

Unusual Modes of Inheritance

Wayne Lam

wayne.lam@ed.ac.uk

New Genetics

- **Non-Mendelian**
 - Genomic Imprinting
 - Digenic Inheritance
 - Triallelic inheritance
- **Mitochondrial Inheritance**
- **Chromosomal**
 - Telomeric deletions
 - Contiguous gene syndrome
- Trinucleotide repeat expansions
- Somatic and Gonadal/Germ line mosaicism

Disorders of disrupted Genomic imprinting

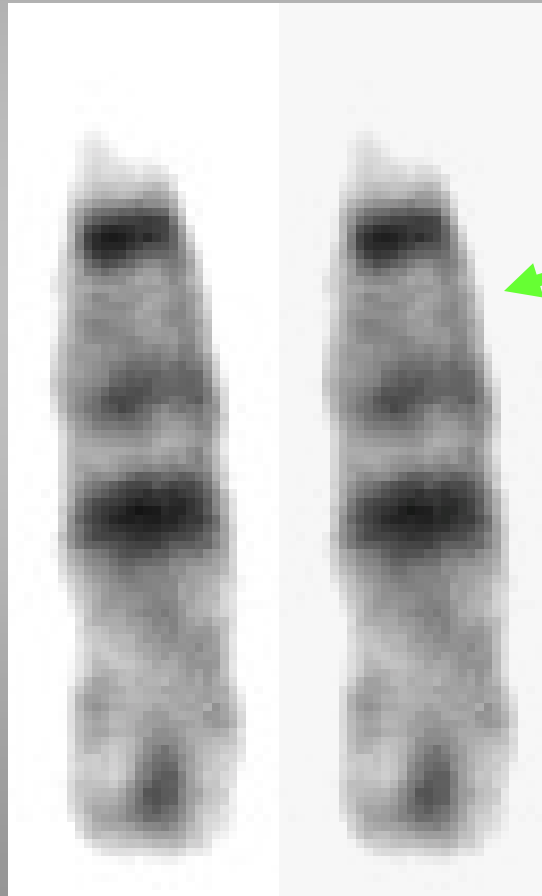
- Severe global developmental delay
- No speech
- Inappropriate laughter
- Drooling
- Seizures
- Cannot walk without help
- No family history

Angelman syndrome

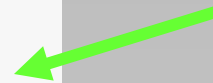
Prader Willi Syndrome

- Floppy at birth, poor feeding
- Short stature, small hands and feet
- Hyperphagia and obesity
- Hyponadism
- Mental retardation (mild to moderate)

Chromosome 15



15q11-13



- Further analysis of these two patients show that the deletion occurred on different chromosomes
- The chromosome that was deleted in Angelman case was derived *from Mother*
- In the Prader-Willi case the chromosome was derived *from Father*

Loss of heterozygosity

Genomic Imprinting

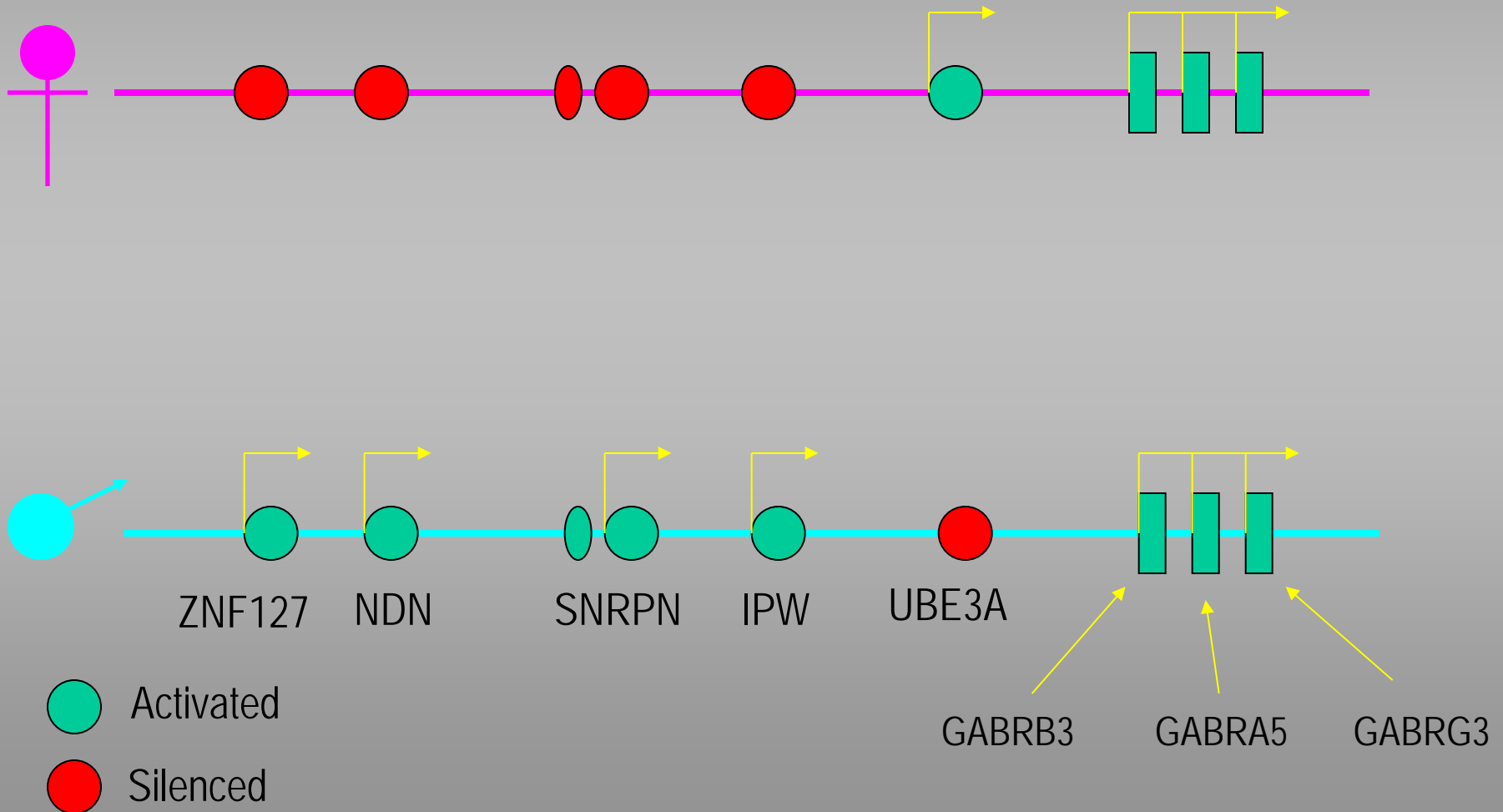
- Defined as differences in gene expression depending on whether a gene is maternally or paternally inherited
- Specific chromosomal regions contain imprinted genes
- Such regions usually contain both maternally and paternally imprinted genes

Genomic Imprinting

- Leads to functional hemizyosity
- Accounts for only a small number of genes
- Importance?
 - many developmental genes are imprinted
 - disruption of imprinting is implicated in several well known genetic disorders and many cancers

