Testicular differentiation factor SF-1 is required for human spleen development

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The transcription factor steroidogenic factor 1 (SF-1; also known as NR5A1) is a crucial mediator of both steroidogenic and nonsteroidogenic tissue differentiation. Mutations within SF1 underlie different disorders of sexual development (DSD), including sex reversal, spermatogenic failure, ovarian insufficiency, and adrenocortical deficiency. Here, we identified a recessive mutation within SF1 that resulted in a substitution of arginine to glutamine at codon 103 (R103Q) in a child with both severe 46,XY-DSD and asplenia. The R103Q mutation decreased SF-1 transactivation of TLX1, a transcription factor that has been shown to be essential for murine spleen development. Additionally, the SF1 R103Q mutation impaired activation of steroidogenic genes, without affecting synergistic SF-1 and sex-determining region Y (SRY) coactivation of the testis development gene SOX9. Together, our data provide evidence that SF-1 is required for spleen development in humans via transactivation of TLX1 and that mutations that only impair steroidogenesis, without altering the SF1/SRY transactivation of SOX9, can lead to 46,XY-DSD.

Introduction
Steroidogenic factor 1 (SF-1; also known as NR5A1) is a transcription factor involved in steroidogenesis, reproduction, and sexual differentiation (1). In mice, it is expressed in all primary steroidogenic tissues and in the embryonic urogenital ridge. SF-1 participates with sex-determining region Y (SRY) and SOX-9 in mammalian sex determination and regulates Müllerian-inhibiting substance (AMH) (2, 3).

SF1 mutations lead to several phenotypes, including disorders of sexual development (DSD) with sex reversal, spermatogenic failure, ovarian insufficiency, and adrenocortical deficiency (1) (OMIM 184757). The only 2 recessive SF1 mutations described to date, D293N and R92Q (4, 5), caused severe 46,XY-DSD as well as adrenal failure in the R92Q homozygote. Here, we report a novel homozygous SF1 mutation, R103Q, presenting with 46,XY complete sex reversal and asplenia, but without AI. This mutation impaired SF-1 activation of the spleen development gene TLX1. It also impaired activation of steroid synthesis, but did not affect synergistic SF-1 and SRY activation of SOX9, a gene considered to be crucial for testicular differentiation.

Results and Discussion
Clinical features and laboratory studies. A 13.5-year-old girl of consanguineous Palestinian parents presented with abdominal pain ultimately ascribed to fecal impaction. History was notable only for delayed puberty and pneumococcal sepsis at 9 months of age. Ultrasound and CT imaging revealed asplenia, bilateral inguinal tests, and absence of the uterus, ovaries, and fallopian tubes (Figure 1, A and B). Peripheral blood smear revealed typical asplenia-associated Howell Jolly bodies and poikilocytosis (Figure 1C). Karyotype was 46,XY. Blood tests showed normal electrolytes, aldosterone, basal and adrenocorticotropic hormone–stimulated (ACTH-stimulated) cortisol, and 17-hydroxylyase–progesterone. Dehydroepiandrosterone, androstenedione, and testosterone levels remained low to undetectable despite ACTH stimulation, while ACTH levels were slightly elevated (Supplemental Table 1; supplemental material available online with this article; doi:10.1172/JCI73186DS1). Estrogen and progesterone levels were prepubertal. These results excluded a precursory major defect in steroid biosynthesis. 17-hydroxylyase deficiency was thought to be an unlikely cause for the phenotype, given the patient’s normal serum electrolytes and normal blood pressure at 13.5 years of age. The severe sex reversal (46,XY-DSD) was therefore postulated to result from a genetic defect affecting testicular differentiation and gonadal function. The patient was reared as a female, given lack of male genitalia, and her gonads were surgically removed and studied for premalignant changes. Gonadal histopathology revealed normal and abundant Sertoli cells, few Leydig cells (consistent with low serum testosterone levels), absence of germinal or pregerminall cells, absence of staining for premalignant markers (e.g., placental-like alkaline phosphatase [PLAP]), and positive inhibin and SOX-9 staining in Sertoli cells (Figure 1, D–F).

