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Germline mutations in the proof-reading domains of *POLE* and *POLD1* predispose to colorectal adenomas and carcinomas

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Abstract

Many individuals with multiple or large colorectal adenomas, or early-onset colorectal cancer (CRC), have no detectable germline mutations in the known cancer predisposition genes. Using whole-genome sequencing, supplemented by linkage and association analysis, we identified specific heterozygous *POLE* or *POLD1* germline variants in several multiple adenoma and/or CRC cases, but in no controls. The susceptibility variants appear to have high penetrance. *POLD1* is also associated with endometrial cancer predisposition. The mutations map to equivalent sites in the proof-reading (exonuclease) domain of DNA polymerases ϵ and δ , and are predicted to impair correction of mispaired bases inserted during DNA replication. In agreement with this prediction, mutation carriers' tumours were microsatellite-stable, but tended to acquire base substitution mutations, as confirmed by yeast functional assays. Further analysis of published data showed that the recently-described group of hypermutant, microsatellite-stable CRCs is likely to be caused by somatic *POLE* exonuclease domain mutations.

Mutations in at least 10 genes are responsible for Mendelian syndromes associated with colorectal cancer. For some of these genes (*APC* and *MUTYH*), the primary predisposition is to multiple adenomas, the benign precursors of many colorectal cancers (CRCs). For other genes (*STK11/LKB1*, *SMAD4*, *BMPRIA* and *GREM1*), CRC risk is mediated through the development of hamartomas or mixed polyps; and for yet other genes (*MSH2*, *MLH1*, *MSH6* and *PMS2*), there is usually no great number of polyps and early-onset CRC or endometrial cancer is the usual presentation. The functions of these 10 genes vary, although it is notable that four encode (*MSH2*, *MLH1*, *MSH6* and *PMS2*) encode DNA mismatch repair proteins and a fifth (*MUTYH*) codes for a glycosylase that effects base excision repair (*MUTYH*). There exists a set of patients who appear *a priori* to have a strong chance of carrying a high-penetrance CRC predisposition allele, but who have no mutations in these genes. One such group of patients is characterised by multiple adenomas, typically 10-100 in number, often presenting before the age of 60 and frequently progressing to CRC unless treated. Some of these individuals come from extensive CRC pedigrees, but many have no significant family history of colorectal tumours.

As part of the Oxford-Illumina WGS500 project, we undertook whole-genome sequencing (WGS) of 15 probands who had been diagnosed with at least 10 colorectal adenomas by 60 years of age (Supplementary Table 1). For three probands, a relative with more than 5 adenomas was also sequenced, and for one proband two additional affected relatives were sequenced. Eight of the 20 sequenced individuals had developed colorectal carcinoma (CRC) and all of the remainder had a first-degree relative with CRC. Known Mendelian cancer syndromes had reportedly been excluded previously in the clinical diagnostic setting, by mutation screening for *APC*, *MUTYH* and the mismatch repair genes, together with microsatellite instability (MSI) testing and immunohistochemistry for mismatch repair proteins in some cases. The pedigrees of the 15 families showed a degree of heterogeneity in their phenotypes and patterns of inheritance, and we anticipated that this might reflect underlying genetic heterogeneity.

RESULTS

Identification of colorectal tumour susceptibility variants

Following standard quality assurance procedures, whole-genome sequencing reads were mapped and called using the established local pipeline based on the STAMPY¹ and PLATYPUS programs (further details in Methods). We initially excluded two individuals who were found, despite previous testing, to have pathogenic heterozygous germline mutations in genes known to cause high-penetrance predisposition to colorectal tumours (Supplementary Table 1). One of these individuals had attenuated familial adenomatous polyposis (FAP) owing to a splice site germline mutation in the *APC* gene (c.423 -2 A>G) and the other had Lynch syndrome caused by an *MSH6* mutation (R911X).

In the absence of information regarding the underlying genetic architecture of the multiple adenoma phenotype, including the mode of inheritance in our families, we treated analysis of the remaining 13 WGS families as the Discovery Phase of our project. We then used a pragmatic approach to prioritise genes for further investigation in a larger Validation Phase of individuals with a similar phenotype. Based on the assumption that at least some individuals would carry mutations with direct, strong effects on protein function, we filtered the data so as to examine only protein-coding and splice site sequence. We filtered variants further using the algorithm shown in Supplementary Figure 1 and then searched for genes that harboured probably pathogenic variants across 4 or more families. However, no genes matched these criteria.

We therefore switched focus to single families. We initially examined the pedigree (SM2702, Figure 1) from which 3 individuals had been sequenced. We used pre-existing linkage data from 5 SM2702 individuals with ≥ 5 early-onset colorectal adenomas^{2,3} to restrict our search to 8 shared regions of the genome. There were 6 non-silent coding variants present in 4 different chromosomal regions that were shared by the 3 sequenced members of SM2702 (Supplementary Table 2). Further genotyping determined that the additional affected members of SM2702 (Figure 1) only shared one of these variants, *POLE* L424V (NM_006231:c.C1270G). *POLE* encodes the catalytic and proof-reading sub-unit of polymerase ϵ . The L424V amino acid is highly conserved (Supplementary Figure 2a) and the L>V change has predicted severe functional consequences for protein function (SIFT score=0.01, Polyphen2=0.993, PhyloP=1.000, cons46=607, LOD=390 and MutationTaster=0.987).

We genotyped the *POLE*L424V variant in a set of Validation Phase samples. These comprised 3,805 white UK CRC patients enriched for family history of colorectal tumours, multiple adenomas and early-onset disease (see Methods). For comparison, we genotyped 6,721 white UK controls, of whom about two-thirds were population-based and one-third, selected for absent personal history of colorectal tumours. We found 12 additional unrelated cases and no controls who were L424V heterozygotes ($P=2.46 \times 10^{-6}$, Fisher's exact test, one-tailed). In addition, L424V was not present in 10,755 controls sequenced as part of the NHLBI GO Exome Sequencing Project (<http://evs.gs.washington.edu/EVS/>), despite >50X median read depth at this site in the genome. We confirmed that L424V mRNA is expressed, without any evidence of allele-specific instability (details not shown).

