Ten Novel Mutations in the NR5A1 Gene Cause Disordered Sex Development in 46,XY and Ovarian Insufficiency in 46,XX Individuals


Context: Steroidogenic factor-1 (SF-1/NR5A1) is a nuclear receptor that regulates adrenal and reproductive development and function. NR5A1 mutations have been detected in 46,XY individuals with disorders of sexual development (DSD) but apparently normal adrenal function and in 46,XX women with normal sexual development yet primary ovarian insufficiency (POI).

Objective: A group of 100 46,XY DSD and two POI was studied for NR5A1 mutations and their impact.

Design: Clinical, biochemical, histological, genetic, and functional characteristics of the patients with NR5A1 mutations are reported.

Setting: Patients were referred from different centers in Spain, Switzerland, and Turkey. Histological and genetic studies were performed in Barcelona, Spain. In vitro studies were performed in Bern, Switzerland.

Patients: A total of 65 Spanish and 35 Turkish patients with 46,XY DSD and two Swiss 46,XX patients with POI were investigated.

Main Outcome: Ten novel heterozygote NR5A1 mutations were detected and characterized (five missense, one nonsense, three frameshift mutations, and one duplication).

Results: The novel NR5A1 mutations were tested in vitro by promoter transactivation assays showing grossly reduced activity for mutations in the DNA binding domain and variably reduced activity for other mutations. Dominant negative effect of the mutations was excluded. We found high variability and thus no apparent genotype-structure-function-phenotype correlation. Histological studies of testes revealed vacuolization of Leydig cells due to fat accumulation.

Conclusions: SF-1/NR5A1 mutations are frequently found in 46,XY DSD individuals (9%) and manifest with a broad phenotype. Testes histology is characteristic for fat accumulation and degeneration over time, similar to findings observed in patients with lipoid congenital adrenal hyperplasia (due to StAR mutations). Genotype-structure-function-phenotype correlation remains elusive. (J Clin Endocrinol Metab 97: E1294–E1306, 2012)
Effects remain to be elucidated (2). The human SF-1 protein consists of 461 amino acids and is encoded by the \( \text{NR5A1} \) gene (3). It is expressed in the fetal and adult adrenal cortex as well as in fetal and adult testes and ovaries (2).

Human \( \text{NR5A1} \) mutations were first described in 46,XY individuals with combined adrenal failure and disorders of sexual development (DSD) (4, 5). To date, only one case with apparently isolated primary adrenal failure has been reported in a 2-yr-old 46,XX girl (6). By contrast, many \( \text{NR5A1} \) mutations have been found in a large number of 46,XY DSD individuals with apparently normal adrenal function (7–16), as well as in several 46,XX individuals with normal female sexual development but premature ovarian failure (17, 18). Some cases were familial (5, 10–12, 17–20), and some were sporadic (12, 17). Besides the aforementioned phenotypes, \( \text{NR5A1} \) mutations are associated with a very wide range of phenotypes related to reproductive function and development (21), such as hypospadias (13, 22), anorchia (10), isolated micropenis (23), male infertility (24), and primary ovarian insufficiency (POI) (2, 10, 17, 18, 21).

Since the first description of \( \text{NR5A1} \) mutations in 1999 (4), over 50 mutations have been reported. Most subjects carry mutations in a heterozygote state (4, 6, 7, 9, 10, 12–18, 20, 22–26), some are compound heterozygous (8, 11, 12, 17, 24), and only a few are homozygous (5, 27). Although many patients with \( \text{NR5A1} \) mutations have been studied extensively, no clear genotype-phenotype and SF-1 protein structure-function correlation has been found. The search for modulating factors explaining the broad range of clinical manifestations of \( \text{NR5A1} \) mutations continues.

In this study, 10 novel \( \text{NR5A1} \) mutations are described. Nine mutations were identified in 46,XY DSD patients and one in a 46,XX POI patient. Clinical, biochemical, histological, and genetic data of the patients are presented. Functional studies and protein structure analyses of the novel \( \text{NR5A1} \) mutations were performed to study phenotype-genotype correlations.

