Single Gene Disorders with non-classic Inheritance

Mohammed Ismail Syed Ali Group-1, 5th course.

Medical genetics

Single Gene Disorders with non-classic Inheritance

They fall into four categories: Diseases caused by

- 1.Trinucleotide repeat mutation
- 2. Mutation in mitochondrial genes
- 3. Genomic imprinting
- 4.Gonadal mosaicism

- Expansion of trineuclotide repeats is an important genetic cause of human disease, particularly neurodegenerative disordersfirst recognised in 1991
- Till now there are 40 diseases under this category

- Associated with the expansion of trinucleotides in the genome
- These trinucleotides usually share the G and C
- This makes DNA unstable, and may impair gene function
- Expansion depends strongly on the sex of the transmitting parent
 - Fragile X syndrome: Expansions occur during oogenesis
 - Huntington disease: Expansions occur during spermatogenesis

Table 5-8 Examples of Trinucleotide-Repeat Disorders

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Disease	Gene	Locus	Protein	Repeat	No. of Repeats	
					Normal	Disease
Expansions Affecting Noncodin	g Regions					
Fragile X syndrome	FMRI (FRAXA)	Xq27.3	FMR-1 protein (FMRP)	CGG	6-55	55-200 (pre); >230 (full
Friedreich ataxia	FXN	9q21.1	Frataxin	GAA	7-34	34-80 (pre); >100 (full)
Myotonic dystrophy	DMPK	19q13.3	Myotonic dystrophy protein kinase (DMPK)	CTG	5-37	34-80 (pre); >100 (full)
Expansions Affecting Coding Re	egions					
Spinobulbar muscular atrophy (Kennedy disease)	AR	Xq12	Androgen receptor (AR)	CAG	9-36	38-62
Huntington disease	НТТ	4p16.3	Huntingtin	CAG	6-35	36-121
Dentatorubral-pallidoluysian atrophy (Haw River syndrome)	ATNL	12p13.31	Atrophin-1	CAG	6-35	49-88
Spinocerebellar ataxia type 1	ATXN1	6p23	Ataxin-1	CAG	6-44	39-82
Spinocerebellar ataxia type 2	ATXN2	12q24.1	Ataxin-2	CAG	15-31	36-63
Spinocerebellar ataxia type 3 (Machado-Joseph disease)	ATXN3	14q21	Ataxin-3	CAG	12-40	55-84
Spinocerebellar ataxia type 6	CACNA2A	19p13.3	α _{1A} -Voltage-dependent calcium channel subunit	CAG	4-18	21-33
Spinocerebellar ataxia type 7	ATXN7	3p14.1	Ataxin-7	CAG	4-35	37-306

There are <u>three mechanisms</u> by which unstable repeats cause diseases:

- •Loss of function of the affected gene the repeats are generally in non-coding part of the gene
- A toxic gain of function by alterations of protein structure
- the repeats are in the coding regions of the genes
- Huntington disease and
- Spinocerebellar ataxia
- •A toxic gain of function mediated by mRNA: noncoding parts of the gene are affected
- fragile X tremor-ataxia syndrome

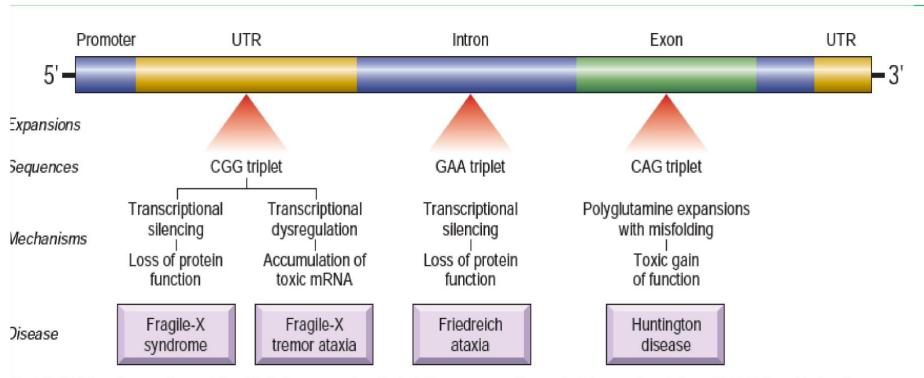


Figure 5-23 Sites of expansion and the affected sequence in selected diseases caused by nucleotide-repeat mutations. UTR, Untranslated region.