Prader-Willi / Angelman region

Normal expression pattern

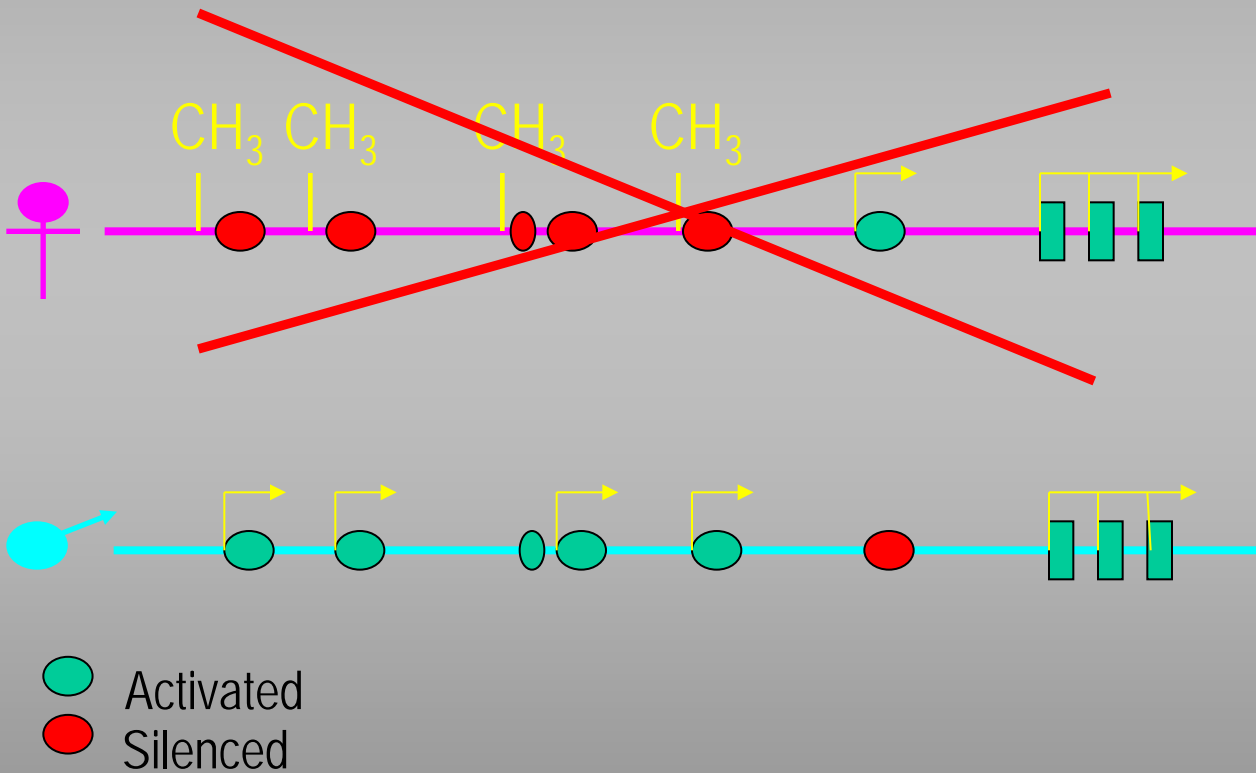


Mechanism of loss of imprinting: 1

Chromosome deletion of maternal chromosome

Angelmans syndrome

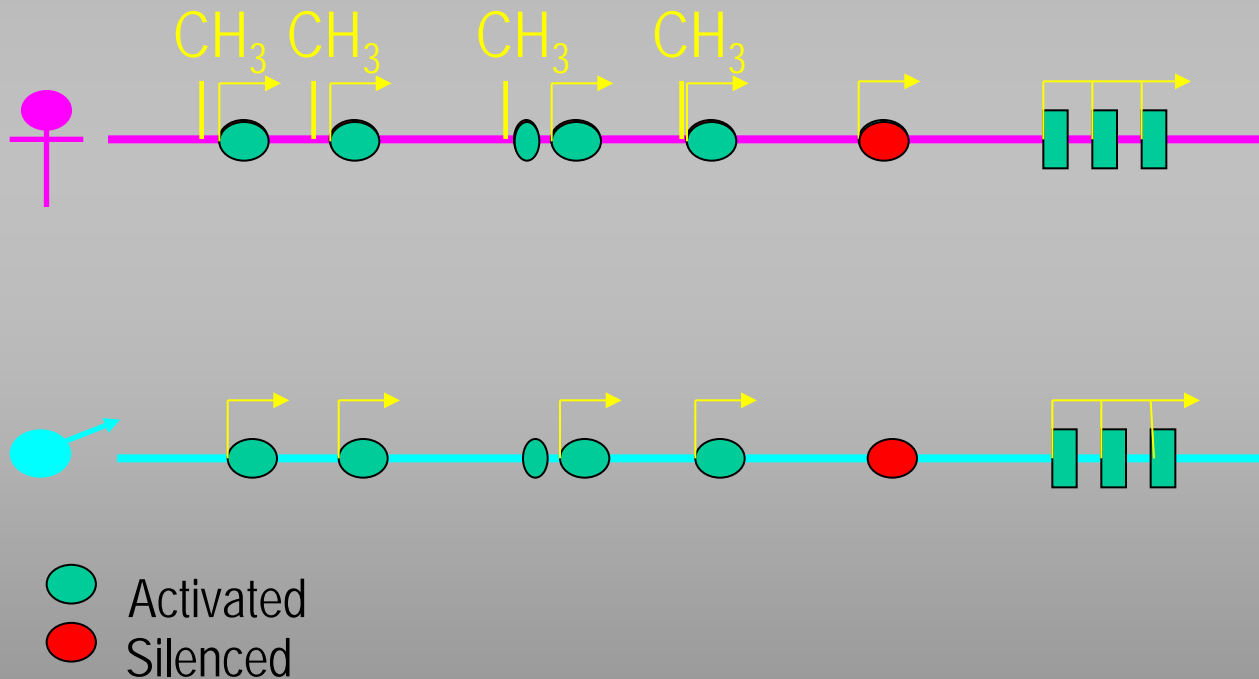
70% of cases



Mechanism of loss of imprinting: 2 Methylation abnormality

Angelmans syndrome

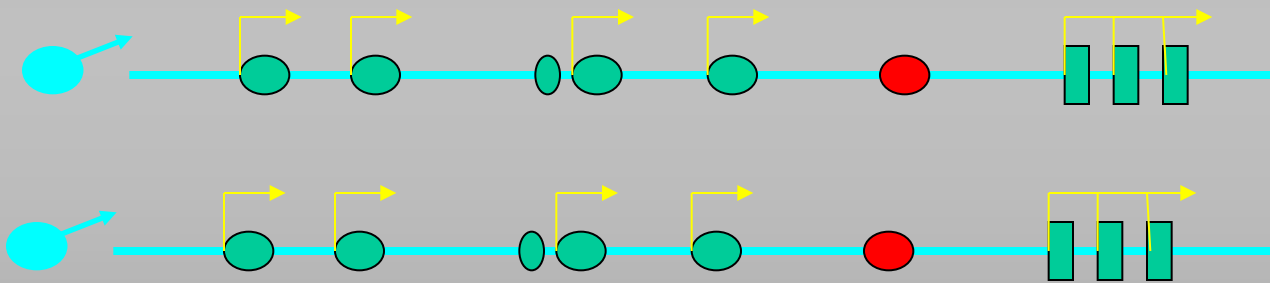
2% of cases



Mechanism of loss of imprinting: 3 Uniparental Disomy

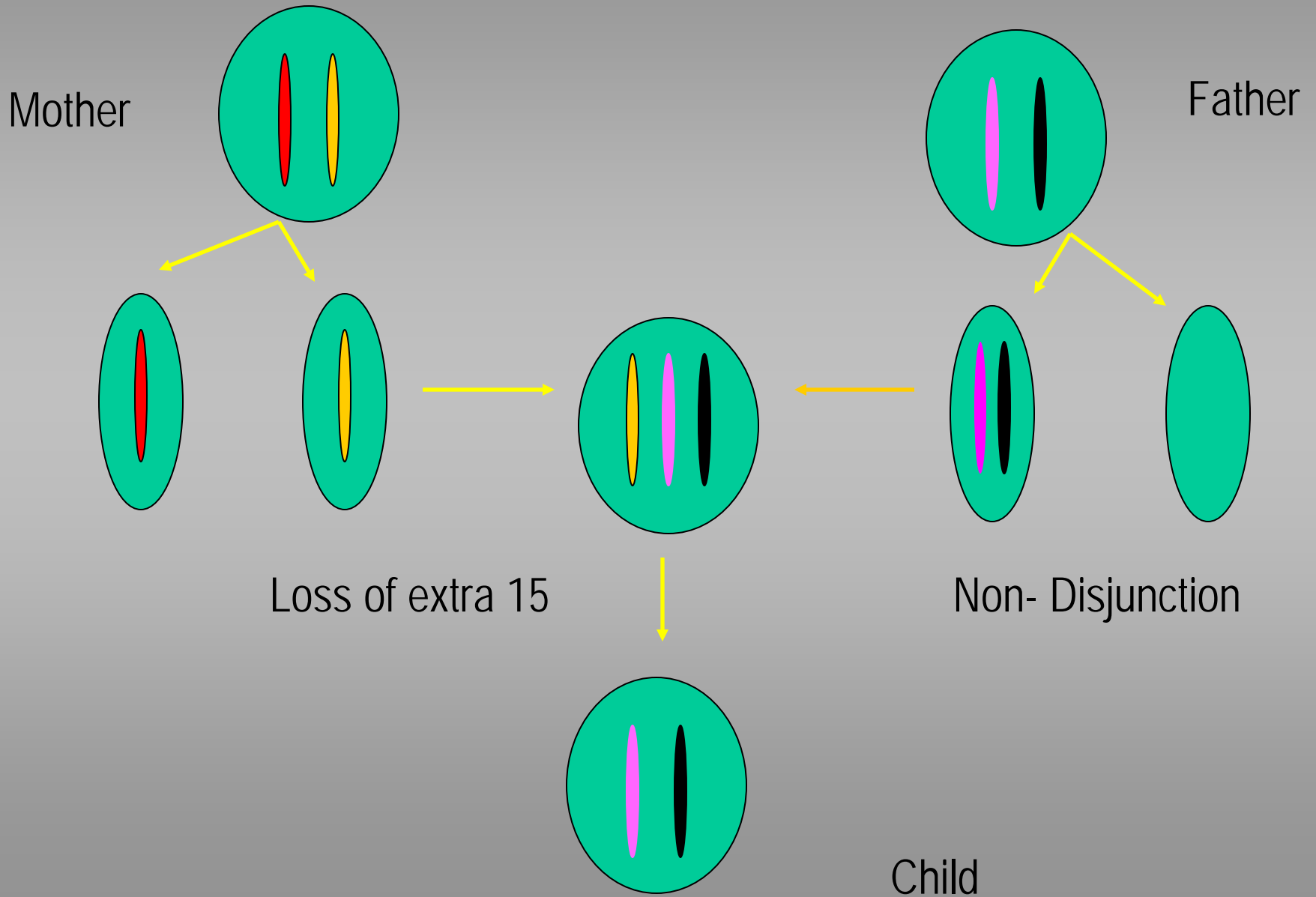
Angelmans syndrome

2% of cases



- Activated
- Silenced

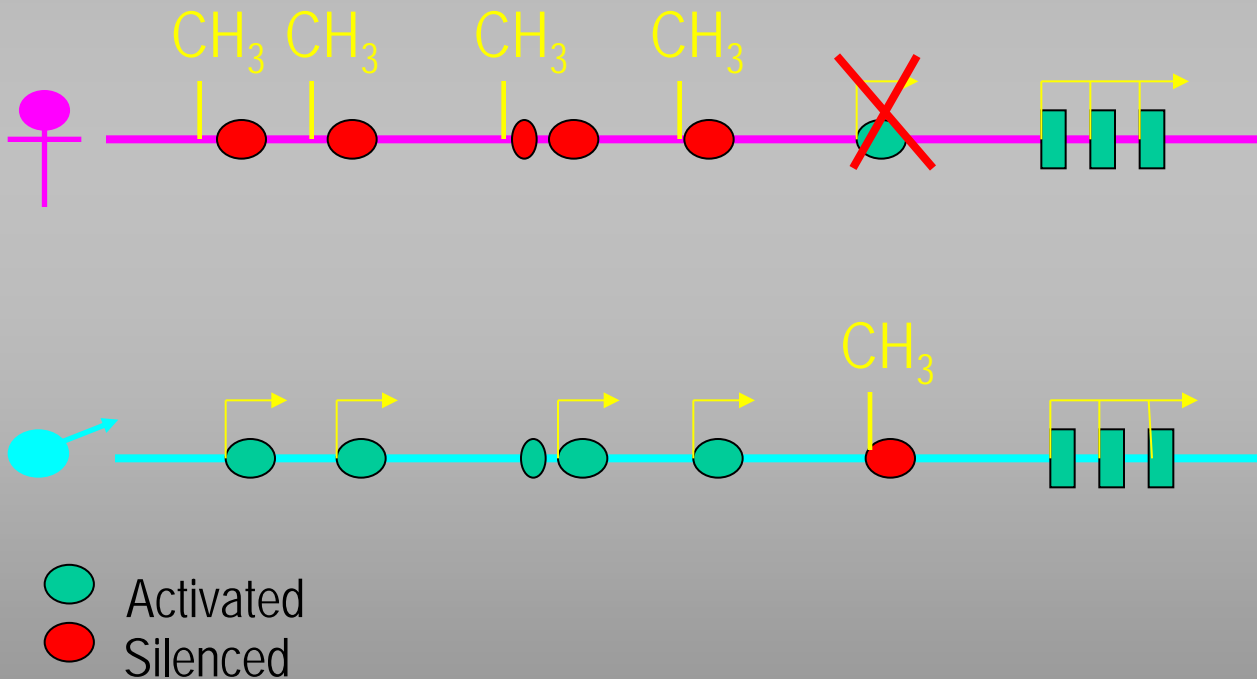
Paternal Uniparental Disomy



Mechanism of loss of imprinting: 4 Mutation in UBE3A gene

Angelmans syndrome

2% of cases



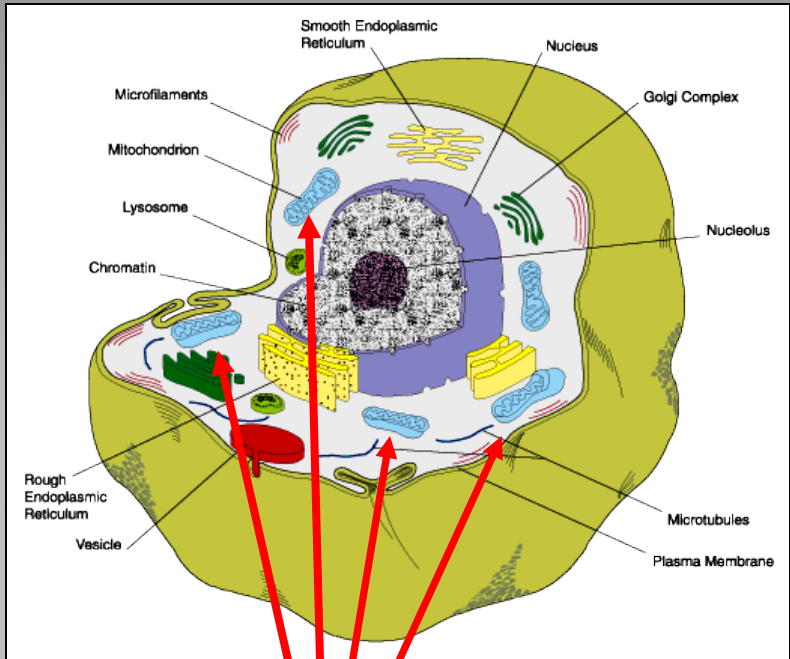
Disruption of Genomic Imprinting

- Parent specific chromosome deletion
- Methylation abnormalities
- Uniparental disomy
- Gene mutations

