Disorders of Sex Development in Indonesia:
Natural course and the implications of a stepwise multidisciplinary approach

Achmad Zulfa Juniarto
1. In the Indonesian community, the etiological spectrum of Disorders of Sex Development (DSD) is broad. 46,XYDSD being most common in contrast to observations in Western societies. (this thesis)

2. Determination of salivary androstenedione and 17-hydroxy progesterone levels is a useful and inexpensive alternative to measurements of those hormones in serum for monitoring of treatment of patients with congenital adrenal hyperplasia. (this thesis)

3. The incidence of Germ Cell Cancer (GCC) is low in most Asian populations, while it is similarly high in Caucasian and Indonesian DSD patients indicating DSD to be a dominant risk factor for GCC. (this thesis)

4. The full implementations of the current consensus statement on DSD (Hughes I et al 2006) in a resource-poor environment is very difficult and necessitates a tailored approach. (this thesis)

5. There is an urgent need for education of primary health care workers in Indonesia on recognition of DSD and urgent clinical assessment of DSD patients in order to prevent morbidity and mortality. (this thesis)

6. Social and community support and the existence of a support group are essential to help individuals with DSD to cope with social stigmatization and the prospect of poor quality of life.

7. The development of a robust and secure e-consultation service within the international community with the objective of providing expert opinion on a worldwide basis will broaden access to healthcare for all patients with rare diseases.

8. Cultural differences between the various tribes in Indonesia pose difficulties in handling and follow-up of patients.

9. Free availability of gluco- and mineralocorticoids is mandatory for a satisfactory treatment of Indonesian children suffering from adrenal insufficiency such as congenital adrenal hyperplasia.

10. The best of people are those that bring most benefit to the rest of mankind. (Al Hadits)

11. No one makes a lock without a key, that’s why The one won’t give you problems without solutions and diseases without cure.
Disorders of Sex Development in Indonesia: Natural course and the implications of a stepwise multidisciplinary approach

Stoornissen van seks ontwikkeling in Indonesië: Natuurlijk beloop en de gevolgen van een stapsgewijze multidisciplinaire aanpak
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Soornissen van seks ontwikkeling in Indonesië:
Natuurlijk beloop en de gevolgen van een stapsgewijze multidisciplinaire aanpak

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“The best of men are the most useful for others”

Hadith

For my family and teachers
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Chapter 1
General Introduction
When a child is born, the question most often being asked is about its gender. Gender, whether male or female, affects almost every aspect of our lives. How profound the distinction between males and females is, and how these differences come about, are seemingly simple questions, however, are demanding a complex answers.

The process of development of the differences between males and females from an undifferentiated zygote is called sexual differentiation. As male and female individuals develop from zygotes into foetuses, infants, children, adolescents and eventually into adults, differentiation of sex and gender also develop at many levels: chromosomes, genes, gonads, hormones, anatomy, psychology, and social behaviours.

The purpose of sexual differentiation or the development of any male or female specific physical or behavioural characteristic is to equip the organism with the necessary anatomy and physiology to facilitate sexual reproduction.

Differences in sex may be absolute or may become only obvious by statistical analysis. Some aspects of development are typically sex-dichotomous characterizing one sex only. Examples of sex-dichotomous differences are the sex specific genital organs such as ovaries, uterus or phallic urethra. In contrast, sex-dimorphic differences may be mainly statistical differences, a matter of degree (e.g., size of phallus) with overlap between male and female populations. Nonetheless in the human, even sex-dichotomous differences are not an absolute matter. There are individuals who demonstrate exceptions, for example: males with a uterus, or phenotypic females with an XY karyotype, and those who exhibit biological and/ or behavioural characteristics of both sexes.

The very early phase of human differentiation seems to be quite similar in males and females. During the first weeks of life, the embryo has no anatomic or hormonal sex and can only be differentiated by karyotype. Specific genes initiate gonadal differentiation, gonads produce different hormones leading to anatomic differences as well as psychological and behavioural differences, some of which are innate while others are socially induced.
Disorders of Sex Development (DSD) in Indonesia

Disorders of sex development (DSD) are defined as congenital conditions in which development of chromosomal, gonadal or anatomical sex is atypical, and where previously referred to as intersex conditions (1). A new classification of DSD was proposed following a consensus meeting in Chicago in 2005. The primary root of this classification is based on the chromosomal constitution consisting of three main groups, namely; 46,XY DSD, 46,XX DSD, and sex chromosome DSD. Although this classification has its limitations and has been the subject of intensive discussions, it is considered less offensive than the use of different earlier terminologies and it prevents misunderstanding.

Babies born with DSD or children presenting with DSD at a later age are a challenge for both parents and physicians. Integrated handling, careful decision-making and counselling are indispensable for such patients.

In Indonesia, patients presenting with DSD most often do not receive a diagnostic evaluation and options for medical and surgical treatment are limited. A standardized management protocol for patients is not yet available. This makes the management of patients with DSD highly variable and dependent on the experience of the experts and on facilities available in a particular health centre.

