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Introduction: Retinal dystrophies (RD) is a group of blinding diseases that are characterized by clinical variability and pronounced genetic heterogeneity. Although the various forms of RD can be distinguished clinically, disease progression is difficult to predict and may vary even within the same family. Also, same mutation could induce different phenotypes.

The aim of this study was to identify the gene causing retinitis pigmentosa (RP) in a Tunisian family.

Methods:

Two members of a consanguineous family with RP were clinically examined. Patients underwent:

- BCVA,
- Slit lamp biomicroscopy,
- Fundus photography, and electrophysiology.

DNA sample from the index patient was subjected to whole exome sequencing (WES). Variants localized in homozygous regions were validated by Sanger sequencing. Familial segregation was performed.

Results:

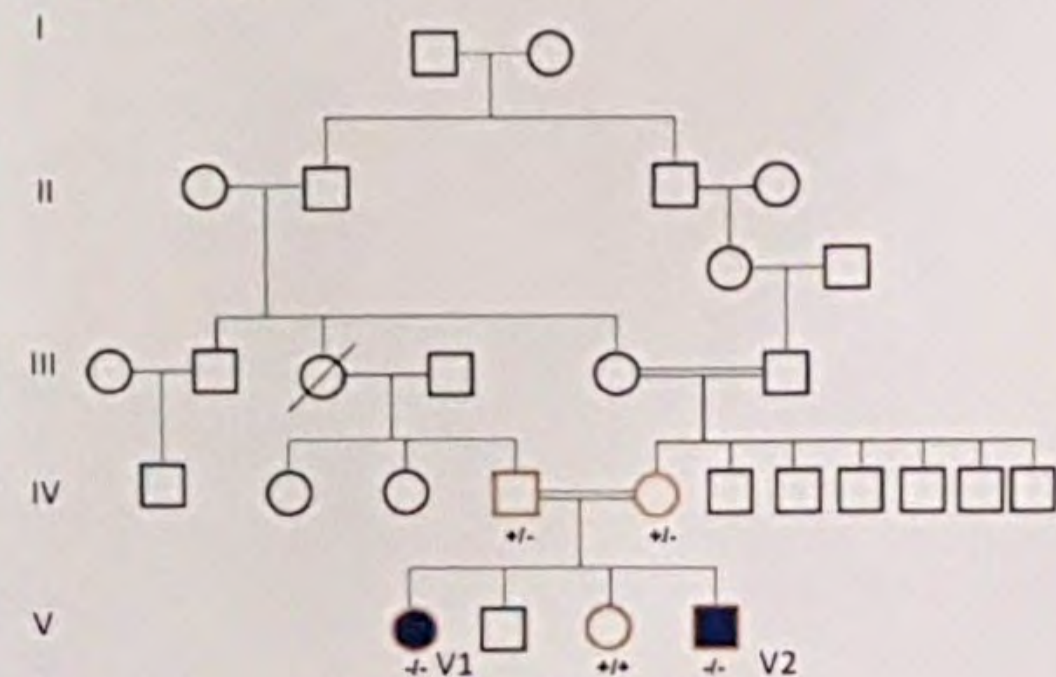


Figure 1: Color fundus photography of patient V.1 showing preserved posterior pole with peripheral retinal atrophy and spicule shaped pigment deposits.

