Genetic Analysis of NR0B1 in Congenital Adrenal Hypoplasia Patients: Identification of a Rare Regulatory Variant Resulting in Congenital Adrenal Hypoplasia and Hypogonadal Hypogonadism without Testicular Carcinoma in situ

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Key Words
Carcinoma in situ · Congenital adrenal hypoplasia · DAX1 · Hypogonadotropic hypogonadism · NR0B1 · OCT3/4 · Testis

Abstract
There have been few testicular histology reports of adult patients with congenital adrenal hypoplasia/hypogonadal hypogonadism (AHC/HH), but Leydig cell hyperplasia has been observed, an indicator of the possibility of malignant transformation. We aimed to define the basis of AHC/HH in 4 pedigrees of different ethnic backgrounds. One patient was elected to have testicular biopsy which was examined for evidence of carcinoma in situ (CIS). NR0B1 mutation analysis was performed by sequence analysis. NR0B1 expression was investigated by RT-PCR. Testicular biopsy sections were stained with HE or immunostained for OCT3/4, an established marker of CIS. We identified NR0B1 variants in the 4 AHC pedigrees: pedigree 1 (United Arab Emirates), c.1130A>G predicting p.(Glu377Gly); pedigree 2 (English Caucasian), c.1168+1G>A, a regulatory variant within the NR0B1 splice donor site. This last male patient, aged 30 years, presented with evidence of HH but incomplete gonadotrophin deficiency, following an earlier diagnosis of Addison’s disease at 3 years. Hormonal therapy induced virilisation. Testicular biopsy was performed. The c.1168+1G>A variant abrogated normal splicing of testicular mRNA. Histological examination showed poorly organised testicular architecture and absence of spermatozoa. Morphological analyses and the absence of immunohistochemical staining for OCT3/4 excluded the presence of malignant germ cell cancer and its precursor lesion, CIS. These studies add to the knowledge of the types and ethnic diversity of NR0B1 mutations and their associated phenotypes, and provide insight into the assessment and interpretation of testicular histology in AHC and HH.

A.P.W. and R.C.F. contributed equally to this work.
The atypical orphan nuclear receptor NR0B1 (OMIM 300473, previously called DAX1, dosage-sensitive sex-reversal adrenal hypoplasia critical region on the X-chromosome protein 1) is a critical regulator of adrenal and gonadal development, where it is the major negative regulator of steroidogenic factor-1 (NR5A1) [Zanaria et al., 1994; Phelan and McCabe, 2001; Achermann, 2005]. The NR0B1 gene was identified by a positional cloning strategy which mapped partially overlapping deletions associated with a contiguous gene deletion syndrome involving congenital adrenal hypoplasia (AHC), hypogonadal hypogonadism (HH), Duchenne muscular dystrophy and glycerol kinase deficiency [Monaco et al., 1992; Walker et al., 1992]. Point mutation of NR0B1 was demonstrated to cause both phenotypes of AHC and HH (OMIM 300200), highlighting its importance in the development and function of the adrenal gland and testis [Muscatelli et al., 1994]. Expression of missense variants in vitro resulted in translation of non-functional or functionally impaired NR0B1 protein [Brown et al., 1994; Phelan and McCabe, 2001; Achermann, 2005]. Only 3 regulatory variants have been reported and the molecular consequences of NR0B1 mutation upon testis mRNA levels have not been investigated previously.