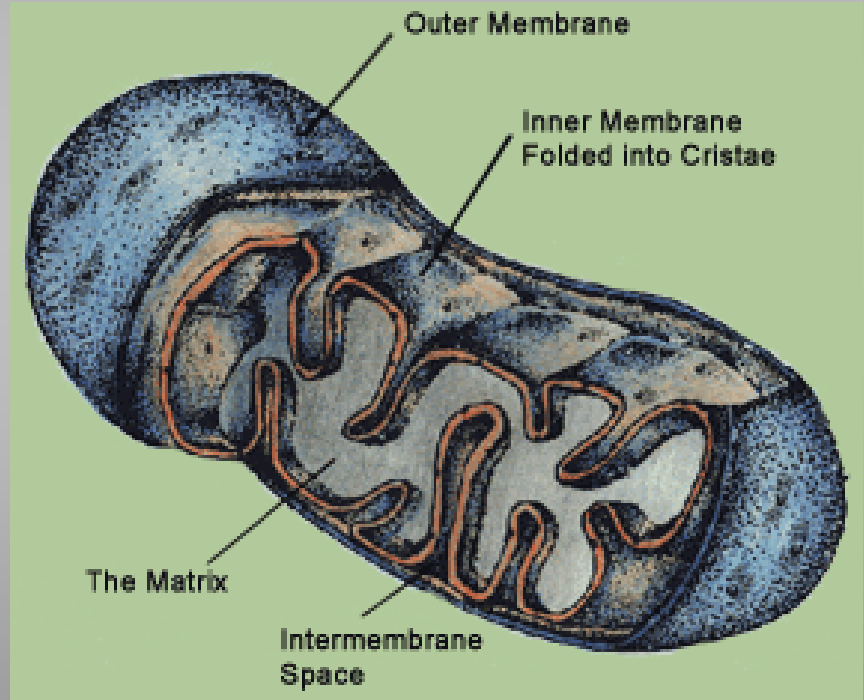
Imprinting and Cancer

- Wilm's tumour – maternal chrom 11p15
- Neuroblastoma – maternal chrom 1p36
paternal chrom 2
- Acute Myeloblastic Leukaemia – paternal chrom 7
- Rhabdomyosarcoma – maternal chrom 11p15.5
- Osteo-sarcoma – maternal chrom 13

Mitochondrial Inheritance



Mitochondria



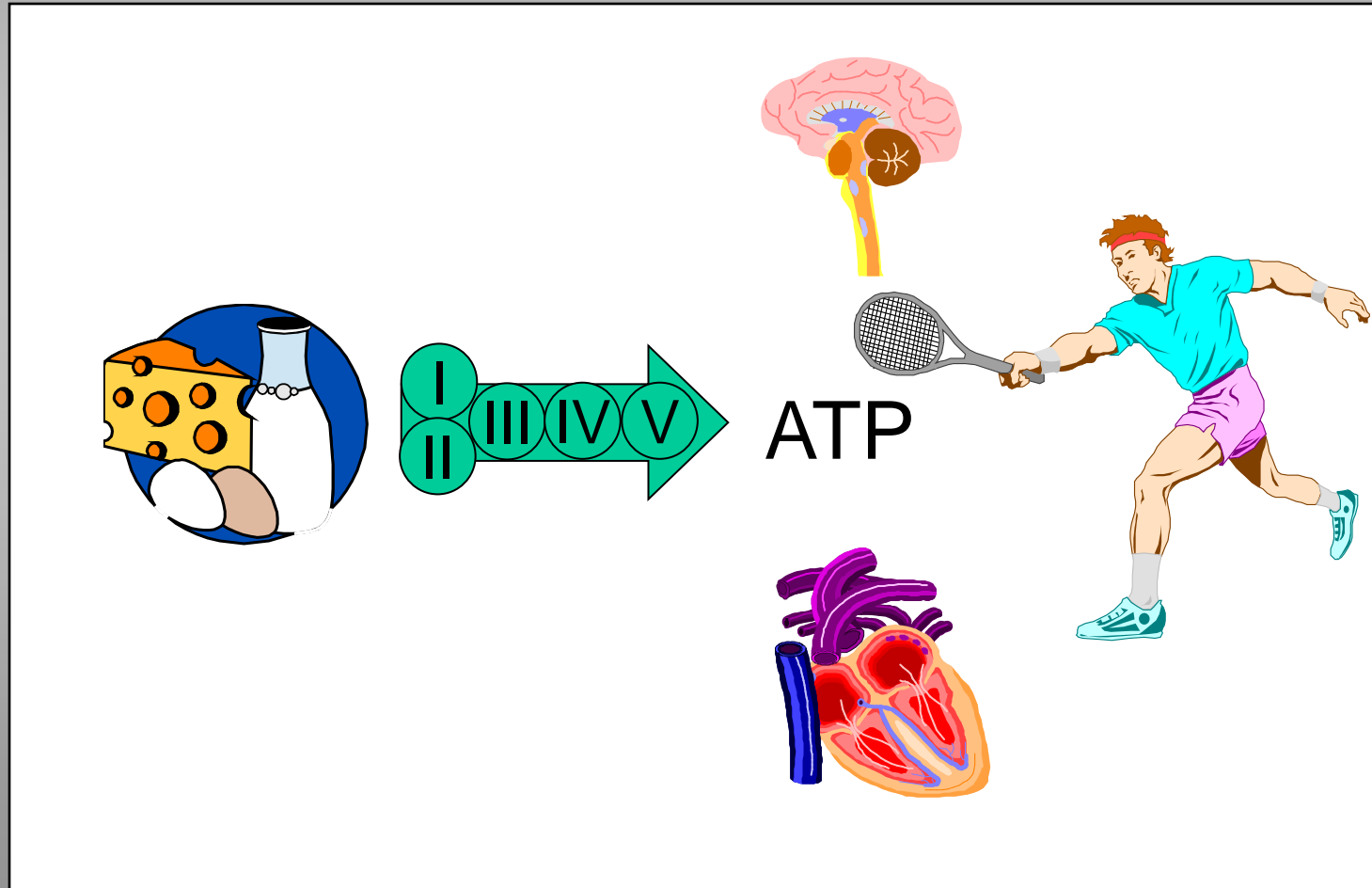
Mitochondrial DNA

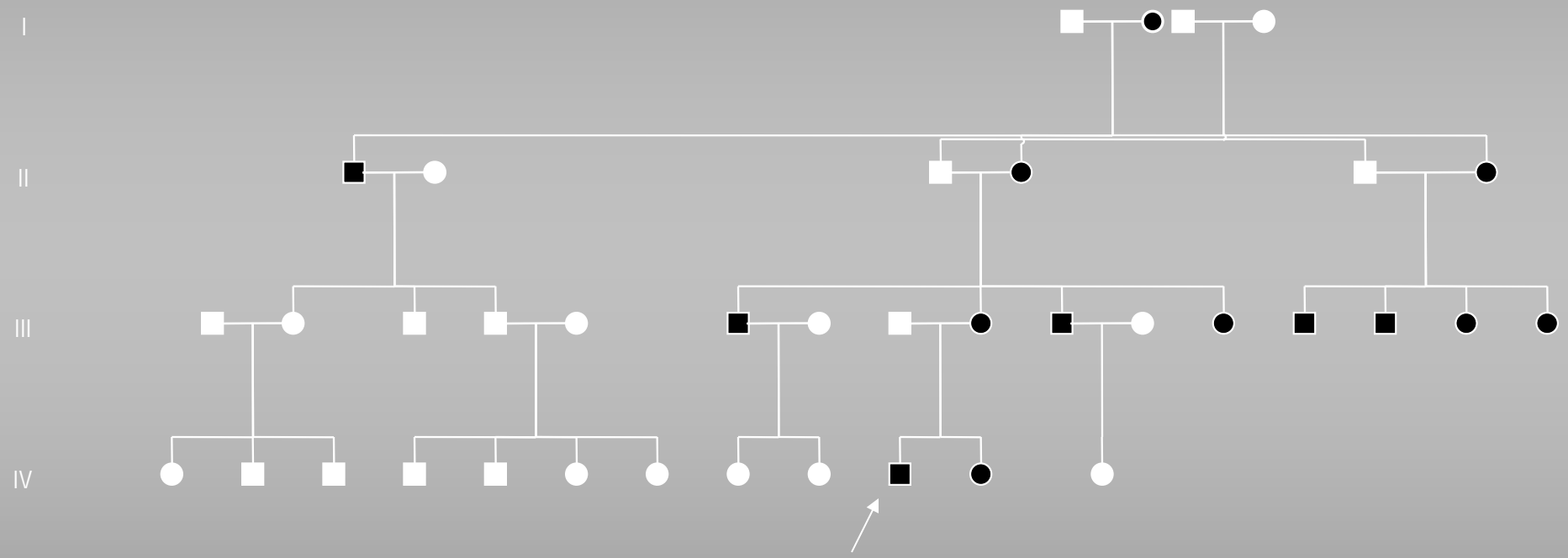
- 16,559 base pairs
- Many copies in a cell, dependent on energy requirement of cell/tissue
- Contains important genes for mitochondrial metabolic pathways and ribosomal RNAs
- Inherited almost exclusively maternally
- High rate of mutations
 - Point mutations and deletions occur

Mitochondrial DNA

- Double stranded
- Ring structure
- No Introns
- Genes are tightly packed together
- Few or no non-coding nucleotides between genes
- Approx 92% of the mitochondrial genome has coding function.

"Mitochondrial Diseases" = Respiratory Chain Disorders





■ Affected
□ Unaffected

Jack H.

