Less Familiar Cancer Genes and Syndromes

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Ataxia-Telangiectasia

- Incidence: 1 in 40,000 to 1 in 100,000
- Autosomal recessive inheritance
- Caused by mutations in the ATM gene, found on the long arm of chromosome 11 (11q22.3)
- Diagnostic testing
 - Serum AFP
 - Colony survival assay
 - Karyotyping (translocation 7;14)
 - Immunocompetence assays



Ataxia-Telangiectasia

Clinical features

- Progressive cerebellar ataxia
- Facial and conjunctival telangiectasia
- Combined immunodeficiency
- Growth retardation
- Usually normal intelligence

Associated malignancies

- Lymphoma/leukemia (in ~40%)
- Increased risk for solid tumors (e.g., ovary, breast, melanor stomach)

Jones KL. In: Smith's Recognizable Patterns of Human Malformation. 5th ed. Philadelphia: WB Saunders Co; 1997: 196-197.
Olsen JH, et al. J Natl Cancer Inst. 2001;93:121-127.

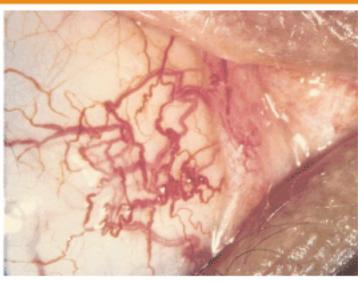
Swift M, et al. N Engl j Med. 1991;1831-1836.



Ataxia-Telangiectasia (cont.)









Heterozygous *ATM* Mutation Carriers

- Ataxia-telangiectasia is an autosomal recessive condition
- ATM gene on chromosome 11 cloned in 1995
- Early studies suggested that female carriers have an elevated risk of breast cancer
- Two ATM mutations identified in Australia: T7271G, IVS10-6T → G
 - 15.7-fold elevated risk of breast cancer in carriers
 - Found in families with multiple cases of breast cancer

Heterozygous *ATM* Mutation Carriers

- This issue is of importance in view of the frequency of ATM heterozygotes in the general population, estimated as $\sim 2-3\%$
- The summary estimated relative risk of breast cancer in *ATM* heterozygotes is ~4 (D Easton: Int J Radiat Biol 1994; 66 [Suppl 6]:177-182)
- If both estimates are correct, 3-4% of all breast cancer might be attributable to ATM heterozygosity
- Problem: more recent epi studies have yielded conflicting results regarding whether this risk estimate is correct (RM Tamimi et al: Breast Cancer Res 2004; 6:R16-R22)
- The strongest data in support of there being a relationship between ATM and breast cancer risk are found in studies targeting female family members from AT kindreds (JH Olsen et al: JNCI 2001; 93:121-127)

Nijmegen Breakage Syndrome

- Clinical features
 - Microcephaly
 - Growth retardation/short stature
 - Mental retardation
 - Irregular pigmentation
 - Immunodeficiency
 - 1° ovarian failure
 - Congenital malformations
- Associated malignancies
 - Lymphoma, especially B cell
 - Other lymphoreticular cancers



Concannon PJ, Gatti RA. GeneTests [database online]. Available at: http://www.geneclinics.com. Accessed November 11, 2002.

The International Nijmegen Breakage Syndrome Study Group. Arch Dis Child. 2000 82:400-406. Photos reprinted with permission fro BMJ Publishing Group.

OMIM78. Available at: http://www.ncbi.nlm. nih.gov/omim. Accessed November 11, 2002.



Nijmegen Breakage Syndrome (cont.)

- Incidence: ~1 in 100,000
- Autosomal recessive inheritance
- Associated with mutations in NBS1 (8q21.3)
 - Almost 100% of Slavic patients and ~70% of North America patients are 657del5 homozygotes
 - Clinical testing available for 657del5
- Gene product is nibrin, which complexes with the protein products of hMre11 and hRAD50 to aid in DNA repair

Carney JP et al. Cell. 1998;93:477-486.

Concannon PJ, Gatti RA. GeneTests [database online]. Available at: http://www.geneclinics.com. Accessed November 11, 2002.
Varon R et al. Cell. 1998;93:467-476.

