INTRODUCTION

The struggle to understand the origins of human cancers has captured the imagination of many investigators. The epidemiology of human cancers and the availability of many laboratory models of cancer could give the casual observer the impression that all cancers are a result of exposures to chemical carcinogens in the environment. This is only part of the story, and in most instances environmental exposures are very different in scale from what is required in laboratory animals to induce tumours. Actually, most laboratory models have been carefully developed to match the carcinogen with the host. For example, several alkylating agents can induce intestinal cancers in rodents. However, the distribution of the neoplasms throughout the gut varies from one mouse strain to another, and in some instances the carcinogens induce tumors only outside the gut. Lower doses—perhaps those more relevant for human cancers—may be tolerated, and not induce cancer at all. The mechanisms for tumour development in the human gastrointestinal tract appear to be a much more complicated issue.

This review of recent advances in basic science will focus on newly discovered mechanisms involved in the development of colorectal cancer (CRC). This is potentially a very broad topic, and therefore we have selected two novel mechanisms for emphasis. Firstly, a virus carried by most healthy individuals has been implicated as a possible cause for chromosomal instability (CIN), the process that leads to aneuploidy. Chromosomal aberrations and this form of genomic instability play a major role in the development and progression of multistep carcinogenesis, such as occurs in CRC. Secondly, it is abundantly clear that inflammation is carcinogenic, and furthermore, endogenous processes that can modify the ability of the host to cope with inflammation appear to modify the risk of cancer to the host. There is growing evidence that this may be germane to cancer risk in inflammatory bowel disease (IBD). Almost certainly, additional mechanisms will be found in the future but these may be particularly pertinent for CRC, and perhaps cancer elsewhere in the gut.

VIRAL INFECTION AND GASTROINTESTINAL CANCER

There has been gradual acceptance that viruses can participate in the induction of some cancers. This concept is nearly a century old, and dates back to the observation by a New York farmer that his chickens were highly prone to tumours. Subsequent experiments conducted by Peyton Rous eventually revealed that an avian retrovirus carries a mutated proto-oncogene, which is linked mechanistically to these sarcomas. Although the links between viruses and cancer are less obvious in humans, it is generally agreed that hepatitis B virus and hepatitis C virus are aetiologically linked to the development of hepatomas. Similarly, human papillomaviruses have been linked to human genital tract tumours by virtue of the coordinated action of two oncogenes encoded by this virus, and vaccination against this virus has begun in the hope of preventing those cancers.

The role of polyomaviruses in human cancer has been much more controversial. Safety studies performed on the human polio vaccine in the early 1960s revealed contamination by SV40 virus, which originated in the simian kidney cells used to culture the poliovirus. Large numbers of humans were exposed to SV40 while receiving their polio vaccines. Although the virus is present in some cancers, evidence for its role in carcinogenesis is inconclusive. However, injecting SV40 into rodents clearly causes cancer. The small number of genes encoded by this virus, and the unequivocal oncogenic activity of the T antigen, have raised the possibility that human polyomaviruses may cause cancers in the human host by virtue of encoding a potent oncogene.

There are two viruses closely related to SV40 in which the natural host is humans rather than monkeys. These are JC virus (JCV) and BK virus (BKV). SV40 has evolved into a useful laboratory tool for transforming cells, and its presence in the genome leads to chromosomal aberrations and
genomic instability. Based on close structural similarity, it is reasonable to speculate that these human viruses may play a role in human carcinogenesis.

**JCV structure and epidemiology**

JCV was first isolated from the spinal fluid of a patient suffering from progressive multifocal leukoencephalopathy, or PML. JCV belongs to the subfamily of non-enveloped DNA viruses with icosahedral capsids that contain small (40–60 nm), double stranded, negatively supercoiled, circular DNA genomes. The 5.13 kb circular genome of JCV encodes only six genes, and has two regions of approximately equal size known as early and late transcription units, as illustrated in fig 1. The early and late coding regions are separated by a bidirectional transcriptional control region (TCR), which is the most divergent DNA sequence among the polyomaviruses JCV, BKV, and SV40. The late region encodes the capsid structural proteins VP1, VP2, and VP3 through alternately spliced mRNAs, and a small regulatory protein known as “agnoprotein” which is involved in viral assembly. The early region encodes the alternatively spliced transforming proteins large T-antigen (T-Ag) and small t-antigen (t-Ag). T-antigen plays a critical role in the life cycle as it directs viral early and late gene expression, as well as viral DNA replication during lytic infection.