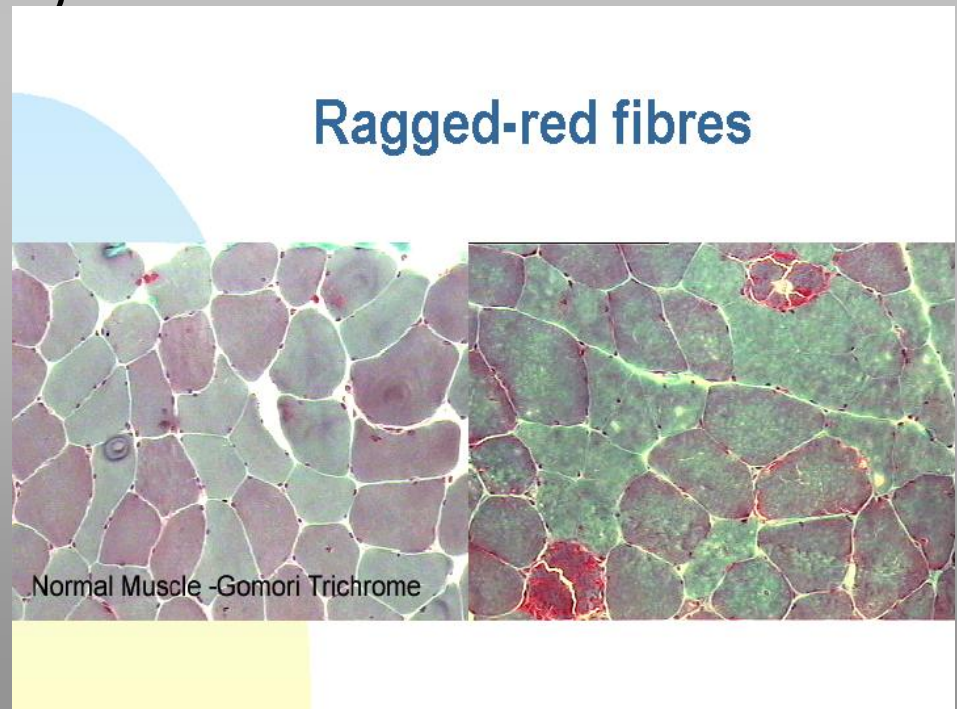
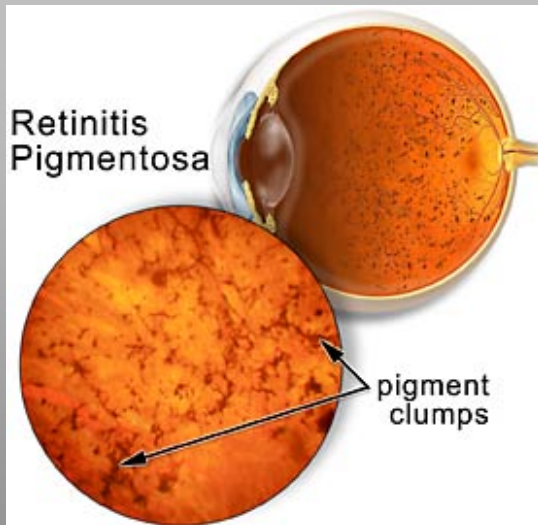
- 21 year old art student
- Presented with diplopia
- Progressive muscle weakness
- Deteriorating vision
- Exertional dyspnoea
 - Echocardiogram: Dilated Cardiomyopathy

Jack H.

- Serum lactate
 - Raised
- Mitochondrial DNA mutation
 - Blood analysis normal
- Muscle biopsy
 - ragged red fibres
 - 4,977 base pair deletion in muscle mitochondrial DNA

Kearns Sayre Syndrome

- Ophthalmoplegia
- Cardiomyopathy
- Myopathy with ragged red fibres
- Pigmentary retinopathy



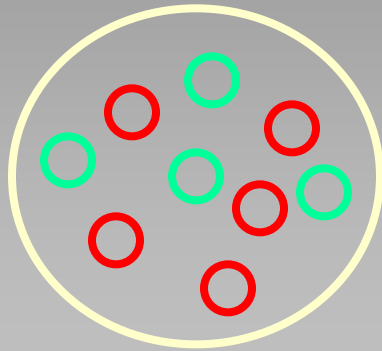
Mitochondrial Mutations

- Multiple phenotypes (clinical heterogeneity)
 - Pearson (Marrow-Pancreas) Syndrome
 - Kearns Sayre Syndrome
 - Myopathy
 - Ataxia
 - Cardiomyopathy
 - Leighs encephalopathy
 - Liebers Hereditary optic neuropathy

Heteroplasmy

- Different daughter cells contain different proportions of mutant mitochondria

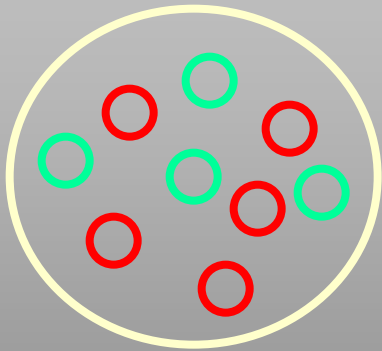
Heteroplasmy



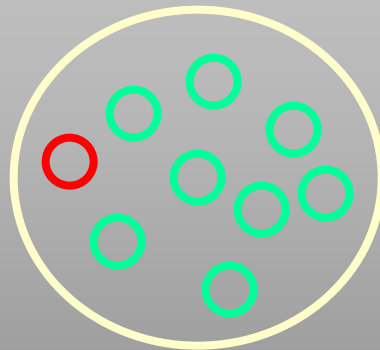
Oocyte



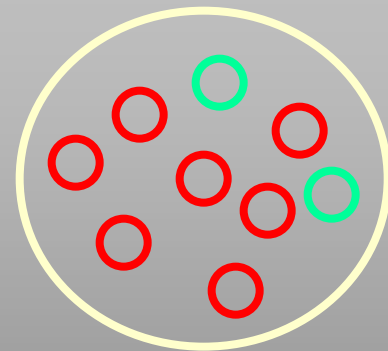
- Mutant
- Wild type



Child with mild disease



Child with no disease



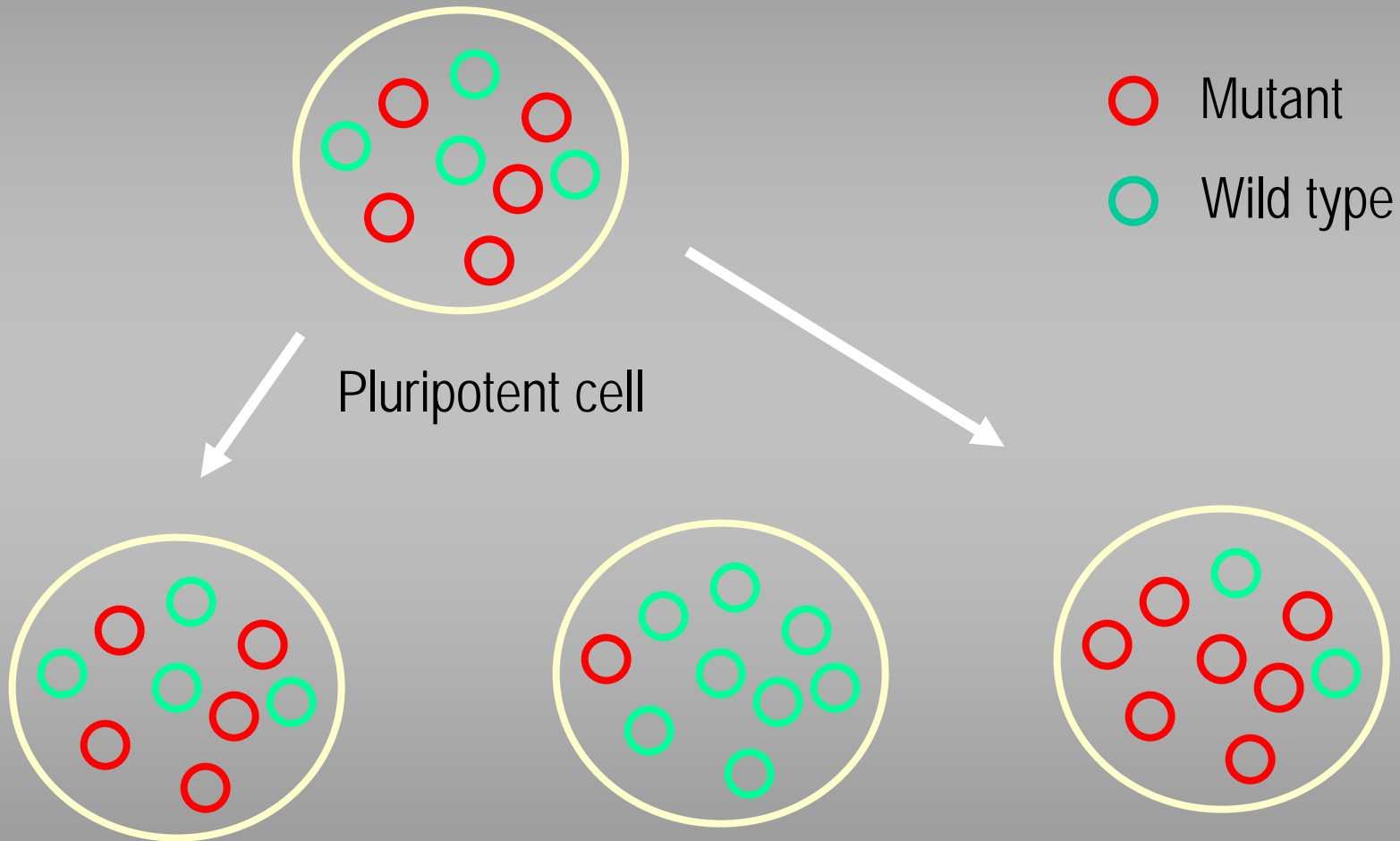
Child with severe disease

Heteroplasmy

- Different daughter cells contain different proportions of mutant mitochondria
- Severity and nature of phenotype depends on
 - type of tissue involved
 - proportion of mitochondria carrying a mutation
 - type of mutation

Threshold of onset

Heteroplasmy



Inheritance patterns in mitochondrial disorder

- Maternal inheritance only if affected gene is from mitochondrial DNA
- Mitochondrial DNA does not code for all mitochondrial protein
- If abnormal mitochondrial protein is coded from genomic DNA then genetic disorders follow mendelian patterns of inheritance

Triplet repeat expansion
Dynamic mutations

Dynamic mutations

- Mutations are evolving
- Not stably inherited
- Mutations are (usually) increasing in size with successive generations
 - But can also contract in size
- Has a threshold effect
- Exhibit a relationship between severity and copy number
 - Explains the clinical phenomenon of Anticipation
 - More severe in succeeding generations