### Patients and Methods

#### Patients and ethical approval

A total of 102 patients of Spanish, Turkish, and Swiss origin were analyzed for mutations in the \( \text{NR5A1} \) gene. The 65 Spanish

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Origin, YOB</th>
<th>Karyotype/assigned sex</th>
<th>Genital anatomy</th>
<th>Testes histology (age)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Spanish, 2008</td>
<td>46,XY/male</td>
<td>Scrotal hypospadia. Bilateral cryptorchidism. No Müllerian ducts</td>
<td>ND</td>
</tr>
<tr>
<td>2</td>
<td>Spanish, 1981</td>
<td>47,XY/female</td>
<td>Female external genitalia. Bilateral inguinal hernia. No Müllerian ducts</td>
<td>Abnormal (3.5 yr), Fig. 3A</td>
</tr>
<tr>
<td>3</td>
<td>Spanish, 1971</td>
<td>46,XY/female to male at 18 yr</td>
<td>Ambiguous external genitalia at birth. Progressive virilization at puberty with nonpalpable gonads. No Müllerian ducts</td>
<td>Cryptorchidic, dygenetic testes (19 yr)</td>
</tr>
<tr>
<td>4</td>
<td>Turkish, 1997</td>
<td>46,XY/female</td>
<td>Ambiguous external genitalia. Bilateral inguinal hernia. No Müllerian ducts</td>
<td>Seminiferous tubules devoid of spermatogonia</td>
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<td>Spanish, 1998</td>
<td>46,XY/female</td>
<td>Female external genitalia. Bilateral inguinal hernia. No Müllerian ducts</td>
<td>No histology upon gonadectomy (1 yr)</td>
</tr>
<tr>
<td>7</td>
<td>Spanish, 2003</td>
<td>46,XY/female</td>
<td>Female external genitalia. Gonads in labia majora. No Müllerian ducts</td>
<td>Abnormal (2 yr), Fig. 3, B and C</td>
</tr>
<tr>
<td>8</td>
<td>Spanish, 2003</td>
<td>46,XY/female to male at 8 months</td>
<td>Ambiguous genitalia (Prader 3). Palpable gonads. No Müllerian ducts</td>
<td>Abnormal (2 yr), Fig. 3D</td>
</tr>
<tr>
<td>9</td>
<td>Swiss, 1994</td>
<td>46,XX/female</td>
<td>Normal female at birth. Pelvic US (16 yr), prepubertal uterus, nondetectable ovaries</td>
<td>ND</td>
</tr>
<tr>
<td>10</td>
<td>Turkish, 2009</td>
<td>46,XY/male</td>
<td>Ambiguous genitalia (Prader 3). Palpable gonads. No Müllerian ducts</td>
<td>ND</td>
</tr>
</tbody>
</table>

| YOB, Year of birth; F, father; M, mother; (N), normal sequence; SRDS2A, 5a-reductase type 2 gene; LHCGR, LH receptor gene; CYP17A1, cytochrome P450 17a-hydroxylase/17,20-lyase gene; US, ultrasound; ND, not done; T, testosterone; E2, estradiol; AMH, anti-Müllerian hormone.

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patients included 61 subjects with 46,XY DSD, one with 47,XY,Y DSD, and three 46,XY patients with anorchia. AR (androgen receptor) and SRD5A2 (5α-reductase type 2) genes had been previously analyzed in these patients and were normal in all except one carrying the P378R AR mutation (28). In some, the CYP17A1, HSD17B3, and LHCGR genes were analyzed for mutations, but none were found (Table 1). Similarly, a group of 35 Turkish patients with 46,XY DSD and two Swiss POI 46,XX patients were evaluated. AR and SRD5A2 genes were analyzed in all 35 Turkish patients, but no mutations were detected. The Swiss patients were only analyzed for NR5A1 mutations.

All studied subjects and/or their legal guardians gave written informed consent for the biochemical and molecular studies, which were approved by the respective ethical committees of the three study centers.

**Genetic analyses**

Genetic analyses of the NR5A1 gene were performed as explained in Supplemental Data and Supplemental Table 1 (published on The Endocrine Society’s Journals Online web site at http://jcem.endojournals.org).

**In vitro functional studies**

In vitro functional studies were performed in human steroidogenic NCI-H295R and nonsteroidogenic HEK293 cells (see Supplemental Data and Supplemental Table 1).

**In silico protein structure analysis**

For bioinformatic studies, the mouse SF-1 DNA binding domain (DBD) NMR structure (PDB no. 2F09; N terminus, AA 10-111, 100% similar to human SF-1) and human SF-1 ligand binding domain (LBD) x-ray crystal structure (PDB no. 1ZDT; C terminus, AA 221-461) were used (see Supplemental Data).