Heterozygous *NBS* Mutation Carriers

- Two founder mutations in NBS occur in Poland, permitting genetic studies to be more efficiently accomplished
- 23 of 1289 (1.8%) subjects with various cancers carried one of the founder mutations, versus 14/1620 (0.9%) controls
 - significantly increased risks of melanoma, NHL and colon cancer were seen
 - (J Steffen et al: Int J Cancer 2004; 111:67-71)
- Another Polish study:
 - 0.6% of 1500 controls were carriers
 - 7% of 305 prostate cancer cases were carriers (OR = 3.9)
 - 9% of 56 familial prostate cancer cases were carriers (OR = 16)
 - (C Cybulski et al: Cancer Res 2004; 64:1215-1219)

Bloom Syndrome

Clinical features

- Prenatal and postnatal growth delay/short stature
- Spotty hypo- and hyperpigmentation
- Facial telangiectatic erythema
- Photosensitivity
- Microcephaly
- Immunoglobulin deficiency



Bloom Syndrome. In: Gorlin RJ, Cohen MM Jr, Levin LS, eds. Syndromes of the Head and Neck. 3rd ed. New York: Oxford University Press; 1990:297-300. Photo reprinted with permission from Oxford University Press.



Bloom Syndrome (cont.)

- Incidence: rare in most ethnic groups; 1 in 100,000 in Ashkenazi Jews
- Autosomal recessive inheritance
- High rate of chromosomal instability
 - Elevated sister chromatid exchange (pathognomonic)

Wamen S et al. Proc Nat Acad Sci U S A. 1581;78:3133–3137.
Roa BB, et al. Genet Test. 1999;3:219-221.



Bloom Syndrome (cont.)

- Gene mutated is RECQL3 (BLM) at locus15q26.1
 - 2281delta6ins7 is a founder mutation in Ashkenazi Jews (~1% are carriers)
- Gene product is a helicase involved in DNA repair

Ellis NA et al. Cell. 1995;83:655–666. Imamura O et al. Oncogene. 2001;20:1143-1151. Marsh DJ, Zori RT. Cancer Lett. 2002;181:125-164. Roa BB et al. Genet Test. 1999;3:219-221.



Bloom Syndrome (cont.)

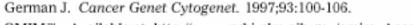
Associated malignancies

- · Very high rate of cancer
- Acute leukemia, lymphoma
- Solid tumors in adults

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tongue breast
esophageal others
colon
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Solid tumors in children

medulloblastoma osteosarcoma Wilms tumor others







Heterozygous *BLM* Mutation Carriers

- Case (n=1244) control (n=1839) study of colon cancer risk in BLM Heterozygotes in Subjects of Ashkenazi Jewish heritage
- Facilitated by the AJ BLM founder mutation
- Colorectal cancer subjects were 2.45 times more likely to carry the AJ BLM founder mutation than were controls

(SB Gruber et al: Science 2002; 297:2013)

- Emerging concept: "HAPLOINSUFFICIENCY"
 - For some genes, a half-dose of its protein is not adequate for full gene function
 - May be a particular issue for genes involved in maintenance of genomic integrity
 - Subnormal levels of protein lead to genomic instability, increased mutation rate in affected cells, and an increased risk of malignant transformation
 - Examples: ATM, NBS, XP, FA

Fanconi Anemia

Clinical features

- Short stature
- Abnormal pigmentation
- Thumb abnormalities; radial hypoplasia (see radiograph)
- Other multisystem congenital anomalies
- Hearing loss
- Progressive bone marrow failure with pancytopenia

