

CLINICAL AND GENETIC ANALYSIS OF A COHORT OF UK CYSTINURIA PATIENTS



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Background

Cystinuria is an inherited renal stone disease

The inability to reabsorb cystine and dibasic amino acids by the proximal tubular cells of the kidney leads to crystalluria (Figure 1) and the formation of cystine calculi (Figure 2).

- Causes 10% of stones in children and 1% in adults
- Usually presents before 30 years of age
- Prevalence in UK unknown
- Current treatments (Figure 3) are non-curative

Figure 1: Characteristic morphology of cystine crystalluria

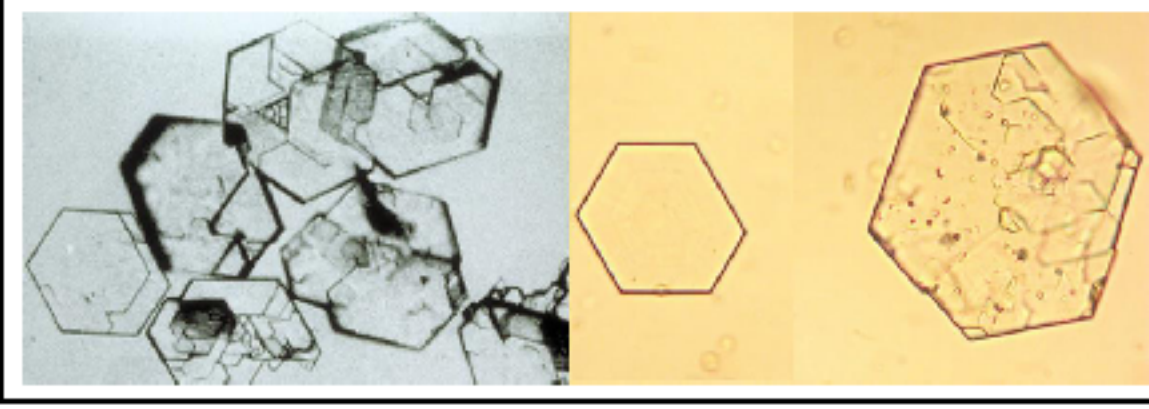


Figure 2: Cystine stones produced by adolescent patient over 3 month period