The pedigrees of the 12 Validation Phase cases with *POLE*L424V are shown in Supplementary Figure 3. They are compatible with a dominantly-inherited trait. All pedigrees except one contained at least one individual with multiple or very large adenomas, multiple CRCs, or early-onset CRC. Microsatellite marker analysis provided no evidence of a recent common ancestor in these families (data not shown). All the L424V mutation carriers were found in our highly-selected groups of patients from the CORGI, multiple adenoma and NSCCG studies (see Methods) rather than in our CRC clinical trial patients (VICTOR and QUASAR2). This suggests that the relatively severe phenotypes of our L424V carriers do not simply reflect ascertainment criteria and also shows that these mutations are likely to be a rare cause of CRC in the general population. Genotyping of additional members of these 12 families showed that all L424V carriers developed colorectal tumour(s) and that no tumour-free blood relatives of cases carried L424V. One non-carrier, from a kindred whose other affected members developed tens of adenomas or multiple carcinomas, had developed a single tiny (~0.5mm diameter) colorectal polyp by 33 years of age, a phenotype compatible with a sporadic occurrence or an additional "complex" genetic predisposition in the family. Based on a relatively stringent definition of affection status – ≥ 5 colorectal adenomas, ≥ 1 large (>2cm diameter) adenoma, ≥ 2 CRCs, or CRC at ≤ 40 years of age – and on the reasonable assumption that all L424V alleles within each family were identical by descent, the probability of each affected non-proband sharing L424V in the 12 Validation Phase families was 1.22×10^{-4} after ascertainment correction.

Overall, the phenotypes of our L424V pedigrees were consistent with dominantly-inherited, high-penetrance predisposition to colorectal adenoma and carcinoma, with a variable tendency to develop multiple and large tumours. Therapeutic or prophylactic colectomy had occurred in several cases, thus attenuating the phenotype, and it is also likely that some tumours were under-reported, especially in early generations. However, even allowing for these factors, tumour multiplicity appeared to vary among individuals (Figure 1a, Supplementary Figure 3). Moreover, adenomas did not, in general appear to progress rapidly to carcinoma in all individuals. The histological features of the L424V carriers' colorectal

tumours were unremarkable, mostly comprising conventional adenomas and carcinomas without specific morphology or obvious site predilection in the large bowel. No conclusive evidence of a predisposition to extra-colonic tumours or non-tumour phenotypes was found in the L424V-mutant families (Figure 1a, Supplementary Figure 3).

We examined 39 tumours from 11 *POLE*L424V carriers for somatic mutations. “Second hits” by LOH involving the germline wildtype allele were found in some tumours, including adenomas (Supplementary Figure 4). In contrast to Lynch syndrome, all tumours were microsatellite-stable (MS-stable), and the two carcinomas analysed had chromosomal instability. Most tumours were screened for *KRAS* and *BRAF* driver mutations, and a subset of tumours was screened for somatic mutations of established pathogenicity in *APC*, *CTNNB1*, *PIK3CA* and *FBXW7* (Table 1, Supplementary Table 3). Mutations were found in all genes apart from *CTNNB1*, suggesting that the tumours at least partly followed the classical pathway of colorectal tumorigenesis. Mutations were all base substitutions. For *APC*, this was a notable difference from sporadic tumours in which ~60% of mutations are frameshifts⁴. Moreover, certain sites not commonly mutated in sporadic colorectal tumours seemed to be mutation hotspots, for example codons 1114 and 1338 of *APC* and codon 146 of *KRAS*. Unlike in *MUTYH*-associated polyposis, where somatic driver mutations are almost all G:C>T:A changes, our patients’ tumours showed no evidence of a predominant type of substitution in the 6 genes analysed, although at this stage, we could not exclude more subtle biases in this regard (see below).

We then considered variants shared by the two affected individuals sequenced in our other large family, SM1645. Using the same strategy as used for SM2702 – searching for shared functionally important variants and filtering using linkage analysis (Supplementary Table 4) – we identified two SM1645 cases who shared a heterozygous *POLD1* mutation (S478N; NM_002691:c.G1433A). We also found the same variant in another proband (SM1412) who had undergone whole-genome sequencing in the WGS500. This variant was stably expressed in mRNA (details not shown) and was predicted to have a severe effect on protein function (SIFT score=0.01, Polyphen2=0.992, PhyloP=0.987, cons46 (607, LOD=390) and MutationTaster=1.000). Moreover, the equivalent of *POLD1* 478 is *POLE* 428, very close to the site of the L424V mutation (Supplementary Figure 5).

We typed S478N in all available members of SM1645 and SM1412 (Figure 1b,c). All S478N carriers developed colorectal tumour(s) and all affected individuals (see above for criteria) carried S478N (P=0.008 after ascertainment correction). Affected members of SM1645 and SM1412 shared alleles at microsatellites D19S867 and D19S904, consistent with a common ancestor. No tumour-free blood relatives of cases carried the mutation. We noted that a formally unaffected non-carrier from SM1645, whose other members had multiple polyps (Figure 1b), had developed one, very small (<1mm diameter) colorectal adenoma by 43 years of age. We then genotyped the *POLD1* S478N variant in the Validation Phase and found one additional carrier, a case diagnosed with colorectal carcinoma at age 28 whose father also had colorectal cancer at 44 years of age. No control carried *POLD1* S478N, and the variant was also absent from the NHLBI GO Exome Sequencing Project database.

The colorectal phenotypes of *POLD1* S478N mutation carriers were generally similar to those of the *POLE*L424V mutants (Figure 1, Supplementary Figure 3). However, 7 patients with *POLD1* mutations had developed endometrial carcinoma, some at relatively young ages, and one had developed two primary brain tumours. No cases of either tumour type were present in the 13 families with *POLE* mutations. As a result of this finding, we screened 386 early-onset endometrial cancer cases without a reported family history of CRC for *POLD1* S478N, but did not find any further mutation carriers.

