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LETTER TO THE EDITOR

Genetic sequencing of a patient with Kallmann syndrome plus 5α -reductase type 2 deficiency

Wen Ji¹, Lu-Yao Zhang¹, Fu-Cheng Li², Yu Wang¹, Wei He¹, Qi-Qi Yin¹, Zhi-Hong Liao¹

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Dear Editor,

Kallmann syndrome (KS) is a phenotypically and genetically heterogeneous disorder featured by hypogonadotropic hypogonadism and congenital hyposmia or anosmia, accompanined with renal dysplasia, hearing loss, and craniofacial defects sometimes. More than 20 genes have been identified causing KS either alone or in combination.

 5α -reductase type 2 deficiency (5α -RD) caused by *SRD5A2* gene mutation is a rare disease characterized by elevated ratio of testosterone (T) to dihydroteststorone (DHT). The clinical spectrum of 5α -RD is heterogeneous, ranging from the classic phenotype to males with hypospadias and even isolated micropenis. Here, we report a male KS patient accompanied with mild 5α -RD diagnosed from genetic sequencing and clinical analysis.

A 28-year-old male (46, XY) was referred for no secondary sexual characteristics and anosmia. At birth, he had bilateral cryptorchidism, anosmia, and deafness in the left ear. Figure 1a shows the patient's olfactory bulbs and tracts while Figure 1b shows the normal individual. Figure 1c shows his flat pituitary. Bilateral orchidopexy was performed at age five, and there is no prior treatment. The distance between the top of the head to the superior margin of the symphysis pubis was 87.2 cm and from the inferior margin of the symphysis pubis to the sole of the foot was 93.0 cm, and distance between outstretched arms was 187.0 cm. He had bilateral cubitus valgus, and his bone age was 16 years old (Figure 1e). No remarkable frontotemporal hairline recession or acne was noted. Each testicle was in the scrotum without hypospadias. Genital development was Tanner genital stage 1. His pelvic MRI showed prostate dysplasia, mullerian duct cyst (Figure 1f), and seminal vesicles dysplasia (Figure 1g). The MRI of normal seminal vesicles is given in Figure 1h.

Normal respond of follicle-stimulating hormone (FSH) and luteinizing hormone (LH) was seen after the subcutaneous injection of triptorelin 100 mg. The results of the triptorelin stimulation test at baseline and 15, 30, 60, 90, and 120 min after injection were LH 0.08, 1.30, 1.48, 1.67, 1.81, and 2.26 (normal: 2–12) IU l⁻¹; FSH 1.02, 2.03, 2.47, 3.03, 3.13, and 4.20 (normal: 1–8) IU l⁻¹, respectively. T, DHT, and T/DHT ratio were 0.32 (normal: 1.58–8.77) μ g l⁻¹, 47.58 (normal 57.5–355.0) ug l⁻¹,



Figure 1: Image characters (**a**) Fat-saturated coronal T2-weighted MR image shows bilateral agenesis of the olfactory bulbs and tracts (arrows). (**b**) Coronal T2-weighted MR image shows normal olfactory tracts and bulbs (arrows). (**c**) Sagittal postcontrast T1-weighted image shows a flat pituitary but no lesion (4 mm height, arrow). (**d**) Direct sequencing of the *SRD5A2* gene shows c. 680G> A (p.R227Q) substitution at exon 4 in the patient (top arrow) and the sequence of a normal control subject (bottom arrow). (**e**) X-ray picture of the patient's left wrist shows a 16-year-old bone age. (**f**) Sagittal T2-weighted MR image shows a Mullerian duct cyst (the upper arrow) and a dysplastic prostate (the lower arrow). (**g**) T2-weighted axial MR image shows the patient's bilateral agenesis of seminal vesicles. (**h**) Axial T2-weighted MR image shows normal seminal vesicles. MR: magnetic resonance.

and 6.78 at baseline, and 4.41 ug l^{-1} , 168.5 ug l^{-1} , and 26.40 after human chorionic gonadotropin (HCG) stimulation, respectively. Other hypothalamic-pituitary-axes' functions were normal.

The patient was treated with HCG 2000 U i.m. 3 times every week for 9 months, and then human menopausal gonadotropin (HMG) 75 U i.m. was added 3 times a week for another 3 months. Mild

¹Department of Endocrinology, 1st Affiliated Hospital of Sun Yat-sen University, Guangzhou, 510080, China; ²Department of Medical Genetics, Genome Research Center, Zhongshan School of Medicine, Sun Yat-sen University, Guangzhou, 510080, China.

Correspondence: Prof. ZH Liao (liaozhh@mail.sysu.edu.cn)

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All exons and splice junctions of 23 related genes were screened using Panel or Sanger sequencing. The results were validated by Sanger sequencing. The screened genes were *KAL1*, *FGFR1*, *FGF8*, *PROKR2*, *PROK2*, *GNRHR*, *GNRH1*, *KISS1R*, *KISS1*, *TACR3*, *TAC3*, *CHD7*, *WDR11*, *HS6ST1*, *SEMA3A*, *NR0B1*, *LHB*, *LEP*, *LEPR*, *FSHβ*, *PCSK1*, *SRD5A2*, and *NSMF*. *SRD5A2* gene variant (c. 680G>A) (**Figure 1d**) was identified in addition to two nonpathogenic variants in *KAL1* and *GnRH1* (rs808119, rs6185). **Supplementary Table 1** shows genes information and sequencing results. The failure to find pathogenic genes involved in KS could be due to the mutations mapping outside the coding regions or other candidate genes.