The Sexual Adjustment Team (Tim Penyesuaian Kelamin) of the Faculty of Medicine, Diponegoro University-Kariadi Hospital in Semarang, Indonesia is one of six hospital based teams appointed by the Indonesian Government to handle patients with DSD. Since its founding in 1989, this team has been receiving patients with genital abnormalities from almost all over Indonesia.

The multidisciplinary team consist of specialists from various departments: paediatric endocrinology, urology, andrology, obstetric and gynaecology, genetics, psychology, psychiatry, social services, law and ethics. Significant progress has been made since the collaboration with the gender team of the Erasmus Medical Centre Rotterdam, The Netherlands starting in 2004. Out of the total patient number of 583 referred since 1989 not less than 347 patients were evaluated in the period 2004-2010. Due to inclusion criteria of the research, 286 of these patients were included in the present study.
Scope of the thesis

The final goal of management of DSD is to provide appropriate gender assignment and to optimize the quality of life of the patients. In the process of gender assignment of DSD patients many factors, both related to the patient him or herself and to the psycho-social environment of the patient should be taken into consideration.

For all of these reasons a stepwise diagnostic evaluation of patients with DSD referred to the Sexual Adjustment Team of the Faculty of Medicine, Diponegoro University-Kariadi Hospital in Semarang, Indonesia was initiated. This thesis reports not only on results of this evaluation but also on various aspects of management of DSD notably the management of congenital adrenal hyperplasia (CAH) and on gonadal tumor risk of patients with DSD. Furthermore, since in Indonesia, options for treatment of DSD are limited and often patients are referred at a later age, it was possible to study the natural course of DSD.

It is well recognised that DSD has a great impact on psychological and psychosexual development. Separately but in parallel with this thesis Mrs. Annastasia Ediati has made a study of these aspects focussing on the psychological and social aspects of DSD: gender development, psychopathology, stigmatization, quality of life and cognitive functioning. From this study conclusions are drawn on the psychological consequences in patients with DSD which should be taken into consideration for further intervention.

Aims of the study

The aims of the various studies reported in this thesis can be summarized as follows:

A. Stepwise diagnostic evaluation of a cohort of patients with DSD

1. Diagnostic spectrum
   - What is the diagnostic spectrum of DSD in Indonesia based on clinical and hormonal data?
   - What is the spectrum of gene mutations within each of the 3 diagnostic DSD categories?
• Are there any novel mutations in the well-known loci or other loci in suspected genes?

2. Value of clinical and laboratory parameters
• Which clinical and laboratory parameters are most contributory in the diagnostic process?

B. Congenital Adrenal Hyperplasia, diagnosis and management
• What is the clinical spectrum of CAH in Indonesia?
• What is the spectrum of gene mutations among CAH patients in Indonesia?
• How should CAH patients be treated comprehensively?

C. Gonadal tumor risk
• Does Germ Cell Cancer (GCC) occur in the Indonesian DSD population and if so what types of gonadal cancer can be found?
• What is the gonadal cancer risk per diagnostic category?
• Is it safe for certain diagnostic groups to leave the gonads in place?

D. Management of DSD
• What is the outcome of the implementation of comprehensive management of DSD in Indonesia?
• What are essential requirements for the management of DSD?

Reference
CHAPTER 2

Disorders of Sex Development

A Literature Review
I. PHYSIOLOGY OF SEX DEVELOPMENT

As one of the most important physiological processes, reproduction leads to the production of new organisms and the perpetuation of the species. Effective reproduction requires a normal development of the sex organs which is strongly influenced by genetic composition and gonadal development.

A. CHROMOSOMAL SEX

Genetic sex, indicated by karyotype, is the chromosomal basis of sex determination and defines the sex-determination system. In man, the normal number of chromosomes is 46, 44 of which are autosomes while 2 distinct chromosomes are acknowledged as the sex chromosomes which define the sex of an organism and various sex-related characteristics. An individual normally has a single pair of sex chromosomes in each cell where males have one Y chromosome and one X chromosome while females have two X chromosomes, making females the homogametic sex. However, other karyotypes do exist.

During meiosis, or the process of gamete formation, the autosomal chromosomes are arranged in arrays and exchange of genetic material between the members of each pair is possible by recombination. In the sex chromosomes, this process is restricted to small regions on the distal ends of the X and the Y, which are called the 'pseudoautosomal' regions.

Nowadays, it is generally accepted that the X and Y chromosomes have evolved from and ancestral pair of homologous autosomes. The Y chromosome is considered to have evolved sometime between 170 and 310 million years ago when a sex-determining locus arose on one of the proto-sex chromosomes which led to the accumulation of other sex-specific alleles nearby. This resulted in deletion of large parts of the Y chromosome, with the shrinking of this chromosome (1). One might think that the Y chromosome would sooner or later lose all homology with the X. However, mice, and humans appear to possess a vital requirement for the preservation of X and Y pairing for the meiotic process and XY chromosomal segregation during spermatogenesis (2).
A.1. X chromosome

The sex chromosomes form one of the 23 pairs of chromosomes in each human cell. Named for its distinctive characteristics by early researchers, the X chromosome was the first of the two sex chromosomes to be described. The other sex chromosome, which was discovered later, was named Y chromosome, representing the next letter in the alphabet. The X chromosome spans about 165 million DNA building blocks (base pairs), and represents approximately 5 percent of the total DNA. It is likely to contain between 900 and 1,500 genes which have a variety of roles in the body. Female individuals have two X chromosomes (one from each parent) while males inherit a single maternal X chromosome. Gene expression on one of the X chromosomes in female somatic cells is deactivated early in development by the process of X-inactivation and this chromosome remains inactive thereafter (3). This X-inactivation warrants that females have one functional copy of the X chromosome in each body cell similar to males. In normal females, due to the random nature of X-inactivation, the X chromosome inherited from the mother may be active in some cells and that inherited from the father in other cells.

