LETTERS

The study of Lynch syndrome in a special population reveals a strong founder effect and an unusual mutational mechanism in familial adenomatous polyposis

We read with interest the study by Møller and colleagues.1 The isolation and relative homogeneity of the Saudi population enhance the potential to discover founder mutations, while its high rates of consanguinity enhances homozygosity even for typically dominant disease genes.2 3 We have previously explored the contribution of Lynch syndrome (LS) to colorectal cancer (CRC) based on ~800 Saudi patients.4 We have since expanded our cohort to 1207 CRC patients. Of the 112 mismatch repair deficient (dMMR) cases, MMR gene mutations were identified in 26 cases and these varied in their cancer risk by age 50 years (figure 1). Three founder mutations were observed, accounting for 42.3% (n=11) of LS cases, and none is listed in gnomAD. The PMS2:c.1376C>G;p.S459X variant was the most commonly encountered LS variant (n=6), and we calculated its minor allele frequency at 0.0001. Importantly, we were able to identify a homozygous individual for PMS2:c.1376C>G;p.S459X through a large scale whole-exome sequencing (WES) study.2 This individual presented at age 8 years with haematochezia and a typical picture of familial adenomatous polyposis (FAP) with thousands of polyps but negative adenomatous polyposis coli (APC) testing for germline mutations and dMMR (figure 2). High depth capture sequencing of APC on three independent polyps showed at least one pathogenic APC variant per polyp (one had two variants, while one variant was shared by two polyps) completely absent in blood (figure 2). We also performed WES on one of the polyps and compared it to the WES performed on blood-derived DNA and observed no apparent enrichment for dinucleotide or trinucleotide repeat-derived mutations.

Thus, while our study shows a comparable prevalence of LS and associated lifetime risk of CRC between Saudi and other populations, the genetic landscape of LS was distinct. First, the distribution of mutations among the MMR genes is unique since majority of LS cases in the literature are caused by mutations in MLH1 and MSH2 with less than 5% being caused by PMS2.5 7 Second, we note a strong founder effect in our population likely due to the heritage of tribal affiliation. The founder mutation (c.1376C>G;p.S459X) in PMS2...
was previously reported in a single family in which the parents developed LS and one child developed T-cell acute lymphoblastic leukaemia. Here, we show homozygosity for this variant in a young child with typical colonic appearance for FAP. A study of APC-negative FAP cases found that biallelic inactivating mutations in *MutS Homolog 3 (MSH3)* induce somatic APC mutations that are largely consistent with dinucleotide and trinucleotide repeat instability. That study also showed that biallelic PM2 mutations cause FAP but did not analyse APC in those patients. Our patient with a homozygous PM2 truncation, therefore, offers the first evidence to date that PM2-related FAP is mediated by somatic APC mutations as demonstrated by the finding of at least one APC mutation in each of the three polyps. But why was one somatic mutation shared between two physically distinct polyps? This may hint at an earlier developmental onset of that somatic mutation such that a segment of the colon is affected. The resulting FAP phenotype and the unraveling of multiple somatic APC mutations that are not dinucleotide or trinucleotide repeat-derived raise important questions about the underlying mechanism, which should be the subject of future investigations. In the interim, patients with biallelic mutations in MMR genes may benefit from targeted APC sequencing in their colon as part of their cancer screening.


1Department of Genetics, King Faisal Specialist Hospital and Research Center, Riyadh, Saudi Arabia
2Department of Pediatric Surgery, King Faisal Specialist Hospital and Research Center, Riyadh, Saudi Arabia
3Department of Pathology, King Faisal Specialist Hospital and Research Center, Riyadh, Saudi Arabia
4Department of Genetics, King Faisal Specialist Hospital and Research Center, Riyadh, Saudi Arabia

Correspondence to Dr Khawla S Al-Kuraya, Human Cancer Genomic Research, King Faisal Specialist Hospital and Research Center, Riyadh 11431, Saudi Arabia; kkuraya@kfshrc.edu.sa

Contributors FSA and KSA designed and implemented the study. TM, AKS and SS performed WES, critical data analyses, interpretation of results and wrote the manuscript. RB performed DNA extraction and analysed the data. SKP, AA and FAD contributed samples and analysed clinical data. FSA and KSA wrote the original draft and critically reviewed the manuscript.

Funding The authors have not declared a specific grant for this research from any funding agency in the public, commercial or not-for-profit sectors.

Competing interests None declared.

Patient consent for publication Not required.

Provenance and peer review Not commissioned; internally peer reviewed.

Open access This is an open access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited, appropriate credit is given, any changes made indicated, and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/.


Received 19 December 2019
Revised 6 January 2020
Accepted 6 January 2020
Published Online First 10 January 2020


ORCID iD Khawla S Al-Kuraya http://orcid.org/0000-0002-8430-6693

REFERENCES