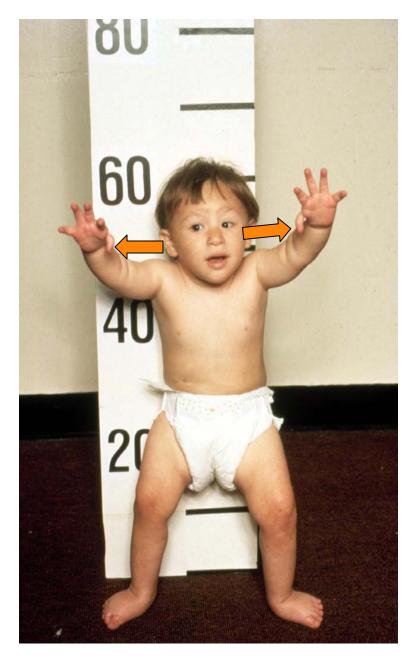


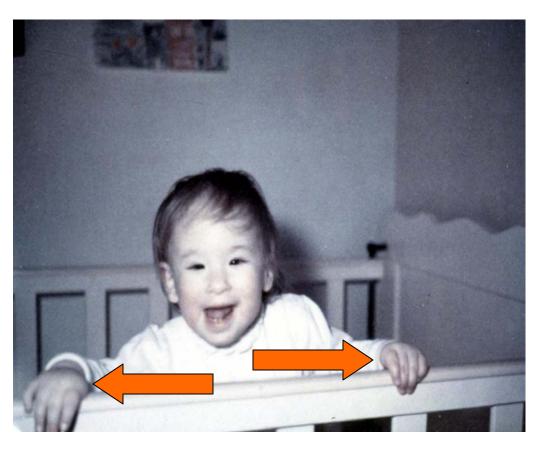
De Kerviler E et al. Clin Radiol. 2000;55:340-345. Figure reprinted with permission from Elsevier.

Giampietro PF et al. Am J Med Genetics. 1997;68:58-61.



Cousins with Fanconi's Anemia





Case 1





Absent thumbs, L pollicization



Wrist Splint

Case 2



Café-au-lait spot



Flat thenar eminence

Fanconi Anemia (cont.)

- Associated neoplasias
 - Myelodysplasia
 - Acute myelogenous leukemia
 - Solid tumors
 - Vulvar Cancer: O/E = 4300
 - Esophageal Cancer: O/E = 2400
 - Head/Neck Cancer: O/E = 700
 - Beware the atypical presentation in young adults!

Butturini A et al. Blood. 1994;84:1650-1655. Giampietro PF et al. Am J Med Genetics. 1997;68:58-61.

Rosenberg P et al: Blood 2003; 101:822-826



Fanconi Anemia (cont.)

- Incidence: 1 in 100,000 live births
- Autosomal recessive inheritance
 - Carrier frequency: 1 in 300; ~1 in 100 in Ashkenazi Jews (IVS4 +4 A→T founder mutation)
- Diagnosis based on chromosomal breaks and other aberrations detected using diepoxybutane or mitomycin C in culture

Auerbach AD. Genet Test. 1997;1:27-33.



Fanconi Anemia (cont.)

- ELEVEN complementation groups identified (A, B, C, D1, D2, E, F, G, I, J, L)
 - FA-A subtype present in >65% affected patients
- NINE genes have been identified, including BRCA2 (FA-I
 - Clinical testing available only for FA-C and FA-D1 group gene mutation (includes Ashkenazi carriers)
- Gene products complex together and interact with other proteins such as those of the BRCA1 and BRCA2 genes to regulate DNA repair and genomic stability

Howlett NG et al. Science, 2002;297:606-609.

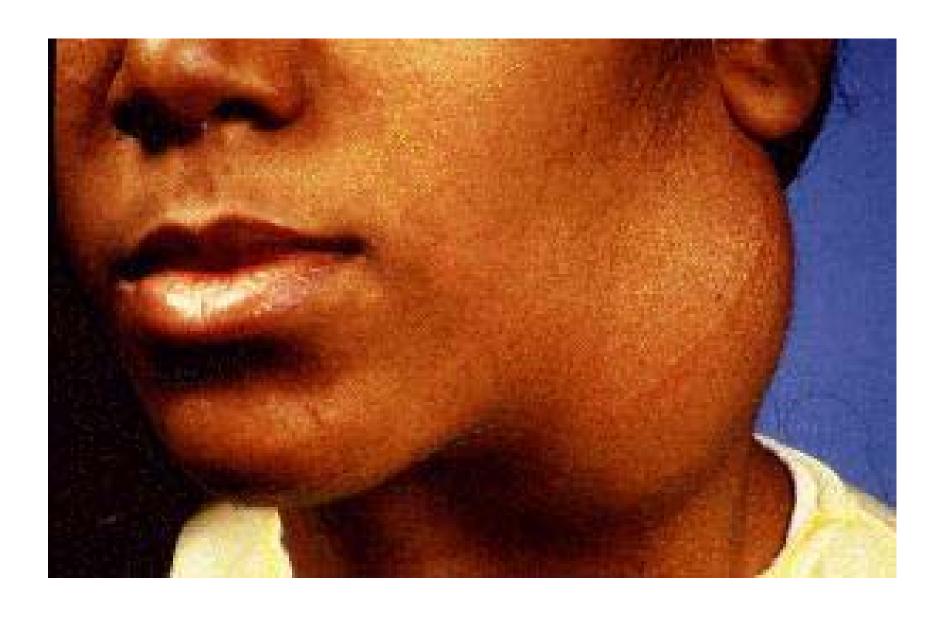
Shimamura A et al. GeneTests [database online]. Availableat: http://www.geneclinics.com. Accessed August 27, 2002.