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Fragile X Syndrome and Fragile X Tremor/Ataxia

- 1 in 1550 for affected males and
- 1 in 8000 for affected females
- FMR1 gene
- CGG repeats:
- In the normal population ranging from 6 to 55 (average, 29)
- Normal transmitting males and carrier females 55 to 200 repeats premutations
- Affected individuals: 200 to 4000 repeats -full mutations

 Anticipation: Clinical features of fragile X syndrome worsen with each successive generation - as it is transmitted from a man to his grandsons and great-grandsons

Fragile X Syndrome and Fragile X Tremor/Ataxia

In fragile X syndrome:

Clinical features:

- •Males are mentally retarded, IQ 20 to 60
- Long face
- Large mandible
- Large everted ears and
- Large testicles (macro-orchidism)
- Hyperextensible joints

- •a high arched palate, and
- Mitral valve prolapse



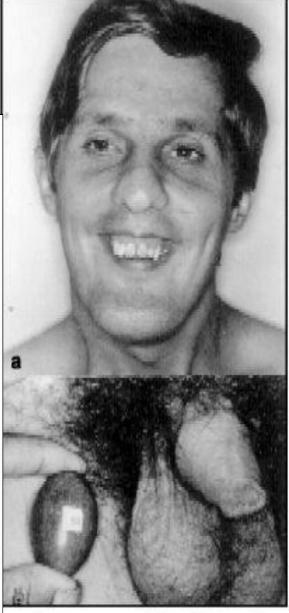
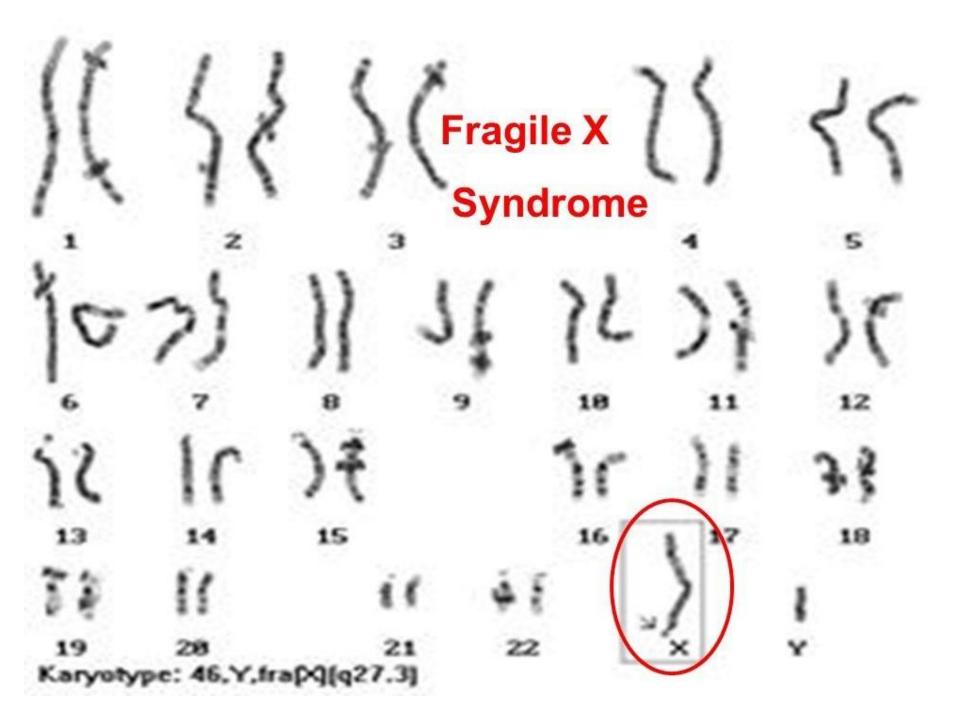


Fig 3. (a) Patient III3 (family 1) with long and narrow face and (b) macro-orchidism (testicular volume= 56 ml).



Fragile X Syndrome

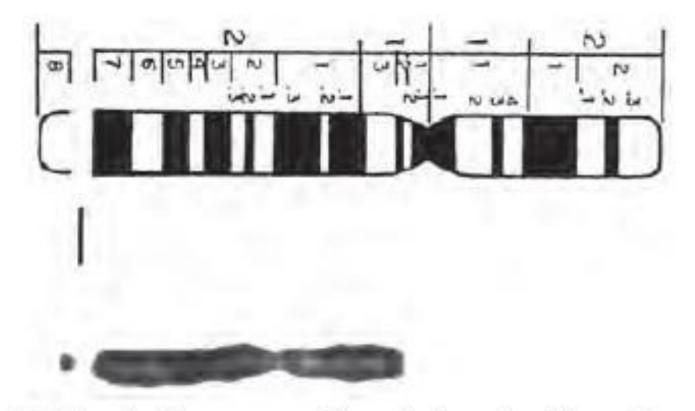
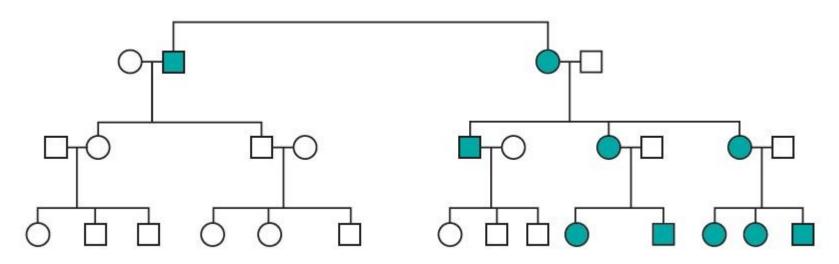


Figure 5-24 Fragile X seen as discontinuity of staining. (Courtesy of Dr. Patricia Howard-Peebles, University of Texas Southwestern Medical Center, Dallas, TX.)