We examined 23 tumours from *POLD1* S478N carriers for LOH and for the somatic mutations that had been tested in the *POLE*-mutant tumours (Table 2, Supplementary Table 5). In most respects, the *POLD1*-mutant tumours resembled *POLE*-mutant tumours: “second hits” occurred at *POLD1* by LOH involving the germline wildtype allele (Supplementary Figure 4), tumours were all MS-stable, carcinomas had chromosomal instability, C>T substitution mutations were most common, and the *APC* mutation spectrum was atypical compared with sporadic CRCs. However, there were also some possible differences: *KRAS* mutations tended to target codons 13 and 61 in the *POLD1* mutants, as compared with codons 12 and 146 in *POLE* mutants, and some *POLD1* tumours had *BRAF* mutations.

Functional and structural assessment of *POLE* L424V and *POLD1* S478N

Human *POLE* is the catalytic subunit of the polymerase epsilon (Pol ϵ) enzyme complex⁵. Pol ϵ is responsible for synthesis of the leading strand during DNA replication. In addition to DNA-binding and polymerase domains, Pol ϵ has proof-reading capacity through the *POLE* exonuclease domain. This capacity is essential for the maintenance of replication fidelity and may act not only on newly misincorporated bases, but also on mismatches produced by non-proof reading polymerases such as Pol α . L424 is conserved in the exonuclease domain of class B DNA polymerases (Supplementary Figure 2a) and a Blast search against the Protein Data Bank (www.pdb.org) revealed that L424 maps directly to the active site of the exonuclease domain (L479 in yeast DNA polymerase [PDB ID: 3IAY])⁶. The importance of leucine 424 for proof-reading has been shown by mutation of the equivalent residue (L479S) in *S. cerevisiae* Pol δ /Pol3. This results in a mutator phenotype similar to that of the *pol3-01* mutation, which has less than 0.5% wild-type exonuclease activity^{7,8}.

POLD1 encodes the catalytic and proof-reading sub-unit of Pol δ , the equivalent lagging strand polymerase to Pol ϵ ^{9,10}, and Pol δ may also participate in the mismatch and base excision repair pathways^{11,12}. *POLD1* serine 478 is highly evolutionarily conserved in eukaryotes including *S. cerevisiae*, although in *S. pombe*, the homologous amino acid is the structurally very similar cysteine (Supplementary Figure 2b). S478N lies close to other mutations that have a mutator phenotype in *S. cerevisiae* Pol3⁸, but mutation of this specific residue has not been reported. We therefore constructed the equivalent mutation in fission yeast and determined its effect on reversion of the *ade6-485* allele, which is a C to G transversion that reverts by base substitution¹³. The Pol3-C462N strain (equivalent to human *POLD1* S478N) had a mutation rate 12-fold higher than a wild-type strain that was constructed using the same strategy (Table 3, Supplementary Table 6). We also examined a Pol3-C462S strain, equivalent to the human wild-type, and this mutation did not have a significant effect on the *ade6* reversion rate.

POLE and *POLD1* are related B family polymerases that have greatest homology (23% identity, 37% similarity) over the exonuclease domain (residues 223-517 of *POLE* and 245-571 of *POLD1*). Mapping these two mutations onto the structure of yeast DNA polymerase reveals that they pack together at the interface between two helices that form the base of the exonuclease active site. Modelling the ssDNA component of T4 DNA polymerase/exonuclease complex (1NOY) reveals that *POLE* L424 is only ~5Å from the ssDNA, and mutations of *POLE* 424 or *POLD1* 478 will distort the packing of the helices which will be propagated through to the active site, affecting nuclease activity (Figure 2).

Search for additional *POLE* and *POLD1* predisposition variants in the exonuclease domain

We wondered whether additional germline *POLE* and *POLD1* exonuclease domain variants might predispose to colorectal tumours. We screened these regions (codons 268-471 of *POLE*, codons 304-517 of *POLD1*) for germline variants in 469 cases with multiple colorectal adenomas and/or familial CRC (sample sets (i) and (iv) in Methods). We found

three heterozygous *POLD1* variants, each in a single case, that were absent from public control databases and from the non-cancer cases in the WGS500: P327L (c.C981G), S370R (c.C1110G) and G426S (c.G1276A). Structural studies showed that both S370R and G426S were unlikely to be involved in direct DNA binding and were predicted to have only moderate functional effects. By contrast, for P327L, which occurred in a 70 year-old with 10 colorectal adenomas, there was good evidence of functional consequences. The residue is fully evolutionarily conserved and lies on the DNA interface of the *POLD1* exonuclease domain. Moreover, *POLD1* 327 is analogous to *POLE* 286, an amino acid that lies at the DNA-binding interface and is somatically mutated in sporadic CRCs (Figure 2 and Supplementary Table 7).

Assessment of *POLE* and *POLD1* somatic mutations and their consequences in sporadic colorectal cancers

There is currently little evidence of pathogenic somatic *POLD1* mutations in sporadic CRCs (Supplementary Table 7), but there have been some reports of somatic *POLE* mutations in sporadic CRCs¹⁴⁻¹⁶. Of particular interest is the recent TCGA sequencing of 224 CRC exomes¹⁷. The authors highlighted *POLE* as being an important somatic change, but did not demonstrate a significant excess of mutations over background. Moreover, the importance of individual mutations had not yet been assessed and we therefore examined the TCGA *POLE* data in the light of our own findings above (Table 4, Supplementary Table 7). Fifteen TCGA CRCs had one or more *POLE* mutations at locations throughout the gene. Six of these cancers were hypermutated and/or MS-unstable owing to *MLH1* methylation. A further two CRCs were MS-stable without hypermutation, and one of these had an exonuclease domain mutation. Strikingly, all of the remaining 7 *POLE*-mutant cancers were hypermutated and MS-stable or -low, and all of these had a mutation in the *POLE* exonuclease domain ($P < 0.001$, Fisher's exact test; Supplementary Table 7). In some cancers, the exonuclease mutation was accompanied by a second nonsense (sample 17) or missense mutation elsewhere in the protein (Table 4). Structural analysis showed that the exonuclease domain mutations cluster around the DNA-binding site (Figure 2), including one mutation, P436R (P327L in *POLD1*), that lies in a disordered loop which becomes ordered on DNA binding (sample #15, Supplementary Table 7). All of these mutations will have a direct effect on either DNA binding and/or activity. The 2 exceptions are S370R and G426S that lie on the periphery of the domain, and mutations at these sites must act indirectly, if they are pathogenic.

