





Polyposis and Colon Cancer Predisposition Syndromes

- Familial Adenomatous Polyposis, Hereditary Nonpolyposis Syndrome, Juvenile Polyposis
 - Genetic analysis of these syndromes has identified their genetic causes and led to understanding of sporadic colorectal cancer

Familial Adenomatous Polyposis

- Autosomal dominant
- Multiple benign adenomas of the colon and rectum
- · Increased risk of colon cancer
- Patients develop adenomas in 2nd and 3rd decade
- Inherited deletion of chromosome 5q

Adenomatous Polyposis Coli









Hereditary Nonpolyposis Colon Cancer Syndrome

- At least three affected family members in two generations
- Autosomal Dominant
- One member diagnosed under age 50
- Right sided colon cancer most common
- · Also associated with endometrial carcinoma



Microsatellite DNA

- Repeats of simple single, double, triple or tetra nucleotides
- Commonly (A)_n or (CA)_n/(GT)_n repeats
- $>10^4$ -10⁵ found throughout genome

Linkage analysis in HNPCC Families

- Log of the Odds (LOD) ratio of greater than 5 seen in HNPCC pedigrees
- Linkage to 2p16 and 3p24

 Inheritance of phenotype was linked with specific allele

Microsatellite Instability and HNPCC

- Simple repeated sequences such as CA_n and A_n are mutated in tumors from HNPCC patients
- Mutations typically delete or insert repeat sequence
- Point mutations occur at high frequency

HNPCC Tumors Have Mutations in Microsatellite DNA



Mismatch repair and Microsatellite Instability

- Resembles mutator phenotype seen in e. coli and s. cerevesiae that are deficient in mismatch repair
- Cells with microsatellite instability also have increased rate of point mutations
- Cells with microsatellite instability have no functional mismatch repair

E. Coli Mismatch Repair

- E coli: MutS, MutL and MutH
- MutS binds mismatch
- MutL binds MutS and DNA repair machinary
- MutH recognizes daughter strand
- Mismatches can be repaired with purified factors in a cell free system



Eukaryotic Mismatch Repair

- MSH2 and (MSH3 or MSH6) bind DNA
- MLH1 binds MSH complex and recruits DNA repair machinery
- Mutation of one subunit inactivates repair
- Purified factors able to repair mismatches





















Predictions of the Nowell's Hypothesis

- Mutations of oncogenes are rare events
- Solid tumors require multiple genetic alterations within a single clone
- Multiple waves of mutation require increased mutation rate







K-RAS Mutations

- •Mutated in 50% of sporadic colorectal cancer
- •Mutated in 50% of sporadic adenomas
- •Mutations are somatic
- •Mutations affect only one allele
- •Mutations are dominant and oncogenic
- •Mutations are not seen in small adenomas or aberrant crypts
- •Mutations inactivate GTPase activity of K-RAS



























Genomic Instability in Colon Cancer

- APC inactivation causes a mitotic checkpoint defect
- p53 mutations cause G1 and G2 checkpoint defect
- MMR defects associated with diploid karyotype and 1000 fold increase in mutation rate
- Cause of aneuploidy remains poorly understood but likely to involve mitotic checkpoint pathways







Comparison of MMR deficient and Aneuploid Tumors: The TGF-β pathway

- 100% inactivation of TGF β type II receptor in MMR-deficient cases.
- Typically, frame shift mutation in A₁₀ tract in open reading frame
- Not mutated in aneuploid tumors.
- Chromosome 18q lost in 80% of aneuploid cases.
- Both alleles altered for SMAD4 and SMAD2 in substantial proportion of cases.

Comparison of WNT pathway Alterations (MMR + v. MMR -)

- β-catenin mutations more common than APC mutations in MMR-deficient tumors
- APC mutation occur in MMR proficient tumors
- Mutations are mutually exclusive
- WNT pathway is targeted in all colorectal cancers

Therefore:

- Different genetic instabilities reveal distinct "hot-spots" within different genes on a pathway.
- The pathways are the target
- Multiple pathways are activated in an invasive carcinoma