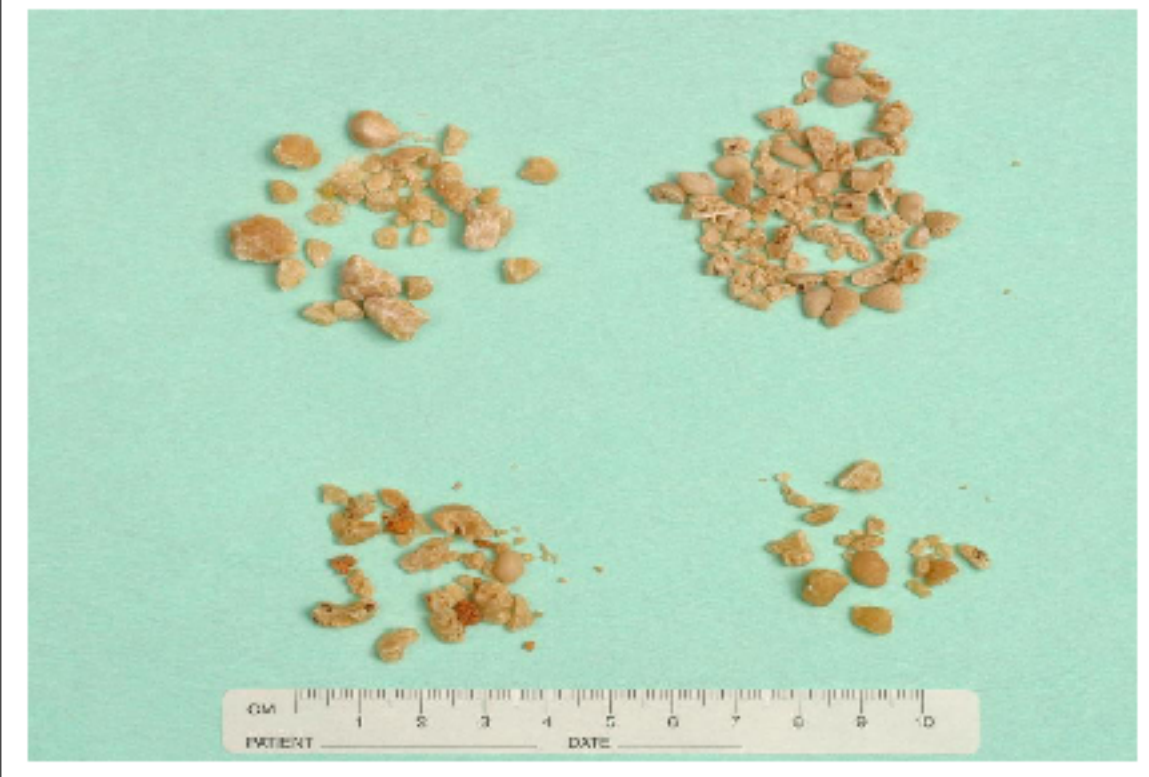
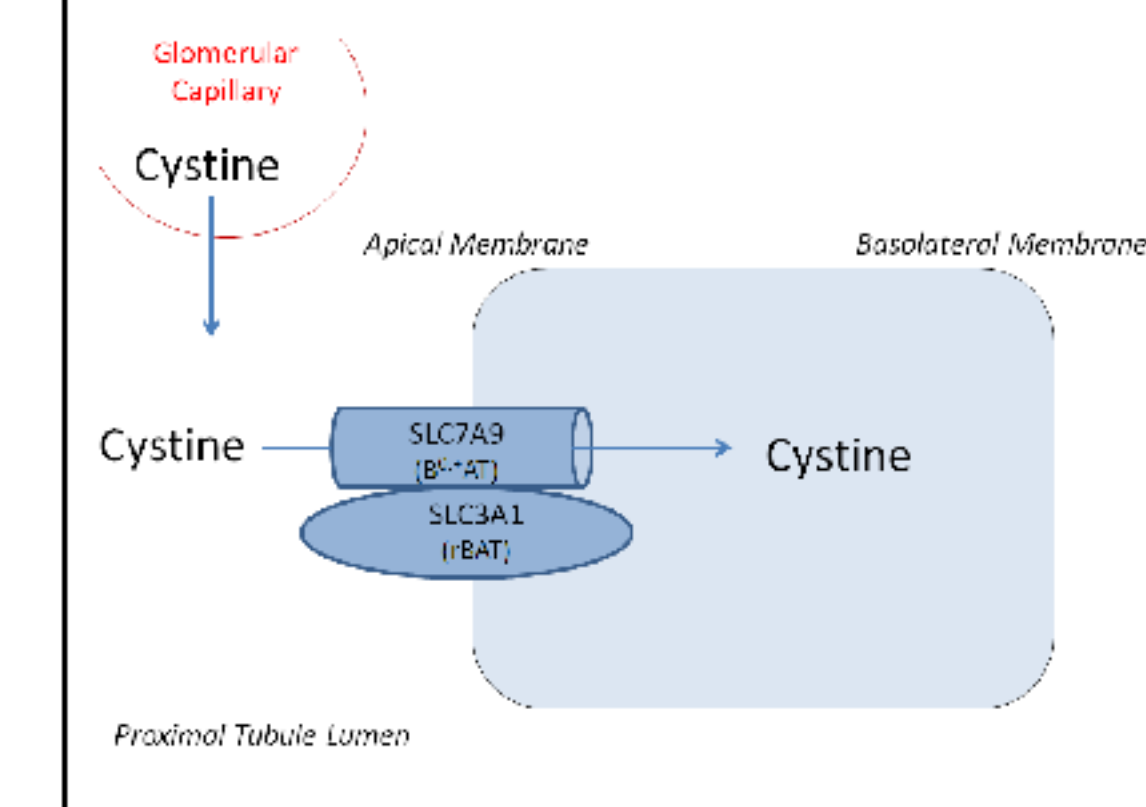


Figure 3: International Treatment Guidelines (AUA,EAU):

- Increased fluid intake (urine output >3L/day)
- Urine alkalinisation – Potassium citrate, sodium bicarb.
- Addition of cystine-binding drug – tiopronin
- Surgical removal of problematic urinary tract stones

Figure 4: Cystine transport in proximal tubular cells via the rBAT/ b⁰⁺AT heterodimer



Mutations in SLC3A1 and/or SLC7A9 cause cystinuria

- SLC3A1 and SLC7A9 genes encode the two subunits of the cystine transporter, rBAT and b⁰⁺AT, (Figure 4)
- Patients with mutations in SLC3A1 have Type A, SLC7A9 Type B, and Type AB has been more rarely observed, see Figure 5 for nomenclature.