FA Complementation Groups/Genes

Group	Locus	cDNA	Exons	AA	%
А	16q24.3	5.5	43	1455	~70
В	Xp22.31	2.8	10	859	Rare
С	9q22.3	4.6	14	558	~10
D1/BRCA2	13q12.3	11.4	27	3418	Rare
D2	3p25.3	5	44	1451	Rare
Е	6p21-22	2.5	10	536	~5
F	11p15	1.3	1	374	Rare
G	9p13	2.5	14	622	~10
I	-	-	-	-	Rare
J	-	-	-	-	Rare
L	2p15-16.1	1.7	14	375	Rare

Carotid body is the most common location of PGL tumors

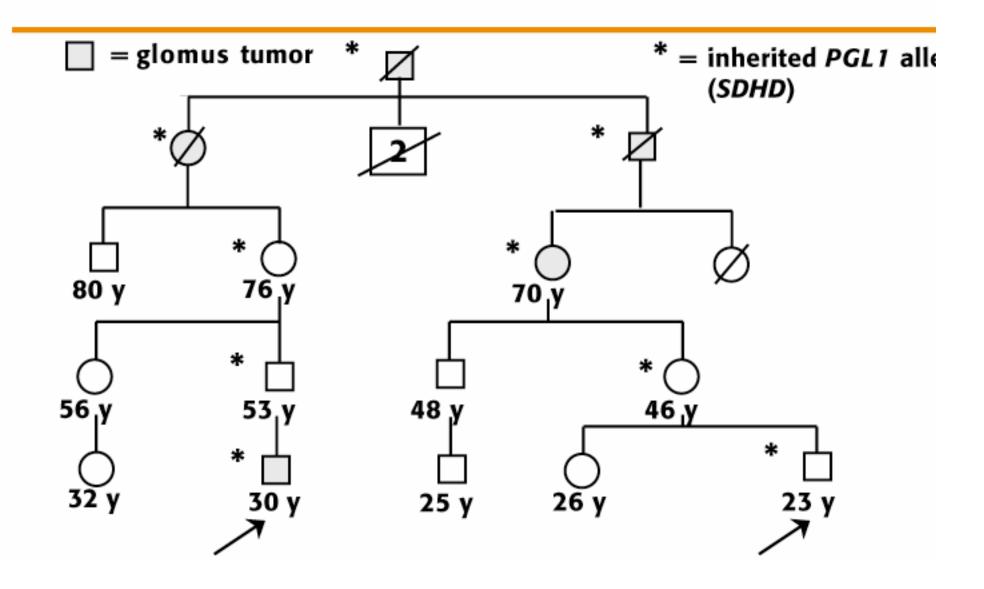


Hereditary Paraganglioma

- Genes: SDHB, SDHC, and SDHD (encode subunits of mitochondrial complex II)
- Inherited as an autosomal dominant disorder
- Characterized by imprinting: affected individua inherit the gene from their fathers
- Genetic heterogeneity:
 - SDBH: chromosome 1p36.1-35
 - SDHC: chromosome 1q21
 - SDHD: chromosome 11q23



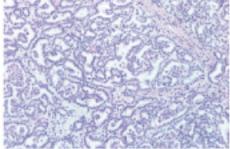
Hereditary Paraganglioma: Autosomal dominant inheritance with imprinting (affected individuals inherit the disease gene from their fathers)



Hereditary Papillary Renal Cell Carcinoma

- Young age at diagnosis (median age is 45 years)
- Up to 3000 tumors per kidney! Difficult to detect by US, CT hypovasc
- Primarily type 1 papillary RCC
- Multiple affected family members
- Met Proto-oncogene
- Encodes hepatocyte growth factor





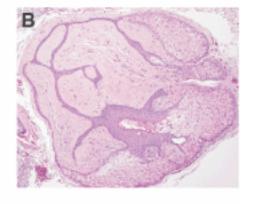
Figures courtesy of Jberton Zbar, MD, National Cancer Institute.