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### TABLE 1. Continued

<table>
<thead>
<tr>
<th>Gonadal function (age)</th>
<th>Adrenal function (age)</th>
<th>NR5A1 gene mutation</th>
<th>Family</th>
<th>Previous genetic studies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal baseline (1 d and 1 yr)</td>
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<td>c.58G&gt;T; Val20Leu</td>
<td>F = carrier, M = WT</td>
<td>AR (N), SRD5A2 (N)</td>
</tr>
<tr>
<td>Abnormal (T slightly decreased and normal precursor response to hCG) (3 yr)</td>
<td>Normal baseline (30 yr)</td>
<td>c.70C&gt;T; H62Y</td>
<td>Brother and sister = WT</td>
<td>AR (N), SRD5A2 (N)</td>
</tr>
<tr>
<td>Abnormal (normal T and precursors, high LH and FSH) (18 yr)</td>
<td>Normal baseline (18 yr)</td>
<td>c.70delC; His24ThrfsX51</td>
<td>Sister = carrier (infertility). (History of early menopause in M and of ambiguous genitalia in maternal great aunt)</td>
<td>Patient AR (N), SRD5A2 (N). Patient and sister, LHCGR (c.51_52insTGACG polymorphism)</td>
</tr>
<tr>
<td>Abnormal (no T response to hCG) (1 yr)</td>
<td>ND</td>
<td>c.90T&gt;G; Cys30Trp</td>
<td>M = carrier. (History of ambiguous genitalia in maternal great uncle and of early menopause in M and grandmother)</td>
<td>AR (N), SRD5A2 (N)</td>
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<tr>
<td>Abnormal (low T and normal precursor response to hCG) (7 months)</td>
<td>ND</td>
<td>c.389delC; Pro130ArgX165</td>
<td>F = WT, M = WT</td>
<td>AR (N), SRD5A2 (N)</td>
</tr>
<tr>
<td>Abnormal (no T response to hCG) (14 d)</td>
<td>Abnormal? (slightly increased ACTH and decreased precursor response to Synacthen) (6 yr)</td>
<td>c.614_615insC; Gln206ThrfsX20</td>
<td>F = WT, M = WT</td>
<td>AR (N), CYP17A1 (N)</td>
</tr>
<tr>
<td>Abnormal (no T response to hCG) (1 month)</td>
<td>ND</td>
<td>c.690_691insC; Gln206ThrfsX20</td>
<td>F = WT, M = WT</td>
<td>AR (N), SRD5A2 (N)</td>
</tr>
<tr>
<td>Abnormal (increased LH and FSH and undetectable E2 and AMH) (15 yr)</td>
<td>Normal (15 yr)</td>
<td>c.704C&gt;T; Pro235Leu</td>
<td></td>
<td>AR (N), SRD5A2 (N)</td>
</tr>
<tr>
<td>Normal baseline (2 months)</td>
<td>ND</td>
<td>c.905G&gt;; A; Trp302Stop</td>
<td></td>
<td>AR (N), SRD5A2 (N)</td>
</tr>
</tbody>
</table>

**Results**

**Identification of 10 novel NR5A1 gene mutations in patients presenting with 46,XY DSD or 46,XX POI**

We found 10 novel, disease-causing mutations in the NR5A1 gene in a combined group of 102 patients presenting with 46,XY DSD (eight of 99; 8%), 47,XY,Y DSD (one of one), or 46,XX POI (one of two). All details of the patients’ characteristics are summarized in Table 1, and individual case reports are available as Supplemental Data.

Six of nine 46,XY subjects harboring NR5A1 mutations presented with ambiguous genitalia at birth and were assigned either male (two of six) or female (four of six) sex of rearing. Patients 3 and 8, who were initially assigned to female sex, were assigned to male sex at age 18 yr and 8 months. Three 46,XY subjects presented with normal external female genitalia but were noted to have either inguinal hernia at the age of 2–3 yr or palpable gonads in labia majora at age 2 wk. Gonadal function was tested in nine subjects and found to be abnormal in seven of the 46,X(Y)Y. Six subjects were gonadectomized at ages 2–19 yr, and a testis biopsy was performed in one aged 4 yr. The single 46,XX female patient presented with absent pubertal signs at age 15 yr due to POI/hypergonadotropic hypogonadism. None of the patients had a history of adrenal insufficiency, but adrenal function was only evaluated in six patients, suggesting normal function in five (using vari-
able assessments, e.g. basal or stimulated tests) and minor abnormalities such as slightly increased ACTH and decreased cortisol precursor secretion in subject 7. Family history and/or genetic testing of relatives revealed other affected family members in at least two subjects (one healthy 46,XY carrier excluded), but it was only available from six families.