Exonuclease domain-mutant (EDM) CRCs in the TCGA data set tended to have nonsense mutations in the *APC* gene, including some of the same hotspots that we observed in the patients with germline *POLE* or *POLD1* mutations (Table 4, Supplementary Table 7). For example the *APC*R1114X mutation was found in 6 of 224 TCGA CRCs, 3 of which had *POLE* exonuclease domain mutations ($P < 0.001$, Fisher's exact test). Genome-wide analysis showed that the set of 7 *POLE* EDM CRCs from the TCGA data had an increased tendency to acquire all types of base substitution compared with cancers that had *POLE* mutations outside the exonuclease domain and with all the other TCGA cancers. Indeed, non-EDM *POLE*-mutant cancers were MS-unstable and showed no difference in mutation spectrum or frequency from MS-unstable cancers without *POLE* mutations (Supplementary Table 8). The EDM-associated mutator phenotype did not, however, affect all substitutions equally. Hence, whilst C>G>T:A changes remained the most common type of mutation in EDM tumours, with an ~30-fold excess over other cancers, there was a particularly large (~100-fold) relative excess of G>C>T:A changes (Supplementary Table 8). An analysis of individual EDM cancers (details not shown) demonstrated that they all showed this mutation spectrum, further suggesting that each of these exonuclease domain changes was functionally deleterious. However, within the EDM group, two CRCs had acquired

strikingly large numbers of mutations (over 6,000 each), these being the tumour with the mutation in the loop that became ordered on DNA binding and the tumour that had both an exonuclease domain mutation and a truncating mutation in *POLE*. We therefore speculate that these cancers may have had particularly deficient proof-reading.

A very recent study by Seshagiri *et al*¹⁸ analysed 74 CRC exomes. Although a direct comparison between large-scale sequencing studies using non-identical platforms and analysis pipelines must be performed with caution, we found that the data of Seshagiri *et al* provide support for our conclusions from the TCGA data. Although Seshagiri *et al* did not highlight *POLE* in their manuscript, their data set included two hypermutated MS-stable cancers, both of which were EDM (P286R in both cases) and had an genome-wide mutation spectrum similar to that of the EDM TCGA cancers (details not shown).

We examined four tumours from our *POLE*L424V and *POLD1* S478N carriers using an extended Ion Torrent panel based on 150 cancer gene exomes (see Methods). These tumours all showed mutation spectra similar to the *POLE* EDM cancers (Supplementary Table 8).

DISCUSSION

We have shown that the germline *POLE* variant L424V predisposes to multiple colorectal adenomas and carcinomas. The allele shows dominant inheritance, apparently with high penetrance, and tumours occur predominantly or exclusively in the large bowel. Some individuals have a predominantly multiple adenoma phenotype, similar to *MUTYH*-associated polyposis (MAP) that results from defective base excision repair. In other patients, the phenotype is one of large adenomas or early-onset carcinoma, thus resembling Lynch syndrome that results from defective DNA mismatch repair. This phenotypic variation is found in both MAP¹⁹ and Lynch syndrome²⁰, and is consistent with the action of genetic modifiers. However, it may have other causes (for example, random mutation, different environments, reduction in risk owing to therapeutic surgery or other tumour prophylaxis, under-reporting of adenomas especially in older family members, or premature death). The evidence strongly suggests that the mechanism of tumorigenesis is decreased fidelity of replication-associated polymerase proof-reading, leading to an increased mutation rate by base substitution.

We have also shown that *POLD1* S478N predisposes to colorectal tumours, endometrial cancer and, perhaps, to brain tumours. The colorectal phenotype cannot be distinguished from that of *POLE*L424V mutants in the current data set. The apparently different tumour spectrum between *POLE* L424V and *POLD1* S478N carriers is unexplained, but similar differences are found in Lynch syndrome, in which carriers of *MSH6* mutations, for example, seem relatively prone to endometrial cancer²¹. One possible explanation is that a mutator phenotype is not the only tumour-promoting consequence of *POLE* and *POLD1* – and indeed, mismatch repair gene – mutation.

It is highly plausible, based on theoretical considerations and the TCGA data in sporadic CRCs, that a variety of germline *POLE* or *POLD1* variants in the exonuclease domain can influence CRC risk. A strong candidate from our own analysis is *POLD1* P327L. The effects of these mutations might vary depending on the degree to which they impair proof reading. Other pathogenic mutations might occur in the non-proof-reading domains of *POLE* or *POLD1* or in genes that encode the other components of Polε and Polδ (*POLE2*, *POLE3*, *POLE4*, *POLD2*, *POLD3* and *POLD4*). Such mutations might act a little differently from those in the proof-reading domain, for example if they caused a tendency for the polymerase to incorporate mispaired bases into the growing strand. Of note, we have previously shown

that common variation at the *POLD3* locus is associated with CRC risk in the general population²².

Mice that carry double *Pole* mutations (D272A;E274A) close to the exonuclease active site impair proof reading and cause a mutator phenotype in both the heterozygous and homozygous states^{23,24}. The proof-reading mutations cause a tendency to base substitutions, but not to MSI. *Pole* homozygote mutants are specifically predisposed to developing intestinal adenomas and carcinomas. Mice with germline *Pold1* D400A mutations (equivalent to human D380A) had a similar mutator phenotype in both the heterozygous and homozygous states, and homozygous mutant animals had a tendency to develop a variety of cancers, although, intriguingly, the tumours spectrum differed from that of the *Pole* mutants, with most tumours being of cutaneous, rather than intestinal, origin^{23,25-28}. There was also evidence of different, but overlapping mutation spectra in the *Pole*- and *Pold1*-mutant animals.

The question remains as to whether *POLE* and *POLD1* mutations act as classical tumour suppressors, with “second hits”, as haploinsufficient alleles, or through some hybrid mechanism, such as loss of a specific protein function. We cannot resolve this issue yet from our own data or the TCGA findings, but we note the following: (i) “second hits” do occur in some of our patients’ tumours, including early lesions, at frequencies greater than the background expected from other studies²⁹, but many *POLE*- or *POLD1* EDM tumours do not have identified “second hits” (Supplementary Tables 3, 5 and 7); (ii) the L424V and S478N alleles produce stable mutant mRNA, and there is no evidence from our data that protein-truncating or null *POLE* or *POLD1* mutations predispose to tumours; and (iii) bi-allelic *Pole* or *Pold1* mutations that cause complete loss of enzyme function are probably cell-lethal in null mice. One intriguing mechanism to consider is that mutations are only pathogenic when they couple functional polymerase activity to non-functional proof-reading in the same molecule.