Genetic analysis. Analysis for XY-DSD included testing for SRY (by PCR) and sequencing of STAR and SF1 as candidates for nonclassic steroidogenic failure or gonadal dysgenesis. SRY was present, and no mutations were identified in STAR, consistent with the patient’s normal mineralocorticoid and glucocorticoid levels (Supplemental Table 1). However, in SF1, we identified a homozygous G-to-A transition (c.308G>A) resulting in a substitution of arginine to glutamine at codon 103 (p.R103Q). Both parents and all 5 unaffected brothers of the patient were heterozygous for this mutation (Figure 2, A–C), which was not detected in 190 ethnically matched controls (Supplemental Figure 1). This novel amino acid substitution, the
third recessive SF1 mutation reported to date, results in loss of posi-
tive charge in the otherwise basic sub-domain of the cross-species
conserved Fushi-tarazu (Ftz-F1) box of SF1 (Figure 2, D and E, and
ref. 6). In a 3D model derived from SF-1 solution structure, the posi-
tively charged R103 appears to be in close proximity to the nega-
tively charged sugar-phosphate backbone of the DNA site bound
by SF-1 (Figure 2F and ref. 7). Replacement with a noncharged residue
is likely to affect DNA binding, as previously shown for similar sub-
stitutions in the Ftz-F1 box (8).

The unique finding of asplenia in this patient (Figure 1A), togeth-
er with impaired spleen development reported in Sf1 knockout mice (9), raised the hypothesis that the R103Q mutation may alter
expression of SF-1–regulated genes important for spleen develop-
ment. We therefore searched for SF-1 recognition elements in genes
previously implicated in spleen development, and identified 2 such
bona fide elements in the first exon of TLX1 (OMIM 186770). A
similar cluster of SF-1 binding sites was not found in the promoters
of other spleen-development genes (PBX-1, NKX2-5, NKX3-2, WT-1,
and POD-1). TLX-1 is a homeodomain-containing transcription
factor critical for embryonic spleen development, as Tlx1 knockout
mice have isolated asplenia (10, 11); in contrast, the other above-
described spleen development genes also affect the development
of other organs. To determine whether SF-1 regulates TLX1, and
whether this effect is altered by the SF1 R103Q mutation, we engi-
nereed and tested the activity of a luciferase reporter construct
controlled by the minimal promoter and first exon of TLX1 (Fig-
ure 3A). Whereas WT SF1 promoted TLX1 transcription, the SF1
R103Q mutation dramatically decreased this transcriptional activ-
ity by 2.7-fold in COS-7 cells and similarly in CHO cells (Figure
3A and Supplemental Figure 2). Interestingly, previously reported
SF1 mutations, G35E and R92Q, also decreased SF-1 activation
of the TLX1 promoter, whereas the D293N mutation, associated
with a milder phenotype, had no significant effect (Figure 3A and
refs. 5, 12, 13). This may explain the early demise of a homozygous
R92Q patient, who died of sepsis, a well-known complication of
hyposplenism, at 4–5 months of age (14). While SF-1 is charac-
terized as a transcription factor involved in human gonadal and
adrenal development, it was not previously known to be important
for human spleen development. Such a role for SF-1 was surmised
from tissue expression studies (15) and from the splenic pheno-
type of SF7 knockout mice, which have small and maldeveloped
spleens, but not complete asplenia (9). Interestingly, another case
of asplenia in a patient with a SF1 mutation was presented after our
study was completed (16). Our finding that the SF1 R103Q muta-
tion impaired SF-1 transactivation of the TLX1 promoter provides
a mechanism for the observed asplenia and suggests a role for SF-1
as a facilitator of normal spleen development in humans.

SF-1 plays a critical role in many aspects of gonadal development
and testicular differentiation, including steroidogenesis (17). SF-1 is
thought to induce SRY expression in the early gonad, leading to syn-
ergetic activation (by SRY and SF-1) of SOX9 transcription through
its testis-specific enhancer, TES, and when sufficient levels of SOX9
are achieved, SOX9 replaces SRY and binds its own enhancer together
with SF-1 to help maintain its own expression. Failure of this SF-1–
duced SOX9 activation may lead to sex reversal (3, 18). In the next
stage of testicular differentiation, SF-1 in Leydig cell progenitors also
regulates expression of key testosterone synthesis genes, including \textit{STAR} and \textit{CYP17A1}. \textit{SF1} mutations can lead to XY sex reversal by impairing any of these functions, but most reported mutations have not been evaluated for their effects on \textit{SOX9} expression.

Based on the developmental roles of \textit{SF-1}, we examined the effects of \textit{SF1} mutations R103Q, G35E, R92Q, and D293N on SOX9 gene expression using the luciferase reporter system designed by Sekido et al. (3), which assays transactivation of the core mouse \textit{SOX9} enhancer, TESCO. In the absence of \textit{SF-1}, neither SRY nor SOX-9 overexpression stimulated TESCO-dependent reporter activity (Figure 3B). Recapitulating the known sequence of testicular development requiring a synergistic effect of \textit{SF-1} and SRY on the \textit{SOX9} promoter, expression of SRY or SOX-9 together with WT \textit{SF1} stimulated TESCO reporter activity ∼4.5- and ∼8.5-fold, respectively (Figure 3B). \textit{SF1} mutations, in the absence of SRY or SOX-9, reduced TESCO activation: R103Q reduced activation compared with WT \textit{SF1} (by 65%), as did the R92Q and D293N mutations (by 72% and 39%, respectively), and G35E drastically decreased TESCO activity by 93% (Figure 3B). However, the synergistic effect of \textit{SF-1} with either SRY or SOX9 was not impaired by the novel R103Q mutation or by the 2 previously clinically reported recessive mutations, R92Q and D293N (Figure 3B).

