Clinical and genetic study of leukodystrophies in Tunisian cohort

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INTRODUCTION

 Leukodystrophies hereditary disorders are affecting central nervous system white matter (WM) with or without damages in peripheral nervous system (1,2)

•Brain Magnetic resonance imaging is the major tool to detect WM abnormalities (2)

•Clinical and radiological correlation can help to provide an accurate diagnosis (2)

•Confirmation of diagnosis is based on **molecular study** (1,2)

•In Tunisia, rare studies had focused on this subject and clinical and genetic spectrum of LD remain not defined

OBJECTIVES

•To determine the clinical and mutational spectrum of Tunisian patients with LD without apparent biochemical markers

•To implement a targeted diagnostic strategy for the most frequent forms

MATERIALS AND METHODS

•Descriptive, longitudinal and prospective study over 5 years (2014-2019) which included all the patients followed for "leukodystrophy"" defined as bilateral, symetrical and confluent involvement of the WM

•We expertized the patient files with a clinical and radiological correlation and we carried out molecular investigations by targeted sequencing of genes either by the classic Sanger technique or by new-generation sequencing techniques



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Figure 1: Forms of LD and different mutations identified in our patients

REFERENCES



RESULTS

•45 Tunisian patients belonging to 39 families with LD without biochemical marker were included

- 26 hypomyelinating LD vs 19 demyelinating LD
- 8 forms of LD (figure 1)

•27 different mutations (Figure 1)

- 10 novel mutations
- 2 founder mutations
- 2 recurrent mutations

DISCUSSION AND CONCLUSIONS

•Our study contributed to a better knowledge of leukodystrophies in Tunisia and focused on the genetic clinical, and strong heterogeneity of these conditions

•In our study, we identified a novel form of hypomyelinating leukodystrophy by impairing biogenesis of RNA polymerase III related to a homozygous mutation of the POLR1D gene described only with Treacher Collins syndrome (3)

• Identification of novel, recurrent, and founder variants is crucial for targeted research, patient's care and genetic counselling

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