A.2. Y chromosome

As one of the two sex chromosomes in the human, the Y chromosome spans about 60 million base pairs and represents almost 2 percent of the total DNA in cells. It contains about 50 or 52 genes (1, 4). The genes on this chromosome are involved in male sex determination and development, which is stimulated by the expression of the SRY gene, a testis-determining factor. As one of the important genes related to male fertility, the SRY gene is placed in the non-recombining portion of the Y chromosome (NRY), a specific region that encompasses 95% of the human Y chromosome (5). Other genes on the Y chromosome are also important for male fertility.

It is expected that at least 27 distinct proteins or protein families are encoded by the NRY region. Most of these contribute to sex determination and specific male functions e.g. spermatogenesis (6).
Defects or deletions of the SRY gene are likely to be the cause of the clinical picture of XY females in 15% of the cases. In contrast, males with an XX karyotype usually present with a tiny piece of the Y chromosome, containing the SRY gene, added to the X chromosome. This sex reversal is often associated with other developmental malformations (7).

Abnormalities in the sex chromosomes will lead to disorders of sex development. The most widely known sex chromosomal abnormalities are Turner syndrome (45,X) and Klinefelter Syndrome (47,XXY). Although both abnormalities represent variations in sexual differentiation, they are often not categorized as intersex conditions, since there is usually no discordance between elements of sexual differentiation. Variant karyotypes of these syndromes are also possible, in which different cells from the same individual have different karyotypes (mosaicism) such as 45,X/46,XY; 45,X/47,XYY.

**B. PHENOTYPIC SEXUAL DIFFERENTIATION**

Determined by endocrine influences, phenotypic sex includes gonadal sex, defined by the presence of ovarian or testicular gonads and morphological sex, determined by the morphology of the external and internal genitalia.

Hormones secreted by the gonads determine the secondary sex characteristics, which will affect the physical phenotype outside the gonads. A female body possesses a vagina, cervix, uterus, oviducts, and mammary glands, and a male body features a penis, seminal vesicles, and a prostate gland (8).

**B. 1. Sexual differentiation of the internal genitalia**

The first phase of gonadal development is marked by the appearance of the indifferent, bipotential gonad, or genital ridge which is identical in males and females and remains so until the 7th week of human gestation, when the migration of the primordial germ cells begins.

The next stage is the development of the indifferent gonad into a testis or an ovary (9). The bipotential gonad consists of four presumptive cell lineages: the germ cells (which have an extra-embryonic origin) and three types of somatic cells.
These somatic elements include the supporting cell precursors, which will create Sertoli cells in the male or granulosa cells in the female; secondly the steroidogenic precursors, which differentiate into Leydig cells (male) and theca cells (female), and finally the connective tissue cells which accommodate other important structures (10).

This process of gonadal sex determination marks the first step in sexual development and includes a unique decision to make a testis or an ovary out of a bipotential primordial gonad. The differentiation process of the gonad is the primary step on which all other aspects of sexual differentiation depend. This has been known as the ‘central dogma’ of the sexual differentiation process (11).

In male fetuses, at the 7th week of gestation the testicular development begins. A vital event in this process is marked by $SRY$ gene expression in cells destined to differentiate into Sertoli cells (12-14), which in turn coordinate the differentiation of all other cell types in the testis. These cells also affect spermatogenesis, which is followed by the differentiation of seminiferous tubules and the formation of Leydig cells (9, 15). Later in life, Sertoli cells will nurture the development of germ cells into sperm. Concurrent with the differentiation of Sertoli cells, the size of gonad increases significantly because of increased proliferation and migration of cells from the adjacent mesonephros. This progression occurs only in males, after the inception of $SRY$ expression (16).

The development of the primordial germ cells in the testis stops at the stage of pro-spermatogonia as a result of paracrine action of mediators secreted by the Sertoli cells (17). At the same time, anti-Müllerian Hormone (AMH) is also secreted by the Sertoli cells. AMH is a member of the transforming growth factor $\beta$ (TGF$\beta$) family and is also referred to as Müllerian inhibiting substance (18). It elicits male sexual differentiation by signaling via two cell-surface receptors: AMH receptors I and II (18).

