The genetics of hereditary colon cancer

Anil K. Rustgi1

Department of Medicine (Gastrointestinal), Department of Genetics, and Abramson Cancer Center, University of Pennsylvania, Philadelphia, Pennsylvania 19104, USA

The genetic basis of sporadic colorectal cancer has illuminated our knowledge of human cancer genetics. This has been facilitated and catalyzed by an appreciation and deep understanding of the forms of colorectal cancer that harbor an inherited predisposition, including familial adenomatous polyposis (FAP), hereditary nonpolyposis colorectal cancer (HNPCC) or Lynch syndrome, the hamartomatous polyposis syndromes, and certain other rare syndromes. Identification of germline mutations in pivotal genes underlying the inherited forms of colorectal cancer has yielded many dividends, including functional dissection of critical molecular pathways that have been revealed to be important in development, cellular homeostasis, and cancer; new approaches in chemoprevention, molecular diagnostics and genetic testing, and therapy; and underscoring genotypic–phenotypic relationships.

Colorectal cancer is a common cancer in the United States and worldwide. There are nearly 150,000 new cases annually in the United States [http://www.cancer.org/docroot/stt/stt_0.asp] and ~900,000 cases worldwide [http://www.who.int/en]. Colorectal cancer-related mortality comprises nearly 55,000 cases annually in the United States [http://www.cancer.org/docroot/stt/stt_0.asp]. The lifetime risk of colorectal cancer in the average-risk person, defined as without personal history or family history of colorectal cancer and above the age of 50, is 5%–6%. This increases anywhere up to 20% when there is involvement of first-degree and/or second-degree relatives with colorectal cancer, and reaches a lifetime risk of 80%–100% in hereditary colorectal cancer syndromes, such as in hereditary nonpolyposis colorectal cancer (HNPCC) and familial adenomatous polyposis [FAP], respectively.

An explosion of information and insights into the molecular pathogenesis of sporadic colorectal cancer dates back to the late 1980s, and since has served as a paradigm for the investigation of cancer genetics in general, and the emergence of novel diagnostics and therapeutics in cancers as well. Much of this was fueled by the identification, characterization, and elucidation of probands and families with hereditary forms of colorectal cancer. In parallel fashion, an appreciation of the biological underpinnings of colorectal cancer has been transformed through mouse models and delineation of molecular pathways that were predicated upon how these pathways operate to foster different forms of hereditary colorectal cancer.

In assessing the annual cases of colorectal cancer in the United States, it is clear that a distinction should be made for what is truly hereditary and what is in actuality familial. The former connotes a distinct genetic basis that has been defined, whereas the latter comprises an increased predisposition to cancer but without determination, as of yet, as whether there is a hereditary basis with discovery of pertinent tumor suppressor genes that are inactivated in the germline or whether the predisposition is stochastic. In that context, it is estimated that perhaps 20%–30% of all colorectal cancers have a familial basis. A study of 34 kindreds revealed that there is genetic susceptibility to sporadic colorectal adenomatous polyps and colorectal cancer (Cannon-Albright et al. 1988, 1989). Ongoing efforts should be fruitful in deciphering the potential polygenic basis for familial colorectal cancer. These will be achieved through careful selection of families for genome-wide studies. An example is found in the study of nearly 60 kindreds in which siblings less than age 65 had colorectal cancer but without evidence of hereditary colorectal cancer syndromes. This led to genetic linkage to human chromosome 9q22.2-31.2 (Wiesner et al. 2003).

Hereditary colorectal cancer syndromes, especially with an emphasis on biology and genetics and their relationship to phenotypic manifestations, form the basis for this review (Table 1). Approximately 3%–4% of colorectal cancer cases are attributable to HNPCC or Lynch syndrome, and the slight variation is due likely to geography and ethnicity. Nearly 1% of colorectal cancer cases are due to FAP. Less than 1% of cases are due to a panoply of conditions, namely, MYH-associated polyposis [MAP], the hamartomatous polyposis syndromes, and hyperplastic polyposis.

FAP

FAP is an autosomal dominant mode disorder that affects one in 13,000 births [Bisgaard et al. 1994]. The most compelling feature is the onset and progression of hun-
Hyperplastic polyposis syndrome (genetic basis unknown)

Hamartomatous polyposis syndromes

Familial adenomatous polyposis (FAP) [APC]
Attenuated FAP [APC]
Turcot syndrome (nearly two-thirds with germline APC mutation; one-third with germline MMR mutation)
MYH-associated polyposis syndrome (MYH)
Hereditary nonpolyposis colorectal cancer (HNPCC) or Lynch syndrome [MSH2, MLH1, MSH6, PMS2]
Muir-Torre syndrome
Familial colorectal cancer X (genetic basis unknown)
Hamartomatous polyposis syndromes
Peutz-Jeghers (PJ) syndrome [LKB1]
Familial Juvenile Polyposis [FJP] [SMAD4, BMPRIA, ENG]
Cowden’s syndrome [PTEN]
Bannayan-Ruvalcaba-Riley [BRR] syndrome [PTEN]
Gorlin’s syndrome [PTCH]
Hereditary mixed polyposis syndrome (genetic basis unknown)
Hyperplastic polyposis syndrome (genetic basis unknown)