Inheritance of Cystinuria

- SLC3A1 autosomal recessive**
 - Heterozygotes of SLC3A1 have normal urinary cystine and dibasic amino acids
 - Except some heterozygotes with the duplication of exons 5-9
- SLC7A9 autosomal dominant with variable penetrance**
 - 86% of SLC7A9 heterozygotes have abnormal urinary dibasic amino acid levels
 - Some heterozygotes develop cystine stones

Figure 5: Nomenclature for Cystinuria Genotypes

- Type AA = 2 mutated SLC3A1 alleles
- Type BB = 2 mutated SLC7A9 alleles
- Type A = 1 mutated SLC3A1 allele
- Type B = 1 mutated SLC7A9 allele
- Type AB = 1 of each mutated allele
- Type AA(B) or BB(A) = more than 2 mutated alleles present

Aims

- Identify large cohort of UK cystinuria patients
- Estimate prevalence of cystinuria
- Analyse clinical features of cystinuria cohort
- Undertake genetic analysis of SLC3A1 and SLC7A9
- Determine if genotype predicts disease severity

Patient cohort

- Cystine stone(s) confirmed on chemical analysis**
- Hospitals throughout the South West and North West regions
- Detailed clinical data collected for genotype/phenotype analysis
- Population estimates from 2011 UK Census

Methods

Genetic Analysis

- Sanger sequencing** of all coding exons and flanking intronic regions (including splice sites and branch points) of SLC3A1 and SLC7A9 using bidirectional automated high-throughput sequencing (Beckman NX/ABI3730), and analysed with Mutation Surveyor software Alamut (version 2.3 rev 1)
- Multiplex Ligation-Dependent Probe Amplification (MLPA)** of coding exons utilising an in-house high-throughput automated MLPA assay (Beckman NX/Beckman CEQ8000). Probes for SLC3A1 & SLC7A9 as per Bisceglia et al (2010) with control P200 probe kit from MRC-Holland.

Ethics: Informed consent and ethical approval obtained: 12/SC/0456 and 11/NE/0259.

Statistics: Mann Whitney U test (2-tailed) to compare two independent groups of non-Gaussian data using Graphpad Prism v5

Results

Cohort of 76 patients with cystinuria:

- 55% male, 97% white British
- Median age at 1st stone 24 years (range 2-62 years)
- 21% aged over 40 years at presentation
- Median stone frequency per year 0.45 (range 0.06-78.2)
- 15 patients (20%) had staghorn stones
- 53 (70%) had eGFR < 90ml/min/m² (Table 2)
- 54 received medical therapy following international guidelines (Figure 3) of whom 27 (50%) continued to form cystine stones
- Prevalence of cystinuria ~1 in 100,000 (population size 7,886,100)

Genetic Analysis

- 125 mutated alleles identified
- 37 distinct variants detected (distribution shown in Figure 6)
- 12 novel mutations; 8 in SLC3A1 and 4 in SLC7A9 (Figure 6)
- 22% (27/125) are large gene rearrangements
- 20% (15/76) are homozygous for mutant alleles
- Frequency of genotypes detected is shown in Table 1

Table 1: Frequency of genotypes

Genotype	N ^o	% of total
AA	27	36
BB	20	26
AAB	1	1
BBA	1	1
BBB	1	1
A	5	7
B	17	22
Unsolvd	4	5
Total	76	