These findings were consistent with the normal histological appearance and inhibin staining of Sertoli cells in the gonads removed from the patient. Furthermore, staining of these gonadal sections with antibodies against SOX-9, the critical protein for male gonadal sexual development (19), demonstrated, for the first time, SOX-9 protein expression in gonadal Sertoli cells of a 46,XY DSD patient (Figure 1F). In contrast to the recessive \textit{SF1} mutations, impairment of TESCO activation by G35E (which is known to cause autosomal-dominant DSD; ref. 20) remained even with coexpression of SRY or SOX-9, and similar results were obtained in CHO cells (Figure 3B and Supplemental Figure 3). This qualitative difference between recessive mutations and a severe dominant \textit{SF1} mutation was not
distinguishable in a previous study conducted with the human TES (hTES) element, most probably because SRY alone is sufficient for hTES activation (21).

Finally, to understand the XY sex reversal phenotype and the patient’s lack of blood testosterone, we studied the effect of the SF1 R103Q mutation on transcriptional activation of 3 steroidogenic (CYP11A1, CYP17A1, and HSD3B2) promoter reporter constructs (27) transfected into nonsteroidogenic HEK293 cells. Activation of CYP11A1 was not significantly affected by the mutation, and HSD3B2 promoter activity was slightly elevated (1.3-fold; Figure 3C). It therefore appeared that XY sex reversal in this patient was due to a defect in steroidogenesis, rather than impaired SOX9 activation. This is consistent with the general observation that the degree of hypoandrogenism in SF1 mutant patients is greater than the degree of testicular dysgenesis, as well as with examples of sex-limited dominant inheritance of SF1 mutations from unaffected mothers to affected sons (22).
We hypothesize that the different phenotypes observed with SF1 mutations may be explained by their different effects on SRY and SOX9 activation and testicular steroidogenesis. The recessive SF1 mutations R92Q and D293N may be similar to R103Q in enabling sufficient activation of SRY to thus activate SOX9 (Figure 1E and Figure 3B), leading to early gonadal and testicular differentiation and inhibin expression (Figure 1, E and F). However, the defect in testosterone synthesis caused by the R103Q mutation was apparently sufficiently severe to lead to undescended testes and phenotypic sex reversal. Severe mutations such as G35E may act earlier in development to curtail SOX9 activation altogether.

In conclusion, our present study describes a unique clinical phenotype of severe 46,XY-DSD with asplenia, caused by a novel homozygous SF1 mutation, R103Q. Transactivation studies of TLX1 demonstrated for the first time that SF-1 is required for spleen development in humans, which shows that SF1-DSD and asplenia are not simply coincidental. We also found that SF1 mutations can lead to sex reversal due to a defect in testosterone synthesis without disrupting the SFR-SRY-SOX9 activation cascade. Because asplenia has therapeutic consequences, the splenic status of individuals with DSD harboring SF1 mutations should be actively examined.

Methods

Further information can be found in Supplemental Methods.

Genetic studies. Standard Sanger sequencing was performed on genomic DNA extracted from the proband and her nuclear family. We sequenced the coding regions of both SF1 and STAR (Supplemental Table 2). The SF1 mutation identified was tested in ethnically matched controls by PCR and ApaI digestion (Supplemental Figure 1).

Antibody staining. SOX9 and inhibin. Paraaffin-embedded sections of the patient's gonads were stained with mouse anti–SOX-9 and monoclonal mouse anti-inhibin, as previously described (23), and visualized by fluorescence and DAB staining, respectively.

Functional analysis of the SF1 R103Q mutation. Promoter activity assays were performed by transfecting luciferase reporter vectors controlled by various gene promoters into cells, and used to assay for SF1 activity as a transcription factor.

Statistics. For transfection experiments, 2-tailed paired t test was used to compare WT and mutant SF1 vectors. A P value less than 0.05 was considered significant.

Study approval. Histological and molecular analysis of the patient's tissues and blood, as well as genetic analysis of the patient's family, were under informed written consent of the subjects themselves and/or the legal guardians thereof. The study was approved by the institutional Helsinki board of Shaare Zedek Medical Center (approval no. 20/10).

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