Formed by invagination of a tube from the surface epithelium of the mesonephros, the Müllerian (or paramesonephric) ducts are the precursor of the female ductal system whereas the Wolffian (or mesonephric) ducts are the progenitors of the male duct system. The Müllerian duct runs parallel to the Wolffian duct in both male and female embryos (Figure 1). The
differentiation of an indifferent gonad into a testis or ovary will determine which one of the two duct systems will develop. In the human embryo, this process starts at the 7th week of gestation.

In the absence of AMH, the Müllerian ducts will develop and differentiate into oviducts, uterus, and upper third of the vagina; but on the development of male sex, AMH causes these ducts to regress instead of developing (18). At the 8th week of gestation, the masculinization process of the male fetus is initiated when Leydig cells appear in the differentiating testis and start secreting androgens. Under the influence of testosterone, the Wolffian ducts develop into epididymis, vasa deferentia and seminal vesicles(19).

There are two stages of testicular descent during sexual development. The first is caused by development of the gubernacula rather than actual movement and the testes reach the internal inguinal ring by week 24. Insulin-like Factor 3 (INSL3), produced by Leydig cells, regulates this trans-abdominal phase of descent by stimulating the development of the gubernaculum (20). In the last two months of fetal life, the second stage occurs where the testis passes through the inguinal canal to reach the scrotum. Androgens are a primary requirement for this migration and in 97% of normal infants, the testes are in scrotal position at the time of birth (19).
The two main roles of the ovary are firstly to produce hormones and secondly to generate mature oocytes that are capable of being fertilized and of developing into an embryo. Surrounded by granulosa and theca cells, the ovarian follicle is the functional component of the ovary, where the oocyte matures (9). Unlike the seminiferous tubule, the functional part of the testis, the ovarian follicles commence differentiation only after birth.

The development of the ovary seems to be based upon a number of genes and transcription factors: DAX1 and WNT4 are known as genes that are likely to suppress testicular development (21, 22).
B. 2. Sexual differentiation of the external genitalia

Similar to the development of the gonads, but unlike that of the internal reproductive tracts, the external genitalia of both female and male are formed from the same initially identical structures: The genital or labioscrotal swelling, the genital or urethral folds, the genital tubercle and the urogenital sinus.

Testosterone is essential in the development of the male external phenotype. However, to allow normal differentiation, it must be converted into its active metabolite, 5α-dihydrotestosterone (DHT) within the cells of the anlagen by the enzyme steroid 5α-reductase type 2 (SRD5A2) (19).

Figure 2. Diagram of the development of the male (bottom left) and female (bottom right) external genitalia. In males, the genital tubercle grows and forms the shaft and glans of the penis. The urogenital sinus becomes continuous with a groove that develops on the caudal face of the genital tubercle and this groove closes to become the penile part of the urethra while the fused urogenital folds enclosing the sinus become the prostate part of the urethra. In the most distal part of the penis, invagination of a cord of epithelial cells covering the glans meets the penile urethra and when this cord canalizes the formation of the urethra is complete. The line of fusion along the urethra and scrotum is called the raphe. The labioscrotal folds form the scrotum (19).
In the female fetus, the genital tubercle folding inferiorly will form the clitoris, whereas the urogenital folds become the labia minora and the genital swellings develop into the labia majora. The vagina and the urethra open into the vestibule of the urogenital sinus. Until 15 weeks of gestation the size of external genitalia of the male and female is the same. In the male the growth of the external genitalia is not to begin until the last two thirds of pregnancy which will be followed by the descent of the testes into the scrotal sac (19).

C. GENES INVOLVED IN SEX DETERMINATION AND DIFFERENTIATION

The process of an undifferentiated gonad passing through a complicated series of steps to develop into a testis or an ovary is called the differentiation of the gonad and depends on the sex-determining pathway succeeding in determining the sex (23).

Numerous investigators have tried to discover genes that are vital in sex determination and differentiation. Their work led to the conclusion that a number of genes are essential for normal sex differentiation. Later studies revealed that mutations of some of these genes perturb the normal differentiation process and can be causative for various forms of Disorders of Sex Development (DSD).
C.1. Undifferentiated state (bipotential)

**Pax2**: Pax2 is a transcriptional regulator of the paired-box family and is extensively expressed in the development of ductal and mesenchymal components of the urogenital system (24). Expression of Pax2 within the mesonephros is limited to the Wolffian ducts and mesonephric tubules. Pax2 homozygous mutant newborn mice are found to be lacking kidneys, ureters and genital tracts. These defects might be associated with dysgenesis of both ductal and mesenchymal parts of the developing urogenital system (25). In either sex in Pax2/- mice, no defects in gonadal development have been found, indicating that the formation of the mesonephric tubules is not a prerequisite for gonadal development. Genetic defects in PAX2 in humans are known the in renal-coloboma syndrome, without genitourinary abnormalities (9, 24).
**Emx2**: *Emx2* (Empty spiracles homolog 2) encodes a homeobox-containing transcription factor that is a homolog of the Drosophila head gap “empty spiracles” gene and is expressed in the developing dorsal telencephalon and in the epithelial parts of the urogenital system (26). In *Emx2*−/− mice, the migration of the primordial germ cells (PGCs) occurs as normal. However, the first stage of the gonadal development which is marked by the thickening of the coelomic epithelium, is poor: the Wolffian ducts degenerate and the Müllerian ducts never form. Thus the mutants have neither gonads nor genital tract (27). Mutations in *EMX2* are a rare cause of schizencephaly. Somatic mutations in *EMX2* have been found in endometrial carcinomas (28). However, there is no report on defects of human sex development due to *EMX2* mutations until now.