Epidemiological studies have demonstrated that JCV is ubiquitous in the human population, and approximately 60–80% of adults have specific antibodies to JCV. The virus is believed to be transmitted by close contact during early childhood years, and primary infections are typically harmless. Reappearance of the virus in the urine of pregnant women has led to the hypothesis that latency may be maintained, at least in part, in the kidney. The presence of viral genomic sequences in the gastrointestinal tract and in raw urban sewage suggests possible faecal-oral transmission of JCV, and emphasises the relative stability of the viral particles and the potential for interpersonal spread.

**JCV and human cancers**

In addition to its primary role in the development of PML, in recent years mounting evidence has suggested that JCV may be associated with human neoplasms in the absence of immunosuppression or PML. This has been possible through the use of sensitive techniques and the availability of more reliable immunohistochemical reagents, which have allowed the detection of JCV genomic sequences and T-antigen expression in a variety of human malignancies, including brain tumours of glial origin, medulloblastomas, colon carcinoma, and oesophageal cancers.

Although the aetiological role for JCV in the development of human malignancies remains to be established, it is believed that the early proteins of the virus, and particularly the T-antigen, play a critical role in malignant transformation by associating with several cellular proteins.

Similar to SV40 T-antigen, JCV T-Ag is a multifunctional protein that possesses the ability to bind and break DNA, and has helicase and ATPase activities, which are needed for DNA replication. Furthermore, JCV T-antigen can also dysregulate control of the cell cycle by interacting with the tumour suppressor proteins p53 and pRb, making it unique in its ability to simultaneously disrupt chromosomal integrity and inactivate cell cycle checkpoints. This coordinated action permits the replication and proliferation of cells with damaged DNA (fig 2). Moreover, T-antigen may distort control of cellular proliferation by deregulating the Wnt signalling pathway through stabilisation of β-catenin, interacting with IGF-IR signalling, and inducing chromosomal instability in B lymphocytes.

**JCV and genomic instability: implications for colorectal carcinogenesis**

Molecular pathways responsible for genomic instability in CRC include microsatellite instability (MSI), CIN, and CpG island methylator phenotype (CIMP). Approximately 12–15% of all CRCs demonstrate MSI, a reasonably well understood
Figure 2  Interaction of JC virus (JCV) T-antigen with key growth regulatory pathways. JCV large T-antigen (T-Ag) is believed to drive the oncogenic process of malignant transformation by associating with several cellular proteins. T-Ag has the capacity to interact with two tumour suppressor proteins that regulate cell cycle progression, pRb and p53. (A) Under normal physiological conditions, pRb is maintained in a hypophosphorylated state and sequesters the S phase specific transcription factor E2F-1, in a pRb:E2F-1 complex. On JCV infection, T-Ag binds to the pRb protein releasing E2F-1, permitting it to induce cellular proliferation by promoting transcription of S phase genes. E2F-1 induces p14ARF gene expression, which interferes with the activity of MDM2, a negative regulator of p53 protein. Consequently, p53 is stabilised, which would inhibit the cell cycle and promote apoptosis (see fig 6 for additional details). (B) T-Ag binds to and inactivates p53, which prevents inhibition of the cell cycle or apoptosis. (C) T-Ag binds to IRS-1, a key member of the IGF signalling pathway, leading to uncoupling of IGF-1R from IRS-1, and its translocation to the nucleus. In the nucleus, IRS-1 may be important in Rad51 trafficking and homologous recombination directed DNA repair. (D) Finally, T-Ag can be oncogenic by deregulating the Wnt signalling pathway. In normal cells, β-catenin levels are regulated by a multiprotein complex of GSK3β, Axin-1, and APC, which phosphorylate β-catenin and trigger its degradation. On JCV infection, T-Ag binds to β-catenin, leading to its stabilisation, and providing a nuclear localisation signal. Once in the nucleus, stabilised β-catenin complexes with transcription factors such as TCR/LEF, which stimulates the transcription of cell cycle regulatory genes, including c-myc and cyclin D1.