The 10 novel mutations in the NR5A1 gene were scattered throughout exons 2 to 5 (Figs. 1 and 2). Nine mutations were single nucleotide changes that led to six point mutations (five missense and one nonsense) and three frameshift mutations (two deletions and one insertion). A duplication of nine nucleotides (in-frame) was also detected, leading to an insertion of three amino acids and a prolongation of the protein sequence.

Three mutations were found in other family members (cases 1, 3, and 5), whereas the mutations Pro130ArgfsX165 and Leu231-Leu233dup appeared to be de novo mutations.

FIG. 1. Diagram of the NR5A1 gene and chromatograms of the 10 novel mutations. The mutations identified in patients and their exact location in the NR5A1 gene sequence are shown. In the NR5A1 gene diagram, numbers refer to exons 1 to 7 and noncoding sequences are shown in gray.
in patients 6 and 8 because both of their parents were non-carriers (Table 1).

In addition, the polymorphism Gly146Ala (c.437G>C) (rs1110061) was identified in seven of 102 (6.8%) 46,XY DSD subjects (Table 2). Six were heterozygous, whereas one was homozygous (subject 17). Subject 17 also carried two other sequence variations: Pro125Pro (rs1110062) in the NR5A1 gene, and Pro378Arg in the AR gene (28).

Histopathology findings of testes in patients with heterozygote NR5A1 mutations

Testis tissue for histopathological studies was available from five patients aged 2 to 4 yr (patients 2, 4, 6, 7, and 8; Fig. 3 and Table 1). Gonadal function in those subjects appeared to be abnormal (Table 1). Tissue sections were compared with normal control tissue and testis tissue originating from a patient with lipid congenital adrenal hyperplasia owing to StAR mutations (Fig. 3). Morphology of testis tissues obtained before puberty from patients harboring heterozygote NR5A1 mutations revealed diminished tubular diameter and absent or decreased spermatogonia. Interstitial tissue was remarkable for cell nests with vacuolized, xanthomatous, or adipoblast-like Leydig cells (Fig. 3, A, B, and D). Osmium staining revealed osmium-positive lipid deposits (Fig. 3C), not present in control testis (Fig. 3F), and which resembled the Leydig cells typically observed in prepubertal testes of patients with lipid congenital adrenal hyperplasia (Fig. 3E).

In vitro functional studies of the novel NR5A1 mutations

Functional activity was tested by studying transactivation of wild-type (WT) and mutant NR5A1 on promoters of genes for steroidogenic enzymes regulated by SF-1 in steroidogenic and nonsteroidogenic cell models (Fig. 4).

Transfection of human adrenal NCI-H295R cells with WT and NR5A1 mutants together with a CYP17A1 promoter reporter construct revealed that all 10 NR5A1 mutations had impaired ability to stimulate the CYP17A1 promoter (Fig. 4A). Among the 10 mutants, Pro235Leu (identified in a 46,XX POI patient; Table 1) was most active, having 80% of WT activity. Overall, mutations located in the DBD (cases 1–5) appeared to be functionally less active than mutations in the LBD (cases 8–10). Studies of SF-1 transactivating the CYP11A1 and HSD3B2 promoters were not possible in NCI-H295R cells because background activity of endogenous SF-1 was too high and promoter stimulation using WT overexpression too low (data not shown). Therefore, we performed further studies in nonsteroidogenic HEK293 cells, which do not express SF-1. Similar to NCI-H295R cells, all 10 NR5A1 mutations had impaired activity on the CYP17A1 promoter (Fig. 4B). Again, the Pro235Leu mutant displayed highest activity (80% of WT), and mutations in the LBD seemed slightly more active than mutations in the DBD.
However, studies of SF-1 activating the CYP11A1 and HSD3B2 promoters in HEK293 cells confirmed these results only partially (Fig. 4, C and D). NR5A1 mutations located in the DBD (1–4) showed a profound loss of CYP11A1 and HSD3B2 promoter stimulation similar to the CYP17A1 promoter. But in contrast to the CYP17A1 promoter, all NR5A1 mutants located in the LBD (8–10) had either unchanged activity in stimulating the CYP11A1 or HSD3B2 promoters or even higher activity (Trp302X had either unchanged activity in stimulating the CYP11A1 promoter). But in contrast to the CYP17A1 promoter, all NR5A1 mutants located in the LBD (8–10) had either unchanged activity in stimulating the CYP11A1 or HSD3B2 promoters or even higher activity (Trp302X had either unchanged activity in stimulating the CYP11A1 promoter). But in contrast to the CYP17A1 promoter, all NR5A1 mutants located in the LBD (8–10) had either unchanged activity in stimulating the CYP11A1 or HSD3B2 promoters or even higher activity (Trp302X had either unchanged activity in stimulating the CYP11A1 promoter).

