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Genotype and phenotype Alport syndrome

differences in the same family

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Alport syndrome is a hereditary disorder caused by variants in genes for chains of collagen type IV:COL4A3, COL4A4, **COL4A5.Variants** inCOL4A3 andCOL4A4causean and autosomal recessive type of disease, while inCOL4A5cause a classic, X-linked disease.

Methods

c.2881+1G>A in COL4A3 gene. The proband presented with end-stage renal disease(ESRD) and had a history of hematuria and renal injury (RI). We have made a family pedigree and gathered all family members for urinalysis and blood sampling for genetic analysis. Genetic testing was performed using NGS (next generation sequencing) for COL4A3, **COL4A4 and COL4A5 genes.**



Results All patients tested positive for hematuria and proteinuria.			Hematuria +/N	Proteinuria +/g	Creatinine/GFR	NGS	Renal biopsy	Ocular signs	Hearing loss Audiometric check-ups	Blood pressure over 140/90
Four patients underwent kidney biopsy. Mother had hematuria and non-nephrotic proteinuria, 2 children had	Mother	N Q	+ 10	+ 0,51gr/24h	74 μmol/L 90 mL/min	No	No	No	No	Jiiiiiig √
ESRD, 3 had nephrotic proteinuria and 1 son had subnephrotic proteinuria. 3 children had sensorineural	Child	M ♀	0	0	ESRD/Tx 2010/normal graft	COL4A3 c. 2881+1G> A	x2	No	Yes	✓
kidney biopsy specimen and a pathogenic 'splice site' variant c.2881+1G>A in COL4A3 gene was found in 3 children.	Child	₽ ♀	+ 20	++ 1.46gr/24h 3.5 gr/24h	114 µmol/L 80 mL/min	COL4A3 c. 2881+1G> A	x2	No	Yes	√
Mother hasn't been tested. Family members with the same variant, despite the same genotype, had different clinical presentation [Table 1.]It is not	Child	B ♂	+ 12	++ 4.64 gr/24h 8.31 gr/24h	CAPD 2020	COL4A3 c. 2881+1G> A	x 3	No	Yes	✓
yet clear what causes phenotype variability. It is possible that some other, not detected variant in COL4 genes which is not nathogenic by itself, but in co-inheritance with the pathogenic	Child	Lð	+ 4-6	+ 1.2 gr/24h	76 μmol/L 136.4 mL/min	COL4A3 c. 2881+1G> A	x1	No	0	✓

variant contributes to more severe phenotype. Possible cause are also variants in other genes connected with the structure and function of the glomerular filtration barrier that were not sequenced by this method. Finally, environmental factors and diseases (smoking, obesity, hypertension) surely play the role with the same variant point to the need for patients to in kidney damage and in accordance with that, contribute to be monitored more, early detection and prevention of severe phenotype and worse prognosis.

Hematuria +/N (qualitatively/quantitatively), proteinuria +/g (qualitatively/quantitatively) creatinine/GFR (creatinine/glomerular filtration ratio)



Clinical and morphological differences among patients the progression to ESRD