When added to the DNA mismatch repair defects that underlie Lynch syndrome and the base excision repair defects that cause MAP, the mutations in *POLE* and *POLD1* emphasise the critical role of replication errors and coupled repair of base pair-level mutations in predisposition to colorectal and endometrial cancer. This is in contrast to cancers of the breast and ovary, in which double strand break repair is more important in predisposition. *POLE* L424V and *POLD1* S478N mutations can be easily tested and should be considered in any individual with an unexplained personal or family history of multiple or large colorectal adenomas, and/or multiple or early-onset colorectal (or endometrial) carcinoma. Whilst further data are required, it may be prudent in the short term to manage mutation carriers in a fashion intermediate between Lynch syndrome and MAP, with regular and frequent colonoscopic polypectomy and consideration of prophylactic surgery.

Methods

Samples

All cases and controls were UK residents and had self-reported European ancestry. For most individuals, large-scale genotyping data were available that allowed ethnic clustering with HapMap CEU samples to be checked. None of the groups described below overlapped. All studies were performed with UK national ethical committee approval (MREC/06/Q1702/99).

Discovery Phase cases—These were obtained from the COloRectal tumour Gene Identification (CORGI) study³⁰. The study has recruited through Clinical Genetics Departments from throughout the United Kingdom since 1999 and has to date enrolled

1,698 families. General eligibility criteria for the study are given below. Discovery Phase cases were selected from among the set of CORGI probands for a disease phenotype that was most strongly reminiscent of a high-penetrance predisposition. We specifically enriched for multiple tumours and/or an early age of presentation and/or multiple family members with CRC or adenomas. Formal criteria were not set owing to the impossibility of weighing these different features against each other and the heterogeneity of clinical data (for example comparing an individual who had had fewer adenomas but also a colectomy against one who had more adenomas but only polypectomies). Our prioritisation resulted in the identification of a set of 15 unrelated individuals who had been diagnosed with ≥ 10 colorectal tumours before the age of 60 years (Supplementary Table 1). All individuals had CRC or a first- or second-degree relative with CRC, but they were not otherwise selected for family or personal history of other tumour types. All individuals had been screened for *APC* and *MUTYH* mutations by their local Genetics service and Lynch syndrome had been screened by microsatellite instability and/or mismatch repair protein expression in tumours and/or direct *MSH2*, *MLH1*, *MSH6* and *PMS2* mutation testing. DNA from these samples and 5 additional family members was sequenced across the entire genome as part of the Oxford University-Illumina WGS500 collaboration.

Validation Phase cases—These samples comprised the following non-overlapping collections, all comprising white individuals from the United Kingdom.

- i. *Multiple adenoma cases* comprised 271 individuals who had developed ≥ 5 colorectal adenomas at any age, irrespective of family history of colorectal tumours. Germline *APC* and *MUTYH* mutations had been excluded. These individuals were recruited principally from St Mark's Hospital, London and were included in the study irrespective of other personal or family history. The mean number of adenomas was 16 (range 4-65), mean age of presentation was 54 (range 23-80); 21% had had CRC and 31% reported a family history of CRC.
- ii. *CORGI cases* comprised 1,476 individuals from the COloRectal tumour Gene Identification study³⁰. All recruits had developed CRC at age ≤ 80 , and/or "significant" colorectal adenoma(s) that fulfilled one or more of the following criteria: ≥ 3 in number; severe dysplasia; villous histology; and presentation at < 45 years of age. All adenoma-only cases (N=503) had a first or second degree relative with CRC. Mean age of participants was 58 years (range 18-80).
- iii. *National Study of Colorectal Cancer Genetics (NSCCG) CRC cases* (N=300) were selected from the main NSCCG study to be aged < 55 at diagnosis and to have at least one first-degree relative affected with CRC. The main NSCCG study recruited any individual with CRC from Oncology clinics throughout the United Kingdom³¹.
- iv. *Whole-genome sequencing case data* were obtained using the Complete Genomics platform³² from 198 CRC cases previously selected for early age of presentation and family history from the CORGI and NSCCG studies.
- v. *VICTOR/QUASAR2 samples* comprised 1,560 cases from the VICTOR and QUASAR2 clinical trials of stage II/III CRC treated with curative intent³³. VICTOR was a post-primary therapy randomised controlled trial of rofecoxib and QUASAR2, a randomised trial of adjuvant 5-fluorouracil±bevacizumab. The mean age of patients derived from these trials was 61 years (range 44-70).

Validation Phase controls—These comprised the following collections, all comprising white individuals from the United Kingdom

- i. *CORGI* controls were 1,666 spouses/partners of *CORGI* cases and reported no personal or family history of colorectal tumours.
- ii. *1958 Birth Cohort sequencing set* controls ³⁴ (N=300) had undergone whole-exome sequencing.
- iii. *Population controls* (N=3,812) were obtained from the population-based, publicly-available 1958 Birth Cohort and National Blood Service ³⁵ sample sets.
- iv. *GLACIER* controls without cancer (N=943) were derived from the *GLACIER* study of lobular breast cancer predisposition and were cancer-free spouses, partners or friends (E. Sawyer, I. Tomlinson, R. Roylance, unpubl.).
- v. Although not used for primary statistical comparisons, additional population-based control data were derived from the Exome variant Server (NHLBI GO Exome Sequencing Project).

Endometrial cancer cases—386 cases with primary carcinoma of the endometrium and without a family history of CRC were derived from the National Study of Endometrial Cancer Genetics (NSECG) that recruited white UK cases with endometrial cancer under the age of 70 years old ³⁶.

