

بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ

Pathophysiology and Genetics of Tyrosinemia Disorders

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Tyrosinemia Disorders

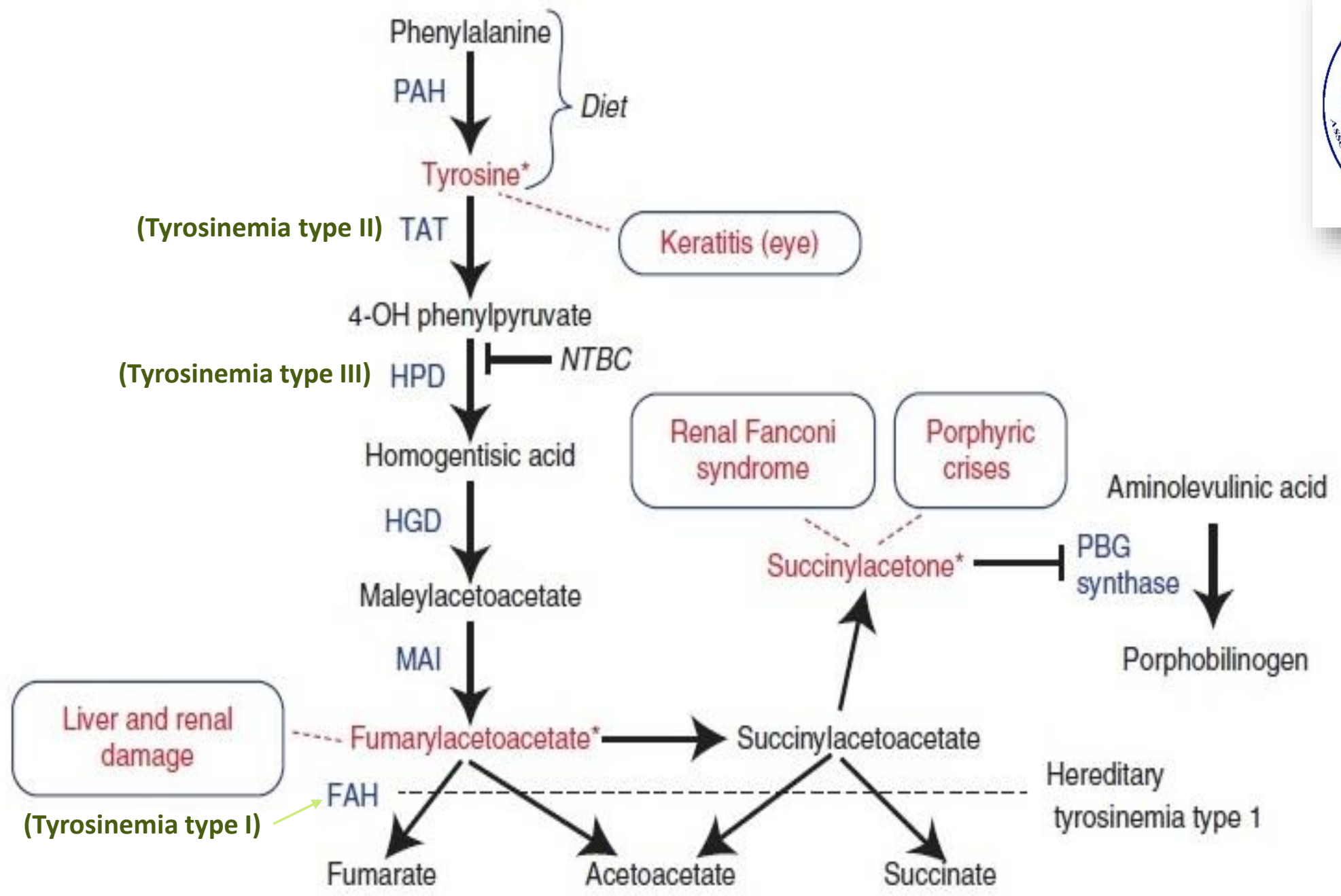


- **Hereditary Tyrosinemia Type I (HT1)** (OMIM276700) is a severe inherited metabolic disease affecting mainly hepatic and renal functions that leads to a fatal outcome if untreated.
- In 1977, fumarylacetoacetate hydrolase (FAH) was identified as the deficient enzyme responsible for HT-1.

Tyrosinemia Disorders



- **Tyrosinemia type II** is caused by a defect in tyrosine aminotransferase (TAT) (EC 2.6.1.5).
- **Tyrosinemia type III**, the rarest of the tyrosine disorders, is caused by a deficiency of *p*-hydroxyphenylpyruvic acid dioxygenase (EC.1.13.11.27)



Pathway of Tyrosine Metabolism

- In Fah mutant mice the mRNA for tyrosine amino transferase (Tat), the rate-limiting enzyme in tyrosine degradation, is absent.
- The activity of 4-hydroxyphenylpyruvic dioxygenase (HPD), the second step in the tyrosine degradation pathway, is decreased in human HT-1 liver samples.
- These observations suggest that the clinical effects associated with HT-1 are due to other metabolites resulting from FAH deficiency, not the elevation of tyrosine in the blood.