**Lhx9**: At embryonic day 9.5, the expression of the gene *Lhx9*, a member of the LIM homeobox gene family, commences in the urogenital ridges of male mice. It is also localized in the interstitial region during morphological differentiation. In mice lacking functional *Lhx9*, somatic cells of the genital ridge are somehow unable to proliferate and a discrete gonad fails to form despite normal migration of germ cells. The steroidogenic factor 1 (*Sf1*) expression which is essential for gonadogenesis, is reduced to minimal levels in the *Lhx9*-deficient genital ridge. Biochemical analysis shows that *Lhx9* can attach directly to the *Sf1* promoter and has an additive effect to its *Wt1*-induced activation in vitro (29). These results indicate that *Lhx9* may be an initial point for the coordination of a network of gene regulation during the undifferentiated stage of gonad development which may lie upstream of *Sf1* in a developmental cascade. The absence of testosterone and AMH will make a genetically male mouse to have the phenotype of a female. *Lhx9* mutants do not show additional major developmental defects. Despite the fact that *LHX9* mutations may underlie certain forms of isolated gonadal agenesis in humans, no such mutation has been found to date (30).

**WT1**: The *WT1* gene encodes a zinc finger DNA-binding protein that is expressed widely throughout the urogenital ridge, in the mesonephros, the kidney, and the gonad (9).
Both mutation analysis in human patients and genetic experiments in mice indicate that \textit{WT1} plays an important role in development as well as in tumor suppression. In the development of the gonad, \textit{Wt1} is expressed in both the coelomic epithelial cell layers and the developing Sertoli cells in males and in granulosa cells in females. Although the gonadal primordium is visible in 11 dpc \textit{Wt1-/-}-mutant mouse embryos, it degenerates afterwards due to increased apoptosis (9) Because the gonads and adrenal cortex share a common primordium, the adrenal glands are also affected in \textit{Wt1-/-} mice. Expression of \textit{Sf1} and expression of \textit{Wt1} in the gonad begins concurrently and might be interdependent (31). In vitro, a number of genes including \textit{Sf1}, are activated by \textit{Wt1} and in research with transgenic mice, it was found that \textit{Sf1} is likely to be a genuine \textit{Wt1} target (29). \textit{Wt1} might also stimulate an \textit{Sf1}-independent pathway necessary for adrenogenital survival, including the anti-apoptotic factor \textit{Bcl2} (24). In gonad formation, \textit{WNT-4}, \textit{DAX 1} and AMH also appear to be activated by WT1. It appears that \textit{WT1}'s function as a transcriptional activator is vital for the survival and differentiation process of gonadal cells (9). As an influencing gene in male sexual development in mouse and man, \textit{Dax1} was proposed to be a repressor of the \textit{AMH} promoter that could remove \textit{Wt1} from its complex with \textit{Sf1} (24). Mutations in the \textit{WT1} gene have been discovered in patients with a variety of disorders such as Wilms’ tumor and isolated diffuse mesangial sclerosis (IDMS), as well as in complex diseases such as aniridia and genito-urinary anomalies. In addition, \textit{WT1} mutations have been described in mental retardation syndrome (WAGR syndrome), Frasier syndrome, Denys–Drash syndrome (DDS) and Meacham syndrome (24).

\textbf{GATA-4}: \textit{GATA-4}, a member of the GATA family of transcription factors, is found in the gonad and possibly plays a role as a regulator of gonadal gene expression. It is vital for the establishment of Sertoli cell localization as well as for proper testis cord formation. \textit{GATA-4} is found in the developing somatic cell lineages specifically (Sertoli cells in testis and granulose cells in ovary) but not in primordial germ cells (23, 24).
C.1. a. Testes

**SRY**: *SRY* belongs to a large family of nuclear proteins characterized by a DNA-binding domain known as high mobility group (HMG) box, which functions as a transcription factor (33). To activate testis determination and consequent development of male sexual characteristics, *SRY* alone is necessary and sufficient. Whenever *SRY* is impaired or non-existent, ultimately an ovary will be formed. In the mouse embryo, a restricted and limited spatiotemporal profile of expression of *SrY* has been demonstrated in the precursors of Sertoli cells of the XY gonad (34). Previous literature shows that *SrY* is expressed initially around 10.5 days post coitum (dpc) in the mouse, soon after the genital ridges appear, and reaching maximal levels of expression at 11.5 dpc shortly after 12.5 dpc expression begins to regress. *SrY* obviously instigates a molecular switch to perform a male-specific cascade of molecular events. However, for these events to surface, continued expression of *SrY* is not required (24). *SrY* appears to affect the expression of one single gene, *SOX9*, which is then rapidly enhanced by positive regulatory loops. Subsequently, *SOX9* induces Sertoli cell formation which leads to testis differentiation. Whenever *SrY* fails to act timely, or when it is totally absent, *SOX9* expression is shut down and follicular cells start to develop resulting in ovarian differentiation. The condition of 46,XY DSD caused by an *SrY* gene mutation leads to pure gonadal dysgenesis, originally referred to as 46,XY, female with gonadal dysgenesis (35).