process caused by inactivation of the DNA mismatch repair (MMR) system. However, the majority of CRCs acquire genomic instability by one of two other pathways. CIN is characterised by aneuploidy and loss of heterozygosity (LOH), and leads to losses of tumour suppressor genes on chromosomes 5q, 18q, and 17p. In a completely novel pathway, CIMP leads to cancer by silencing tumour suppressor genes through hypermethylation of CpG sequences in the promoters of these genes. The biological bases of these two critical processes are not currently understood. It has long been appreciated that CRCs are commonly aneuploid and have CIN, but the molecular mechanisms causing CIN are poorly understood, and are currently an issue of controversy and intense investigation.

CIN produces large scale chromosomal losses, eliminating millions of base pairs at once, and unlike point mutations, which can create a variety of silent or innocuous alterations at the amino acid level, deletions unambiguously inactivate genes. Colon cancers typically have multiple LOH events that occur diffusely throughout the genome. In some instances, more than 50% of assayed loci have experienced LOH. Losses of the APC gene have been proposed as a cause of CIN. However, LOH is commonly the mechanism for inactivation of APC, so it would seem circular to propose that CIN is both the result of losing APC and the cause of LOH at APC. This argues for the primary occurrence of some form of genomic instability, the random generation of genomic diversity, the consequent loss of tumour suppressor genes, and the expansion of favoured clones in an evolutionary fashion. However, there is no convincing evidence for a genetic event that accounts for CIN in most, or even a large proportion of, CRCs.

We hypothesised that a transforming virus, such as JCV, which ubiquitously infects most humans and encodes the highly oncogenic T-antigen, would interact with key signalling pathways, simulate Wnt signalling, and abrogate the functions of p53 and pRb, which would provide the right milieu of cellular resources and opportunity for this virus to induce CIN in CRCs. Armed with the speculation that JCV might cause CIN, our laboratory first determined that JCV DNA sequences were present in human colon cancers and adjacent normal colonic tissues. In pilot studies, we found that the native supercoiled JCV was difficult to amplify by polymerase chain reaction (PCR). PCR amplification following pretreatment of viral DNA with topoisoasemerase I (which relaxes supercoiling) and the use of degenerate primers (anticipating microheterogeneity) allowed us to detect JCV in 89% of colon cancers, but also in 89% of normal adjacent colonic epithelia from the resected matched tissue specimens. These findings have been confirmed in another laboratory, in which JCV DNA sequences were found in 81% of colon cancers. Furthermore, expression of several viral proteins, including T-antigen and agnoprotein, occurs in benign adenomas and tumour specimens, but not in any normal colonic tissues, suggesting that JCV may play a role in the earliest stages of neoplastic development in the colon.
Subsequently, using a semiquantitative PCR assay, we found at least 10-fold more copies of the virus in colon cancers than in the adjacent normal colon.17

Encouraged by these findings, and cautiously optimistic, we tested the hypothesis that JCV latently infects the gastrointestinal tracts of individuals without neoplasia. We obtained biopsy samples from the oesophagus, stomach, duodenum, colon, and rectum from patients undergoing routine diagnostic examinations and found that 75.8% of patients harboured JCV sequences (70.6% of the upper gastrointestinal samples and 81.2% of the colorectal samples). These data were subsequently confirmed using nested PCR, Southern blot analysis, and direct DNA sequencing analysis.11 We concluded that the gastrointestinal tract is a reservoir for JCV and proposed that ubiquitous infection of humans with this virus may be due to faecal-oral transmission during childhood. More recently, we sequenced the TCR reservoir for JCV and proposed that ubiquitous infection of APC, p53, and CIN in RKO cells, which is a diploid CRC cell line with tested the hypothesis that JCV T-antigen may directly induce CIN in colonic epithelial cells transfected with plasmid DNA containing the Mad-1 strain of JCV in these cells led to expression of T-antigen and viral capsid proteins. These cell lines developed CIN within seven days of transfection, providing direct experimental evidence for the ability of T-antigen to induce CIN in colonic epithelial cells.

