0.63 to 3.66, p = 0.059)</td>
</tr>
<tr>
<td>Sijmons et al.</td>
<td>Dutch hereditary non-polyposis colorectal cancer registry</td>
<td>Contact with family members known at the Hereditary Cancer Institute Erasmus MC, Rotterdam, and the Finnish Cancer Registry</td>
<td>Contact with family members known at the Hereditary Cancer Institute Erasmus MC, Rotterdam, and the Finnish Cancer Registry</td>
<td>Yes</td>
<td>CR70* overall</td>
</tr>
</tbody>
</table>

FDR, ﬁrst degree relative; MC, mutation carrier; PMC, probable mutation carrier; CR, cumulative risk; NS, not signiﬁcant; F, female; M, male.

References


6. Lynch HT, Taylor RJ, Lynch JF, Knezevic JA, Barrows A, Fodde R, Wijnen J, Wagner A. Multiple primary cancer, including transitional cell carcinoma of the upper urinary tract cancer. In conclusion, our data suggest that in addition to upper urinary tract cancer, urothelial cancer of the urinary bladder is part of the Lynch syndrome tumour spectrum. Carriers of an MSH2 mutation are particularly at increased risk of urinary tract cancer including cancer of the bladder. In these cases we consider surveillance necessary.

Competing interests None.

Provenance and peer review Not commissioned; externally peer reviewed.

Recomendations for urothelial carcinomas surveillance in Lynch syndrome

1. Surveillance with a combination of ultrasound of the bladder and upper urinary tract, urinary cytology and sediment.
2. In every MSH2 mutation carrier
3. From age 40 and up
4. Performed every 1–2 years

ultrasonography. It was shown to be as accurate in the detection of renal masses and bladder filling defects as intravenous urography and computed tomography scanning.35,36 Further studies are needed to develop an optimum early detection strategy concerning the appropriate interval, methods to be used, and patient groups to be included. Until then, we propose a combination of ultrasonography of the bladder and upper urinary tract, urinary cytology and urine sediment (erythrocytes) every 1–2 years. We recommend a surveillance programme for UC of the bladder and upper urinary tract for all MSH2 mutation carriers starting at the age of 40, which is based on the youngest Lynch syndrome patient with bladder cancer reported in the literature (age 40) and observed in our study (age 41).35 The top age limit of surveillance for UC can be similar to that of surveillance for colorectal cancer. Surveillance should not be limited to families with a history of UC, because in our study clustering of urinary tract cancer was only observed in five families, while 19 patients had a negative family history of urinary tract cancer.

In conclusion, our data suggest that in addition to upper urinary tract cancer, urothelial cancer of the urinary bladder is part of the Lynch syndrome tumour spectrum. Carriers of an MSH2 mutation are particularly at increased risk of urinary tract cancer including cancer of the bladder. In these cases we consider surveillance necessary.

Acknowledgements We would like to thank Irene Reimerink and Marsha Voorendt (genetic counselors), Dr Ernie Bongers (clinical geneticist), Riki Willems, Monique Link, Monique Goossens, Sandra Hendriks-Comelissen and Evelien Haenselaar (technical assistance).

Provenance and peer review Not commissioned; externally peer reviewed.