**SOX9**: *SOX9* is a member of the *SOX* family of transcription factors and is proposed to be the best candidate for a direct *SrY* target gene for the following reasons (36). First, *SOX9* is initially expressed at low levels in the indifferent gonad, and gradually expression is increasing until it becomes up-regulated in the Sertoli cells immediately after the start of *SrY* expression, whereas it is down-regulated in the ovary. *SOX9* expression is preserved in the Sertoli cells until birth.

Second, *SrY*-positive cells exclusively become *SOX9*-positive Sertoli cells. Third, in most cases of campomelic dysplasia XY patients have male to female sex reversal. It is well known that the sole factor that accounts for this human skeletal malformation syndrome is a heterozygous
mutation of SOX9. In the male sexual development process, SOX9 is not only necessary but also sufficient (9). SOX9 expression in the genital ridge is not entirely reliant on SRY, the normal gonadal SOX9 transcriptional regulation consists of an SRY-independent initiation; an SRY-dependent up-regulation and finally an SRY-independent maintenance in adult life (24). SF1 is a suitable candidate to instigate or sensitize SOX9 expression further. It initiates a low level of expression in the genital ridge in both sexes at 10.5 dpc in the mouse. SF1 also activates SRY expression, presumably jointly with other factors such as WT1 (24). By joint action of SRY and SF1, SOX9 expression is up-regulated. In contrast, it is down-regulated in the female. This down-regulation tends to be an active process, caused by the presence of one or more currently unknown repressors. When the transient expression of SRY is finished, high levels of SOX9 are controlled by its direct auto-regulation and via FGF9 signaling (24). DAX1 and FGF9 are also affecting the up-regulation of SOX9 expression in pathways parallel to SRY. Up until now, there is only limited information on the genes which are stimulated by SOX9 and are important in testis determination. One study revealed that joint effects of Sox9 and Sf1 are responsible for the regulation of anti-Müllerian hormone (Amh) gene expression. However, where Sox9 is vital in the initiation of Amh transcription, Sf1 appears to act as a quantitative regulator of the level of Amh transcription (37).

**SF1/NR5A1** : The expression of SF1 in the developing urogenital ridge, hypothalamus, and the anterior pituitary gland, emphasizes its importance for the development of the hypothalamic-pituitary-gonadal axis. After the completion of sexual differentiation, SF1 can be detected in steroidogenic (Leydig) and non-steroidogenic (Sertoli) cells in the testis (9). The pattern of SF1 expression, starting in the human adrenal gland and bipotential gonad at 32-33 dpc, is consistent with its pivotal task, which is to regulate adrenal development, and gonadal determination and differentiation. In the hypothalamic-pituitary system it controls reproduction and metabolism (24). From approximately day 42 onwards, SF1 expression in the human is consistently preserved in the somatic cells of the early testis. Jointly with SRY, SF1 plays a critical role in supporting SOX9 expression (24, 36). In Sertoli cells of the developing male fetus, SF1 is involved in regression of Müllerian structures due to activation of AMH expression from around
7 weeks of gestation. In Leydig cells, SF1 activates the expression of steroidogenic enzyme systems from 8 weeks of gestation, which leads to androgenisation of the external genitalia (24). SF1 can also be detected in somatic cells (granulosa and theca cells) of the female adult ovary (38). The phenotypic spectrum caused by mutation in the human SF1/NR5A1 gene ranges from complete testicular dysgenesis with Müllerian structures, through individuals with mild clitoromegaly or genital ambiguity to severe penoscrotal hypospadias or anorchia (39, 40). A recent study found that heterozygote mutations of the SF1 gene are associated with ovarian insufficiency although it is not essential for ovarian determination (41). Like SF1/NR5A1, NR5A2/LRH1 also plays an important role in induction of steroidogenic enzymes and factors. This liver receptor homolog is strongly expressed in the Leydig cells of the testis but only weakly in Sertoli cells, where SF1 predominates (42, 43).

**DAX1/NR0B1**: As an orphan member of the nuclear hormone receptor family of transcriptional regulators, DAX1 is encoded by an X-chromosomal gene. The key model of the molecular mode of action of DAX1 is presumably related with that of other nuclear receptors such as SF1, recruiting co-repressors or co-activators to the appropriate transcriptional complex, thus affecting nuclear receptor-mediated transcriptional activation (44, 45). Interaction between DAX1 and SF1 during gonadogenesis occurs in a similar manner as seen during steroidogenesis. A common function for DAX1 as a repressor of SF1 ‘trans’-activation has been implied in both adrenal and gonadal tissues. Expression of DAX1 is found in the developing adrenal gland, the gonads, the hypothalamus, and the pituitary (46). In testicular development in mice, Dax1 is expressed in somatic cells prior to Sry expression, with a strong up-regulation in Sertoli cells by 12.5 dpc, which declines subsequently. Inactivating mutations in DAX1 lead to adrenal insufficiency with glucocorticoid and mineralocorticoid deficiency. These mutations account for most patients with adrenal hypoplasia congenita (AHC) (47). Duplication of the region in the X chromosome containing DAX1 leads to dosage-sensitive sex reversal (24, 48). Therefore, it is unexpected that loss of function in female mice had no reproductive consequences, while the testicular development in XY animals was impaired (49). The molecular mechanism underlying this testis-
promoting versus anti-testis function of DAX1 is not clear. In gonadal differentiation of man and mice, dosage sensitivity seems to be crucial, in which a proper balance of DAX1 levels at the right time could tip the balance in one of the two ways (50).