Table 1. Hereditary gastrointestinal polyposis syndromes

<table>
<thead>
<tr>
<th>Syndrome</th>
<th>Genetics</th>
</tr>
</thead>
<tbody>
<tr>
<td>Familial adenomatous polyposis (FAP) [APC]</td>
<td></td>
</tr>
<tr>
<td>Attenuated FAP [APC]</td>
<td></td>
</tr>
<tr>
<td>Turcot syndrome (nearly two-thirds with germline</td>
<td>APC mutation; one-third with germline MMR mutation)</td>
</tr>
<tr>
<td>Hereditary nonpolyposis colorectal cancer (HNPCC)</td>
<td>[MSH2, MLH1, MSH6, PMS2]</td>
</tr>
<tr>
<td>Lynch syndrome</td>
<td></td>
</tr>
<tr>
<td>Muir-Torre syndrome</td>
<td></td>
</tr>
<tr>
<td>Familial colorectal cancer X</td>
<td>(genetic basis unknown)</td>
</tr>
<tr>
<td>Hamartomatous polyposis syndromes</td>
<td></td>
</tr>
<tr>
<td>Peutz-Jeghers (PJ) syndrome [LKB1]</td>
<td></td>
</tr>
<tr>
<td>Familial Juvenile Polyposis [FJP] [SMAD4, BMPRIA,</td>
<td>ENG]</td>
</tr>
<tr>
<td>Cowden’s syndrome [PTEN]</td>
<td></td>
</tr>
<tr>
<td>Bannayan-Ruvalcaba-Riley [BRR] syndrome [PTEN]</td>
<td></td>
</tr>
<tr>
<td>Gorlin’s syndrome [PTCH]</td>
<td></td>
</tr>
<tr>
<td>Hereditary mixed polyposis syndrome (genetic basis</td>
<td>unknown)</td>
</tr>
<tr>
<td>Hyperplastic polyposis syndrome (genetic basis</td>
<td>unknown)</td>
</tr>
</tbody>
</table>

Table associated FAP with an interstitial deletion on human chromosome 5q21 [Herrera et al. 1986], which was further expanded on by independent genetic linkage analyses to 5q21. Positional cloning verified the gene responsible for FAP to be the Adenomatous polyposis coli [APC] gene, a landmark effort [Groden et al. 1991; Kinzler et al. 1991; Nishisho et al. 1991]. The APC gene contains 15 exons (ORF of 8538 nucleotides) with exon 15 being the largest coding region (6.5 kb). Sundry studies yielded information that germline APC mutations were distributed throughout its 15 exons (especially exon 15, however), and the preponderance of these were nonsense mutations, resulting in a truncated protein with a broad range of molecular masses less than the predicted 310-kDa (2843 amino acids) wild-type APC protein. Some of these germline mutations correlated with phenotypic manifestations, such as CHRPE, the severity of polyposis, and an attenuated form of FAP, designated as attenuated APC (AAPC) or attenuated FAP [Fig. 1]. Alternative splicing of the APC gene 5’ to exon 1 generates isoforms that may regulate cell growth and differentiation [Carson et al. 2004]; additionally, other exon[s] can be alternatively spliced. Attenuated FAP is highlighted by mutations in either the extreme 5′ or 3′ ends of the APC exons [Spirio et al. 1993], and this may influence potentially the stability of the APC protein with markedly delayed onset of and a diminished range of clinical manifestations (e.g., fewer colonic adenomatous polyps in patients in their 50s or 60s). An APC mutation (T to A at nucleotide 3920 or APC 11307K) was found in 6% of Ashkenazi Jews and ~28% of Ashkenazi with a family history of colorectal cancer [Laken et al. 1997]. Interestingly, this mutation creates a small hypermutable region, indirectly causing cancer predisposition [Laken et al. 1997, Syngal et al. 2000]. However, this mutation has low penetrance in the general population.

In parallel fashion, often at a feverish pace, the biology of the APC protein was unraveled. One critical finding related to the premise that nearly 70% of sporadic (average-risk) colorectal adenomatous polyps harbor somatic APC mutations [Powell et al. 1992]. Domains of the APC protein have been dissected and shown to correlate with functional relationships [Fig. 1]. The APC protein, together with glycogen synthase kinase-3β, phosphorylates cytoplasmic β-catenin, thereby leading to β-catenin’s degradation [Fig. 1; Su et al. 1993; Korinek et al. 1997; Morin et al. 1997]. Most of the β-catenin is bound to E-cadherin to facilitate cell–cell contact through the adherens junctions [Gumbiner and McCrea 1993]. However, germline or somatic APC mutations render cytoplasmic β-catenin stable, resulting in nuclear translocation, where in concert with T-cell factors (TCF), certain target genes are activated transcriptionally. A partial list of the target genes is c-myc, cyclin D1, MMP-7, Axin2/conductin [Leung et al. 2002], and EphB/ephrinB [Batlle et al. 2002].