The phenotypic spectrum of patients with NR0B1 sequence variants is broad, but usually involves adrenal insufficiency presenting either neonatally or during infancy and HH in adulthood. However, normal puberty has been reported and even instances of precocious puberty. In adult male patients with AHC and HH due to NR0B1 mutation, histological analyses of testicular biopsies have shown Leydig cell hyperplasia, indicating the possibility of malignant transformation [Seminara et al., 1999; Ozisik et al., 2003]. Male patients with a range of reproductive disorders collectively termed testicular dysgenesis syndrome are screened for the presence of the precursor of malignant germ cell tumour, carcinoma in situ (CIS) [Sonnier et al., 1999; Ozisik et al., 2003]. 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and a control individual without symptoms of AHC (RNeasy Mini Kit, Qiagen, UK). cDNA was synthesised and amplified using a touchdown PCR protocol to examine expression of NR0B1 and ACTB. The NR0B1 primers used were RTEX1BF-NEW (GCTTTCTTTCCAAATGCTG) and RTEX2R-NEW (ATGATGGGCCTGAAGAACAG) for amplification of the predicted 271-bp product. The RT-PCR was performed twice using 2 independent RNA preparations from separate portions of the testicular biopsy.

For immunohistochemistry, 3-μm sections were cut from the prepared testis biopsy block. Parallel sections were stained with haematoxylin and eosin (H&E) or immunostained for OCT3/4 (an established marker of CIS) [Looijenga et al., 2003; de Jong et al., 2005], using a mouse monoclonal antibody directed against amino acids 1–134 of human OCT3/4 (SC-5279, Santa Cruz, Heidelberg, Germany; 1:350 dilution). The sections were evaluated by a pathologist experienced in germ cell tumour pathology (J.W. Oosterhuis, Erasmus MC Rotterdam, The Netherlands) [Oosterhuis and Looijenga, 2005; van Casteren et al., 2008]. Evidence of CIS was assessed on both H&E and OCT3/4 staining. CIS was morphologically defined as the presence of large, atypical intra-tubular cells with large hyperchromatic nuclei containing several prominent nucleoli [Oosterhuis and Looijenga, 2005; van Casteren et al., 2008].

### Results

In pedigree 1, sequence analysis for the 2 cousins (1-IV:6 and 1-IV:4) identified the presence of a novel missense variant in exon 1, c.1130A>G, predicting p.(Glu377Gly). A different missense mutation predicted to affect the same amino acid residue has been reported in AHC patients: c.1129G>A, predicting p.(Glu377Lys) [Zhang et al., 1998; Achermann et al., 2001]. The residue corresponding to E377 is conserved in 3 related nuclear receptors, and modelling implicated a salt bridge between E377 with R425, a residue which has also been identified as affected by sequence variation in AHC: p.(R425G) [Zhang et al., 1998].

In pedigree 2, the c.327C>A nonsense variant p.(Cys109*) was detected in the 2 cousins tested (2-III:1 and 2-III:5); this variant has been identified previously in a patient with AHC [Phelan and McCabe, 2001].

In pedigree 3, the 3 brothers tested (3-III:14, 3-III:17 and 3-III:18) were found to have a novel deletion of 6 nucleotides located within a short direct repeat sequence in exon 1, c.857_862delTGGTGC, predicting p.(Leu286_Val287del) in the nuclear receptor-like domain; this variant was heterozygous in their mother. A missense variant of residue 287, c.860T>G, predicting p.(Val287Gly), has
been previously reported to result in AHC and HH, with additional features of inappropriately tall stature and renal ectopy, features not previously described in AHC [Franzese et al., 2005]. These rare features were not present in the 3 brothers with p.(Leu286_Val287del) described in this report.

In pedigree 4, DNA sequence analysis revealed a novel variant within the NR0B1 splice donor site for patient 4-II:1 (c.1168+1G>A; fig. 4A). Both the location of this variant within the conserved 2 bp of the splice site consensus sequence and its rarity, evidenced by its absence from the 1000 Genomes database (http://browser.1000genomes.org/index.html), indicated a likely functional variant [The 1000 Genomes Project Consortium, 2010]. Testicular RNA was prepared from the biopsy sample and reverse transcribed for PCR analysis of NR0B1 expression using primers located in exons 1 and 2. A product of 271 bp was amplified from the control, but no NR0B1 product could be amplified from the patient’s testicular RNA, despite amplification of β-actin (ACTB) as an internal positive control for RNA integrity, indicating absence of the cognate NR0B1 mRNA transcript (fig. 4B).