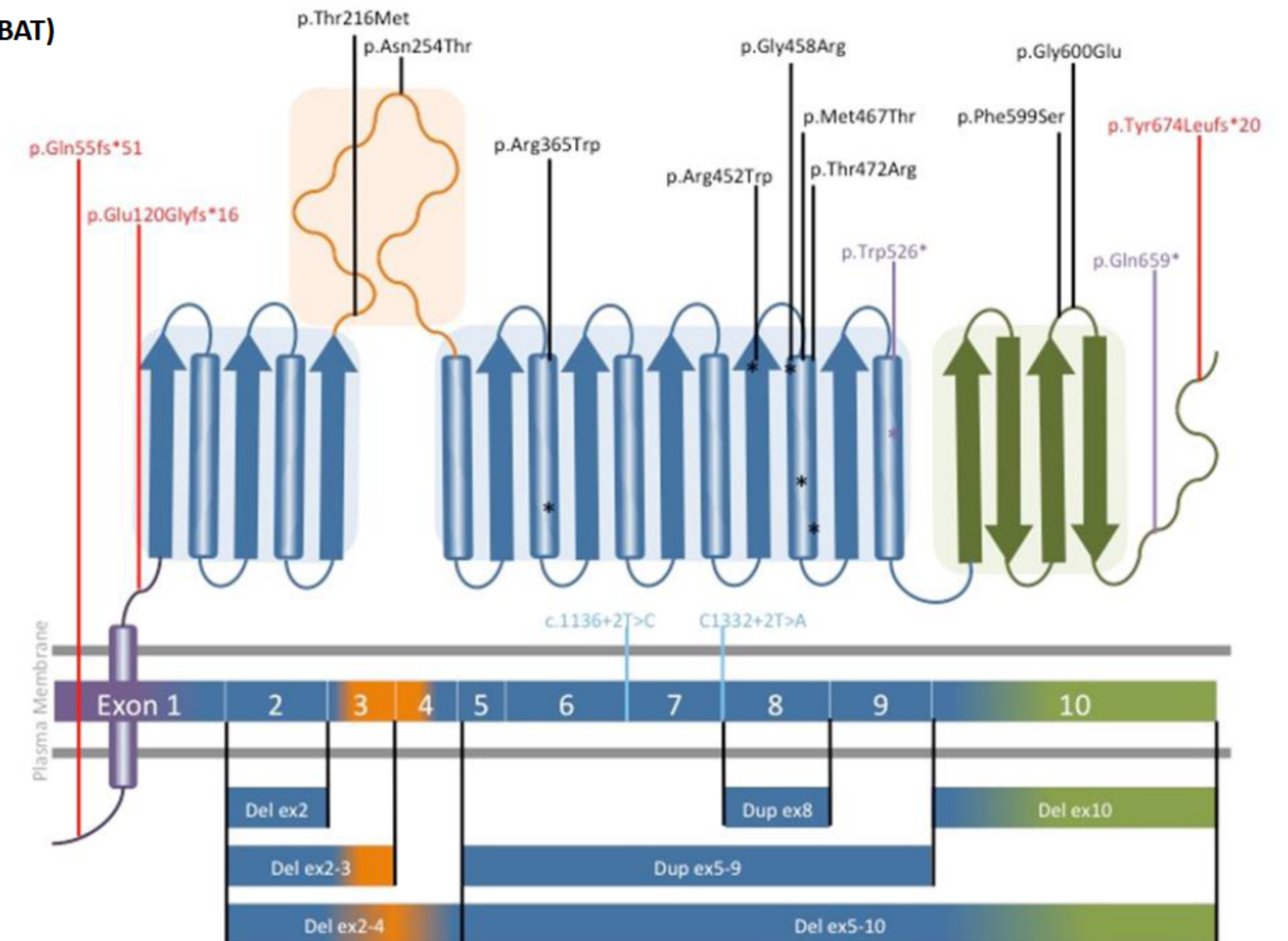
Table 2: Comparison of renal function by genotype

eGFR	N ^o	%	AA	A	BB	B	AB	?*
>90	23	30	8	6	8			1
60-89	37	49	16	4	7	5	3	2
30-59	9	12	2	3	3			1
<30	4	5	1	1	2			
ESRD (with transplant)	3	4		2	1			

