MUTATIONAL ANALYSIS OF AGXT IN TUNISIAN ADULT POPULATION WITH PRIMARY HYPEROXALURIA TYPE 1

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BACKGROUND

Primary hyperoxaluria (PH) is an autosomal recessive metabolic disorder caused by inherited mutations in the AGXT gene, which controls the production of liver peroxisomal alanine: glyoxylate aminotransferase (AGT). These mutations result in either a deficiency of AGT or its misplacement into mitochondria. PH is mainly characterized by an excess of oxalate production, excretion and progressive deposition of calcium oxalate in the kidney.

Aims: We focused on studying the four most common mutations (I244T, 33-34insC, G190R and R360Q) in our patients suspected of having PH.

PATIENTS AND METHODS

Study population:

- ✓ A total of 158 suspected PH patients were referred from the adult nephrology departments of university hospitals of Sahloul, La Rabta, and Monastir.
- ✓ The diagnosis of PH was based on clinical findings (urolithiasis, nephrocalcinosis, and end-stage renal failure), elevated plasma oxalate, and urinalysis (raised oxalate)
- ✓ **Methods**
- ✓ PCR-RFLP: Genotyping of the most common mutations (I244T "**rs121908525**" , 33-34insC, G190R "**rs180177239**" and R360Q "**rs730880415**") and the haplotypes were determined by screening for the 33dupC duplication
- ✓ SPSS26: statistical analysis

RESULTS

- ✓ In our study population, 69% were index cases, while the remaining individuals were parents and siblings referred as part of a family investigation

Table 1: Clinical characteristics of our study population

Characteristics of our study population		N= 158
Sex ratio (male/female)		1.29
Age (years) mean ± SD		26.8 ±16.5
Hospitalization	Lithiasis	5.5 %
	RF	37.6 %
	RF + lithiasis	7.3 %
	ESRD	20.2 %
	RF + anemia	3.7 %
	RF + lithiasis+ anemia	1.8 %
Family history	Oxalosis	4.6 %
	Lithiasis	17.4 %
	RF+lithiasis	7.3 %
Dialysis	HD	25.7 %
	PD	9.2 %

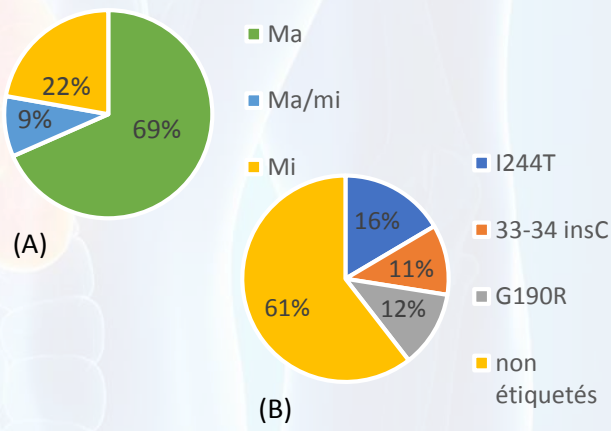

Figure 1: Frequencies of identified haplotypes (A) and mutations (B)

- ✓ We found that the Maghrebien mutation I244T is the most frequent

CONCLUSION

Targeted mutation analysis serves as a valuable initial investigation for PH. Mainly the I244T and G190R mutations were the most identified mutations causing PH disease in our cohort. Identifying these mutations can offer a precise method for prenatal diagnosis in affected families, facilitate genetic counseling, and enable the detection of presymptomatic individuals.