



PROFILING A BRAZILIAN COHORT IN SOTOS SYNDROME: A REVIEW OF 9 INDIVIDUALS

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INTRODUCTION

Sotos syndrome (SS, OMIM #117550) is an autosomal dominant overgrowth syndrome characterized by macrocephaly, distinctive facial features, and variable intellectual disability, caused by haploinsufficiency of the Nuclear Receptor SET Domain—containing protein 1 (*NSD1*) gene located at 5q35.

OBJECTIVES

In this study, we aimed to characterize the clinical and molecular spectrum of a Brazilian cohort of 9 individuals with SS.

METHODS

A multicentric retrospective study of clinical and molecular findings in individuals presenting with clinical features of SS investigated through whole genome sequencing or cytogenomic techniques.

RESULTS AND DISCUSSION

The sex ratio was 6:3 (M:F), ages at first consultation ranged between 5 months and 14 years, and the mean age at molecular diagnosis was 17,1 years (2-33y). All exhibited variable degrees of intellectual disability (6 with mild, 2 with moderate ID, and 1 with severe) and long face, 8 presented with prominent forehead (88%), 6 patients with sparse frontotemporal hair (66%), and 5 with dolichocephaly (54%), findings that collectively define the *Gestalt* of SS (Figure 1).



Figure 2: Serial photos of patients 2 and 3 from childhood to adulthood.

Eight patients exhibited central nervous system anomalies (88%), four patients with congenital heart defects (44%), the most frequent defect being mitral and tricuspid regurgitation (3/9). Additionally, renal abnormalities were observed in 4 patients, all of them presenting with hydronephrosis.

Our molecular data were consistent with the profile of SS, with a clear predominance of *NSD1* nonsense variants amongst single-nucleotide variants (50%) (Figure 2) and only one patient harboring a 5q35 microdeletion, aligning with the molecular profile of non-Japanese SS patients.

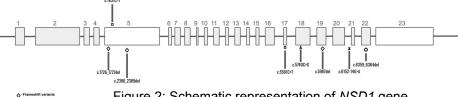
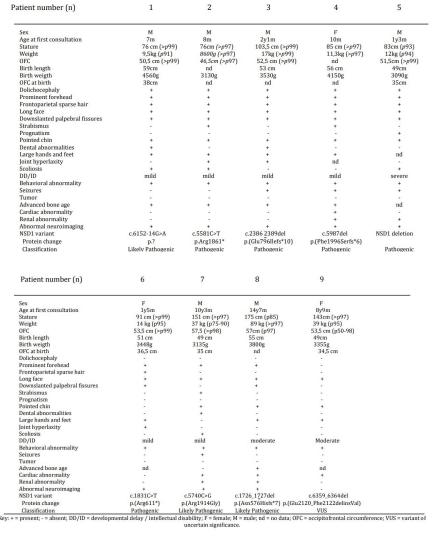


Figure 2: Schematic representation of *NSD1* gene structure and single nucleotide variants found in this cohort

Table 1 summarizes the clinical and molecular findings.

Table 1: Molecular data and clinical features of the patients



CONCLUSION

This case series expands the clinical and molecular data on SS, presenting a novel variant and shedding light on uncommon manifestations, as well as a previously unreported feature in this condition associated with syndromic overgrowth that could be attributed to a multiple diagnoses scenario.

REFERENCES



ACKNOWLEDGEMENTS