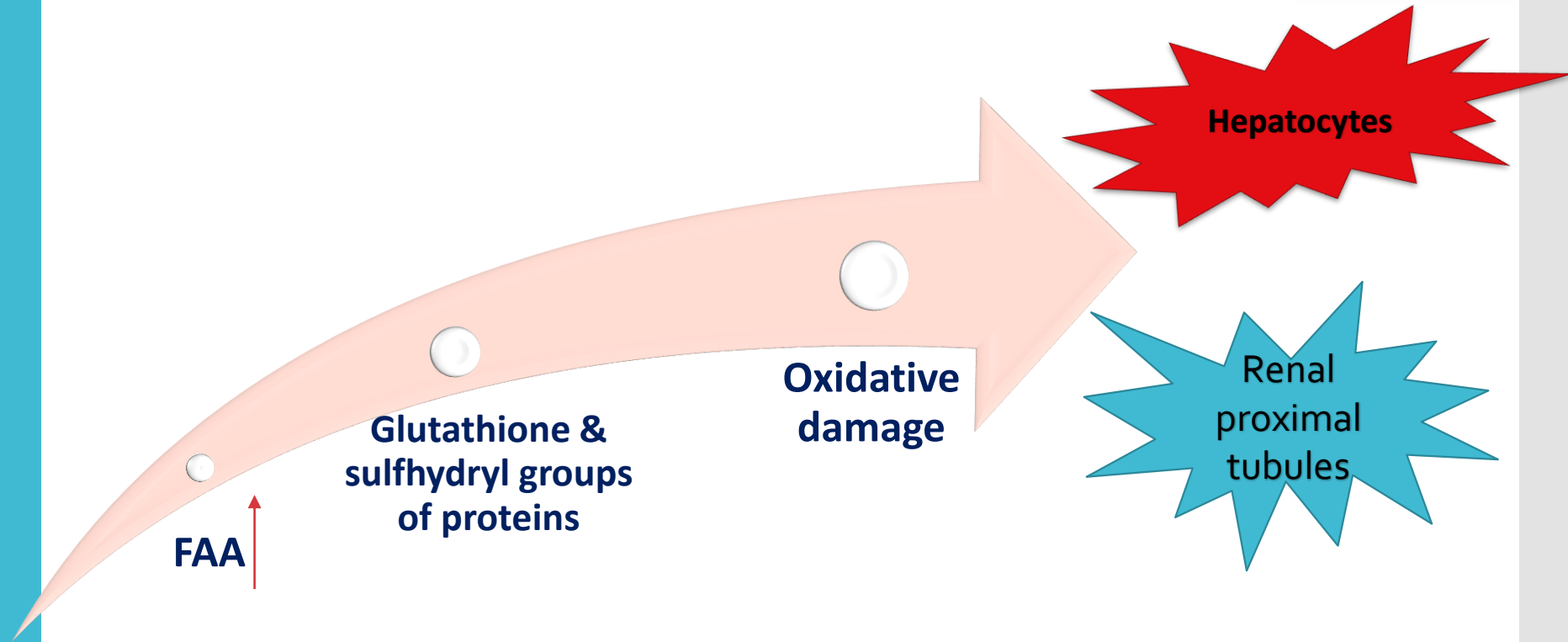
Tyrosinemia Type I



- In FAH deficiency, fumarylacetoacetate (FAA), the immediate precursor which appears to accumulate in hepatocytes, causing cellular damage and apoptosis.