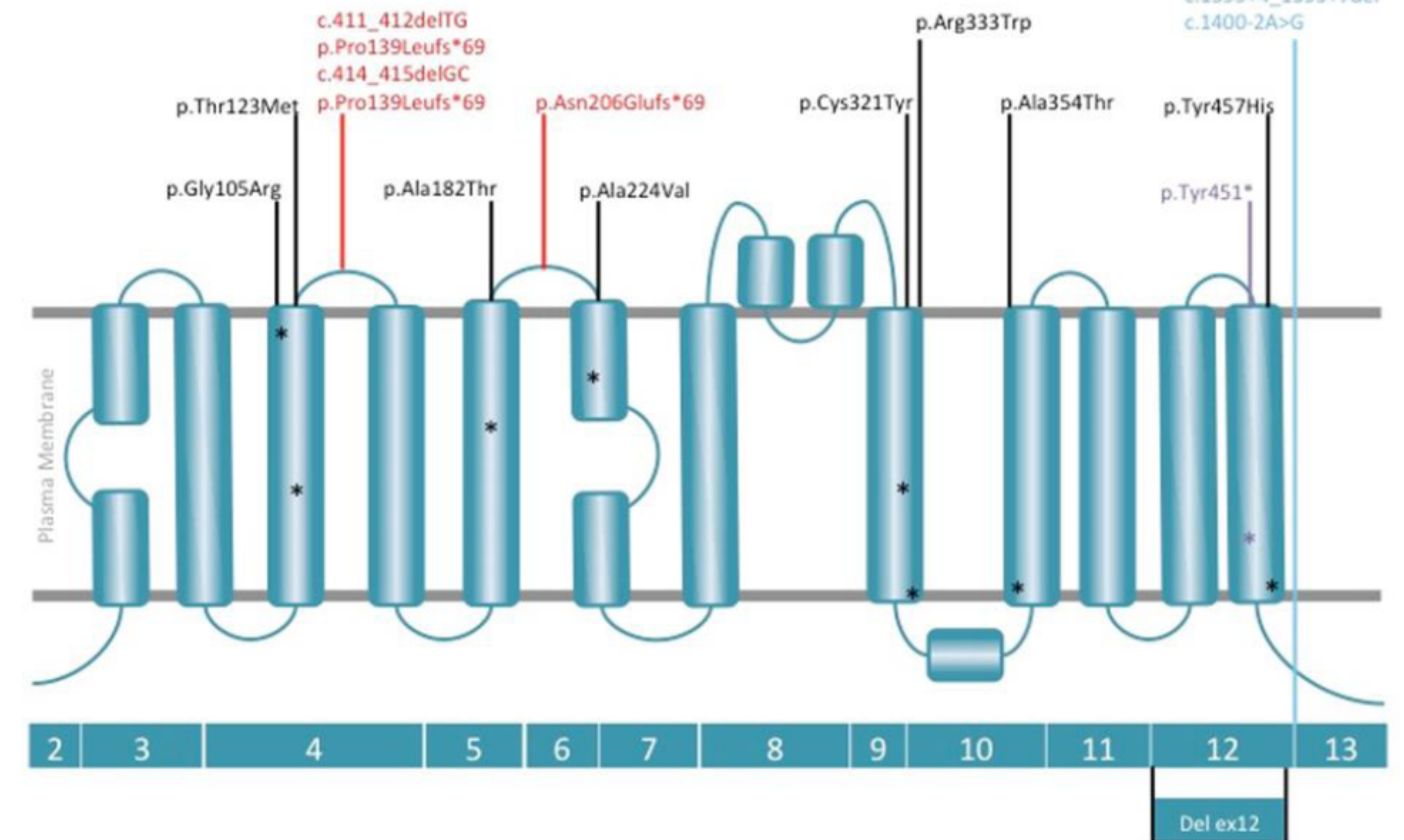
Results

Figure 6(a): Distribution of mutations detected in SLC3A1 (rBAT) throughout all exons and protein domains. Schematic diagram of rBAT based upon a figure by Eggemann *et al.* (2012) and a homology model of the extracellular domain of rBAT based on the crystal structure of oligo-1,6-glucosidase from *Bacillus cereus* (PDB code 1UOK). The three domains of rBAT are shown in purple (TMD), blue (Domain A), orange (Domain B (subdomain)), and green (Domain C). **Figure 6(b): SLC7A9 (b⁰⁺AT) mutations distributed in exons 4-6, 9, 10, and 12-13.** Schematic diagram of b⁰⁺AT based upon figures by Eggemann *et al.* (2012) and Yamashita *et al.* (2005), and a homology model of b⁰⁺AT based on the crystal structure of AdiC, an Arginine:Agmatine Antiporter from *E.coli* (PDB code 3L1L). Mutations are labelled as follows: Missense (black), Nonsense (purple), Frameshift (red), Splice-site (pale blue). Mutations predicted to fall within alpha helices are denoted by * of the appropriate colour.

(a) SLC3A1 (rBAT)



(b) SLC7A9 (b⁰⁺AT)



Genotype/Phenotype Analysis

- Overlap between all the genotype groups regarding age at first stone event, see Figure 7(a)
- Variability both between and within the genotype groups for the level of urinary cystine at first presentation (Figure 7(b))
- Renal impairment present in all genotype groups (Table 2)

Figure 7: Genotype-phenotype. (a) shows the age in years at first stone event for each genotyped group, (b) shows 24 hour urinary cystine at first presentation demonstrating the considerable overlap between the genotype groups.

