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Is Lynch syndrome a pediatric onset cancer predisposition syndrome: a systematic review

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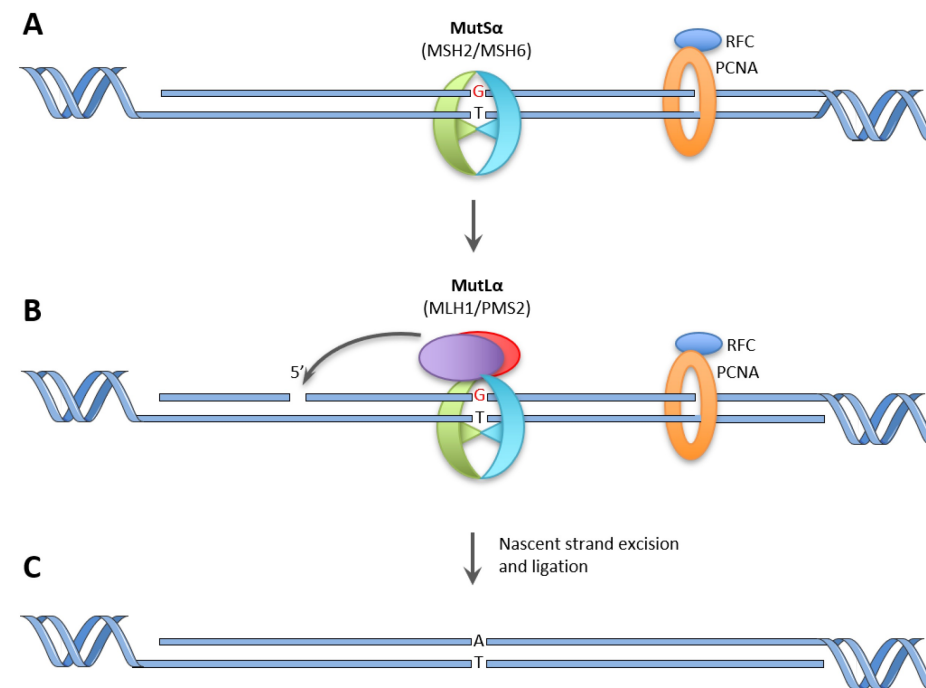
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Background: Lynch syndrome

- Heterozygous, autosomal dominant variant in one of the DNA mismatch repair genes: ¹
 - *MLH1, MSH2, MSH6, PMS2*
- Failure to correct mismatching leads to hypermutation and subsequent errors in cell replication ¹



Background: Lynch syndrome

- Cancers of the colon and rectum, stomach, small intestine, biliary tract, genitourinary tract, reproductive organs and brain ³
 - Most commonly occur > age 40 years
 - Cancer risk is high: 66% of men develop colorectal cancer, 39% of women develop endometrial cancer
- Widened availability of genomic testing across the lifespan has revealed a growing collection of children with Lynch Syndrome but relevance is not well understood

Genomic sequencing in Quebec

- Since 2020 all pediatric cancer patients in Quebec are offered paired germline and tumour sequencing as part of research initiatives (Signature, Triceps & others ⁴)
- A unique opportunity to determine the prevalence and relevance of Lynch syndrome in unbiased children and adolescents with cancer
- To date, 599 patients have undergone successful germline analysis including WES/targeted cancer gene panel including MMR genes
 - 0.5% have been found to have a heterozygous, pathogenic germline variant in one of *PMS2*, *MSH6* and *MLH1*

Case example (MCH)

- Previously healthy 7-year-old boy newly diagnosed with SR B-ALL with favorable cytogenetics
- Family history:
 - Maternal grandmother - colorectal cancer (62)
 - Maternal great-grandmother - colorectal cancer (92)
 - Maternal great aunt – ovarian cancer (35)
 - Maternal great aunt – endometrial cancer (70s)
 - PGM breast cancer (61)
- Family consented to *Signature* study → found to have a pathogenic germline variant in *PMS2*
- Many questions arise from this case:
 1. **Are there other patients like him?**
 2. What does this finding mean for the patient?
 3. Is this finding relevant to his current cancer diagnosis and management?

Study aims

Primary objective:

What proportion of pediatric oncology patients who have undergone genetic sequencing have a pathogenic or likely pathogenic variant in a gene associated with Lynch Syndrome?