**DMRT1**: One of the characteristics found in patients with XY gonadal dysgenesis, Swyer Syndrome, is the absence of DMRT1, which maps to a region of chromosome 9p (51). This is supported by evidence that DMRT1 expression in humans is detected only in the developing gonads, and at higher levels in testes compared with ovaries, usually in the late sex-determining or early testis-differentiation period (52). However, null mutant mice show only a moderately mild phenotype in postnatal testis differentiation which signifies that either Dmrt1 is not crucial for primary sex determination or that other factors are able to compensate for its loss (53). However, results of a more recent study indicate that DMRT1 is essential to maintain testis determination in mammals (54). Differentiation of Sertoli cells into granulose cells can be reprogrammed by deletion of DMRT1 in adults through activation of FOXL2 (13).

**SOX8**: SOX8 is also a member of the family of SOX proteins. The temporal and spatial expression patterns in the developing gonad are similar to those of Sox9 and the expression is upregulated in Sertoli cells 12 h after Sox9, but prior to Amh expression. Similar to Sox9, Sox8 can attach to the Amh promoter and jointly with Sf1 it activates Amh expression in vitro (55).

**FGF9**: FGF9 is a signaling molecule secreted by Sertoli cells, an essential factor in influencing Sertoli cell differentiation. Broadly expressed in the mouse embryo with a sex-specific pattern in the developing gonad, Fgf9 can be found from 11.5 dpc in male and female mouse fetuses (56). Later, from 12.5 dpc onwards, it is expressed only in the testis cords of the XY gonad, but not in the XX gonad or the mesonephros of both sexes. XY sex reversal is mostly believed to be due to a reduced proliferation rate, presumably combined with impaired differentiation of pre-Sertoli cells, where the threshold number required to direct the differentiation of other cells in the gonad is not sufficient in completing the testis differentiation process. Fgf9 receptor type 2 (Fgfr2) is considered a candidate testis-determining gene. This gene encodes a potential receptor for Fgf9
during male sex determination and knockout mice of the other FGF receptors such as Fgfr1, Fgfr3 and Fgfr4 show no obvious gonadal phenotype whereas FGFR2 protein shows male-specific localization in the nuclei of Sertoli cell precursors during the period between 11.0-12.5 dpc (56).

**DHH**: Desert hedgehog (*DHH*) appears to have a critical role in regulating Leydig and peritubular myoid cell function. Emerging at 11.5 dpc in somatic cells of the testes in XY mice, its expression continues afterwards in Sertoli cells. However, in the developing ovary, no expression is detected at any stage. *Dhh* is attached to its receptor Patched 1 (PTCH1), the expression of which comes shortly later being under the positive control of *Dhh* in Leydig and peritubular myoid cells (57). In mice, null mutation of *Dhh* causes disrupted formation of testis cords due to abnormal peritubular tissue. Furthermore, *Dhh* appears to have an important role in Leydig cell differentiation by upregulating *Sf1* (58). Mutations of the *DHH* gene are associated with the presence of 46,XY complete pure gonadal dysgenesis in men (59).

**ATRX**: Diseases associated with deletions or mutations of *ATRX* are found in alpha thalassemia and mental retardation, X-linked (*ATRX*) syndromes. The involvement of *ATRX* in the development of the human testis was hypothesized because of *ATRX* gene mutations displaying varying degrees of gonadal and urogenital abnormalities (60), ranging from small testes to ambiguous external genitalia in 46,XY individuals. The biochemical role of *ATRX* still remain unclear.

**CBX2/M33**: Known as the murine counterpart of the *Polycomb* gene in *Drosophila*, *M33* maintains a repressed state of homeotic and other developmentally regulated genes. This is done by compressing the chromatin, preventing the binding of transcription activators. Homozygous *M33-/-* mice display a male to female sex reversal in most XY animals with perfectly normal female gonads and genitalia but with invariable sterility (24, 61). It is assumed that *M33* plays a significant role in early gonadal development, i.e. before the time of sex determination. Recent research showed that M33 is involved in the regulation of *Sf1* expression in spleen and adrenal
glands (62). It is assumed to have a similar function in gonadal development, however, its cellular roles or molecular functions are yet to be verified (9).