In summary, we and others have demonstrated that most CRCs contain the DNA of JCV that encodes an oncogenic T-antigen, which is capable of interacting with key growth regulatory pathways in the colon, and has the potential to induce CIN. Current evidence indicates that JCV infection is ubiquitous and remains subclinical throughout the life of most individuals, but can cause serious disease in the setting of extreme immunosuppression. It is proposed that some factor or factors lead to activation of the virus in the colon, induction of the adenomatous phenotype, CIN, and eventually colon cancer. Finally, based on unpublished data, it appears that the virus may be too disruptive for the highly proliferative cancer in its advanced stages, and the infection may be lost in a “hit-and-run” fashion. Thus we are suggesting that JCV is involved in the initiation of colorectal neoplasia, but the instability may be selected against once an optimal reorganisation of the neoplastic genome has been achieved.

**Table 1** Association between chronic inflammation and cancer in the gastrointestinal tract

<table>
<thead>
<tr>
<th>Gastrointestinal location</th>
<th>Type of inflammation</th>
<th>Type of cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oesophagus</td>
<td>Gastro-oesophageal reflux disease</td>
<td>Barrett’s cancer (adenocarcinoma of the distal oesophagus)</td>
</tr>
<tr>
<td>Stomach</td>
<td>Chronic gastritis (autoimmune or H. pylori)</td>
<td>Gastric adenocarcinoma, MALT lymphoma, GIST</td>
</tr>
<tr>
<td>Pancreas</td>
<td>Chronic pancreatitis (familial, autoimmune, alcohol)</td>
<td>Pancreatic cancer</td>
</tr>
<tr>
<td>Bile ducts</td>
<td>Primary sclerosing cholangitis</td>
<td>Cholangiocarcinoma</td>
</tr>
<tr>
<td>Small bowel</td>
<td>Coeliac disease, Crohn’s disease</td>
<td>MALT lymphoma, small bowel adenocarcinoma</td>
</tr>
<tr>
<td>Large bowel</td>
<td>Ulcerative colitis, Crohn’s colitis</td>
<td>Colorectal cancer</td>
</tr>
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**INFLAMMATION AND GASTROINTESTINAL CANCER**

**Association between inflammation and gastrointestinal cancer**

Over 150 years ago, the German pathologist Virchow described a link between inflammation and cancer.19 A number of observations strongly suggest that cancer is a common consequence of chronic inflammation in the gut. Gastrointestinal cancers are more prevalent in disease states that produce a chronically inflamed epithelium (table 1). The emergence of multifocal cancers in inflamed mucosae adds to the speculation that inflammation is mechanistically involved in carcinogenesis.

The best data on inflammation driven carcinogenesis come from studies in ulcerative colitis. Ulcerative colitis affects approximately 0.3% of Western populations and typically starts in the second or third decade of life. The pathogenesis of ulcerative colitis is only partially understood and involves autoimmunity, genetic predisposition (for example, the IBD2 locus on chromosome 12q), and environmental triggers. The first case of CRC in ulcerative colitis was described by Crohn and Rosenberg in 1925.20 Since then, epidemiological evidence has clarified that patients with long term ulcerative colitis have an increased risk of developing CRC. The magnitude of this risk has been difficult to estimate but was considered very high (increased up to 50-fold) in early studies.21–24 Later studies based on population cohorts gave rise to reduced estimates.25–28 The risk increases with disease extent (19-fold in pancolitis),21 severity of inflammation,22 young age at onset,23 family history of colorectal cancer,25 presence of primary sclerosing cholangitis,26 and presence of backwash ileitis.27

Several genetic and epigenetic changes have been described in ulcerative colitis that might be responsible for colon carcinogenesis, and these differ in frequency and timing compared with sporadic cancer.28–30 One can conceptually categorise CRCs by the mutational signature found in the tumour tissue (that is, CIN, MSI, or CIMP), as described above, but colorectal carcinogenesis in ulcerative colitis may
be unique. Early events in colitis associated cancers often involve MSI and p53 mutations, which are present in non-dysplastic chronically inflamed tissue. These features may serve as a starting point to unravel the mystery of inflammation associated CRC.