Both 5α -RD and severe congenital KS could result in low level of DHT in fetus and prostatic dysplasia. When KS co-existed, it is hard to diagnose 5α -RD according to DHT-dependent signs such as facial or body hair, prostate enlargement, and scalp hairline recession. Hence, identification of mild enzyme defect should be based on genetic diagnosis and T/DHT ratio.

Mild 5 α -RD as stated above was due to the heterozygous c. 680G>A in exon 4. Makridakis et al.1 reported that the mutant retained 3.2% of normal enzyme activity and slowed the rate of enzyme-catalyzed reaction to 0.06 nmol·l⁻¹·mg⁻¹ (normal, $1.7-2.2 \text{ nmol } l^{-1} \text{ mg}^{-1}$). Interestingly, the heterozygous state was found in 5% of their normal Chinese controls. Thus, a remote hypothesis of a dominant effect of some mutations, in particular, cellular environments cannot be completely excluded.² Since people with the same mutation may have divergent phenotypes even in one family, genetic and functional heterogeneity (due to the presence of SRD5A1 and some interacting factors) should be taken into account. The elevated T/DHT ratio post-HCG stimulation is more sensitive and reliable in diagnosis of 5α-RD³ and helpful to distinguish between androgen insensitive syndrome and other conditions arising from T synthesis defects. The diagnostic cut-off point of T/DHT ratio has not been precisely defined, varied from 3.6 to 18 in diverse ethnic groups pre or after HCG stimulation.⁴⁻⁶ Obviously, high T/DHT ratio of 26.4 after HCG stimulation is another reason for the diagnosis of mild 5α-RD.

Some authors reported that DHT regulated the expression of genes relevant for normosmia idiopathic hypogonadotropic hypogonadism (nIHH) such as *GnRH1*, *KISS1*, and *KISS1R* and significantly stimulate the migration of FNC-B4 placode *in vivo*.^{7,8} KS might be similar with nIHH in some way. The interaction between KS and 5α -RD need further investigation.

Feyles *et al.*⁹ reported that the earlier the orchiopexy performed the better the restoration of spermatogenesis. In 5 α -RD, the differentiation from spermatogonium to spermatocyte was defective at an age of 4–6 years, which resulted in a lack of spermatocytes but normal spermatogonium.¹⁰ Dysplasia prostate and seminal vesicles epididymis are the primary causes for azoospermia and few semen. Testicular biopsy is an approach to confirm the testicular spermatozoa.

In conclusion, we first reported a male with KS and 5α -RD diagnosed with gene sequencing that will boost the knowledge about geneotype-phenotype connection. If a KS patient had prostate dysplasia, cryptorchidism, unremarkable frontotemporal hairline recession, or a minor response to gonadotropin therapy, *SRD5A2* sequencing might be considered.

Table 1: Clinical features and laboratory data

	Before therapy	After therapy
Voice change	_a	-
Bear hair/pubic hair/armpit hair	_/_/_	Viliform (1-2 mm)/ Tanner P3/–
Testosterone level (ng ml ⁻¹)	0.46±0.15	3.65±1.93
Left testicle/right testicle (length \times width \times thickness) (cm)	1.0×0.4×0.6/ 1.2×0.3×0.6	1.6×0.8×1.1/ 1.3×0.7×0.9
Head of epididymis (left/right) (cm)	Smaller/less clear	0.7×0.4/less clear
Stretched length of penis (cm)	1.4	2.0
Semen	-	Few, no sperm
Not detected		

"Not detected

AUTHOR CONTRIBUTIONS

WJ collected the clinical data, performed the literature search, and drafted the manuscript. LYZ and FCL carried out the molecular genetic studies. ZHL conceived of the study and revised the manuscript. YW, WH, and QQY participated in the follow-up of treatment. All authors read and approved the final manuscript.

COMPETING INTERESTS

All authors declared no competing financial interests.

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Supplementary information is linked to the online version of the paper on the *Asian Journal of Andrology* website.

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Supplementary	Table	1:	Screened	genes	and	sequencing	results
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OMIM ^a	Symbol	Hereditary mode	Nonsynonymous variants	RefSeq	
*•300836	KAL1	XR	c. 1600G>A	NM_000216.2	
*136350	FGFR1	AD	_d	NM_023110.2	
*607123	PROKR2	AR	-	NM_144773.2	
*607002	PROK2	AR? -		NM_001126128.1	
*600483	FGF8	AD/AR	-	NM_033163.3	
*138850	GNRHR	AR	-	NM_000406.2	
*152760	GNRH1	AR	c. 47G>C	NM_000825.3	
*604161	KISS1R	AR	-	NM_032551.4	
*603286	KISS1	AR	-	NM_002256.3	
*608137	NSMF	AD	-	NM_001130969.1	
*162330	TAC3	AR	-	NM_013996.2	
*162332	TACR3	AR	-	NM_001059.2	
*608892	CHD7	AD	-	NM_017780.3	
*606417	WDR11	AD	-	NM_018117.11	
*604846	HS6ST1	AD?	-	NM_004807.2	
*603961	SEMA3A	AD?	-	NM_006080.2	
*300473	NROB1	XD?	-	NM_000475.4	
*152780	LHB	AD	-	NM_000894.2	
*164160	LEP	AR?	-	NM_000230.2	
*601007	LEPR	AR?	-	NM_001003679.3	
*136530	FSHβ	AR?	-	NM_000510.2	
*162150	PCSK1	AR?	-	NM_000439.4	
+°607306	SRD5A2	AR	c. 680G>A	NM_000348.3	

^a: Each MIM entry in the column is designated by the MIM numbering system. ^b:An asterisk (*) before an entry number indicates a gene. ^c:A plus sign (+) before an entry number indicates that the entry contains the description of a gene of known sequence and a phenotype. ^d: No nonsynonymous variant was identified