Histological analyses of the testis biopsy showed some sclerotic seminiferous tubules and other tubules beside Sertoli cells only (fig. 5A–D). Spermatocytic differentiation was noted in some tubules, but there were no spermatozoa. Leydig cell numbers appeared substantially decreased. Some areas showed testicular parenchyma containing a mixture of narrow, immature seminiferous tubules and totally fibrosed tubules. The immature tubules contained germ cells at the following stages: spermatogonia, spermatocytes, and very rare, round spermatids. The interstitial space appeared increased due to edema.

Fig. 3. Pedigree 3 (Oman).

Fig. 4. A Sequence chromatogram showing mutation of the NR0B1 splice donor site (c.1168+1G>A) in patient 4-II:1. NR0B1 sequence was compared to Transcript refseq ID NM_000475.4; the intron sequence is contained in Genomic refseq ID NG_009814.1 on chromosome X. B RT-PCR analysis of RNA extracted from control testis gave the 271-bp cognate NR0B1 band. This could not be amplified from 2 independent RNA preparations from portions of the testicular biopsy of patient 4-II:1. Amplification of the β-actin gene (453 bp) confirmed mRNA integrity.
ma, fibrosis and a dense lymphocytic infiltrate. However, there was no morphological evidence of CIS or an invasive germ cell tumour; this was confirmed by the absence of staining for OCT3/4 in the patient biopsy (fig. 5E), as compared to the positive control section (fig. 5F).

**Discussion**

We report 4 NR0B1 mutations, 3 of which are novel and 1 is a rare regulatory variant, demonstrating the first NR0B1 mutations in patients of Arabic origin. We provide the first investigation of CIS in testicular biopsy tissue from a patient with AHC and HH due to NR0B1 mutation, demonstrating it to be absent in this case. In general, male patients with testicular dysgenesis syndrome are screened for CIS; OCT3/4, an established marker of CIS, is negatively regulated by NR0B1. When testicular biopsy is indicated for HH caused by mutation of NR0B1, CIS should be investigated both morphologically (HE) and specifically by OCT3/4 staining. These data will provide evidence of the risk of CIS and allow guidelines to be established for screening of CIS in NR0B1-related AHC with HH.

Testicular histology associated with NR0B1 sequence variants has previously been described in only 2 prepubertal cases and 3 adults. A neonate who died due to AHC, the sibling of a patient with the c.1197C>A variant, predicting p.(Y399*), had normal testicular architecture [Brown et al., 2003]. A 9-year-old boy with AHC and undescended, prepubertal testes had the c.1355delT variant; this predicts a frameshift with the first premature termi-
nation at codon 461, p.(Ile452 Thrfs*10). This infant also had normal testicular architecture [Morii et al., 2007]. An adult with mild phenotype (adult-onset adrenal insufficiency and gonadal failure) had an amino-terminal NR0B1 nonsense variant, c.109C>T, predicting p.(Gln37*) (fig. 6). In vitro studies showed expression of amino-truncated, partially functional protein from an alternative, in-frame initiation site (M83), deduced to reduce clinical severity. He had been treated with gonadotrophins for 6 months. His testicular biopsy showed disorganized seminiferous tubular structures and moderate Leydig cell hyperplasia [Ozisik et al., 2003]. Another adult patient with AHC and HH and the c.501delA variant predicting p.(Gly169Alafs*95) had a testicular biopsy after 7 years of HCG treatment; Sertoli cell only syndrome was reported, with infrequent spermatogonia, no evidence of spermatogenesis, and Leydig cell hyperplasia (fig. 6) [Seminara et al., 1999]. Recently, an adult with AHC and HH and the NR0B1 c.1210C>T variant, predicting p.(Gln404*) (fig. 6), had 20 months treatment with menotropin and HCG; bilateral multiple-site testicular biopsy was performed. Although histology showed very severe reduction in spermatogenesis, a few spermatocytes were extracted for intracytoplasmic sperm injection and embryo transfer, leading to birth of a healthy boy. Thus, there are very few data on testicular function, but they suggest that patients with NR0B1 variants appear to have a primary defect of the testes which is progressive with increasing age, in addition to testicular defects secondary to central HH [Frapsauce et al., 2011]. We report histological analyses of the adult patient 4-II-1 which confirm an extremely compromised testicular architecture, failure of spermatogenesis at a cellular level with absence of spermatozoa. As our recent evidence suggests that histological examination alone can be insufficient to exclude CIS [van Casteren et al., 2008], we also performed OCT3/4 immunostaining, showing no detectable expression in the biopsy sample. There was neither evidence of malignant germ cell tumour, nor of its precursor lesion, CIS. Although sampling error must always be considered for analysis of single site biopsies, based upon our previous studies of CIS, there is no evidence to suggest that the patient is at future risk for development of a malignant germ cell tumour, either a seminoma or nonseminoma [Looijenga et al., 2003; de Jong et al., 2005; Oosterhuis and Looijenga, 2005; van Casteren et al., 2008].