Other functions have been ascribed to the APC protein, including participation in transcription-independent-mediated apoptosis that involves caspase’s cleavage of APC itself [Qian et al. 2007]. APC is involved also in chromosomal segregation. In this context, APC localizes to the ends of kinetochores during mitosis and forms a complex with the checkpoint proteins Bub1 and Bub3 [Kaplan et al. 2001]. However, APC mutations disrupt microtubule binding and kinetochore–microtubule binding. This may help to explain only partially the chromosomal instability with aneuploidy and enhancement of loss of heterozygosity observed in sporadic colon cancers initiated by APC mutations (for review, see Nathke 2006) and also the chromosomal and spindle errors noted in embryonic stem cells homozygous for ApcMin/+ (multiple intestinal neoplasia) or Apc1638T alleles.
It should be emphasized that the chromosomal instability observed in colon cancers involves also loss of p53 function and telomere dysfunction.

Mouse models that have recapitulated features of FAP have a storied history. Mutagenesis studies revealed that the murine intestinal neoplasia (Min) mouse harbors many small intestinal polyps but also large intestinal polyps, although to a smaller extent (Moser et al. 1990). These mice eventually die due to anemia from gastrointestinal (GI) hemorrhage. The gene responsible for this phenotype was identified as the murine homolog of the APC gene (Su et al. 1992). Gene targeting strategies have also led to the widespread use of the Apc1638N (Fodde et al. 1994) and Apc(H9004716) (Oshima et al. 1995) knockout mice. The Apc1638N mice appear to have a shift of polyps to the colon and certain extraintestinal manifestations that are observed in humans. The Apc(H9004716) mice have microadenomas preceding mature adenomas in the small intestine. Both mouse models, along with the ApcMin/+ mice, have proven useful through numerous studies in colorectal carcinogenesis related to the influence or role of environmental factors (e.g., high-fat diet), chemoprevention agents [aspirin, nonsteroidal anti-inflammatory agents, selective Cox-2 inhibitors], diagnosis (evolving proteomics), therapy, and establishment of intersecting pathways through crossbreeding with other mouse models. Particularly illuminating has been the role of COX-2 (Oshima et al. 1996) and the EP2 prostaglandin receptor (Sonoshita et al. 2001) in the background of Apc deficiency in the mouse and the manner in which this work has stimulated chemoprevention efforts in the human.

Genetic testing has exploited the notion that the APC gene is subjected to truncating germline mutations. Ini-
HNPCC (Lynch) syndrome

Originally described in the early 20th century, elaborated on by Henry Lynch (1974), and refined through consensus conferences (Vasen et al. 1991, 1999), this syndrome is marked by an autosomal dominant mode of inheritance, early onset of colon cancer often with a predilection for the right colon, and an 80% lifetime risk of colorectal cancer. The syndrome is noteworthy for a spectrum of extracolonic tumors, such as those originating from the endometrium, ovary, stomach, bile duct, kidney, bladder, ureter, and skin (in this context, referred to as the Muir-Torre syndrome with sebaceous adenomas, basal cell cancers, and keratoacanthomas). The clinical hallmarks of HNPCC syndrome resulted in a classification scheme designated as the Amsterdam I criteria (Vasen et al. 1991), later modified as Amsterdam II to incorporate the importance of the extracolonic cancers (Table 2; Vasen et al. 1999).

An extraordinary amount of work in bacterial and especially yeast genetics paved the way for illuminating translational genetic discoveries in HNPCC (for review, see Fishel and Kolodner 1995). To that end, HNPCC patients have germline mutations in DNA mismatch repair (MMR) genes. In colonic or extracolonic tumors, the wild-type MMR allele is lost through somatic genetic alterations. As a result, DNA replication errors occur in repeat sequences (Aaltonen et al. 1993; Fishel et al. 1993; Ionov et al. 1993), typically in dinucleotide repeats, and consider other modalities to evaluate other organs where cancer(s) may emerge. In aggregate, the genetic and clinical underpinnings of FAP have served as a platform for the dissection of the molecular properties of the APC protein and its roles in sporadic colon cancer.

Table 2. Criteria for HNPCC (Lynch) syndrome

<table>
<thead>
<tr>
<th>Amsterdam I criteria</th>
<th>Amsterdam II criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td>At least three relatives with colorectal cancer and the following:</td>
<td>At least three relatives with HNPCC-related cancers and the following:</td>
</tr>
<tr>
<td>One should be a first-degree relative of the other two.</td>
<td>One should be a first-degree relative of the other two.</td>
</tr>
<tr>
<td>At least two consecutive generations should be affected.</td>
<td>At least two consecutive generations should be affected.</td>
</tr>
<tr>
<td>At least one case of colorectal cancer should be before age 50.</td>
<td>At least one case of HNPCC-related cancer should be before age 50.</td>
</tr>
<tr>
<td>FAP should be excluded.</td>
<td>FAP should be excluded.</td>
</tr>
<tr>
<td>Verification of tumors’ histopathology.</td>
<td>Verification of tumors’ histopathology.</td>
</tr>
</tbody>
</table>

Original Bethesda criteria

- Individuals with cancer in families that meet the Amsterdam criteria.
- Individuals with two HNPCC-related cancers, including synchronous and metachronous colorectal cancers or associated extracolonic cancers (endometrial, ovarian, gastric, hepatobiliary, or small bowel cancer or transitional cell carcinoma of the renal pelvis or ureter).
- Individuals with colorectal cancer and a first-degree relative with colorectal cancer and/or HNPCC-related extracolonic cancer and/or a colorectal adenoma; one of the cancers diagnosed at <50 yr of age, and the adenoma diagnosed at <40 yr of age.
- Individuals with colorectal cancer or endometrial cancer diagnosed at <50 yr of age.
- Individuals with right-sided colorectal cancer with an undifferentiated pattern [solid/cribriform] on histopathology diagnosed at <50 yr of age.
- Individuals with signet-ring cell-type colorectal cancer diagnosed at <50 yr of age.
- Individuals with adenomas diagnosed at <40 yr of age.