Mechanisms involved in inflammation associated cancer

In aerobic cells, reactive oxygen species (ROS) are generated as a byproduct of normal mitochondrial activity. Major endogenous sources are metabolic processes, primarily oxidative metabolism in the mitochondria, and pathological processes such as inflammation. Exogenous sources of ROS include exposure to ionising radiation or radiomimetic chemicals, and ROS produced by neighbouring cells. Toxic ROS include oxygen species such as the superoxide anion radical (•O₂⁻), hydrogen peroxide (H₂O₂), hydroxyl radical (•OH), as well as nitric oxide (NO). ROS can cause severe damage to cellular macromolecules, especially DNA.

DNA damage is detected in the nucleus by various protein complexes, so called sensor proteins, which initiate the cellular response (fig 3). These sensor proteins activate repair pathways that include transducer, signal, and effector proteins. DNA damage is processed through specific repair pathways, including base excision repair (BER), DNA MMR, and nucleotide excision repair (NER), depending on the type of damage involved. Cell cycle checkpoints function as protective barriers against cytotoxicity and carcinogenesis induced by ROS by providing damaged cells additional time to repair DNA before replication or mitosis (fig 4). When damage overwhelms the ability to repair, checkpoint signalling may cause cells to undergo apoptosis or enter an irreversible G₀ state. It is critical to appreciate that as cancer develops in the setting of oxidative stress, ROS not only damage DNA, they also inactivate some of these intracellular protective mechanisms, a deadly combination (fig 5).

The tumour suppressor, p53

Mutations of the p53 gene are the most common genetic alterations found in human cancers, and these play crucial roles in tumour development and progression. In sporadic CRC, p53 protein stabilisation can be caused by p53 mutations, overexpression, or reduced degradation, and this occurs late in carcinogenesis. However, p53 stabilisation—usually attributed to mutation—is found in early dysplastic lesions in ulcerative colitis, and even in chronically inflamed mucosa without dysplasia. Similarly, p53 mutations have been detected in inflamed non-neoplastic synovia from patients with rheumatoid arthritis. LOH of p53 is also common in ulcerative colitis associated dysplasia or carcinoma. The p53 gene encodes a protein that functions like a transcription factor, and the biological functions of p53, which becomes activated in the nucleus in response to genotoxic stress, are manifested through the activities of its downstream genes (for reviews see Hupp and colleagues, Woods and Lane, and Bartek and Lukas, and also fig 6).
Oxidative stress has been found to initiate checkpoint arrest in several eukaryotic cell types. Tumour suppressor p53 plays a vital role in the G1 checkpoint function and its loss results in near complete ablation of that checkpoint. Cells that have incurred DNA double strand breaks during the G1 phase activate and stabilise p53 primarily via an ATM dependent pathway. ATM regulates p53 accumulation by indirect pathways involving Chk2 phosphorylation of p53 and MDM2, thus blocking the interaction between MDM2 and p53. Exposure to oxidative stress enhances p53 and increases intracellular protein levels. Moreover, p53 is post-translationally modified and accumulates in response to the free radical NO. The latter can also increase BER enzymes AAG and APE1 level and activity.

The majority of mutations in the p53 gene involve exons 7 and 8. Transition mutations in p53 codons 247 and 248 are common in the inflamed mucosa of ulcerative colitis patients. Analysing the mutational signatures provides clues to the links between oxidative stress and cancer. Base transitions are typical consequences of oxidative DNA damage. The intermediates of lipid peroxidation and alkylating agents can induce G to A mutations; C to T transitions may be due to the formation of 5-hydroxycytidine, or to the deamination of 5-methylcytosine at CpG sites. The early appearance of p53 alterations makes this an attractive potential marker to screen for ulcerative colitis associated malignancy and in the assessment of cancer risk.