Germline genotyping and mutation screening

WGS data for *POLE*, *POLD1* and other variants within regions of linkage ^{2,3} were validated by bi-directional Sanger sequencing using standard methods (details available from authors) and variants identified both automatically and manually in the Mutation Surveyor (Soft Genetics) program. For screening the Validation Phase samples, we designed KASPar ³⁷ allele-specific SNV primers for *POLE* L424V and *POLD1* S478N (Supplementary Figure 6), and included two known variant samples in each run in order to facilitate genotype clustering (details available from authors). All potential L424V and S478N variants detected were subsequently checked by bi-directional Sanger sequencing. For screening the full exonuclease domains of *POLE* (codons 269-471) and *POLD1* (codons 304-517), bi-directional Sanger sequencing was used (details available from authors).

Expression of the mutant *POLD1* S478N and *POLE* L424V alleles

mRNA was extracted from pelleted untransformed lymphocytes from one patient from SM1645 and two patients from SM 2702 using the RNeasy kit (Qiagen) following manufacturer's instructions. RNA was treated with DNaseI (Fermentas) and converted into cDNA using the High Capacity cDNA reverse transcription kit (Applied Biosystems). cDNA was tested in triplicate using the KASPar genotyping assays described above. Heterozygous gDNA samples were run alongside these samples together with cloned alleles in various mixtures to determine whether the mRNA expression of the two alleles was balanced.

Loss of heterozygosity (LOH) and common ancestor analysis

Microsatellites mapping close to *POLE* (D12S1723, D12S1628, D12S357, D12S1638) or *POLD1* (D19S867, D19S904, D19S907) were analysed in the Gene Marker (Soft Genetics) program and used to assess whether the L424V or S478N alleles were derived from a common ancestor (PCR conditions available from authors). LOH was assessed using the same set of microsatellites. LOH was scored if the intensity of any allele was reduced by $\geq 50\%$ relative to the other allele after taking account of the relative allelic intensities in paired constitutional DNA. In the case of discordance between microsatellites, precedence was given to the one closest to *POLE* or *POLD1*. For a small sub-set of *POLD1*-mutant

tumours, LOH analysis was performed genome-wide using the Illumina Goldengate HumanLinkage system (Panel V). Briefly, ~1µg of tumour DNA and paired constitutional DNA were amplified as per the manufacturer's instructions and hybridised separately to Sentrix BeadArrays overnight. Each chip was then washed and stained, and scanned immediately using an Illumina BeadArray reader. GenomeStudio software was used to identify regions with loss of heterozygosity (LOH) and/or copy number changes. It should be noted that some tumours in the set analysed were very small and contamination by normal cells may have obscured LOH in some cases. Similarly, it was not possible to screen the large *POLE* and *POLD1* genes for "second hits" other than LOH owing to limiting tumour material.

Somatic CRC driver mutation screening: Ion Torrent cancer hotspot panel

Using the Ion Torrent cancer hotspot panel, we screened CRC-associated mutations for somatic changes in tumours from *POLE*L242V and *POLD1* S478N carriers using direct sequencing. Owing to limited quantities of DNA from the formalin-fixed, paraffin-embedded tumours available from our patients, we focussed on relatively common somatic mutations for which there was excellent pre-existing evidence of pathogenicity. Specifically, based on the existing literature and databases (<http://www.sanger.ac.uk>), we regarded the following as pathogenic: *APC* (reference sequence NM_000038) – protein-truncating mutations between codons 167 and 1580; *CTNNB1* (NM_001904) – missense mutations at codons 32, 33, 34, 37, 41 or 45; *KRAS* (NM_004985) – missense mutations at codons 12, 13, 61 or 146; *BRAF* (NM_004333) – V600E; *PIK3CA* (NM_006218) missense mutations at codons 345, 420, 542, 545, 546, 1025 or 1047; and *FBXW7* (NM_033632) – protein-truncating mutations and missense mutations at codons 465, 479, 505 or 582. *TP53* was not analysed because of the uncertain pathogenicity of some missense variants. Mutations were called using Ion Reporter (Invitrogen) and bam files were additionally inspected manually in order to remove likely artefacts and to detect any mutations - especially insertions and deletions in *APC* - that were not called by the Ion Reporter software. *KRAS* and *BRAF* mutations were additionally screened in an extended sample set using Sanger sequencing.

Somatic mutation spectrum screening: Ion Torrent cancer gene custom panel

One tumour a from *POLE*L242V carrier (family SM2702) and three tumours from *POLD1* S478N carriers (two from a member of SM1645 and one from a member of SM1412) were screened for exonic variants in a custom panel of 150 cancer-related genes using the Ion Torrent Ampliseq method (details available on request). After excluding the above known CRC driver genes and known polymorphisms, the somatic mutation spectrum was determined. All but two in-del mutations were substitutions.

Fission yeast strain construction and mutation rate assays

Strains used in this study are listed in Supplementary Table 6. Standard genetic methods were used for strain construction 38. The *pol3-C462N* mutant strain (equivalent to human *POLD1* S478N) was constructed by amplifying *pol3* segments with primer combinations 1075 & 1077; 1076 and 1078 (see Supplementary Table 6). The products were purified, annealed and amplified using primers 1075 & 1076. The product was digested with BamHI and AscI and inserted into pFA6a-*kanMX6*³⁹. The *pol3-C462S* (equivalent to human *POLD1* wild type) strain was constructed in the same way using initial primer combinations 1075 & 1079; 1080 & 1076. As a control, a *pol3*⁺ (wild-type) strain was also constructed using the same procedure, using primer combinations 1075 & 1076 to amplify the wt sequence. Plasmids were integrated into the *pol3* locus after linearization with CspCI and selecting for G418-resistance. Constructs were verified by sequencing. Mutation rates of the *ade6-485* allele in different strain backgrounds were determined by fluctuation analysis as previously described⁴⁰. Eleven cultures were used for each experiment and plates were

scored after 7 days. Mutation rates were calculated using the MSS-Maximum likelihood estimator⁴¹.

Structural analysis

Human mutations in both *POLE* and *POLD1* were visualised in PyMOL (<http://pymol.org>) on the catalytic subunit of the yeast DNA polymerase δ [PDB ID: 3IAY], with the ssDNA component of the T4 polymerase complex [PDBID: 1NOY], modelled into the exonuclease active site.