Because all our patients harbor heterozygote NR5A1 mutations, the dominant negative effect of mutants over the WT NR5A1 was assessed in our cell model. Similar to other investigators testing various NR5A1 mutations (6–8, 11, 12, 14, 20, 29), our reporter assays did not reveal a dominant negative effect for any mutant (Fig. 4E). Thus, the mechanism of heterozygote NR5A1 mutations causing the phenotype of DSD in our patients remains a conundrum. To assess the expression of NR5A1 variants in our cell model, we performed Western blots (Fig. 4F). These studies showed that transiently transfected cells expressed all WT and mutant SF-1 proteins. Only His24ThrfxX51 seemed to be too small to be detected on our blot. On our Western blots, no significant differences were seen in protein expression of mutant SF-1 when compared with WT. Yet, some mutants rather showed a higher level of expression (Gly90Arg, Pro235Leu).

Studies of the Gly146Ala variant on promoter activity of CYP17A1 in HEK293 cells revealed no effect overall and also no dominant negative effect in particular (Supplemental Fig. 1).

In silico protein structure analysis

Human SF-1 protein has two distinctive domains. The DBD contains a core with two Cys4-zinc-finger motifs and a highly conserved Ftz-F1 box that includes a highly conserved RGGR motif potentially involved in interaction with DNA. Mutants Val20Leu, His24Tyr, and Cys30Trp are present in the DBD core, and Gly90Arg is located in the RGGR motif of the Ftz-F1 box (Fig. 5A). The Pro235 and Leu-Gln-Leu repeats are located at the N terminus of the LBD (Fig. 5B).

In the three-dimensional structure, the four DBD mutations are located in a critical hotspot that comprises the C terminus of the DNA-recognition helix, the β-hairpin loop, and the RGGR motif in the loop before the critical C-terminus helix of DBD required for stability of the SF-1/DNA complex (Fig. 5A). All these mutations are in the region that directly interacts with DNA and may alter the pattern/recognition of specific DNA sequences. A change from Val20 to Leu causes alterations in the side chain packing environment of the N-terminal loop due to interaction of altered Leu20 with Asp10 and Glu11 (Fig. 5C). This may slightly alter the DBD structure and influence the interaction with DNA molecule. However, a major conformational change that could have a major influence on DNA binding was not expected. The His24 residue is crucial for DNA binding, and its substitution with Tyr shifts the Tyr side chain away from the DNA binding site, breaking the hydrogen bond (Fig. 5D). The Cys30 residue is essential for zinc binding and stability of the core DBD. In silico mutagenesis and molecular dynamics simulations were used to change the Cys30 to Trp, and resulting structure shows the disruption of a Cys-zinc contact resulting in an unstable core structure (Fig. 5E). The mutation Gly90Arg is located in the RGGR motif formed by R89R92 in human SF-1 (in the loop before the C-terminus helix in Ftz-F1 box). The mutation of Gly90 to Arg results in a major change at the DNA binding site due to the large positively charged Arg side chain (Fig. 5F). The change from Gly to Arg will alter the binding pattern and may have variable effects depending on sequence of DNA interaction partner. Additional interactions with DNA will be created due to Arg side chain at the binding site that may change binding selectivity and result in activation of dif-

### TABLE 2. Clinical, biochemical, and anatomic characteristics of seven 46,XY DSD patients harboring the Gly146Ala NR5A1 sequence variation