Tyrosine metabolism pathway



Genetics of Tyrosinemia Type I



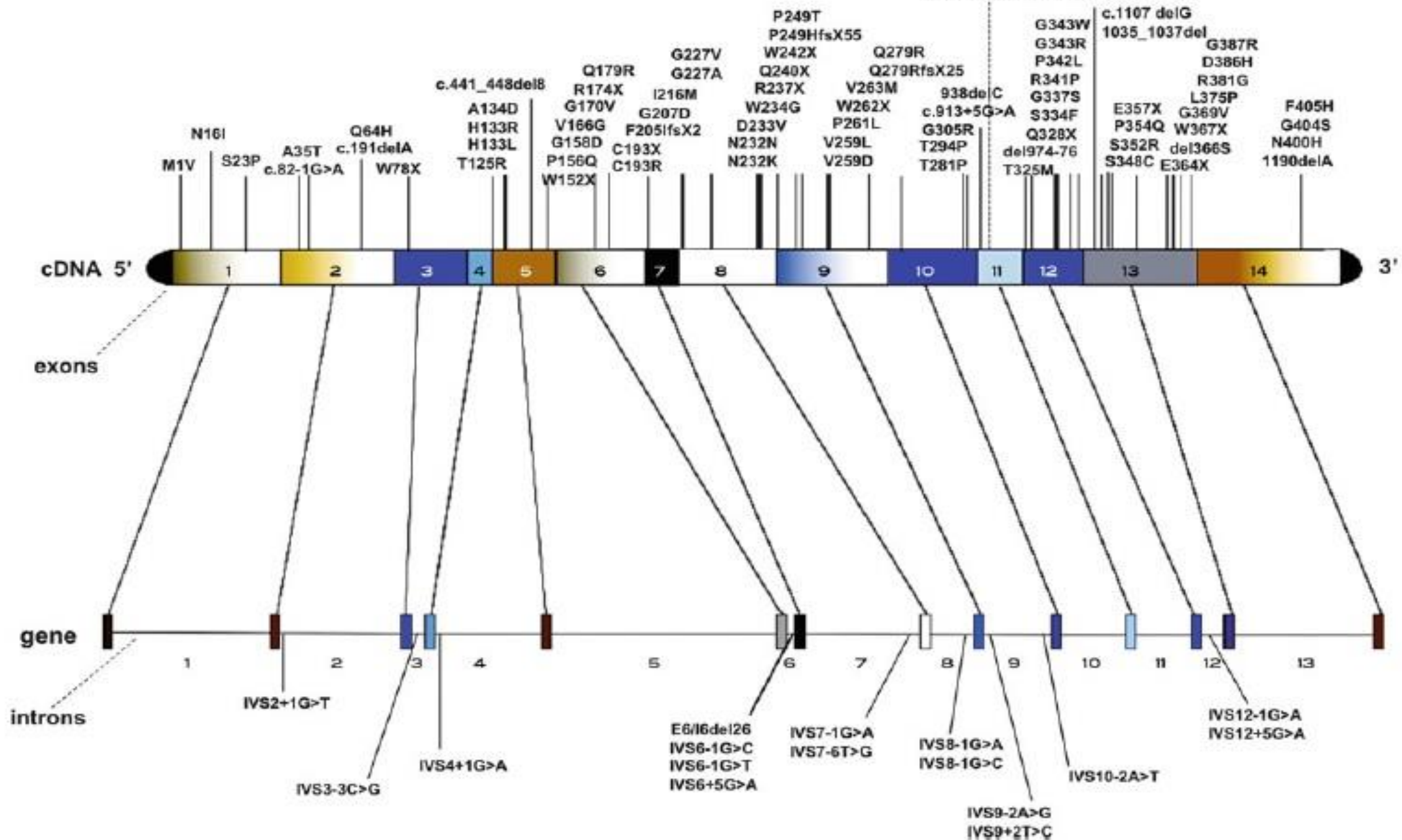
- Tyrosinemia type I is inherited in an autosomal recessive manner.
- The human *fah* gene is located on chromosome 15q23-q25, spans 30–35 kb and consists of 14 exons. The cDNA has an open reading frame of 1,257 bp encoding 419 amino acids

Genetics of Tyrosinemia Type I



- The first mutation reported in the *fah* gene was the c.47A>T (p.Asn16Ile) in a French Canadian patient and was shown to be causative of FAH deficiency.