Mutations in Mitochondrial Genes — Leber Hereditary Optic Neuropathy

- A feature unique to mtDNA is <u>maternal</u> inheritance
- Human mtDNA contains 37 genes
- 22 for tRNA
- 2 for rRNA
- The remaining 13 genes encode subunits of the respiratory chain enzymes
- Hence, mutations affecting these genes exert their deleterious effects primarily on the organs most dependent on oxidative phosphorylation
 - CNS
 - Skeletal muscle,
 - Cardiac muscle
 - Liver, and
 - Kidneys

Typical Pedigree cahrt in mtDNA associated transmission



Genomic Imprinting

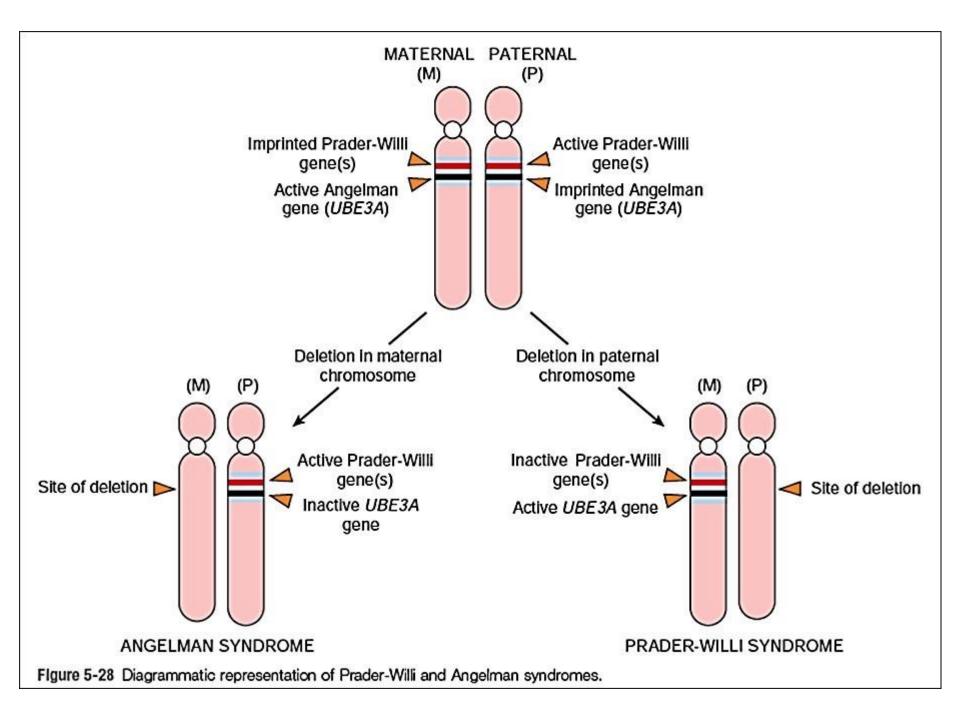
- Imprinting is <u>silencing</u>
- Silencing occurs by methylation of DNA or Histones
- It is an epigenetic phenomenon
- Silencing occurs during gametogenesis

- It is permanent
- Alleles are expressed in a parent-of-origin-specific manner
 - If paternal allele is imprinted (silenced), maternal allele will express and vice versa
- Human diseases involving genomic imprinting include
 - Angelman syndrome and
 - Prader–Willi syndrome

Genomic Imprinting

- Human diseases involving genomic imprinting include
 - Angelman syndrome and
 - Prader–Willi syndrome

- Both are micro deletion syndromes
 - Chr# 15 is involved in deletion
 - -del(15)(q11.2q13)



Prader-Willi syndrome

Characterized by

- Mental retardation,
- Short stature
- •Hypotonia
- Profound hyperphagia
- Obesity
- •Small hands and feet, and
- Hypogonadism

- •In 65% to 70% of cases, an interstitial deletion of band q12 in the long arm of chromosome 15, del(15)(q11.2q13), can be detected
 - (causing a 5-Mb deletion) (Micro deletion)
- •It is striking that in all cases the deletion affects the paternally derived chromosome 15.







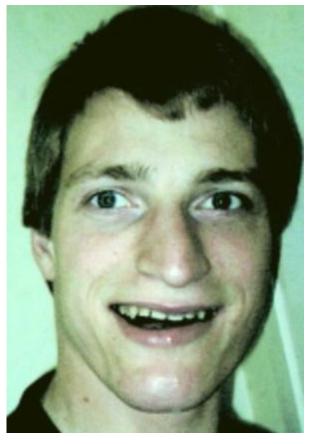




Angelman syndrome

- In contrast patiemts with the phenotypically distinct Angelman syndrome are born with a deletion of the same chromosomal region derived from their mothers
- Patients with Angelman syndrome are:
 - Mentally retarded
 - In addition they have
- Ataxic gait
- Seizures, and

- Inappropriate laughter
- Because of their laughter and ataxia, they have been referred to as "happy puppets"





END