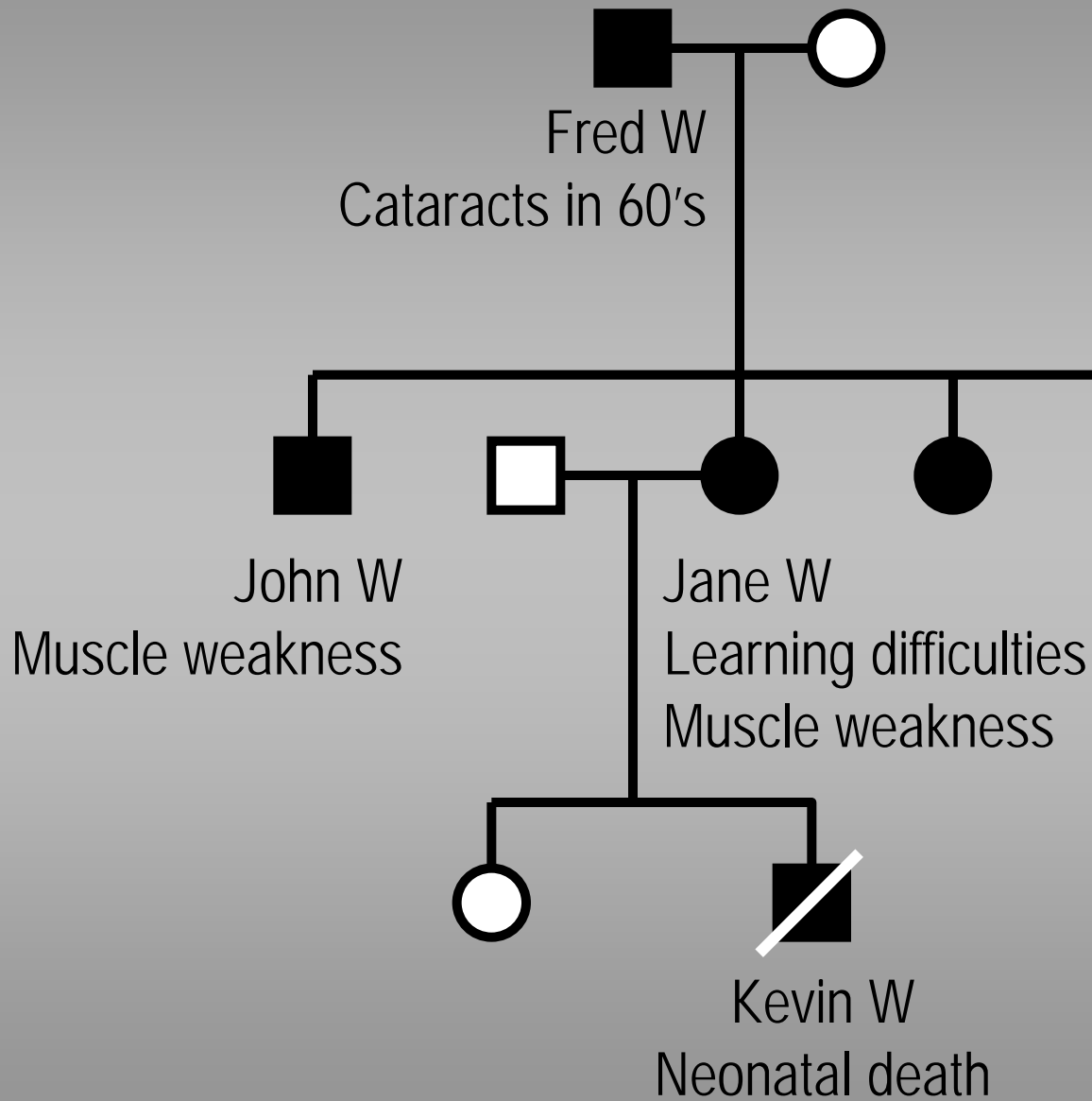
Dynamic mutations

- Most common are triplet repeats
- Expansion of repeats usually has gender bias
 - e.g. HD – expansion when transmitted from paternal line
 - Fragile X – expansion when transmitted from maternal line
- Accounts for over 40 neurological, neuromuscular and neurodegenerative disorder

John W.

- 32 year old window cleaner
- Adverse reaction to muscle relaxant
- Cataracts
- Difficulty getting up in mornings
- On examination
 - Frontal balding
 - Expressionless face
 - Grip myotonia

John W Family Hx



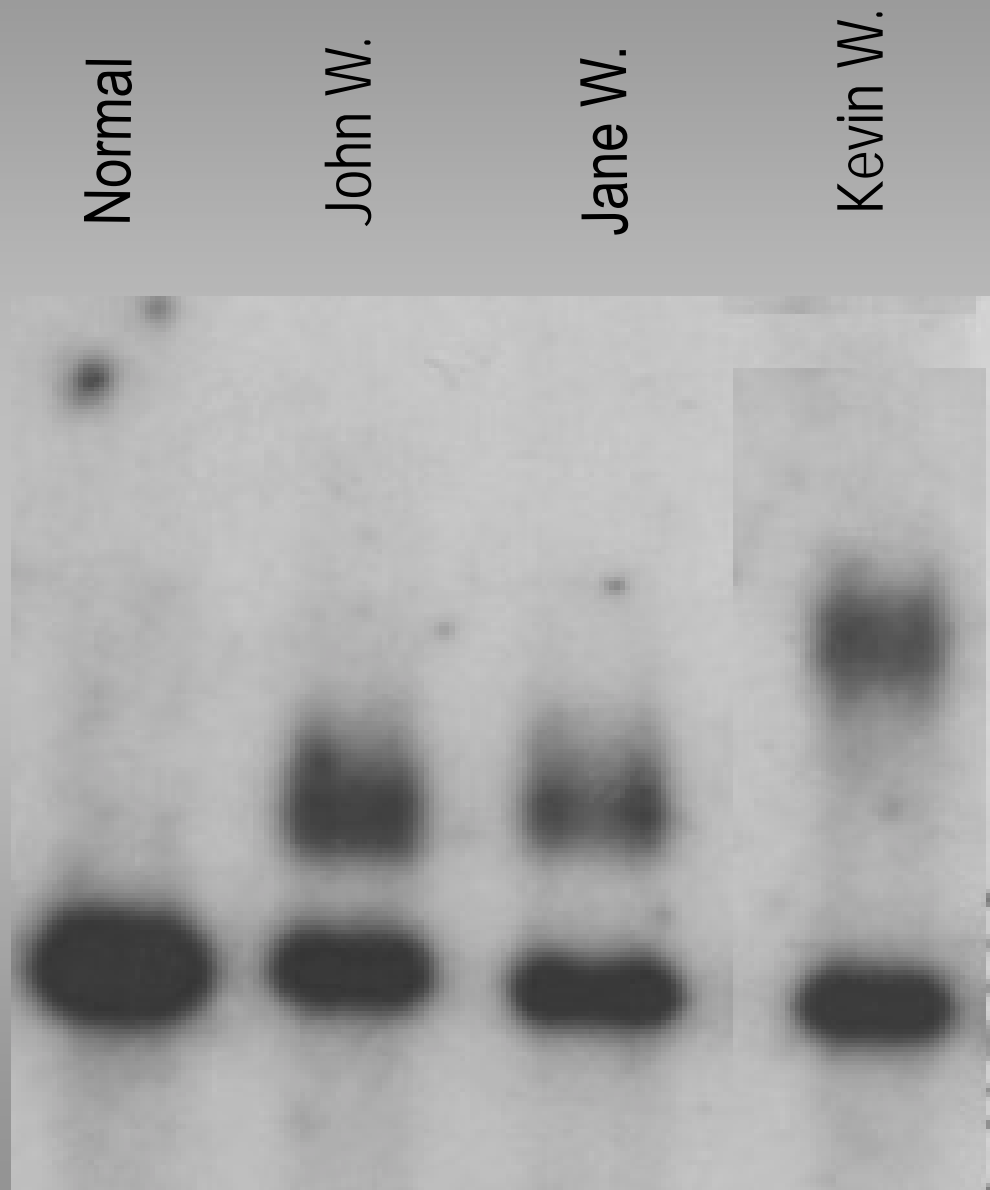
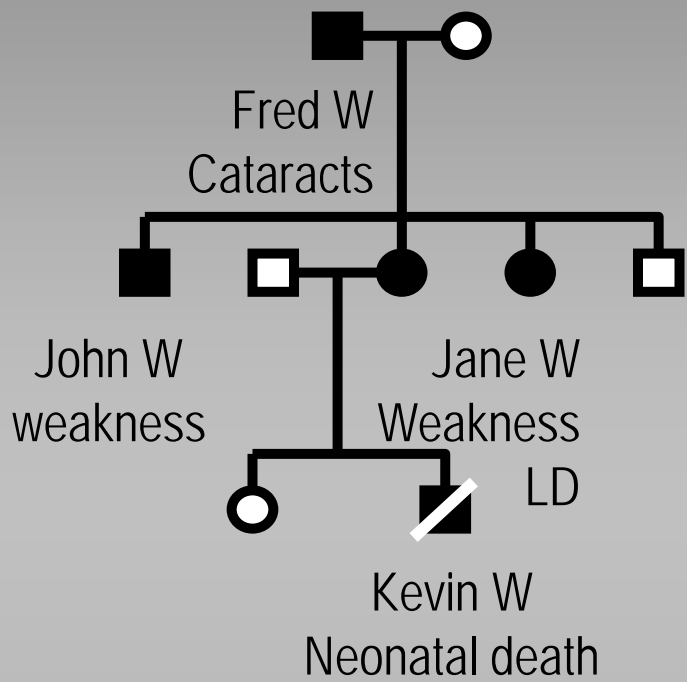
Myotonic Dystrophy

- Frontal balding
- Cataracts
- Muscle weakness
- Myopathic facies
- Myotonia
- Dysphagia
- Intellectual deterioration



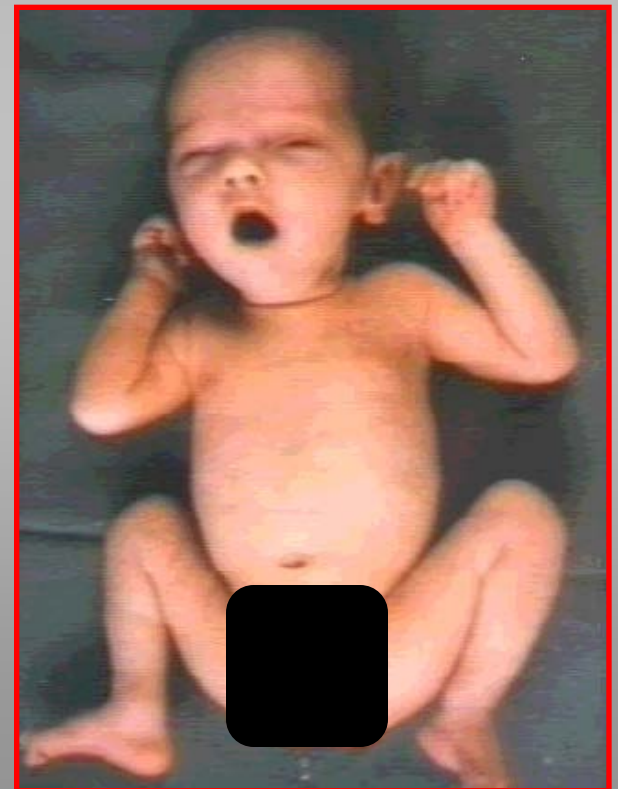
Myotonic Dystrophy

- CTG trinucleotide repeat in 3' UTR of Myotonic dystrophy gene.
- Normally 5-27 copies of repeat
- Disease alleles 50-2000 repeats
- Repeat expands on male or female transmission
- Disease shows anticipation
 - More severe in succeeding generations