<table>
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<tr>
<th>Patient no.</th>
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</tr>
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<tbody>
<tr>
<td>11</td>
<td>Spanish, 1996</td>
<td>46,XY/female to male (1 yr)</td>
<td>Scrotal hypospadias. Bilateral cryptorchidism. No Müllerian ducts</td>
<td>ND</td>
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<tr>
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<td>13</td>
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<tr>
<td>14</td>
<td>Turkish, 2002</td>
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<td>Scrotal hypospadias. Bilateral palpable gonads</td>
<td>ND</td>
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<tr>
<td>15</td>
<td>Turkish, 2005</td>
<td>46,XY/male</td>
<td>Scrotal hypospadias. Bilateral palpable gonads</td>
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YOB, Year of birth; (N), normal sequence; SRD5A2, 5α-reductase type 2 gene; AMH, anti-Müllerian hormone gene; AMHRII, AMH receptor type 2; ND, not done; T, testosterone.
different promoters and may have variable effects on individual promoters.

The Pro235 separates the two N-terminus helices of the LBD of SF-1 (Fig. 5G). The mutation Pro235Leu may abolish the break in between two helices and creates a larger single helix. Such a change will not result in the alteration of the core structure but may cause subtle changes in the neighboring residues near the ligand binding site. A likely effect would be modification of ligand binding and recognition and may have variable effects depending on specific ligands. The dual repeat units of Leu-Gln-Leu located at the N terminus of LBD form the N-terminal helix. The insertion of another Leu-Gln-Leu repeat unit changes the composition of this helix and results in a longer loop structure located in between the two N-terminal helices (Fig. 5H). The addition of extra Leu side chain from Leu-Gln-Leu insertion creates changes in the environment of neighboring residues to accommodate the extra Leu side chain pointing toward the core of the LBD. The specific effect of such a change is unpredictable, and a variable effect depending on specific ligand is expected. Both the Pro235Leu and Leu-Gln-Leu insertion do not appear to alter the ligand-binding properties, and their effects may therefore be related to relatively minor changes caused by altered flexibility of the two N-terminal helixes.

**Discussion**

We found 10 new mutations in the NR5A1 gene in 102 patients studied for either 46,XY DSD or 46,XX POI (9.8%). These mutations were all heterozygous and were predominantly single-nucleotide changes. Individuals with heterozygous NR5A1 mutations present with a broad range of phenotypes covering completely normal phenotype to severe forms of 46,XY DSD or POI in 46,XX subjects (2, 16, 17, 21, 24). Even identical mutations within families may lead to differing phenotypes (10, 17–19). Similarly, our patients presented with a wide clinical spectrum. External genitalia in 46,XY individuals varied from completely female to ambiguous with cryptorchid testes; none presented with Müllerian duct remnants. Gonadal steroid production studied at prepubertal age ranged from apparent lack of testosterone secretion to only slightly diminished testosterone response upon human chorionic gonadotropin (hCG) stimulation with normal steroid precursors. Only one patient developed spontaneous puberty and reached a normal male adult serum testosterone level but had grossly elevated gonadotropin levels. Adrenal function appeared to be normal in most patients but was not assessed in all. However, adrenal function should be followed in patients with NR5A1 mutations because adrenal insufficiency has been described with NR5A1 mutations and may only develop over time.

Family history of two patients (cases 3 and 5) revealed ambiguous genitalia and premature menopause in several relatives, of whom some were also found to have heterozygous NR5A1 mutations. By contrast, the father of a moderately affected 46,XY DSD patient (case 1) was phenotypically normal but was a carrier of Val20Leu. Similarly, normal carriers with heterozygous NR5A1 mutations have been reported (10, 16, 22). Arg281Pro located in the LBD was found in a 46,XY DSD patient who had hypospadias and microopenis and a phenotypically normal carrier father (16). Val335Met was detected in a boy with micropenis and testicular regression syndrome and a normal carrier brother (10). Thus, the wide range of phenotypes of individuals with mutations in the NR5A1 gene includes normal sexual development, or at least normal enough to guarantee fertility.

