Materials and Methods: We analyzed 26 cases of adults with AATD related disease in Costa Rica. We establish presentation based on age, gender, AAT levels, phenotype genetic characteristics and clinical, biochemical and histological features.

Results: 26 patients had either hepatic or pulmonary chronic diseases in relation to AAT enzyme alterations, The proportion by sex was 1:1 and the mean age of diagnosis was 42. Of 21 patients with phenotyping, 9 were homozygous PI*ZZ (7) or PI: NullNull (2). Only this last group had the pulmonary disease. The ones homozygous for the PI*ZZ mutation all developed hepatic disease. Nonetheless, we also found that seven were heterozygous for PI*MNull, 4 for PI*MZ and 1 was PI*SZ. ATT levels were measured in 20 patients, 20% of them had normal levels and 15% were nondetectable. When a biopsy was obtained, the PAS staining was positive in 100% of cases. Several patients had liver steatosis instead of cirrhosis which was handled as NASH due to the similarity in clinical characteristics.

Conclusions: AATD can't only be screened through AAT levels as they can be normal in up to 20% of patients. We should establish the phenotype and keep in mind that heterozygous can develop clinical disease. The association with other forms of liver disease, especially such as MAFLD, is high and so we should screen for AATD in search of possible decompensation.

https://doi.org/10.1016/j.aohep.2023.101048

O-42 COSTA RICA NATIONAL NEWBORN SCREENING LABORATORYS EXPERIENCE IN DIAGNOSING ALPHA-1 ANTITRYPSIN DEFICIENCY

Mariela Solano-Vargas[1,2],
Juan Diego Gutiérrez-Ávila[1,2],
Jessica Arroyo-Hernández[1,3],
Danny Alvarado-Romero[1,2],
Natassia Camacho-Matamoros[1,2],
Mildred Jiménez-Hernández[1,2]

[1] *Costa Rica National Newborn Screening Laboratory, San José, Costa Rica*
[2] *Costa Rican Social Security Fund, San José, Costa Rica*
[3] *Costa Rican Association for the Screening and Prevention of Childhood Disabilities, San José, Costa Rica*

Introduction and Objectives: Alpha-1 antitrypsin (AAT) is an acute-phase glycoprotein encoded by the *SERPINA1* gene. This allele has a codominant expression and Alpha-1 antitrypsin deficiency (AATD) is caused by the inheritance of two affected alleles. The spectrum of the disease depends on the variants and environmental and biological factors. This study aimed to divulge Costa Rica's experience in diagnosing AATD using biochemical and molecular approaches in patients referred to this center between 2014 and 2021.

Materials and Methods: : Forty-three patients (20 males and 23 females) were analyzed.

Biochemical parameters: Serum AAT concentrations were quantified by turbidometry (SPIN200E, ®SPINREACT). Protein electrophoresis and phenotyping isoelectric electrophoresis were performed on the HYDRASYS 2 SCAN FOCUSING (SEBIA).

Genetic characterization: Sanger sequencing of the *SERPINA1* coding regions (NM_000295.5) was performed in 16 patients with rare electrophoretic patterns or MM phenotype with low AAT concentration.

Results: In 43 probands, we found an AAT mean value of 60.7mg/dl and eight different electrophoretic patterns. Most of our affected patients had an MZ or ZZ phenotype. Table 1 shows the main phenotypes and genotypes of our patients (N=25 patients); how some of them share the same electrophoretic pattern; and finally, the correlation between clinical severity and the biochemical phenotype. Our lab found two variants, one related to null phenotype and the other with uncertain clinical significance (VUS).

Conclusions: :

- This laboratory has developed an efficient and comprehensive algorithm diagnosis for AATD that involves biochemical and molecular tools.
- Genetic analysis has allowed the identification of null variants (Q0Cork and Q0Lisbon).
- AATD affects children and adults, with a broad severity spectrum and different clinical presentations.
- Patients with one affected allele (e.g., PI*MZ, Pi*MS) might show some clinical manifestations.
- Accurate diagnosis is essential for optimal clinical attention and to reduce the diagnostic odyssey.

Table 1. Description of main probands phenotypes and genotypes in 25 of our patients

	AAT concentration (mg/dl)	Electrophoretic Pattern (by SEBIA)	Phenotype	Genotype*	
				Allele 1	Allele 2
Severe	0	Null	Pi*Q0Q0	c.611_612delCA	c.611_612delCA
	27	ZZ	PI*ZZ	N/A	
	42				
	23				
	18				
	25				
	30				
	24				
	20				
	8				
	43	MZ	Pi*M3Z	c.1096G>A p.(Glu366Lys) on M1A	WT
	62		PI*M3Z	c.1096G>A p.(Glu366Lys) on M1A	WT
	48		PI*M3Z	c.1096G>A p.(Glu366Lys) on M1A	WT
	69		PI*M1Z	c.1096G>A p.(Glu366Lys) on M1A	WT
	58		PI*M1Z	c.1096G>A p.(Glu366Lys) on M1A	WT
	88		PI*M1Z Augsburg	c.1096G>A p.(Glu366Lys) on M2	WT
	64	M/Rare	N/A	VUS: c.38C>A , p.(Ala13Glu)	WT
	65	SS	Pi*SS	c.863A>T , p.(Glu288Val) on M1V	c.863A>T , p.(Glu288Val) on M1V
	70	M/Null	PI*M3Q0Lisbon	c.275C>T p.(Thr92Ile) on M1	WT
	81	MS	PI*M3T	c.863A>T , p.(Glu288Val) on M3	WT
	84	N/A	PI*M3S	c.863A>T , p.(Glu288Val) on M1V	WT
Normal	77	MM	PI*M2M3	WT	WT
	166		PI*M1M2		
	55		Pi*M1M1		
	49		Pi*M1M1		

* Only in 16 patients genotype was analyzed
N/A: not analyzed.
WT: Wild type.

https://doi.org/10.1016/j.aohep.2023.101049

O-43 RISK FACTORS FOR CANCER DEVELOPMENT IN PATIENTS WITH PRIMARY BILIARY CHOLANGITIS

Michelle Harriz Braga[1],
Guilherme Grossi Lopes Cançado[2,3],
Paulo Lisboa Bittencourt[4,5], Cláudia Alves Couto[2],
Laura Vilar Guedes[1], André Mourão Costa Lima[2],
Maria Lucia Gomes Ferraz[6],
Cristiane Alves Villela-Nogueira[7],
Jorge Nardelli Mateus[2], Luciana Costa Faria[2],
Nathalia Mota De Faria Gomes[6],
Maria Gomes Oliveira Elze[8], Vivian Rotman[7],
Maria Beatriz Oliveira[9],
Simone Muniz Carvalho Fernandes Cunha[10],
Marlone Cunha-Silva[11],
Liliana Sampaio Costa Mendes[12],
Claudia Alexandra Pontes Ivantes[13], Liana Codes[5],