Congenital Myotonic Dystrophy

- Severe neonatal muscle weakness
- Neonatal death from respiratory failure
- Usually > 500 repeats
- Almost invariably mother is affected



Digenic Inheritance

- First came to light in patients with Sensorineural deafness
- >100 genes involved
- Usually conform to mendelian patterns of inheritance
- However a proportion of patients with deafness, were double heterozygotes for known deafness genes
 - ie no hearing deficit were found in patients who were only carriers of a mutation in a single locus but deafness occurred where patients were carriers of mutations in 2 gene loci

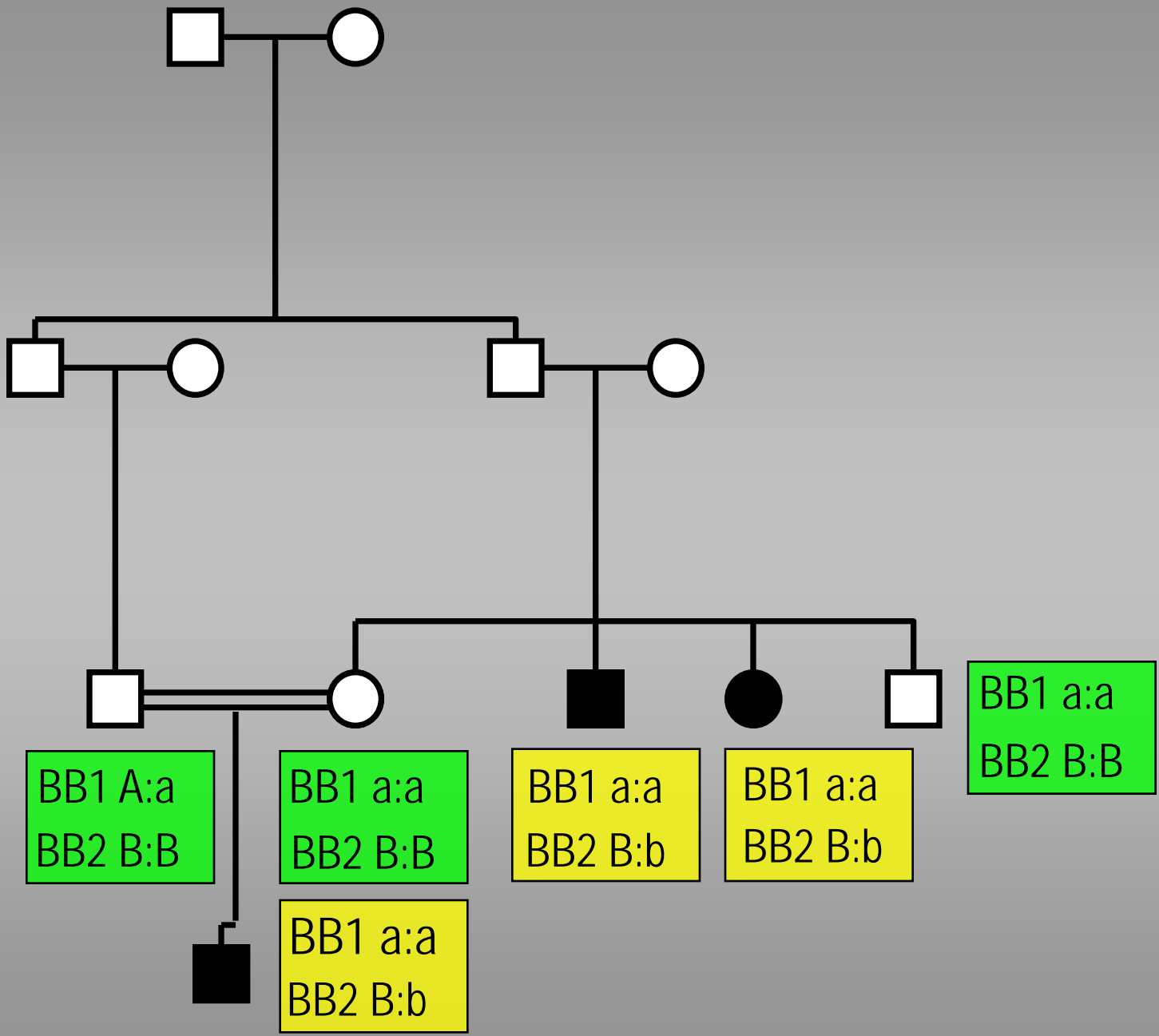
Tri-allelic Inheritance

- Only found in 1 syndrome so far
- Bardet Biedl syndrome
 - multisystem disorder characterized by
 - obesity
 - retinal degeneraton
 - polydactyly
 - gonadal and renal malformations,
 - behavioural and developmental problems



Tri-allelic Inheritance

- 15 loci and 6 genes identified
- Family studies the pattern of inheritance would fit with an autosomal recessive condition
- Found discrepancy in mutation data
- A proportion of patients did not conform to mendelian inheritance pattern
- Found that in some families the condition only manifested if there were 3 mutant genes in 2 locus



Contiguous gene deletion syndromes

What is a contiguous gene deletion syndrome?

What is a contiguous gene deletion syndrome?

“A syndrome caused by a microdeletion that spans two or more genes tandemly positioned along a chromosome”

Well known contiguous gene deletion syndromes:

- Williams-Beuren syndrome 7q11.23
- DiGeorge syndrome 22q11.2
- Wolf-Hirschhorn syndrome 4p16.3
- Smith-Magenis syndrome 17p11.2

Genotype-Phenotype correlations

- Is the clinical manifestations due to the genes which have been deleted
- If so can we attribute particular phenotype to the particular genes which has been deleted
- Or is the syndrome due to just one of the genes that has been deleted

Williams Beuren syndrome 7q11.23

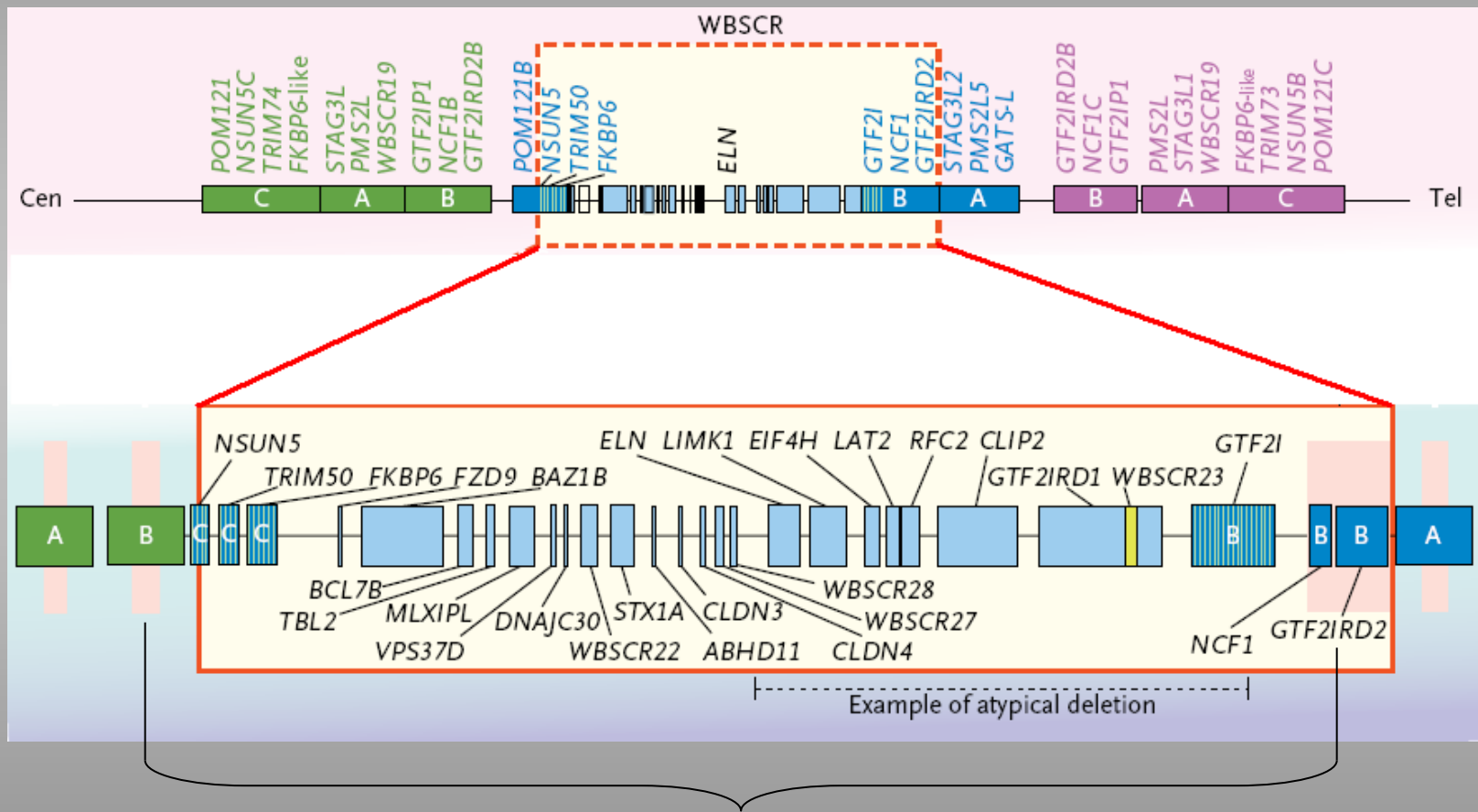
- Common 1.5Mb deletion spanning 24-28 genes
- 320-500Kb highly repetitive sequence flanking the Williams critical region
- Due to defective homologous non-allelic recombination

Williams Beuren syndrome 7q11.23

- Dysmorphic facial features
- “Cocktail party” demeanour
- Excessive non-social anxiety
- Preserved vocabulary
- Cardiovascular problems
- Supravalvular aortic & renal stenosis
- Transient hypercalcaemia (paediatric)



Williams Beuren syndrome 7q11.23



Genes involved in common 1.5Mb deletion (95% cases)

Dissecting the roles of particular genes in WBS

- ***ELN***: Elastin gene. 90-100 % of the WBS patients have hemizygous deletion of *ELN*
=> Cause of supraaortic stenosis (SVAS)
=> ? Cause of facial features
- ***CLIP2***: Encodes cytoplasmic linker protein subunit 2 / 115 (CLIP115); implicated in membranous organelles / microtubules interaction
=> ? A cause of neurological features of Williams syndrome
- ***LIMK1***: Encodes LIM Kinase; strongly expressed in brain
=> some neurological features of WBS

Subtelomeric deletions

del(22)(q13->pter)

- First described as a possible syndrome in 1994 (but first reported case in 1985)
- Submicroscopic deletions detected when looking for deletions at DiGeorge locus
- Characteristic phenotype
 - Global developmental delay
 - Autistic behaviour
 - Absent/severely delayed speech
 - ?Angelman like