Revised Bethesda guidelines

- Colorectal cancer diagnosed in a patient who is <50 yr of age.
- Presence of synchronous or metachronous colorectal or other HNPCC-associated tumors (colorectal, endometrial, stomach, ovarian, pancreas, ureter and renal pelvis, biliary tract, small bowel, brain, and sebaceous gland adenomas and keratoacanthomas), regardless of age.
- Colorectal cancer with the MSI-high histology (presence of tumor infiltrating lymphocytes, Crohn’s-like lymphocytic reaction, mucinous/signet-ring differentiation, or medullary growth pattern) diagnosed in a patient who is <60 yr of age.
- Colorectal cancer diagnosed in one or more first-degree relatives with an HNPCC-related tumor, with one of the cancers being diagnosed under age 50 yr.
- Colorectal cancer diagnosed in two or more first- or second-degree relatives with HNPCC-related tumors, regardless of age.

MSI-low or MSI-L with one unstable marker, or MSS stable or MSS when no microsatellite loci are unstable. Of note, MSI may be found in ~15% of sporadic colorectal tumors (Thibodeau et al. 1998). Target genes...
of MSI include TGFβII, E2F4, and Bax, among others. Germline mutations may be found in MLH1, MSH2, and MSH6 MMR genes, and account for perhaps 60%–80% of all detectable germline mutations [Fishel et al. 1993; Parsons et al. 1993; Lynch and de la Chapelle 2003; Vasen and Boland 2005]. However, somatic MLH1 promoter methylation or MSH2 mutation may be found in MSI-H sporadic colorectal tumors. It is the discovery of MSI that led to the re-evaluation of the Amsterdam classification scheme to evolve into the Bethesda, and subsequently revised Bethesda, criteria [Table 2; Boland et al. 1998; Umar et al. 2004]. There are also unique histopathological features of MSI-H colorectal cancers, thereby potentially obviating the need for MSI analysis in evaluating whether a family might satisfy the criteria for HNPCC [Jenkins et al. 2007]. It has been also advocated that the PREMM [Prediction of Mutations in MLH1 and MSH2] model based on a personal and family history might provide an estimate of the likelihood of finding mutations [Balmana et al. 2006].

The MMR system recognizes and corrects base-pair mismatches and small nucleotide [1–4 base pairs [bp]] insertion/deletion mutations that can occur during DNA replication (Chung and Rustgi 2003; Lynch and de la Chapelle 2003; Edelmann and Edelmann 2004; Vasen and Boland 2005). Eukaryotic MMR mechanisms are more evolved and complex than bacterial MMR. The eukaryotic system, best studied in yeast and in mammalian cells, involves more proteins. These include the homologs of bacterial MutS and MutL, namely, MSH [MSH1–MSH6] and MLH [MLH1–MLH3]/Post-meiotic segregation or PMS [PMS1–PMS2], respectively. In eukaryotes, MSH2 and MSH6 [called MutSα] form a heterodimer and recognize 1-bp mismatches and 1-bp insertion/deletion mutations [Fig. 2]. MSH2 and MSH3 form a heterodimer [called MutSβ] and recognize not only what is recognized by MSH2–MSH6 but expand that capability to recognize 2- to 4-bp insertion/deletion mutations. MSH4 and MSH5 participate in the regulation of meiotic recombination [Ross-Macdonald and Roeder 1994]. Upon recognition of DNA mismatches, members of the MLH and PMS gene families are recruited. MLH1 and PMS2 (yeast PMS1) complex with each other [called MutLα] and are recruited to form a complex with MSH2–MSH6 or MSH2–MSH3, and this is mediated via MLH1. MLH1–PMS2 trigger a cascade of events that lead to the excision of the DNA strand carrying the mismatched base, which culminates in DNA resynthesis and ligation. The functional significance of MLH1–MLH3 [called MutLγ] and MLH1–PMS1 [called MutLβ] in MMR remains to be elucidated. Excision and resynthesis of 1-bp mutations/insertions/deletions in part involve EXO1, a 5′–3′ exonuclease that binds MSH2, MSH3, and MLH1 and functions likely through the MSH2–MSH6 correction system [Tishkoff et al. 1997; Schmittje et al. 2001; Tran et al. 2001].

The identification of exoneucleases, apart from EXO1, remains to be determined, especially for 2- to 4-bp mutations/insertions/deletions. The potential role of germline EXO1 mutations and variants in HNPCC has not been conclusive in spite of early notions that they may be important [Wu et al. 2001]. EXO1 deficiency in the mouse has a limited effect on polypl number and size in Apc(1638N) mice (Kucherlapati et al. 2007). Collectively, these data would indicate that other exoneucleases are involved, but their identification and characterization are the subject of ongoing investigation. Proteins autonomous from exoneucleases may be involved in the later stages of DNA repair. Proliferating cell nuclear antigen [PCNA] binds MLH1, MSH3, and MSH6 [Umar et al. 1996] and potentially may serve to bridge MMR with replication. Other functions have been attributed to MMR proteins, which include involvement in apoptosis [Chung and Rustgi 2003; Edelmann and Edelmann 2004].