Secondary (future) objectives:

1. What proportion of pediatric oncology patients identified to have Lynch syndrome variants also have a second hit in tumour DNA?
2. How does this data compare with that of a control (non-oncology) cohort?

Methods

- Systematic review following the Principles of the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) statement
 - Prospero ID: CRD42022359233
- Expert librarian recruited to develop search strategy (PubMed, Embase and Web of Science, grey search with Google Scholar)
- Article review by two independent reviewers → collection and organization via Rayyan software
- Inclusion criteria:

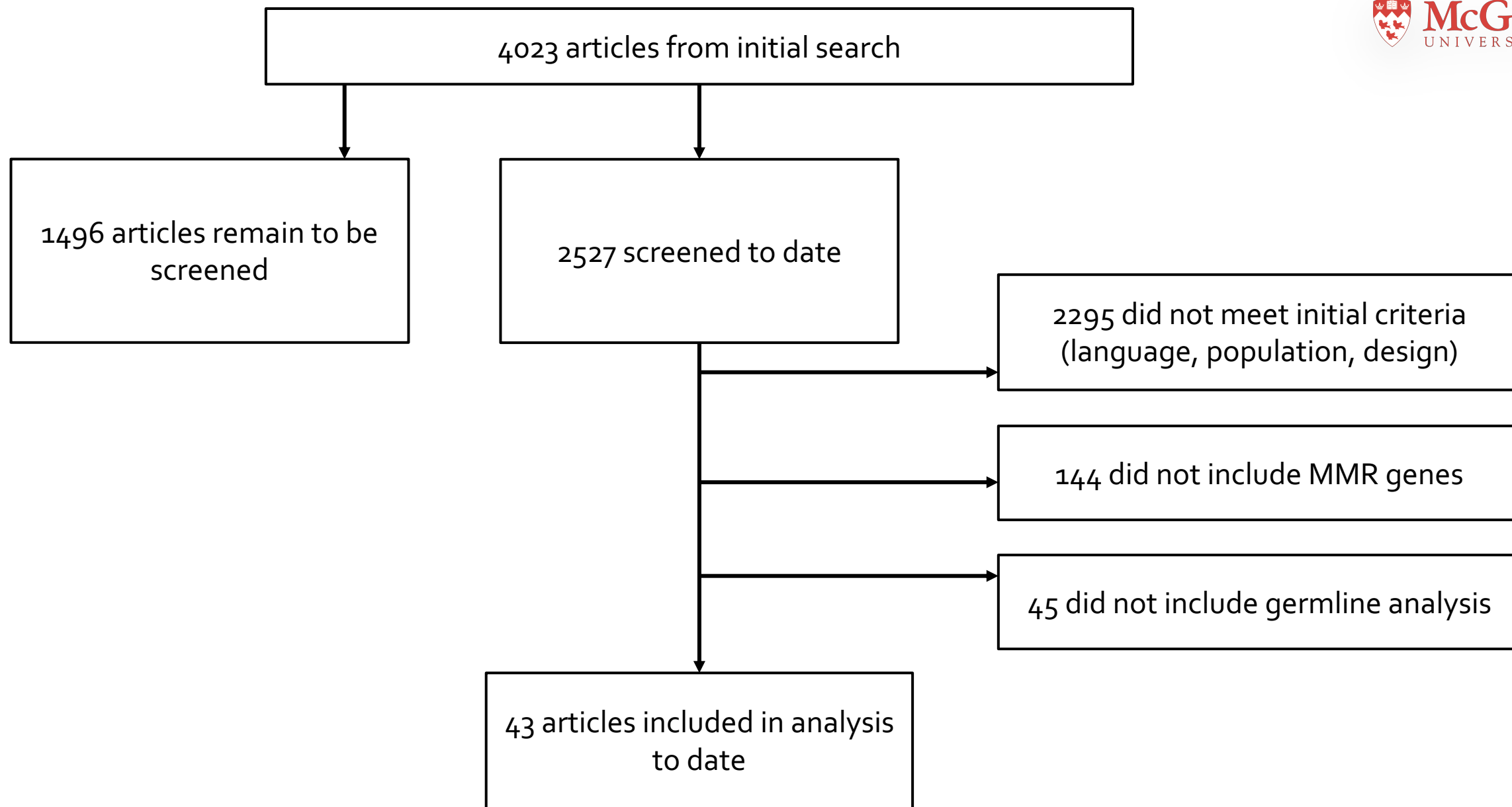
Observational studies (case reports, case series, and cohort) and intervention studies