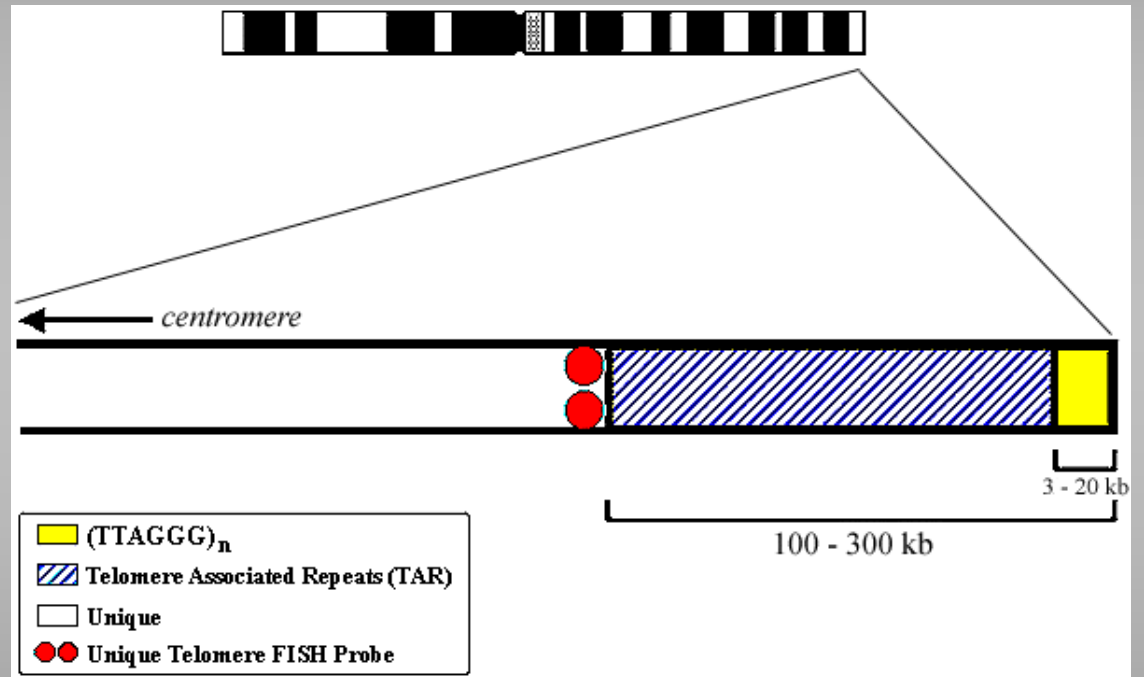
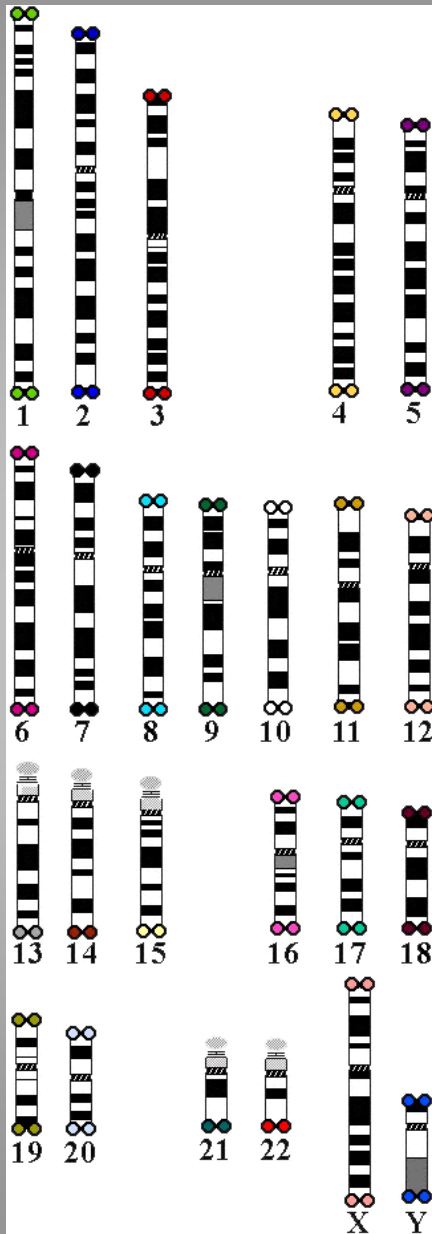
Subtelomeric chromosomal rearrangements

- Mental retardation affects 3% of population, but diagnosis is obtained in less than half of all cases
- Cause remains unknown in 34% of moderate-severe and 80% of mild cases

Subtelomeric chromosomal rearrangements

- Why focus on telomeres?
 - Majority of translocations involve chromosome ends (shared telomere-associated repeats)
 - Gene rich adjacent regions (rearrangements likely to have phenotypic consequences)
- Moderate-severe MR
 - for sporadic cases (7%)
 - for familial cases (25%)

Telomeres



Cellular Mosaicism

Mosaicism

- When an individual is made up of populations of cells with different genetic constitutions.

Can be mosaic for

- Chromosomal Aneuploidy
- Molecular Mutations

Somatic Mosaicism

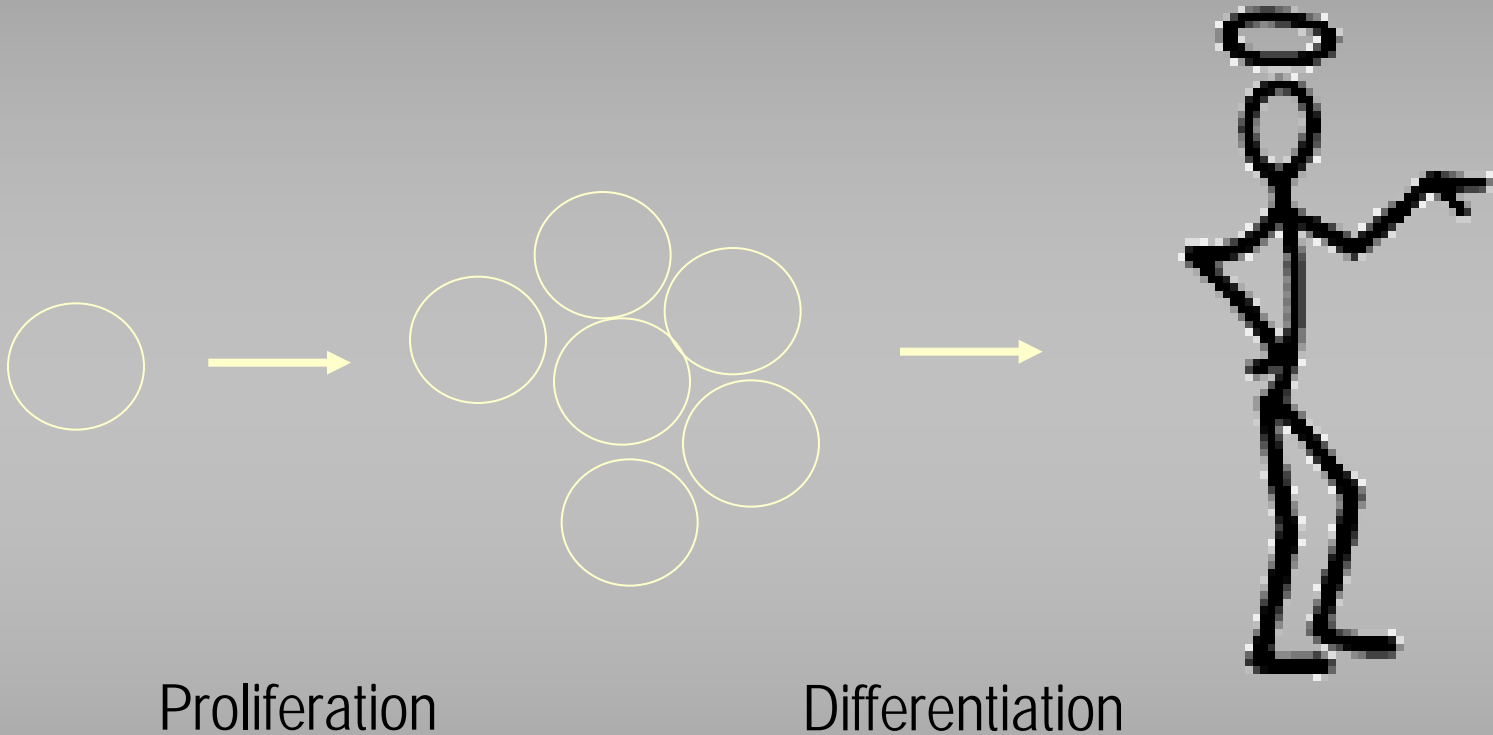
- All cells suffer mutations as they divide
 - At meiosis and at mitosis
 - Approximately 10^{-6} per gene per cell division
- Repair Mechanisms Exist
 - Can give rise to reversion
- Given the numbers of cells in the body
 - everybody will have some cells which has a mutation of some sort