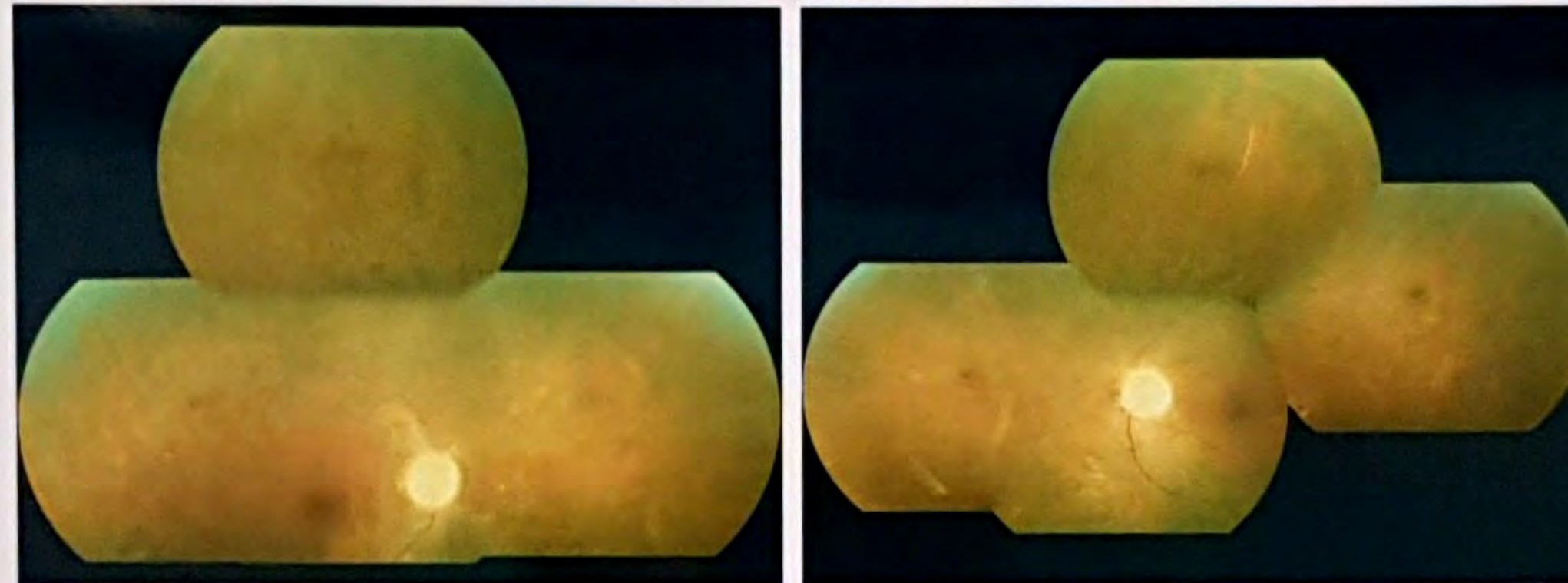
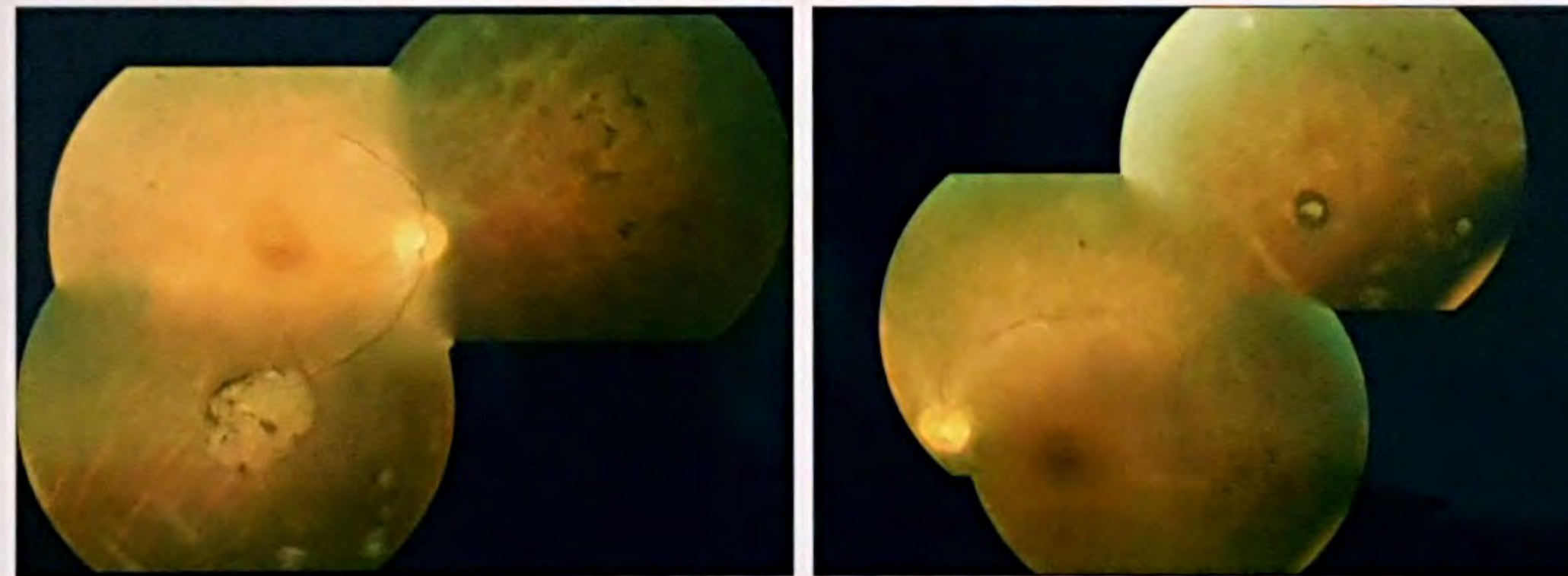