Other methods are provided in the Supplementary Material.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Footnotes

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Accession numbers APC: NM_000038; CTNNB1: NM_001904; KRAS: NM_004985; BRAF: NM_004333; PIK3CA: NM_006218; FBXW7: NM_033632.

Competing financial interests None declared.

URLs PLATYPUS program: <http://www.well.ox.ac.uk/platypus>

dbSNP: <http://www.ncbi.nlm.nih.gov/projects/SNP>

HapMap: <http://www.hapmap.org>

1000Genomes: <http://www.1000genomes.org>

Wellcome Trust Case Control Consortium: <http://www.wtccc.org.uk/>

Exome Variant Server: <http://evs.gs.washington.edu/EVS/>

COSMIC: <http://www.sanger.ac.uk/COSMIC/>

SIFT: <http://sift.jcvi.org/>

PolyPhen: <http://genetics.bwh.harvard.edu/pph>

Mutation taster: <http://www.mutationtaster.org/>

Cancer Genome Atlas project: <http://cancergenome.nih.gov>

OMIM: <http://www.omim.org/>

HGMD Professional: <http://www.hgmd.org/>

GeneCards: <http://www.genecards.org/>

Clustal: <http://www.ebi.ac.uk/Tools/msa/clustalo/>

Pymol: <http://www.pymol.org>

NCBI Structure server: <http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi>

Life Technologies: http://tools.invitrogen.com/content/sfs/brochures/IonAmpliseq_CancerPanel_AppNote_CO32199_06042012.pdf

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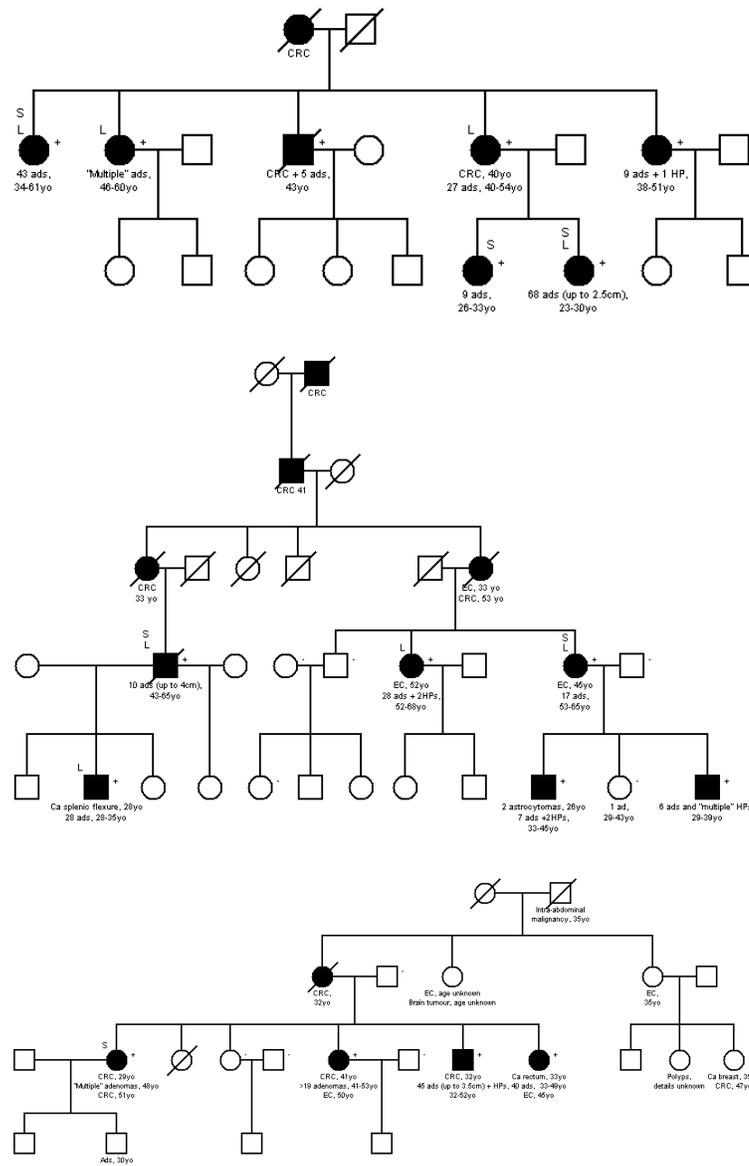


Figure 1. Pedigrees of the *POLE* L424V and *POLD1* S478N families in the Discovery Phase Families (a) SM2702 (*POLE*), (b) SM1645 (*POLD1*) and (c) SM1412 (*POLD1*) are shown. [•]=affected, [+]=mutation carrier and [-]=wildtype. S=whole genome-sequenced, L=genome-wide linkage analysis. For colorectal adenomas (ads), we show the cumulative tumour numbers from age at first presentation or screening colonoscopy to age at last contact. Diameter of the largest adenoma is also given where reported. Hyperplastic polyp (HP) numbers are also shown. For colorectal carcinomas (CRCs), endometrial carcinomas (ECs) and brain tumours, age at first presentation is given. Location of the CRC (colon, caecum, rectum) is also given where reported.



Figure 2. Modelling of the germline and exonuclease domain mutations

- a) Composite model of the catalytic subunit of the yeast DNA polymerase δ (in ternary complex with DNA and an incoming nucleotide [PDB ID: 3IAY]) and the ssDNA component of the T4 polymerase complex [PDBID: 1NOY], modeled into the exonuclease active site. The polymerase is coloured blue, the exonuclease domain is shown in green, the dsDNA in orange and magenta, and the ssDNA in the exonuclease active site in yellow. Mutations map to the active site of the exonuclease domain.
- b) Germline mutations *POLE*L424V (in red) and *POLD1* S478N (magenta) map to a helix (478-487) and pack against another helix, forming part of the base of the exonuclease active site. Mutations will disrupt this packing of helices and distort the active site. The active site is defined by the ssDNA substrate shown in yellow.
- c) Mapping of the possibly pathogenic germline and somatic mutations to the exonuclease domain. All the *POLE* mutations (exonuclease domain somatic changes from the TCGA colorectal cancer data), and *POLD1* P327L (germline variant from our patient, same location as *POLE*P286H) cluster around the active site (in red), whilst the *POLD1* mutations S370R and G426S (germline variants from two other patients, shown in magenta) are more peripheral.