Mosaicism

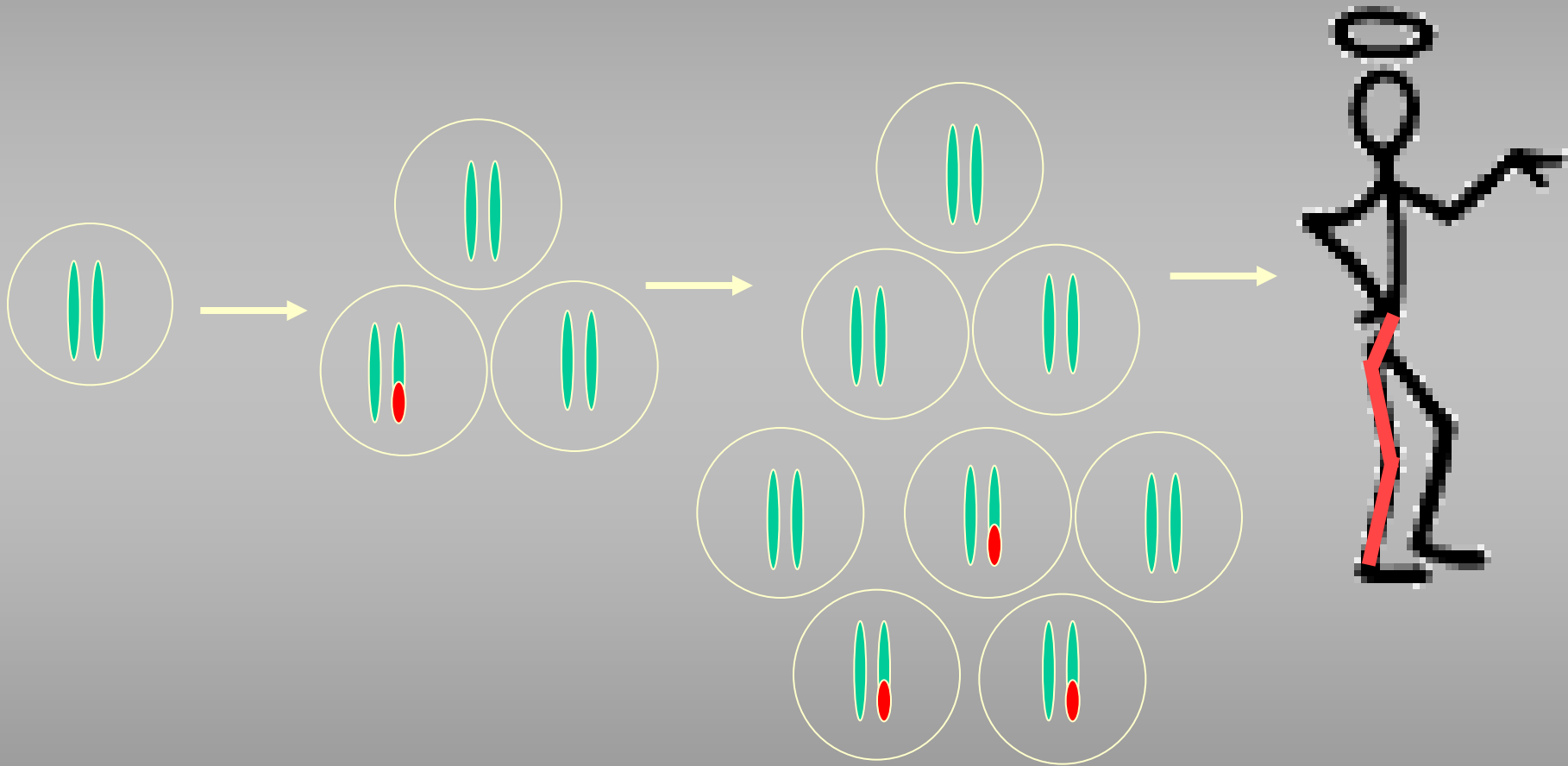
May become clinically important

- If mutant cells have a tendency to grow and replace normal cells (cancer cells)
- If the mutation arose early in embryonic development, so becomes a large proportion of the whole body
- If the mutation occurred in the germ line

Somatic Mosaicism

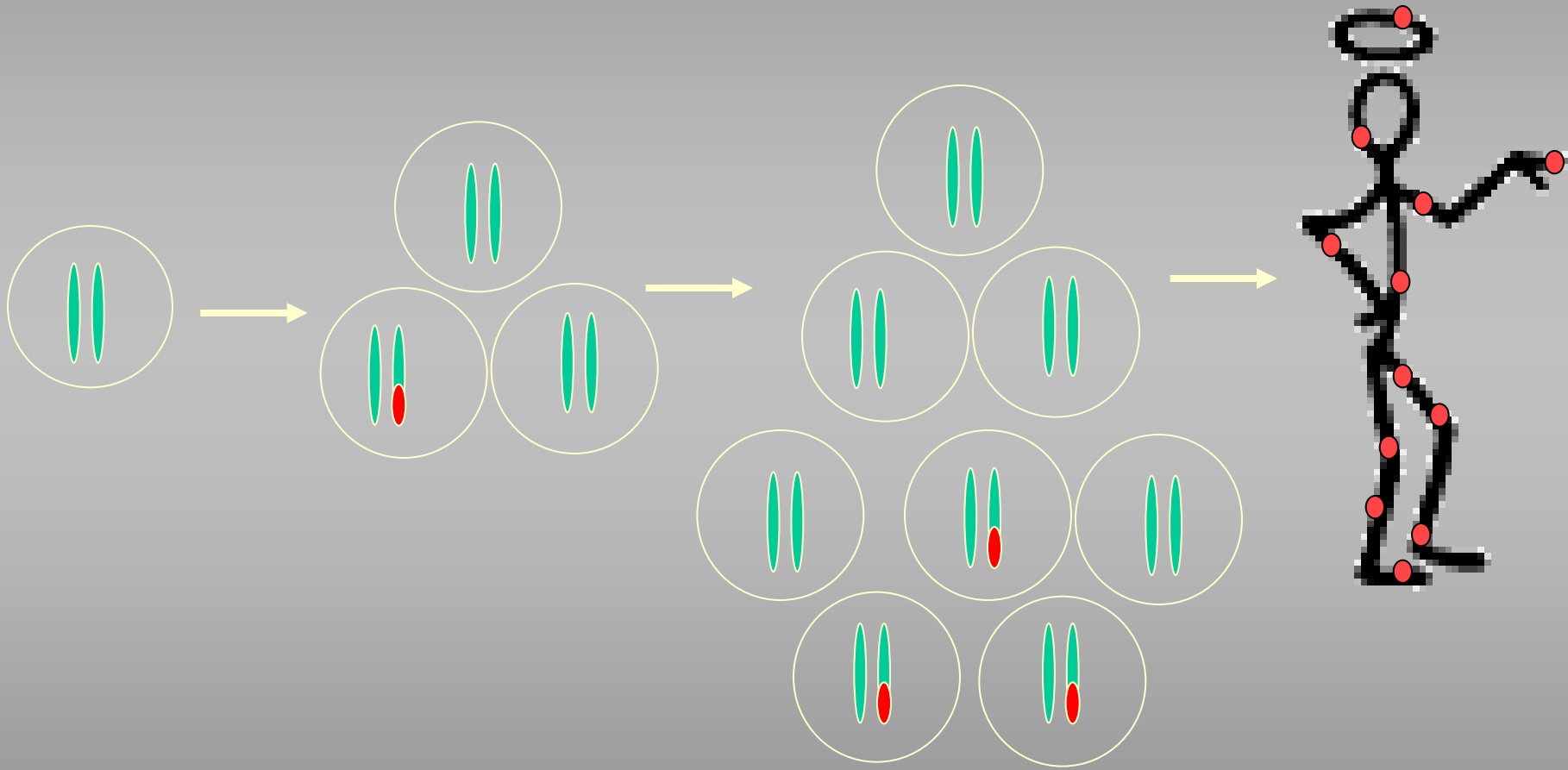


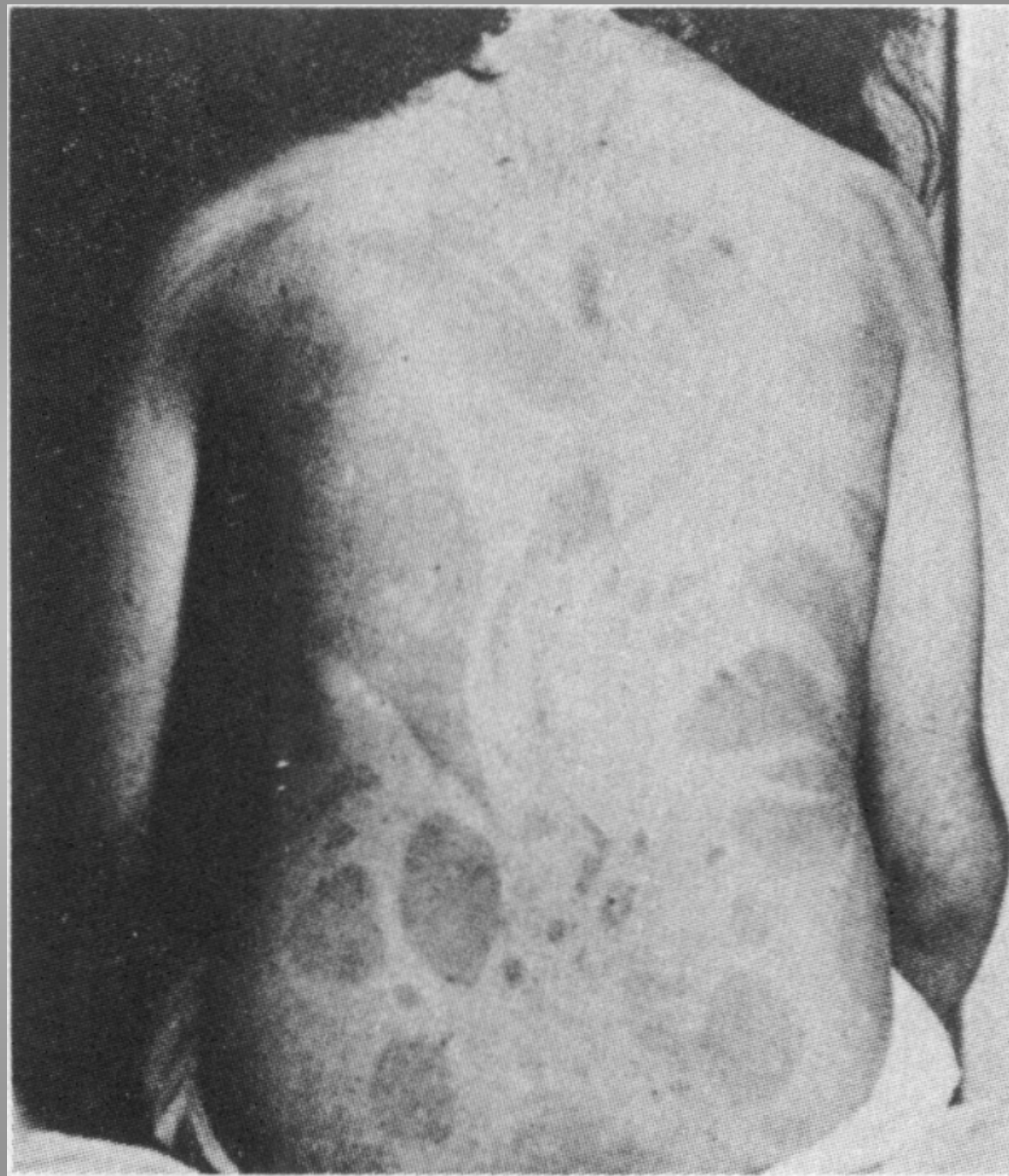
Somatic Mosaicism



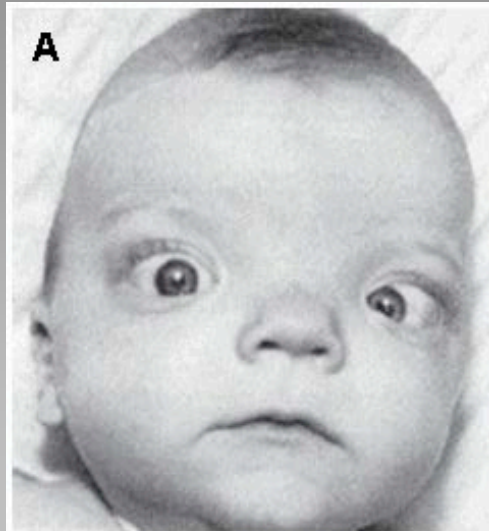


Somatic Mosaicism





Pallister
Killian
syndrome
mosaic
tetrasomy
12p



Gonadal Mosaicism

- Commoner in some diseases
 - Duchenne Muscular Dystrophy
 - Osteogenesis Imperfecta
- Can offer pre-natal diagnosis for a second child, even when parents are unaffected (if a mutation is identified)
- Causes recurrence risk for fatal dominant conditions

New Genetics

- Non-Mendelian
 - Genomic Imprinting
 - Digenic Inheritance
 - Triallelic inheritance
 - Mitochondrial Inheritance
- Chromosomal
 - Micro/telomeric deletions
 - Contiguous gene syndrome
- Trinucleotide repeat expansions
- Somatic and gonadal mosaicism

- Multifactorial inheritance