Overall, we analyzed testis tissue of five heterozygous NR5A1 patients (Table 1 and Fig. 3) and found similar alterations as seen in patients with mutations in the steroidogenic acute regulatory protein (StAR). StAR mediates cholesterol transfer into the mitochondrion toward the P450ssc enzyme cleavage system (30, 31). Therefore,
FIG. 3. Histology findings of testes of patients 2, 7, and 8 with heterozygous NR5A1 mutations. A, Hematoxylin eosin stain (HE) Image originates from patient 2 (47,XYY DSD) at the age of 3.5 yr and shows interstitial tissue (between two seminiferous tubules) with some Leydig cells (one is circled) with cytoplasmic vacuoles (arrow). B and C, Images belong to patient 7 (46,XY DSD) at the age of 2 yr. B, Trichrome stain image shows interstitium surrounded by different seminiferous tubules. In these tubules, with a thin tunica propria, there are predominantly Sertoli cells but no spermatogonia; only a few nests of xanthomized Leydig cells (arrow) can be seen in the interstitium. C, Osmium staining reveals that the cytoplasmic vacuoles of Leydig cells contain lipids (dark brown staining indicates osmium deposits). D, Image originates from patient 8 (46,XY DSD) at the age of 2 yr and shows seminiferous tubules full of pre-Sertoli cells but without germ cells. As in patient 7, the interstitium contains some nests of Leydig cells (circled) with a xanthomatous appearance. None of these structures can be seen in normal testes. E, Image depicts testis histology (HE) of a patient with STAR mutations at age 3 yr showing similar histological findings as seen in our NR5A1 patients. F, Image corresponds to an osmium histochemical staining of normal testis tissue originating from a 2-yr-old subject without any positivity in Leydig cell cytoplasm (circle).

Relatively preserved testicular architecture progresses to dysgenesis in babies and to replacement with connective tissue causing loss of seminiferous tubules and leading to absence of gonadal tissue in adults. Regarding the cellular profile, children of young ages up to puberty have rare germ cells (9, 11, 14, 17, 20, 22, 26) and nests of (vacuolated) Leydig cells (11, 14, 17–20, 26). 46,XY DSD patients carrying heterozygous SF-1 mutations (with undervirilization and diminished fertility index) demonstrate that testosterone secretion is variably affected in fetal life and may progress, probably due to interstitial cell degeneration, similar to what occurs in patients with StAR mutations. Similarly, but at puberty or even later, 46,XX carrier females present with ovarian insufficiency (10, 17, 18). Because this process appears to affect steroidogenesis of only the gonads and not the adrenals, the evolution appears reverse to nonclassic congenital lipid adrenal hyperplasia due to mild StAR mutations, where gonadal function may be preserved into adulthood whereas adrenal insufficiency usually manifests at a young age (32, 33).

The 10 novel NR5A1 mutations described in this paper are located in exons 2 to 5 (Figs. 1 and 2). Generally, mutations in the DBD region that is crucial for transcription factor binding to promoters (2) are more severe. The first four mutations (Val20Leu, His24Tyr, His24ThrfsX51, and Cys30Trp) are located in the first zinc-finger domain of the DBD but not in the P box. Thus, they are involved in the binding of the major groove of DNA but not in the specific recognition of the DNA target sequence (hormone response element) (2). His24ThrfsX51 will result in a truncated protein with total loss of function. Gly90Arg is located in the Ftz-F1 box, which is considered a stabilizing region for the binding of SF-1 to DNA (2, 34, 35). Pro130ArgfsX165 and Gln206ThrfsX20 in the hinge region result in a truncated protein with no LBD, which will lead to an inactive SF-1. The remaining mutations (Leu231_233dup, Pro235Leu, and Trp302Stop) are located in the LBD. This region modulates SF-1 activity owing to its C-terminal AF-2 domain, which binds phospholipid ligands (2, 20, 36, 37) and other cofactors (2). Thus, mutations in the DBD are expected to lead to markedly affected transactivation assays, whereas LBD mutations may have varying effects depending on their location and alterations in the ligand specificity/recognition.

severe StAR deficiency causes intracellular accumulation of lipids and disrupts steroidogenesis. Leydig cells of patients with SF-1 mutations may also be defective in the conversion of cholesterol to pregnenolone (mediated by CYP11A1/P450ssc). In addition, SF-1 deficiency affects further enzymes of steroidogenesis. Thus, similar mechanisms may cause vacuolization of Leydig cells due to accumulation of lipid droplets not processed by steroidogenesis. In our tissue samples, osmium staining confirmed this for the first time, although other reports have presented histological data for testis of subjects with NR5A1 mutations without describing lipid accumulation (4, 7–11, 14, 17–20, 22, 24, 26).

