

Oxidative phosphorylation diseases

- * The clinical pathology may be caused by gene mutations in either mitochondrial DNA (mtDNA) or nuclear DNA (nDNA) that encodes proteins required for normal OXPHOS.
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(A) Mitochondrial DNA & oxidative phosphorylation Diseases:-

- ✓ The mtDNA is a small, 16569 nucleotide-pair, double stranded, circular DNA.... remember its evolution.
- ✓ It encodes 13 subunits of the complexes involved in OXPHOS:-
 - 7 → complex I
 - 1 → complex III (3)
 - 3 → complex IV (4)
 - 2 → Fo portion of ATP-synthase.
- ✓ mtDNA encodes the necessary components for translation of its mRNA: a large and small ribosomal RNA & tRNAs.
- ✓ The genetics of mutations in mtDNA are defined by maternal inheritance, replicative segregation, threshold expression, a high mtDNA mutation rate, & the accumulation of somatic mutations with age.
 - Replicative segregation: when the mitochondria replicate by fission, the mutant or wild-type DNA are distributed to each daughter cell.
 - heteroplasmy: when the cell have a mixture of mitochondria (mutant / wild-type DNA).
 - somatic mutations result in a decline of oxidative phosphorylation capacity with age: accumulation of somatic mutations with age.
 - Threshold expression: the ATP-generating capacity of a tissue falls below the tissue-specific threshold for normal function.
- ✓ In general, symptoms of these defects appear in one or more of the tissues with highest ATP demands: nervous tissue, heart, skeletal muscle and kidney.

(slide 1)

(B) Other Genetic disorders of Oxidative phosphorylation.

- ✓ Most of the estimated 1,000 proteins required for oxidative phosphorylation are encoded by nDNA.
- ✓ Nuclear DNA mutations differ from mtDNA mutations in several important respects.....
These mutations don't show a pattern of maternal inheritance but are usually autosomal recessive.
- ✓ The mutations are uniformly distributed to daughter cells & therefore are expressed in all tissues that contain the allele for a particular tissue - specific isoform.
- ✓ However, phenotypic expression will still be most apparent in tissues with high ATP requirements.

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