Much work has underscored the development and characterization of mouse models that knock out different MMR genes [Edelmann and Edelmann 2004]. Msh2−/− mice have reduced life span and a high incidence of lymphomas [T-cell] and small intestinal adenomas and adenocarcinomas with MSI-H in the tumors [de Wind et al. 1995; Reitmair et al. 1995, 1996; Smits et al. 2000]. A subset of the mice has sebaceous gland tumors, reminiscent of Muir-Torre syndrome. Msh3−−/− mice have a low incidence of late-onset GI tumors with moderate-high MSI [de Wind et al. 1999; Edelmann et al.]

**Figure 2.** DNA MMR system in mammalian cells that perform recognition and editing functions, which have escaped DNA polymerase. A displays the key proteins involved in correction of 1-bp mismatches, whereas B depicts the proteins involved in repair of 2- to 4-bp mismatches [insertions, deletions]. The hMSHS2/hMSH3 complex can also participate in the repair of 1-bp mismatches. Modified from Chung and Rustgi [2003] with permission from *Annals of Internal Medicine*, and from Edelmann and Edelmann [2004] with permission of Wiley-Liss, Inc., a subsidiary of John Wiley & Sons, Inc. (©2004).
2000). Msh6−/− mice develop tumors but with delayed onset compared with Msh2−/− mice [Edelmann et al. 1997]. However, the tumors in the Msh6−/− mice have little or no MSI in their tumors. Interestingly, consistent with the phenotype of msh6−/− mice, it was found that a subset of a slightly older cohort of patients with familial non-HNPCC colorectal cancers had germline MSH6 mutations [Kolodner et al. 1999]. As might be expected, Msh3−/−, Msh6−/− mice develop tumors similar to Msh2−/− mice and have evidence of MSI-H [de Wind et al. 1999, Edelmann et al. 2000]. Mlh1−/− mice behave in a manner similar to Msh2−/− mice with reduced life span and a similar spectrum of tumors [Baker et al. 1996; Edelmann et al. 1996]. Their tumors display MSI-H. Msh4 or Msh5 knockout mice have no tumors. Pms1 knockout mice have no tumors [Prolla et al. 1998], and Pms2 knockout mice develop lymphomas and sarcomas but no GI tumors [Baker et al. 1995; Prolla et al. 1998]. Collectively, these mouse models emphasize the central importance of MSH2, MLH1, and MSH6 in MMR and HNPCC germline mutations and point to potential functional redundancies of the other MMR proteins.

Genetic testing in HNPCC

If a patient’s family satisfies Amsterdam criteria, genetic testing should be offered for MLH1, MSH2, and MSH6 mutational analysis. However, if there is failure to satisfy the criteria, and with an index of suspicion for HNPCC intact, then tumors, if available, can be obtained for either PCR-based MSI testing or MLH1/MSH2/MSH6 immunohistochemistry. Armed with either MSI-H status or lost expression of MLH1, MSH2, or MSH6, then direct genetic testing can be offered and pursued. The options of MSI testing or immunohistochemistry may be equivalent [Pinol et al. 2005], but the precise algorithm may need to be done in accordance with local practice and recommendations. Fulfillment of Amsterdam I criteria, but without evidence of MSI-H status in the tumor(s), prompts the consideration of familial colorectal cancer X syndrome where germline mutations in the known MMR genes do not appear to exist [Lindor et al. 2005]. Clinical monitoring of individuals at risk for HNPCC involves colonoscopy every 2 yr starting between ages 20 and 25, and annually above age 40. Women at risk merit annual endometrial aspiration biopsies and transvaginal ultrasonography to visualize the ovaries, commencing between ages 25 and 35 and occurring annually. Other measures need to be individualized. Patients who are gene mutation carriers should receive counseling about subtotal colectomy given the prominence of colon cancer, and for women, prophylactic hysterectomy and bilateral oophorectomies, especially since endometrial cancer is a defining feature of the disease.

MAP

The MYH gene on human chromosome 1p33-34 is a base excision repair gene in which germline mutations have been found in association with multiple colorectal adenomatous polyps [Sieber et al. 2003]. These mutations may be missense or nonsense, the latter yielding protein truncation. Two common mutations are Y165C and G382D, accounting for >80% of known mutations. Transmitted in an autosomal recessive inheritance pattern, MAP is defined as involving biallelic inactivation and patients harboring multiple colorectal adenomatous polyps without evidence of FAP or attenuated FAP [Sieber et al. 2003]. Monoallelic carriers do not carry an increased risk of colorectal cancer [Balaguer et al. 2007]. 

Clinical findings of an increased number of polyps may trigger suspicion of either MAP or attenuated FAP in the appropriate setting. However, the polyp number can be quite variable in MAP, and it has been demonstrated that if the number of polyps is used as the sole entry criterion, then nearly 25% of cases may be missed in the general population [Jo et al. 2005]. Furthermore, these individuals may have a family history consistent with HNPCC, and thus, MYH gene testing may be necessary for patients who meet clinical criteria for HNPCC and who do not have evidence of DNA MMR gene mutations. These patients warrant regular interval screening and surveillance colonoscopy.

