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## Introduction & Methods

**Lynch syndrome (LS) is a hereditary condition associated with a high risk for colorectal cancer (CRC)**

- LS is caused by germline mutations in DNA mismatch repair (MMR) genes. Incidence 2-4% all CRC

**Deficient DNA MMR can be seen in Lynch syndrome, however can be also seen in sporadic CRC**

- The *BRAF* V600E mutation is associated with *MHL1* promoter hypermethylation
- Sequential *BRAF* V600E and *MLH1* promoter hypermethylation testing differentiates sporadic and LS-associated CRC

**The two screening tests used in the prediction of LS are MMR protein expression assessed by immunohistochemistry (IHC) and DNA microsatellite instability (MSI) analysis**

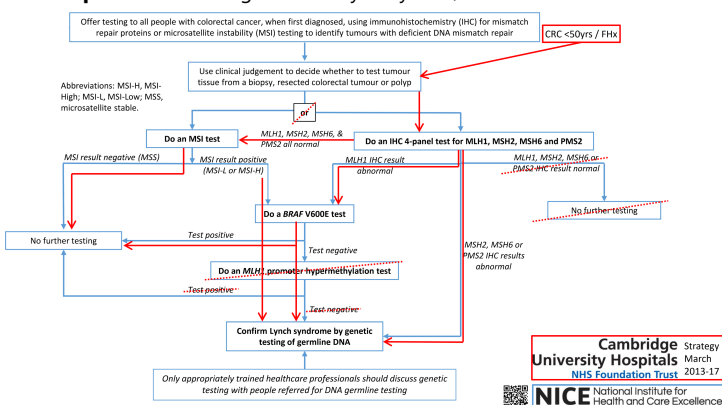
- Previously accepted knowledge had been that MSI was superior to IHC in predicting a germline mutation
- However, later studies showed that, whilst both methods had their limitations, MSI was more sensitive than IHC but slightly less specific

**To ascertain the presence and level of discrepancy between the two methods, we compared our IHC and MSI results retrospectively**

### Patient selection:

- Preselected CRC cases (<50 years or histomorphological / family history criteria suggestive of LS)
- Where MMR IHC testing was performed between March 2013 and March 2017

**Techniques:** MSI: Promega MSI Analysis System; *BRAF*: V600E mutation



## Conclusions

**Discrepancies between MMR and MSI are rare (2/379 (0.5%))**

- Performing either test alone may result in patients warranting further investigation for germline mutations being missed
- This has additional importance in view of recent FDA approval of pembrolizumab for MSI-H/MMR-deficient solid tumours
- Is there a need for MMR IHC guidance for pathologists in view of the difficulties of interpretation?

**Testing on aged FFPE samples can be problematic**

- Limitations in PCR success related to poor DNA quality
- Though aged specimens often show retained MMR IHC, IHC performance can also be affected by prolonged storage
- Failure of successful MSI testing especially on aged specimens should therefore result in routine genetic discussion regardless of MMR IHC status.

## Results: Summary Table

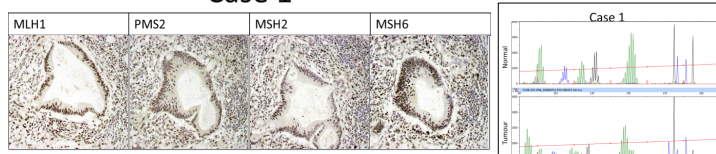
Total cases: 516	MMR proficient: 419 (81%)	MSI not done: 65 (15% of MMR proficient; 13% of total cases)		
		MSI done: 354 (84% of MMR proficient; 68% of total cases)	MS stable: 333/354 (94%)	Likely / suboptimal MSS: 8/354 (2.3%)
			MSI-indeterminate: 2/354 (0.6%) <i>One case indeterminate due to technical failure</i>	Sample unsuitable: 8/354 (2.3%) <i>6 specimens were aged 11-29yrs</i>
Total cases: 516	MMR deficient: 97 (19%)	MSI not done: 72 (74% of MMR deficient; 14% of total cases)		
		MSI done: 25 (26% of MMR deficient; 5% of total cases)	MS stable: 4/25 (16%) <i>(4% of MMR deficient; 0.8% total)</i>	Likely MSI-high: 1/25 (4%) <i>23yrs of storage caused suboptimal DNA quality</i>
			MLH1 and/or PMS2 abnormal: 60/72 (83%) <i>• BRAF V600E mutation 29/50 (58%)</i>	MSI-high: 20/25 (80%) <i>MLH1 and/or PMS2 abnormal: 14/20 (70%)</i> <i>• BRAF V600E mutation 3/8 (38%)</i>

## Results: Identified MMR-MSI Discrepancies

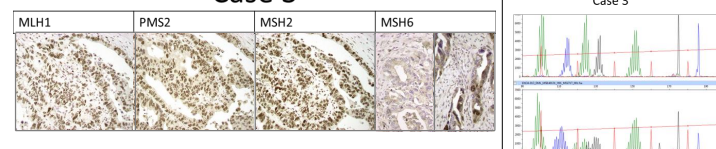
Case	MLH1	PMS2	MSH2	MSH6	Comment
1*	+	+	+	+	No germline mutation in any of the four genes All IHC originally reported as positive.
2	+	-	+	+	Germline mutation in MLH1 All IHC originally reported as positive.
3	+	+	+	-/-	All IHC originally reported as positive. Germline mutation in MSH6

\* true mismatch

### Case 1



### Case 3



Case	MLH1	PMS2	MSH2	MSH6	Comment
4	+(weak)	+(weak)	+/+	+	PMS2 originally reported as negative, no MLH1 germline or loss of heterozygosity (LOH)
5*	-/+/-	-/-/-	+/+/-	-/-/-	No MLH1 germline or LOH
6	+/+	+/+	+	+	Original report states "Interpretation of MLH1 and PMS2 is difficult with focal weak nuclear positivity". BRAF mutation negative
7	+	+	+	+	MLH1/PMS2 originally reported as weak. BRAF not done

\* true mismatch

### Case 5