c.961-1010del50
c.960q1130_*1260q10539del18036



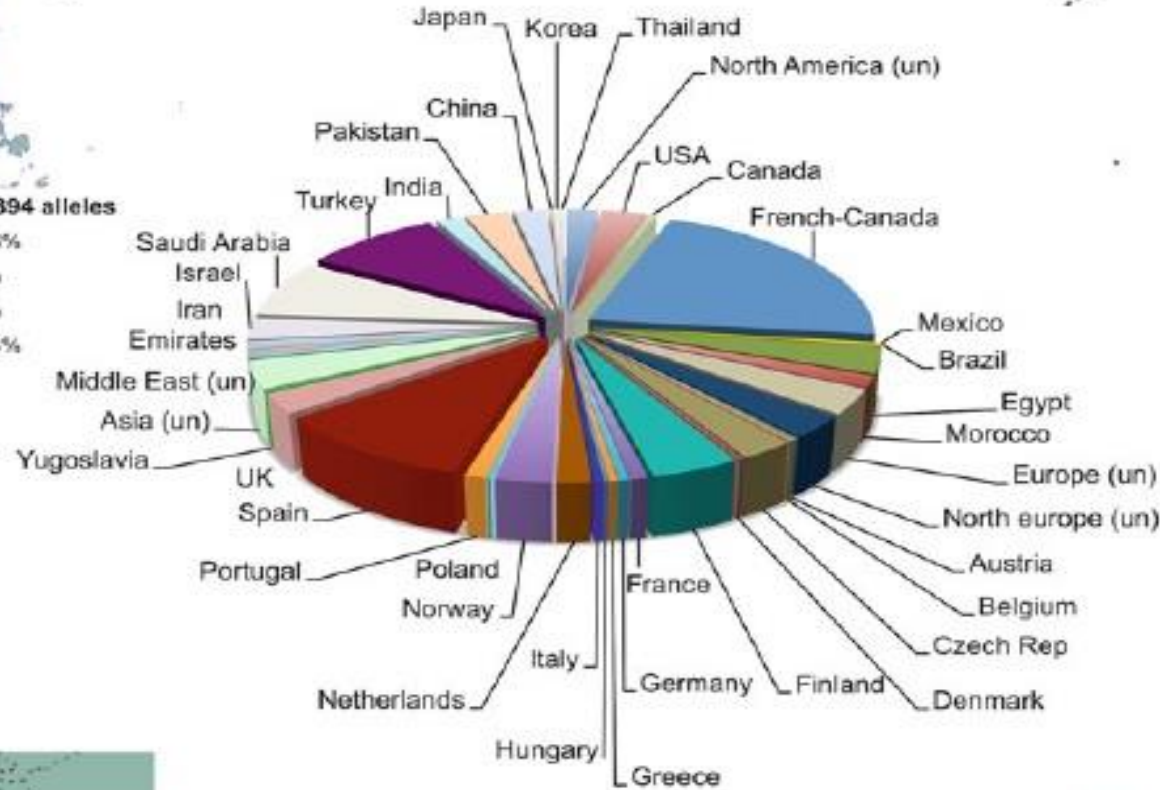


East Asia 29/894 alleles

c.974_976delC AinsGC	20.6%
c.960q1130_*1260q10539del18036	14%
p.Arg237X	14%
others	51.4%

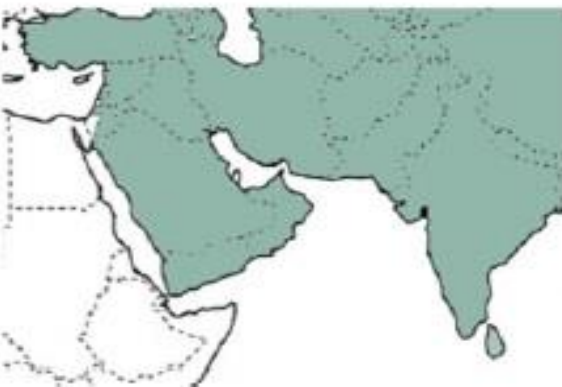
North America 253/894 alleles

IVS12+5G>A	79%
IVS6-1G>T	6.7%
p.Glu364X	4.3%
others	10%



North Africa 46/894 alleles

IVS6-1G>T	24%
IVS4+1G>A	17.4%
p.Thr125Arg	17.4%
others	41.2%



Middle East-South Asia 261/894 alleles

p.Gln64His	15%
p.Arg237X	14%
IVS12+5G>A	11%
others	60%

Europe 332/894 alleles

IVS6-1G>T	29%
IVS12+5G>A	22%
p.Trp262X	14%
others	35%



Mutation distribution of FAH gene

FAH gene mutations in geographic regions

Mutations	Geographic location	Frequency in population
c.1062+5G > A (IVS12+5G> A)*	French Canada	86%
	Northern Europe	46%
p.W262X	Finland	80%
c.554-1G > T (IVS6-1G>T)*	Southern Europe	64%
p.G337S	Norway	58%
p.Q64H	Pakistan	92%
p.D233V	Turkey	94%

Prevalence

- In geographic areas without newborn screening, tyrosinemia type I affects approximately **1 in 100,000 to 120,000** births.



Prevalence



- Two regions of the world have a higher than expected frequency of tyrosinemia type I due to the increased frequency of certain pathogenic variants resulting from a founder effect:
 1. In the Scandinavian countries the birth prevalence is estimated at 1:74,000 and 1:60,000 live births, respectively.
 2. A founder effect from colonization by French settlers is present in the province of Quebec, Canada. The birth prevalence in the province of Quebec is 1:16,000

Prevalence



- **Tyrosinemia, type II (TYR II)** affects fewer than one in 250,000 individuals. The condition may be more common in Arab and Mediterranean regions.
- **Tyrosinemia, type III (TYR III)** is a very rare condition.
Prevalence: $<1 / 1\,000\,000$

Thank You