The tumour promoting gene nuclear factor κB (NFκB)
The NFκB family includes sequence specific transcription factors and consists of a number of related proteins that bind a common sequence motif known as the κB site. Members of the NFκB family exist in unstimulated cells as homo- or heterodimers bound to the inhibitory family of proteins called IκB. Binding to IκB prevents the complex from translocating to the nucleus, thereby maintaining NFκB in an inactive state. NFκB signalling occurs through either a classical or an alternative pathway. In the classical pathway,
NFκB activation may occur in response to stimulation by tumour necrosis factor α, interleukin 1, bacterial lipopolysaccharide, viral double stranded RNA, ionising radiation, etc. Stimulation of this signalling pathway leads to activation of the β subunit of the IkB kinase (IKK) complex, which then phosphorylates IkB proteins. Phosphorylation of IkB leads to ubiquitin dependent degradation of IkBs, which allows NFκB dimers to translocate to the nucleus. NFκB proteins are transcription factors that target expression of inflammatory and immunoregulatory genes, antiapoptotic genes (such as members of the Bcl2 family such as cIAP1/2 and Bcl-XL), cell cycle control genes, and genes that code for negative regulators of NFκB.

Activation of NFκB by mutations, chromosomal rearrangements, or chronic inflammation plays an important role in tumour development by stimulating the dormant KI (IKK) complex, which then phosphorylates IkB proteins. Phosphorylation of IkB leads to ubiquitin dependent degradation of IkBs, which allows NFκB dimers to translocate to the nucleus. NFκB proteins are transcription factors that target expression of inflammatory and immunoregulatory genes, antiapoptotic genes (such as members of the Bcl2 family such as cIAP1/2 and Bcl-XL), cell cycle control genes, and genes that code for negative regulators of NFκB.

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cancer in animal models and the risk of cancer throughout the gut in humans may exert some of their function by inhibiting IKK dependent activation of NFκB. However, the action of these inhibitors is not solely directed towards the NFκB pathway.

DNA repair pathways: BER, NER, and MMR

DNA repair pathways are complex activities that involve excision of the damaged base, restoration of the original DNA sequence by a DNA polymerase that uses the undamaged strand as its template, and sealing of the remaining break in the double helix by DNA ligase (for review see Bartek and colleagues62). The major DNA repair mechanisms, and the types of damage repaired by each, are illustrated in fig 7. The base excision repair (BER) pathway includes enzymes that recognise a specific type of altered base in DNA (such as 8-oxo-guanidines that result from nucleotide oxidation) and catalyse its removal. Another major repair pathway is nucleotide excision repair (NER), which can repair the damage caused by “bulky adducts”, as these will change the structure of the DNA double helix. However, members of the MMR pathway are commonly required to complete the DNA repair.72

Some types of DNA damage require unique repair strategies. Double stranded DNA breaks can be caused by ionising radiation, oxidising agents, replication errors, and certain metabolic byproducts in the cell. Two mechanisms have evolved to repair this damage: non-homologous end joining (NHEJ) and homologous recombination.73 The latter requires factors that recognise areas of DNA sequence matching between the two chromosomes and physically bring them together. Although NHEJ may induce errors in the DNA sequence at the site of breakage, so little of the mammalian genome codes for proteins that this mechanism is an acceptable solution to the problem of keeping chromosomes intact, even at the risk of inducing mutations.

Cells may respond to stress by elevating levels of DNA repair enzymes, as an emergency response to DNA damage.44 Induction of these additional DNA repair enzymes increases cell survival after DNA damage but also transiently elevates the mutation rate by increasing the number of errors made while copying DNA sequences. Such errors may be caused by low fidelity DNA polymerases that are used for DNA synthesis during MMR.74 75 Minor DNA polymerases are specifically called into play to copy unreppaired lesions in the DNA template. These enzymes can recognise specific types of DNA damage and add nucleotides to restore the initial sequence.