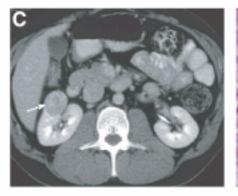
Birt-Hogg-Dubé Syndrome

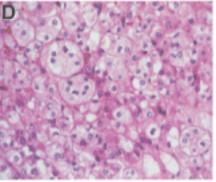
- Rare syndrome characterized by
 - Chromophobe renal cancer (and other histologies)
 - Fibrofolliculoma
 - Spontaneous pneumothorax
- Autosomal dominant
- Gene on chromosome 17p11.2
- Protein Product:FOLLICULIN

Nickerson M et al. Cancer Cell. 2002;2:157-164.









Figures courtesy of Jorge Toro, MD, National Cancer Institu



Birt-Hogg-Dubé Syndrome, con't

- Germline mutations in BHD found in 51/61 (84%) US families
 - 45% of mutation-positive families had ≥ 1 renal cell cancer
- Mutation hotspot in exon 11
 - 27/51 (53%) of mutations occurred in this exon
 - significantly fewer tumors with deletion mutations than insertion mutations
- 3 families affected by renal oncocytomas, first genetic association for this histologic variant of kidney cancer
- VHL, PRCC and BHD managed with observation for tumors < 3cm, partial neprectomy when larger

(LS Schmidt et al: Amer J Hum Genet 2005; 76:1023-1033)

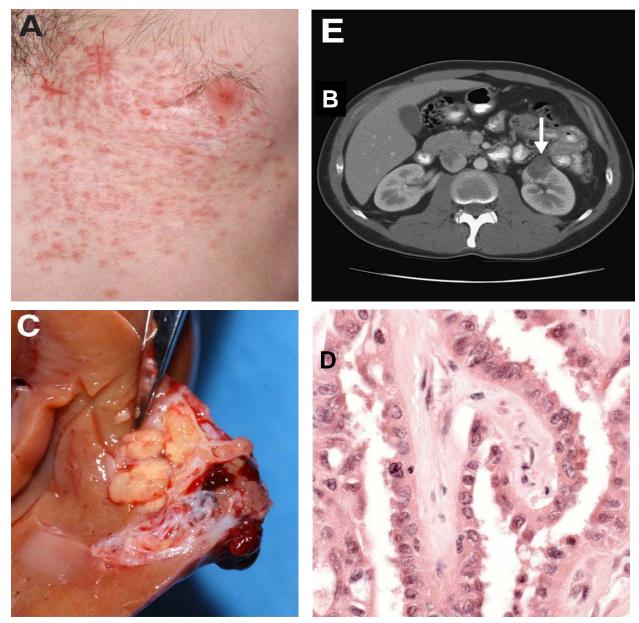
Hereditary Leiomyomatosis and RCC

- Skin nodules (leiomyomata)
- Uterine fibroids (leiomyomas and leiomyosarcomas)
- Unilateral, solitary, VERY aggressive; metastasize early
- Gene on chromosome 1q42.3–43
- Gene identified: fumarate hydratase (Krebs cycle enzyr
- Mutations in FH found in 31/35 (89%) families studied
- 98% of women with skin tumors also had uterine tumor

Tomlinson IP et al. Nat Genet. 2002;30:406-410.

J Toro et al: Amer J Hum Genet 2003; 73:95-106

Hereditary leiomyoma renal cell carcinoma



Photographs courtesy of Dr. Jorge Toro, Genetic Epidemiology Branch, US National Cancer Institute

Histopathology of Hereditary Renal Cancers

- Von Hippel-Lindau.....clear cell renal carcinoma
- Papillary Renal Cell Cancer.....type 1 papillary renal carcinoma
- Birt-Hogg-Dubé......hybrid oncocytic renal tumors; chromophobe renal carcinoma
- HLRCC.....type 2 papillary renal carcinoma; collecting duct carcinoma

Conclusions

- Reviewed a series of less common genetic cancer susceptibility syndromes
 - Ataxia Telangiectasia
 - Nijmegen Breakage Syndrome
 - Bloom Syndrome
 - Fanconi Anemia
 - Hereditary Paraganglioma
 - Familial Papillary Renal Cancer Syndrome
 - Birt-Hogg-Dubé Syndrome
 - Hereditary Leiomyoma Renal Cell Cancer Syndrome
- Recognition of the clinical phenotype is the key
- Theme: potential risk of malignancy in heterozygous carriers of autosomal recessive disorders that involve maintenance of genomic integrity
- Novel mechanisms of inheritance (imprinting)
- Novel etiologic genes (fumarate hydratase; SDHB, C, D)
- Etiologic clues to be found in histopathologic heterogeneity