Peutz-Jeghers syndrome

Peutz-Jeghers is a hamartomatous polyposis syndrome with an autosomal dominant mode of inheritance. The incidence is about one in every 200,000 births, and onset is in early childhood. Clinically, patients have moderate–large sized, but few hamartomatous polyps, typically in the small bowel but also in the colon and/or in the stomach [Fig. 3]. These polyps may enlarge and result in hemorrhage or intussusception with obstruction. However, the pathognomonic features are revealed through histopathology with increased smooth muscle bands.

Figure 3. (A) Gross view of a polyp in a patient with Peutz-Jeghers. (B) Histopathologic confirmation is required for the diagnosis, depicting the cardinal feature of abundant smooth muscle. Courtesy of P. Russo, MD.
vents culture-induced senescence without concordant Lkb1 late Lkb+/− in the epithelium of some of the polyps arising in the digen of (Takeda et al. 2006). The hepatic adenomas have evolved to contain hepatic adenomas and liver cancers develop hamartomatous polyps at a faster rate and also p53 are crossed into a mouse embryonic fibroblasts do not undergo transformation by activated Ha-Ras either alone or with known cooperating transformation-associated oncogenes (Bardeesy et al. 2002).

The biological properties of LKB1 have emerged in recent years, with evidence of unexpected functions in the process. One original theme was that LKB1 is important in regulating cell proliferation and growth, perhaps in part through induction of apoptosis. To that end, ectopic LKB1 overexpression in cells leads to G1 cell cycle arrest (Taichin et al. 1999). Phosphorylation of LKB1 (Ser 431) by PKA or p90 ribosomal S6 is essential for suppression of cell growth (Collins et al. 2000; Sapkota et al. 2001). LKB1 is needed for brahma-related gene-1-induced growth arrest (Marignani et al. 2001), and LKB1 plays a role in p53-dependent apoptosis (Karuman et al. 2001). These initial findings have been supplanted by the discoveries that LKB1 controls cellular polarity (as its Par4 homologs in model organisms) (Martin and St. Johnston 2003) and also cellular metabolism (Woods et al. 2003; Shaw et al. 2004a, b). Seminal studies have enlightened a role for LKB1 as being involved as a sensor for energy stress and nutrient deprivation (Fig. 4). LKB1 binds and activates AMP (α, β, γ subunits) (Shaw et al. 2004b) and related kinases to induce AMP kinase (AMPK), which, in turn, regulates the gene product of TSC2 or tuberin. Tuberin facilitates the generation of Rheb-GDP from Rheb-GTP. Rheb-GTP activates mTOR, which is critical in the regulation of protein synthesis, cell growth, and proliferation through the phosphorylation of S6K1 and rS6 and the inhibition of 4E-BP1 that allows the liberation of eIF4E. Germline LKB1 mutations and somatic LKB1 alterations result in the down-regulation of tuberin, up-regulation of Rheb-GTP, and induction of mTOR (Shaw et al. 2004a). Indeed, the hamartomatous polyps of Lkb1-deficient mice display enhanced activation of downstream effectors of mTOR (Shaw et al. 2004a). It is tempting to speculate that mTOR inhibitors that exist (e.g., Rapamycin), or those in development, might be useful as chemopreventive or therapeutic measures in patients with Peutz-Jeghers syndrome.

Patients suspected to have PJS are candidates for genetic testing with evaluation for germline LKB1 mutations. Those identified patients, or patients at risk, should undergo periodic upper endoscopy, colonoscopy, and small bowel follow-through X-ray series; and meticulous attention to the risk of various cancers (especially pancreatic cancer) is required as the patients reach their third decade of life and beyond.

![Figure 4](Figure 4) The LKB1 tumor suppressor gene pathway in the regulation of energy and nutrients. Modified from Shaw et al. [2004a], with permission from Elsevier (©2004).
Juvenile polyposis

Familial Juvenile Polyposis (FJP) is an autosomal dominant disorder in which 10 or more juvenile polyps are observed in the GI tract. It affects one in 100,000 births, and the phenotypic manifestations are found in childhood to adolescence. The polyps, as with the polyps in Peutz-Jeghers syndrome, may bleed or obstruct [Fig. 5]. The establishment of these hamartomatous polyps as juvenile polyps is predicated on histological interpretation and confirmation of microcysts in the epithelia [Fig. 5]. They are found in the colon, but also other parts of the GI tract. There is an increased risk of colon cancer [Giardiello et al. 2001]. While reports of gastric, small bowel, and pancreatic cancers are found in the literature, it is unclear if these are true associations with juvenile polyposis. It is important to bear in mind that juvenile polyps can be sporadic.