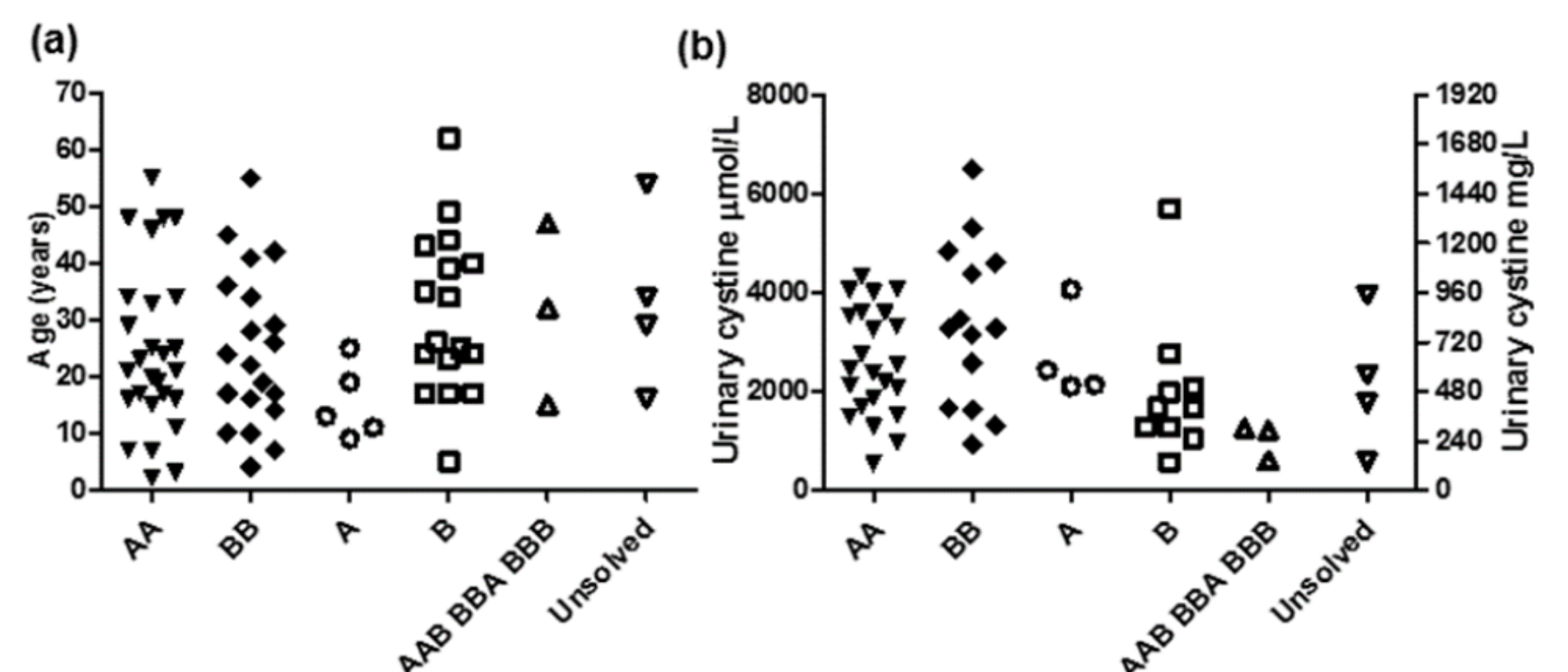


Table 3: Comparison of genotypes AA (SLC3A1) and BB (SLC7A9): no difference between the 27 type AA and 20 BB patients regarding age at first stone, stone episodes per year or renal impairment

Genotype	Median Age at 1 st stone event (range)	Median stone episodes per year (range)	% with renal impairment (eGFR < 90ml/min/m ²)
AA	21 (2-55)	0.44 (0 - 7.13)	70%
BB	23 (4-55)	0.48 (0.09 - 13.3)	82%
p value	0.957	0.392	1.00

Conclusions

- Cystine stones commonly first present in adulthood in cystinuria
- Current treatment options are ineffective
- No genotype-phenotype correlation in these patients
- Presence of a single detectable mutation in both SLC3A1- and SLC7A9-related disease is common and sufficient for a dramatic clinical phenotype
- Several patients do not have an easily identifiable mutation in the known cystinuria genes
- Further sequencing may identify intronic mutations or disease-modifying SNPs
- Collaboration underway for larger study via national registry