Germline analysis of MMR genes (*MSH2*, *MSH6*, *PMS2*, *MLH1*) via targeted sequencing/WES/WGS

Pediatric (≤ 18 years) patients with a diagnosis of malignancy

Published from 2012 onwards

Published in English



Preliminary results

- 43 studies
- 3246 pediatric oncology patients who have undergone germline MMR gene testing
- 23 (0.7%) patients found to have pathogenic or likely pathogenic Lynch syndrome variants
- 8 females, 8 males, 7 not defined

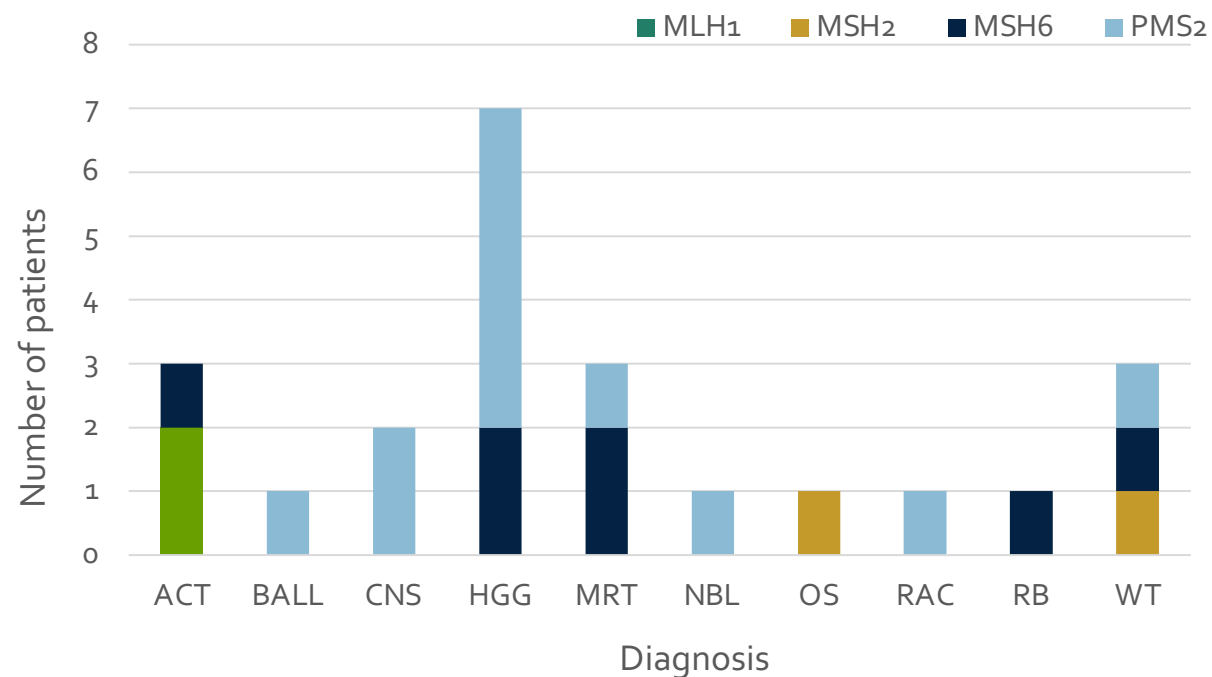


Figure 1. Lynch syndrome variants per pediatric oncologic diagnosis

ACT = adrenocortical tumour, **BALL** = B-cell acute lymphoblastic leukemia, **CNS** = central nervous system tumour,
HGG = high-grade glioma, **MRT** = malignant rhabdoid tumour, **NBL** = neuroblastoma, **OS** = osteosarcoma,
RAC = rectal adenocarcinoma, **RB** = retinoblastoma, **WT** = Wilms tumour

Conclusions

- Prevalence of Lynch syndrome in pediatric oncology patients in Quebec (0.5%) appears to be comparable to that of literature reports (0.7%)
- Findings may be relevant for families but evidence of causality is lacking
- Next steps:
 - Complete oncology cohort analysis & consideration of somatic second hits
 - Conduct genotype/phenotype correlation
 - Compare with a non-oncology cohort
 - Follow ongoing *Signature* data collection
 - Distribute findings beyond the oncology setting

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