

Genetic Diagnosis of 46,XY Disorders of Sex Development (DSDs): Insights for Personalized Management

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INTRODUCTION & AIM

The 46,XY disorders of sex development (46,XY DSDs) are congenital anomalies in which there is a discordance between chromosomal, gonadal, or phenotypic features of the internal and/or external genitalia. Diagnosis may occur in the neonatal period or during adolescence. The 46,XY DSD spectrum is broad and of variable severity. Patients present with overlapping clinical and biochemical features and exhibit varying degrees of virilization of their external genitalia ranging from a small penis or mild hypospadias to completely female external genitalia. The 46,XY DSD encompasses multiple etiologies such as gonadal dysgenesis, defects in androgen synthesis or action, and disorders of anti-Müllerian hormone (AMH) synthesis or action, all of which impair typical male virilization. The genetic cause is found in approximately 30% of cases; However, ongoing advances in molecular diagnostics hold the promise of solving a greater proportion of currently unexplained cases. Genetic investigation typically begins with targeted analysis of candidate genes guided by patients' clinical presentation and biochemical findings. Identifying the underlying genetic etiology of these patients is crucial as it provides prognostic information regarding gonadal function, tumor risk, fertility potential, and gender identity development.

This study focused on 14 Tunisian patients diagnosed with 46XY DSD.

METHOD

14 patients with 46,XY DSDs from unrelated families were recruited for this study at the Department of Medical Genetics, Hedi Chaker University Hospital (Sfax, Tunisia), between 2022 and 2024. Informed written consent was obtained from all participants, or from parents/guardians for those under 18 years of age.

Each patient underwent detailed clinical and hormonal assessments, and data were extracted from their medical records.

Clinical presentation and hormonal evaluation led to the following diagnoses within the cohort:

Complete/partial androgen insensitivity syndrome

- Androgen receptor (AR) gene (NM_000044.6)
- 9 patients (P1 -> P9)

17β-hydroxysteroid dehydrogenase type 3 deficiency

- HSD17B3 gene (NM_000197.1)
- 1 patient (P10)

Gonadal dysgenesis

- SF1/NR5A1 gene (NM_004959.4)
- 2 patients (P11, P12)

5α-reductase type 2 deficiency

- SRD5A2 gene (NM_000348.4)
- 2 patients (P13, P14)

DNA extraction : salt-based protocol

PCR amplification of all exons and splice regions

Sanger sequencing

Assessment of variants

- Homozygous/heterozygous variants
- MAF < 1 % in public databases: 1000 Genomes, GnomAD ...
- Impact on protein function : SIFT, PolyPhen-2, Provean...
- Variants pathogenicity : ACMG/AMP guidelines

RESULTS & DISCUSSION

Rare variants

AR gene

Patient P2

rs1186031724; HOMOZYGOTE; exon 1; c. 1886G>T; p.Gly454=; MAF: 7.1e-06

Patient P3

rs2060100891; HOMOZYGOTE; exon 7; c.3017T>C; p.Leu831=; MAF: Absent in GnomAD

=> Pathogenic effects on splicing ?

=> Further functional investigation is required to evaluate the role these novel or rare synonymous AR gene variants in the phenotype of carrier patients.

Screening of HSD17B3, SF1 and SRD5A2 genes

Patients P10 -> P14

=> Absence of mutations

Common variants: SRD5A2 rs632148 (HETEROZYGOTE), SRD5A2 rs142200057 (HOMOZYGOTE) and HSD17B3 rs408876 (HOMOZYGOTE) were found in patients P10, P13, P14

Polymorphisms

AR gene (Exon 1)

* rs6152

Patients P2, P4, P6

HOMOZYGOTE; c. 1163G>A; p.E213=; MAF: 0.1640

=> Risk for androgenetic alopecia

* Triplet repeats GGC

Reference allele: (GGC)17Gly; AR N-terminal domain

Patients P3: del(GGC)4; 13Gly; HOMOZYGOTE; MAF: 0.03

Patient P4: del(GGC)3; 14Gly; HOMOZYGOTE; MAF: 0

Patient P6: delGGCGGC; 15Gly; HOMOZYGOTE; MAF: 0

Patient P9: delGGC; 16Gly; HOMOZYGOTE; MAF: 0.007

=> GC repeat sizes are directly correlated with cellular AR protein levels [1]

=> AR GGC alleles under 15 repeats are associated with an increased risk of prostate and oesophageal cancer [2, 3, 4]

CONCLUSION

There are a few limitations in the study:

- The impact of VUSs on protein function was predicted only by *in silico* analysis, highlighting the need for *in vitro* functional validation.
- Whole-exome sequencing is essential to elucidate the genetic etiology in patients with undetermined cause.

The management of patients with 46,XY DSD depends on etiology, gender identity, hormonal therapy, and genital surgery, as well as consequent psychosocial implications, all of which necessitate long-term multidisciplinary follow-up.

FUTURE WORK / REFERENCES

Future Work

Epigenetic analysis was not involved in this study; further investigation with larger cohort are needed.

The authors have no conflicts of interest to declare

References: [1] Ding et al. 2004; [2] Chang et al. 2002; [3] Visakorpi 2003; [4] Dietzsch et al. 2003