Overall, data suggest a progressive degeneration of the testicular tissue in individuals with mutations in NR5A1.
FIG. 4. Functional and expression studies of the 10 novel NR5A1 mutations. A–D, The ability of WT and mutant NR5A1 to activate steroidogenic enzyme promoter luciferase reporter constructs was tested in adrenal NCI-H295R cells (A) and nonsteroidogenic HEK293 cells (B–D). A–C, Cells were transiently transfected with NR5A1 expression vectors and CYP17A1 (A and B), CYP11A1 (C), and HSD3B2 (D) promoter reporter constructs. E, Similarly, the impact of the mutants on the activity of the WT SF-1 was checked by transfecting the 10 different mutants with or without WT NR5A1 expression vector together with the CYP17A1 promoter reporter construct in HEK293 cells. No dominant negative effect was observed. A–E, Luciferase activity was measured with the Promega Dual Luciferase assay system. Results are expressed as percentage of WT activity, which was set at 100% RLU, and represent the mean and SEM of two to four independent experiments performed in duplicate. F, Western blot showing expression of WT and mutant SF-1 proteins. Hemagglutinin-tagged SF-1 was recognized by HA antibody in the Western blot (band at 53 kDa). B-actin was used as a control. Note that His24ThrfsX51 was not detected for its small weight/size. *, P < 0.05; **, P < 0.01; ***, P < 0.001; #, p.Pro235Leu is statistically different from all other mutants (P < 0.001); °, Numbers indicate average fold increase of WT over Ve. RLU, relative light units; Ve, empty vector control; HA, hemagglutinin.
In vitro promoter transactivation assays have been used previously to assess the functional impact of sequence variations (4, 6). Therefore, we tested the 10 novel SF-1 variants for their ability to transactivate different promoters of steroidogenic enzymes in steroidogenic adrenal NCI-H295R and nonsteroidogenic human embryonic kidney HEK293 cells. We found that SF-1 mutations in the DBD consistently showed impaired transactivation activ-
ity when studied on different promoters and in different cell systems. By contrast, promoter studies of mutations located outside the DBD showed a more variable picture with different promoters or cell systems. For NR5A1, Pro235Leu minor changes in activity were found leaving the question open whether this mutation may be disease causing. The observation that functional tests correlate poorly with phenotype was also made by several other investigators (6, 7, 10, 20, 38) indicating that results from these studies may be of limited value and that testing of several promoters in different cell systems may be necessary to assess the functional impact of NR5A1 sequence variations. Because most patients harbor heterozygote NR5A1 mutations, dominant negative effect may be considered and was therefore tested. However, we and others (6–8, 11, 12, 14, 20, 29) did not find experimental confirmation for such a mechanism of mutant SF-1 over WT protein in cell models. In vitro protein structure studies have not been able to give a clear picture on the structure-function correlation of sequence variations in LBD.

In addition to the diversity of NR5A1 mutations in the in vitro studies, phenotype variability of NR5A1 mutations in patients make a genotype-phenotype correlation (so far) impossible. Because SF-1 is a transcription factor, (co-)modulators may play a pivotal role, and their number may have been underestimated in the past. In a recent publication, ChIP-on-chip analysis revealed a large number of new SF-1 targets that are currently under further investigation (39). Thus, the conundrum of variability in SF-1 mutations may be explained by additional variations in cofactors.

In our group of 46,XY DSD patients, we found the NR5A1 polymorphism Gly146Ala (rs1110061) in 6.8% (Table 2). It has been detected in other 46,XY DSD patients (8, 11, 12) and 46,XX subjects with sporadic POI (17). Its allele frequency varies depending on the control population studied (http://www.ncbi.nlm.nih.gov/) and occurs frequently in Japanese patients with adrenal disorders (40). It has been associated with micropenis (23, 41) and cryptorchidism (42). Gly146Ala leaves SF-1 transactivation activity unaltered (Supplemental Fig. 1) and does not affect cofactor interaction and cellular localization (11, 40). Therefore, it has been considered a polymorphism only. However, after finding this polymorphism in so many 46,XY DSD subjects, and knowing that in vitro functional tests are poor predictors, its causal role remains elusive.

In conclusion, the detection of 10 novel NR5A1 mutations in nine of 100 46,XY DSD patients and in one of two 46,XX patients with ovarian insufficiency highlights the crucial role of SF-1 in sexual development and function. Clinical and biochemical phenotypes of these 46,XY DSD patients are variable and genotype-phenotype correlation remains elusive. Although functional studies help in defining the impact of NR5A1 sequence variations, results differ depending on the in vitro systems employed. Overall the SF-1 system is very complex and appears to involve as yet unknown modulators, whereas dominant negative effects may be excluded.

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References


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