Approximately 15% of sporadic CRCs have a mutational signature called microsatellite instability (MSI). The MSI pathway is a consequence of losing the activities of enzymes that repair DNA base pair mismatches that occur during the normal process of DNA replication. These errors preferentially target genes such as TGF-βRII or BAX, because exons in these genes contain repeated sequences of mononucleotides (that is, An,Gn, etc.) that are intrinsically unstable and prone to be mutated during DNA replication. If the repetitive sequence is more than six or seven consecutive nucleotides, it is highly dependent on DNA MMR activity for faithful replication, and will be mutated once in every 10²–10³ replications in the absence of this repair system. Germline mutations in the MMR genes are responsible for Lynch syndrome, or hereditary non-polyposis colorectal cancer,76 but this does not cause the MSI that is frequently found in ulcerative colitis. Therefore, something other than germline mutations cause defective MMR in the chronically inflamed colon.

Chang et al found that H2O2 inactivates the DNA MMR system, apparently by damaging the enzymes at the protein level.77 More direct evidence for the role of oxidative stress in colon carcinogenesis via MMR inactivation has come from experiments that induce frameshift mutations in a reporter gene after exposure of cells to hydrogen peroxide.78 This effect
occurs in both MMR proficient and MMR defective cell lines. These findings suggest that oxidative stress may temporarily “relax” the MMR pathway, which permits MSI in the absence of inactivating germline mutations in the MMR genes. This may contribute to the MSI-low (MSI-L) phenotype (with a lower frequency of microsatellite mutations80), and in this instance, the microsatellite mutations are found in dinucleotide repeats.80 Dinucleotide repeats are very rarely found within exons but are very common in non-coding DNA. Importantly, this mutational signature is present in non-neoplastic80 as well as in neoplastic mucosa81. It was initially assumed that MSIs are related to the genomic instability caused by the mutations. However, the implication of MSI in the prevention of sporadic cancers such as those due to chronic inflammation or low replication fidelity (as in Lynch syndrome).

SUMMARY AND CLINICAL IMPLICATIONS

Our appreciation of the basic mechanisms of carcinogenesis has moved from a description of the mutated gene targets to an understanding of the mechanisms by which these mutations are generated, and the exogenous influences that modify the rates of mutation. One can only understand CRC in the context of the processes that lead to the evolution of neoplasia. Analysis of the “mutational signatures” in neoplastic tissue permits classification of CRCs, and raises the perplexing possibility that CRC might be at least three different diseases. The possible role of the common polyomavirus, JCV, in the genesis of CRC with chromosomal instability raises new possibilities for our understanding of this disease, and possible novel opportunities for prevention. Inflammation is clearly associated with an increased risk of mucosal neoplasia throughout the gut but the mechanisms by which this occurs are just beginning to be clarified. This appears to be a complex process, and preventive strategies may depend on the clinical context. What is appropriate for the prevention of sporadic cancers may be inappropriate for the prevention of colitis associated neoplasia. The transition of cancer research from the realm of descriptive pathology to molecular biology has been revolutionary, and will continue to modify our understanding of gastrointestinal cancer.

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cancer by patterns of genomic instability.


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EDITOR’S QUIZ: GI SNAPSHOTS

Answer

From question on page 1272
The magnetic resonance cholangiopancreatography scan showed hepatic fibrosis, multiple renal cysts (fig 1A), and multiple ectatic, dilated, irregular intrahepatic biliary ducts (fig 1B). The unifying diagnosis was that of Caroli’s disease with autosomal recessive polycystic kidney disease (ARPKD) and congenital hepatic fibrosis. The patient has not attended for upper gastrointestinal endoscopy to establish the presence of oesophageal varices.

Also known as congenital cystic dilatation of the intrahepatic biliary tree, Caroli’s disease is rare. In most cases inheritance is autosomal recessive. Two types have been described: type I, usually affecting a single lobe, and type II, associated with hepatic fibrosis. Other associations include ARPKD, medullary sponge kidney, and medullary cystic disease. Clinical findings are recurrent right upper quadrant pain, pyrexia, and sepsis. Type II disease presents with signs and symptoms of portal hypertension. Complications include recurrent cholangitis, biliary calculi, and an increased risk of cholangiocarcinoma. Treatment options include antibiotics, endoscopy for evidence of varices, lobectomy, and liver transplantation.