Germline mutations in BMPR1A (bone morphogenic protein receptor 1A), SMAD4, or ENG (endoglin, an accessory receptor for TGF-β) are reported in FJP [Howe et al. 1998, 2001; Sweet et al. 2005], suggesting that the TGF-β pathway is critical in the pathogenesis of FJP. Conditional inactivation of Bmpr1a in mice impairs normal intestinal homeostasis with an expansion of the stem and progenitor cell populations, eventually leading to intestinal polyposis resembling FJP [He et al. 2004]. Inhibition of BMP signaling by transgenic expression of noggin results in the formation of numerous ectopic crypt units [Haramis et al. 2004]. These changes phenocopy the polyps observed in FJP [Haramis et al. 2004]. Targeted disruption of Smad4 was pursued by cross-breeding the conditional Smad4 knockout mice and transgenic mice expressing Cre-recombinase under T-cell-specific promoters [Kim et al. 2006]. The T-cell-specific homozygous Smad4 knockout mice developed normally, but life span was shortened. There is thickened mucosa of both the large and small intestines with polyps as well as rectal prolapse. Histology revealed facement of villus architecture and expansion of the stromal compartment containing cystic lesions lined by columnar epithelial cells and plasma cell infiltrates in the intestine [Kim et al. 2006]. In contrast, conditional Smad4 deletion in the intestinal epithelia does not yield intestinal tumors. This highlights the importance of the inflammatory response in the stromal compartment in the regulation of epithelial tumorigenesis.

Genetic testing involves the exploration of germline mutational analysis of BMPR1A, SMAD4, or ENG, recognizing that a subset of FJP patients do not harbor these mutations. Clinical monitoring is similar to that recommended for PJ, but the risk for extracolonic cancers is not observed as noted.

Cowden’s syndrome

Cowden’s syndrome has an autosomal dominant mode of transmission and affects one in 200,000 births. Hamartomatous polyps may be found throughout the GI tract, and these polyps are of a diverse nature: juvenile, lipomas, lymphoid, ganglioneuromas, and inflammatory. The lifetime risk of colon cancer may approach 10%, but this remains controversial. Cutaneous manifestations are of paramount importance in the diagnosis of Cowden’s syndrome. These include acral verrucous papules, the classic trichilemmomas of the face (in particular, eyes, nose and mouth; this distribution is reminiscent of the macules in Peutz-Jeghers), and fibromas of the oral mucosa, gingiva, and tongue [Fig. 6]. About two-thirds of patients have a thyroid goiter, and there is a 10% lifetime risk of thyroid cancer. About 75% of the women have fibrocystic breast disease and fibroadenomas, the lifetime risk of breast cancer is nearly 50%, with typically early-age-onset breast cancer. Soft tissue and internal tumors are present, such as lipomas, neurofibromas, uterine leiomyomas, and meningiomas. Cowden’s syndrome involves germline PTEN mutations, which is a negative regulator of PI3K and AKT [Fig. 4; Liaw et al. 1997]. Pten deficiency in the mouse causes a multitude of tumors, including in the thymus, endometrium, liver, prostate, and GI tract, although the GI tract neoplasms are associated with lymphoid tissue [Podsypanina et al. 1999].

An association between Lhermitte-Ducols disease [cerebellar dysplastic gangliocytoma] and Cowden’s syndrome has been advocated. Bannayan-Ruvalcaba-Riley
[BRR; also called Bannayan-Zonana] syndrome is allelic to Cowden’s syndrome [Arch et al. 1997; Marsh et al. 1997]. Comprising lipomas, pigmented macules of the penis, and macrocephaly, BRR also harbors germline PTEN gene mutations [Arch et al. 1997; Marsh et al. 1997], as is observed with Cowden’s. Clinical suspicion merits PTEN genetic testing in at-risk Cowden’s families with careful screening for thyroid and breast lesions, along with that for GI polyps.

Other hamartomatous polyposis syndromes

Hereditary mixed polyposis syndrome was defined as a potentially new entity through the investigation of large kindred with mixed hamartomatous and hyperplastic polyps, and genetic linkage to human chromosome 6q [Thomas et al. 1996; Whitelaw et al. 1997]. Other potential gene loci have been noted, namely, on chromosomes 15q13-14 [Jaeger et al. 2003] and 10q23 (Cao et al. 2006), although the latter might represent a variant of juvenile polyposis since loss of BMPRIA function was noted in one of the families. Thus, in the consideration of this syndrome, it would appear that the clinical features and types of polyps are important to define, and more studies are needed to establish the genetic underpinnings. Other conditions have involvement of their cognate polyps in different anatomic sites of the GI tract and include neurofibromatosis type I, multiple endocrine neoplasia type 2b, and the Gorlin syndrome [also referred to as the Gorlin-Goltz syndrome or the nevoid basal cell carcinoma syndrome]. In each of these aforementioned conditions, the GI tract is one of multiple sites of involvement and not the cardinal feature.

The Gorlin syndrome has an autosomal dominant mode of transmission with multiple basal cell carcinomas; epidermoid cysts, “pits” on the palms and soles; odontogenic keratocysts; jaw, rib, and vertebral abnormalities; ovarian fibromas; short metacarpals; and hypertelorism. There is increased risk of medulloblastoma, and to a lesser extent, fibrosarcoma of the jaw. The underlying genetic basis is attributable to germline PTCH gene [chromosome 9q22.3] mutations, which is critical in sonic hedgehog signaling. One is struck by the overlap between some features of Gorlin syndrome with FAP [e.g., epidermoid cysts, jaw abnormalities], Turcot syndrome [medulloblastoma with germline APC mutations], and Muir-Torre syndrome [basal cell cancers with MSI]. This raises the possibility of functional interactions between aberrant wnt signaling and sonic hedgehog signaling in some of the hereditary polyposis syndromes, or that MSI may be detectable in tumors with aberrant sonic hedgehog signaling. Of note, MSI has been detected in some sporadic basal cell carcinomas [Sardi et al. 2000].

