



MOLECULAR INVESTIGATION IN 46,XY PATIENTS WITH DIFFERENCES IN SEX DEVELOPMENT

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INTRODUCTION

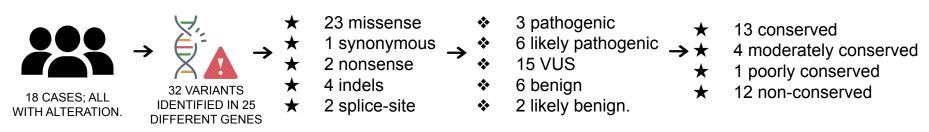
46,XY disorders of sex development (DSD) comprise a heterogeneous group of congenital conditions characterized by abnormalities in chromosomal, gonadal, and/or anatomical development. Phenotypic expressivity is broad, making diagnosis challenging, particularly due to clinical overlap and etiological complexity. In this context, genetic testing is a fundamental tool for the diagnostic and prognosis. In this context, the objective of this paper is to investigate genetic variants in 46,XY DSD cases cared for by the Brazilian Unified Health System in Alagoas.

MATERIALS AND METHODS

CAAE: 59929716.8.0000.5013; 0078620.4.0000.5013



RESULTS



A 8 NOVEL VARIANTS

DISCUSSION

The detection of variants in all participants highlights the importance of large-scale sequencing in the etiological investigation of DSD. The alterations were identified in genes involved in sex determination and differentiation. However, genotype-phenotype correlation could only be established in cases related to defects in androgen synthesis or action and partial gonadal dysgenesis. Eight novel variants were identified, while family recurrence was observed in five cases. Conservation analysis revealed that many variants were located in highly conserved regions, supporting their potential functional impact. The broad diversity of affected genes and clinical manifestations reinforces the diagnostic complexity and heterogeneous nature of these conditions.

CONCLUSION

Despite technological advances, the high prevalence of idiopathic cases and variants of uncertain significance remains a challenge in clinical practice. The integration of clinical, molecular, and bioinformatic data is essential to deepen the understanding of the underlying etiological mechanisms and to improve diagnosis and genetic counseling for patients with 46,XY DSD.

REFERENCES

ACHERMANN, John C. et al. Disorders of sex development: effect of molecular diagnostics. Nature Reviews Endocrinology, v. 11, n. 8, p. 478-488, 2015.

CHOI, Yongwook et al. Predicting the functional effect of amino acid substitutions and indels. 2012.

GARCIA, Felipe Antonio de Oliveira; ANDRADE, Edilene Santos de; PALMERO, Edenir Inez. Insights on variant analysis in silico tools for pathogenicity prediction. Frontiers in Genetics, v. 13, p. 1010327, 2022.

UGHES, L. A. et al. Next generation sequencing (NGS) to improve the diagnosis and management of patients with disorders of sex development (DSD). Endocrine Connections, v. 8, n. 2, p. 100-110, 2019.

HUGHES, I. A. et al. Consensus statement on management of intersex disorders. Journal of pediatric urology, v. 2, n. 3, p. 148-162, 2006.

RICHARDS, Sue et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genetics in medicine, v. 17, n. 5, p. 405-423, 2015.

ZHANG, Junyu et al. Clinical interpretation of sequence variants. Current protocols in human genetics, v. 106, n. 1, p. e98, 2020.