Figure 2: Color fundus photography of the brother V.2 showing same presentation

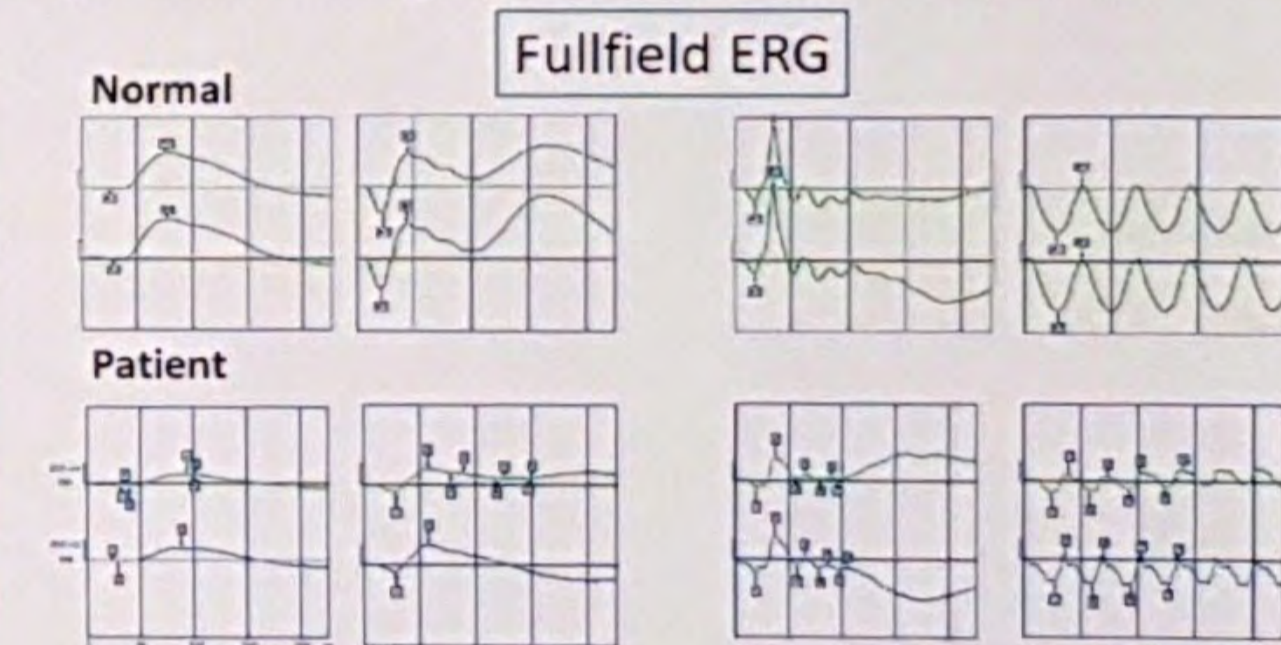


Clinical results:

Affected patients had relatively preserved visual acuity until the third decade. On fundus examination, we found normal macular aspect with few bone spicule shaped pigment deposits and white dot deposits in the mid periphery.

Patient	Gender	Age Years	Age of onset	Visual acuity	
				RE	LE
V.1	F	23	5	5/10	5/10
V.2	M	21	5	7/10	6/10

Figure 3: Fullfield-ERG of patient V.1 :altered scotopic responses with slightly altered photopic responses



Genetic results:

The homozygous mutation NM_001297778.1: c.37G>A, p.A13T in the *NMNAT1*, segregated with the disease in this recessive RP family.

References

*Perrault I et al. Nat Genet. 2012 ; 44(9):975-7.
*Koenekoop RK et al. Nat Genet. 2012 ; 44(9):1035-9.

Discussion and conclusions:

Unexpectedly, two probands in our family with RP had damaging missense mutation, **p.A13T in nicotinamide adenine dinucleotide (NAD) synthase gene *NMNAT1***.

Such mutation have been identified in patients with Leber congenital amaurosis, although the variant is reported only in heterozygote form by the Exome Aggregation Consortium (ExAC) at an allele frequency of 0.0002.

Although the probands' phenotype is consistent with RP and the mutations are predicted to be deleterious, our patients showed preserved visual acuity and RP phenotype with few bone spicule shaped pigment deposits and white dot deposits in the mid periphery.