Hyperplastic polyposis

While long-standing dogma had consigned hyperplastic polyps to incidental occurrences, there has emerged over time a more rigorous histopathological classification of a subset of hyperplastic polyps as serrated polyps and an appreciation that hyperplastic polyposis predisposes to colorectal cancer, albeit without a clear inheritance pattern. The most common types of hyperplastic polyp or serrated polyp are solitary and benign and are not viewed as being subject to malignant transformation, at least directly. These include microvesicular, goblet-rich, and mucin-poor subtypes [Table 3; Fig. 7]. The other types include sessile serrated adenoma (SSA), traditional serrated adenoma (TSA), and mixed polyps [TSA and tubular adenomas] and have replaced older nomenclatures [Table 3; Fig. 7]. All these polyps tend to be flat and diminutive and, thus, may escape recognition at the time of colonoscopy. Magnification chromoendoscopy with indigo carmine may enhance their detection, especially in the context of patients undergoing screening or surveillance due to personal or family history of polyps. This new classification is gaining acceptance but as of yet does not have universal acceptance, in part due to lack of liberation from older nomenclatures and in part due to definition of dysplasia in classic adenomas versus SSAs. SSAs, TSAs, and mixed polyps may progress to cancer. This was appreciated initially in individuals, and even families, with large hyperplastic or serrated polyps, often in the right colon, designated as hyperplastic or serrated adenomatous polyposis. Synchronous colorectal cancers can occur in such settings.

The molecular pathway[s] responsible for the progression of SSAs, TSAs, and mixed polyps to colon cancer deviates from the conventional chromosomal instability pathway observed in the majority of sporadic colon cancers that emerge from adenomatous polyps. Rather, there is evidence of MSI with hypermethylation of MLH1 as part of global hypermethylation or a CpG island methylator phenotype [CIMP] [Park et al. 2003]. It is conceivable that SSAs may be the precursors of MSI-H sporadic colon cancers. Apart from this consideration, SSAs harbor mutations in the BRAF gene, often V600E [Spring et al. 2006]. Similarly, BRAF mutations are observed in MSI-H colon cancers [Tanaka et al. 2006] but are uncommon in MSS colon cancers or in sporadic adenomas. Thus, when encountered, SSAs, TSAs, and mixed polyps should be resected endoscopically since the time interval to colorectal cancer, and the frequency in which this occurs, is not known currently. Nor is it defined whether these types of polyps may, in turn, have their own intermediate lesions before evolving into colon cancer. Interestingly, BRAF mutations may be found in microvesicular and goblet cell-rich subtypes of serrated polyps, raising the intriguing possibility that they

Table 3. Hyperplastic or serrated polyps

|-------------------------|----------------|------------|------------|-------------------------------|-------------------------------------|---------------------------------------|
may progress to SSAs in the correct milieu (Lauwers and Chung 2006).

Summary and future perspectives

The hereditary forms of colorectal cancer have served to illuminate our understanding of the sporadic counterpart, but also provided a critical basis to understand principles of cancer genetics in general. Investigation of hereditary colorectal cancer has, and continues to have, vast translational applications. These include, but are not limited to, chemoprevention, risk stratification and genetic testing, molecular diagnostics, accompanying genetic mouse models, and even more likely in the future, targeted therapeutics. This industrious amount of information to date has made evaluation of patients who have familial colorectal cancer, not defined by the known hereditary forms of colorectal cancer, imperative and increasingly compelling. Such genetic discoveries and insights will lead to new definitions and classifications of subsets of families. Some of these may be inevitably in the continuum with known hereditary forms [especially HNPCC or Lynch syndrome], but others, perhaps the majority even, may be quite distinctive. These in turn will inform us once again about the molecular pathogenesis of sporadic colorectal cancer, and likely other cancers as well, and basic cellular processes, and lead to further translational applications. An ideal scenario would be to risk-stratify the general population based on family history and presence or absence of germ-line genetic mutations and polymorphisms to shape clinical monitoring measures.

Acknowledgments

NIH R01-DK056645 and R01-CA120393, the National Colorectal Cancer Research Alliance, and the Irving A. Hansen Foundation supported this work.

References


The genetics of hereditary colon cancer


ceptible to lymphoid tumours. *Nat. Genet.* **11**: 64–70.


The genetics of hereditary colon cancer

Anil K. Rustgi

Genes Dev. 2007 21: 2525-2538
Access the most recent version at doi:10.1101/gad.1593107

References
This article cites 111 articles, 34 of which can be accessed free at:
http://genesdev.cshlp.org/content/21/20/2525.full.html#ref-list-1

Email Alerting Service
Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or click here.

Topic Collections
Articles on similar topics can be found in the following collections
Cancer and Disease Models (163 articles)

To subscribe to Genes & Development go to:
http://genesdev.cshlp.org/subscriptions

Copyright © 2007, Cold Spring Harbor Laboratory Press