Table 1
Summary of somatic mutation spectra in colorectal cancer driver genes in tumours from POLE L424V patients

For each patient, the data from several tumours are combined. The position of the somatic mutation and the base change are shown for all detected changes. Full details, including numbers of tumours tested, are shown in Supplementary Table 3.

Family	Patient	Somatic mutations
2702	1	<i>APC</i> Q1338X (C>T); <i>FBXW7</i> R465C (C>T)
2702	2	None found
2702	3	<i>APC</i> R1114X (C>T), Q1338X (C>T); <i>KRAS</i> G12D (G>A), A146T (A>C)
A	1	None found
I	1	<i>APC</i> Q1338X (C>T); <i>KRAS</i> A146T (A>C); <i>FBXW7</i> R479Q (G>A)
I	2	<i>APC</i> Q1338X (C>T); <i>KRAS</i> G12D (G>A) × 3
F	1	None found
K	1	<i>APC</i> R1114X (C>T)
C	1	None found
H	1	None found

Table 2
Summary of somatic mutation spectra in colorectal cancer driver genes in tumours from POLD1 S478N patients

For each patient, the data from several tumours are combined. The position of the somatic mutation and the base change are shown for all detected changes. Full details, including numbers of tumours tested, are shown in Supplementary Table 5.

Family	Patient	Somatic mutations
1412	1	None found
1645	1	<i>APC</i> E1309X (C>T); <i>KRAS</i> Q61H (A>C)
1645	2	<i>APC</i> R1114X (C>T), Q1338X (C>T) × 3, Q1367X (C>T); <i>KRAS</i> G13D (G>A) × 4; <i>BRAF</i> V600E (T>A) × 2; <i>FBXW7</i> R465H (G>A), R465C (C>T)
1645	3	None found
1645	4	None found
1645	5	None found

Table 3
Assessment of the functional effects of the *S. pombe* equivalent of human POLD1 S478N

Human S478 is partially conserved in *S. pombe* (C462). The cysteine was therefore mutated to both the human wildtype (S, wt) and mutant (N) alleles. The Table shows reversion rates of the *ade6-485* allele in the genetic backgrounds listed, with standard deviations in parentheses. Numbers are mean values of Ade+ revertants per 10⁹ divisions with standard deviations in parentheses. Reversion rates were determined from three experiments. Strains used were 3176 (wt), 3177 (C462N) and 3178 (C462S).

Site mutated	Mutation rate (x10 ⁹)	Fold increase (mutant/wt)
C462N	72 (9.6)	12
C462S	4.2 (2.1)	0.7
Wildtype	6.0 (4.2)	1

Table 4
Summary of somatic POLE and POLD1 mutations and mutations in known colorectal cancer driver genes from the TCGA colorectal cancer sequencing data

For the *POLE* and *POLD1* mutations: Cat=catalytic domain; Exo=exonuclease domain; DFU-putative C-terminal DNA-binding domain; None=no specific domain; and Loss=protein-truncating mutation presumed to be null. The positions of the driver mutations in *APC*, *KRAS*, *BRAF*, *PIK3CA* and *FBXW7*, and the specific base change, are shown. Full results are shown in Supplementary Table 7.

Tumour	Hyper-mutated?	MSI	MLH1 methylated?	Gene	AA Change	Domain	Somatic mutations
TCGA-AA-3516	Yes	MSI-H	Yes	POLD1	p.A864T	Cat	BRAF V600E (T>A)
TCGA-AA-3710	Yes	MSI-H	Yes	POLD1	p.A145D	None	None found
TCGA-AA-3947	Yes	MSI-H	Yes	POLD1	p.P787L	Cat	APC E874fs; BRAF V600E (T>A), PIK3CA (H1074R (A>G))
TCGA-AA-3949	Yes	MSI-H	Yes	POLD1	p.Q461H	Exo	BRAF V600E (T>A); FBXW7 R367X (C>T)
TCGA-AA-A00J	Yes	MSI-H	Yes	POLD1	p.R808H	Cat	APC R554X (C>T); BRAF V600E (T>A)
				POLE	p.A2056T	None	
TCGA-AA-3518	Yes	MSI-H	Yes	POLE	p.V1368M	None	FBXW7 R465C (C>T)
TCGA-AA-3525	Yes	MSI-H	Yes	POLE	p.A2213V	None	BRAF V600E (T>A)
				POLE	p.K1008N	Cat	
				POLE	p.R762W	Cat	
TCGA-AA-3555	Yes	MSS	No	POLE	p.P286H	Exo	APC R499X (C>T), R1450X (C>T); KRAS A146T (G>A)
TCGA-AA-3678	No	MSS	No	POLE	p.D1752N	DFU	APC E1309fs
TCGA-AA-3710	Yes	MSI-H	Yes	POLE	p.P1421S	None	None found
TCGA-AA-3864	Yes	MSI-H	No	POLE	p.R231H	None	APC R348X (C>T), R564X (C>T), R1432X (C>T)
TCGA-AA-3977	Yes	MSS	No	POLE	p.K777N	Cat	APC R1114X (C>T), E1309X (G>T)
				POLE	p.F367S	Exo	
TCGA-AA-3984	Yes	MSS	No	POLE	p.V411L	Exo	APC R1114X (C>T)
TCGA-AA-A00N	Yes	MSI-L	No	POLE	p.L1255V	None	APC S1281X (C>A), E1408X (G>T); KRAS G13D (G>A)
				POLE	p.V411L	Exo	
TCGA-AA-A010	Yes	MSI-L	No	POLE	p.P436R	Exo	APC R1450X (C>T)
				POLE	p.A189T	None	
TCGA-AG-3892	Yes	MSS	No	POLE	p.S459F	Exo	APC R1114X (C>T)
TCGA-AG-A002	Yes	MSS	No	POLE	p.S459F	Exo	APC R1450X (C>T), E1538X (G>T)
				POLE	p.R150X	Loss	
TCGA-AG-A01W	No	MSS	Not reported	POLE	p.D2013N	None	APC R876X (C>T); KRAS G13D (G>A)