Few variants of regulatory sequences have been reported for NR0B1. Two different NR0B1 splice site variants have been identified in boys with AHC and HH, c.1169–1G>C and c.1168+1G>A [Goto and Katsumata, 2009; Landau et al., 2010]. Over-expression of c.1168+1G>C in COS-1 (monkey kidney) cells and RT-PCR showed multiple alternatively spliced transcripts,
including a band the same size as the cognate NR0B1 product [Goto and Katsumata, 2009], possibly reflecting non-physiological NR0B1 transcriptional regulation under heterologous over-expression. In comparison, in our current study of the novel c.1168+1G>A variant, no cognate NR0B1 transcript was RT-PCR amplified from the patient’s testicular RNA, predicting physiological absence of NR0B1 protein. Lack of sample precluded further analysis of the testicular RNA, so we cannot exclude the possibility that alternative splicing across the region encompassed by the primers, corresponding to amino acids 363–453 in the nuclear receptor-like domain, may have resulted in some level of expression of a transcript encoding a partially functional protein. The only other regulatory variant of NR0B1 described in a patient with AHC and HH was a 60-Mb inversion with 1 breakpoint in a non-coding, conserved element ~4 kb upstream of NR0B1 [Skeinningsrud et al., 2009]. The c.1168+1G>A variant described in patient 4-II:1 in this report, together with the 2 previous splice site variants and the inversion, are the only reported NR0B1 variants affecting non-coding, regulatory sequences.

In summary, we have identified NR0B1 sequence variants in 4 AHC/HH pedigrees. Three are novel, and 2 represent the first NR0B1 variants reported in patients of Arabic ethnic origin. The necessity for clinical suspicion and rapid diagnosis of AHC to avoid familial instances of multiple male neonatal or infant deaths is illustrated by pedigrees 1 and 3 (fig. 1, 3). We have described in patient 4-II:1 a novel splice donor site variant in NR0B1 that abrogated cognate splicing of testicular mRNA. Patient 4-II:1 had clinical features consistent with an incomplete FSH deficiency with some retention of hypothalamic-pituitary signalling, insufficient to spontaneously induce/maintain puberty, but consistent with the observed growth of the testes on HCG treatment and the histological evidence of spermatocytic differentiation, although no mature spermatida were observed. For patient 4-II:1 with the c.1168+1G>A variant, testicular biopsy showed neither malignant germ cell tumour, nor its precursor lesion, CIS. These studies add to knowledge of the types and ethnic diversity of NR0B1 sequence variants and their associated phenotypes, and provide insight into the assessment and interpretation of testicular histology in AHC and HH.

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