**TSPYL1**: Testis-specific protein Y-like-1 (*TSPYL1*) is a member of the TSPY-SET-NAP1L1 family of chromatin modifiers which is involved in nucleosome assembly. *TSPYL1* on chromosome 6p22 lacks introns, and it is assumed to be originating from retroposition of a *TSPY* transcript (63). Mutations in *TSPY* were found to disturb beta globin regulation and to be related to the syndrome of Sudden Infant Death with Dysgenesis of the Testes (SIDDT). SIDDT can occur in genotypic males with fetal testicular dysgenesis and ambiguous genitalia, intra-abdominal dysplastic testes, and deficient fetal testosterone production, but fusion and rugation of the gonadal sac and partial development of the penile shaft can also be found (24, 64, 65).

The sexual development in an 46,XX infant with a *TSPYL1* mutation was reported to be normal at birth. However the child developed signs of viscero-autonomic dysfunction early in life, followed by death prior to the age of 12 months due to abrupt cardio-respiratory distress. One should notice that no mutation in *TSPYL1* has been detected in cases of sudden infant death without testicular dysgenesis, indicating the testis-specific role of this protein (65, 66).

**MAML1**: Mastermind-Like Domain-Containing Protein 1 (*MAML1*), also called Chromosome X Open Reading Frame 6: *CXORF6*, localized on chromosome Xq28, is expressed in several tissues including fetal Sertoli and Leydig cells around the critical period for sex development (67). Most patients with a deletion of this region of chromosome X also had ambiguous genitalia. *MAML1* (*CXORF6*) seems to have an important role in the testosterone production around the critical period for sex development. The protein localizes to the nuclear bodies and has a transactivation function for *Hes3*, increasing testosterone production, assumed to be due to regulation of *Sf1* (68). Recent findings show that a gain of function mutation in *MAMDL1* was present in a 46,XX DSD woman with virilization (clitoromegaly, streak gonads and small uterus), indicating this protein’s involvement in ovarian development (24, 69).

**PGD2S**: Lipocalin-type prostaglandin D2 synthase (L-PGDS) and haematopoietic prostaglandin D2 synthase (H-PGDS) are expressed in the testes and are involved in the nuclear translocation
and expression of SOX9. Knockout of l- and h-Pgds in male mice results in delayed testicular organisation and a uni- or bilateral testis migration defect. Shortly after SRY and SOX9 expression emerge, Pgd2s is expressed in mouse embryonic Sertoli cells. Pgds up-regulation is mediated by SOX9, but not by SRY (70). A large part of the mechanism causing testicular descent is still not understood but several factors, such as Hoxa-10, epidermal growth factor (EGF) and calcitonin gene-related peptide (CGRP), together with androgens and insulin-like factor 3 (Insl3), have been proposed to have a regulatory role (71, 72).

C.1. b. Ovaries

**RSPO1:** In mice, the ovarian phenotype of XX, R-spondin1 (Rspo1) -/- mutants is identical to that of Wnt4-/- female mice, marked by the similar formation of coelomic vessels and the presence of functional steroidogenic cells. This implies that the ovarian phenotype in Rspo1 -/- mice is at least in part because of the failing expression of Wnt4 in XX gonads. Wnt4-/- mice show adrenal or uterine abnormalities, in contrast to Rspo1 -/- female mice, because of the fact that Rspo1 is not expressed in adrenals or mesonephros. This indicates that activation of Wnt4 in these organs is independent of Rspo1 (73). The primary function of R-spondin1 and WNT4 may be to synergize in XX gonadal (ovarian) development to stabilize beta-catenin (74).

**WNT4:** Recent findings in a mouse model contradict the theory of a passive, default pathway of ovarian development. Wnt4 -/-XX mice display a partial sex reversal, indicating that Wnt4 acts to positively regulate ovary differentiation. Wnt4 may also stimulate the proliferation of female germ cells, as shown by the lower number of oocytes in the ovaries of these knock-out mice. Produced in ovarian somatic cells (pre-granulosa cells), WNT4 is a member of the WNT family of secreted molecules acting in a paracrine manner. WNT4 has a significant role in affecting a number of developmental changes. Wnt4 up-regulates Dax1, a gene known to antagonize Sf1, and thereby inhibits steroidogenic enzymes (75). Initially detected in mice in the mesonephric mesenchyme and coelomic epithelium from 9.5 dpc onwards, Wnt4 is also expressed in the mesenchyme of the indifferent gonad and the mesonephros of both sexes at 11 dpc. However, it
is downregulated in the male gonad 12 hours later. The expression is present in both the mesonephroi and in the female gonads as well as the mesenchyme surrounding the Müllerian ducts (76). It appears that Wnt4 has several functions in sexual differentiation. It is needed in the bipotential stage for initial Müllerian duct morphogenesis in both sexes (76). Wnt4 also is an inhibiting factor in the development of the male specific vascularization in the ovary and is vital in separation of adrenal steroidogenic cells from the male and female gonadal primordium (77).

**FOXL2:** FOXL2 is a single-exon gene encoding a nuclear forkhead/winged helix (fkh) transcription factor. In murine gonads, its expression starts from 12.5 dpc in a female specific manner and its pattern is conserved between different phyla. It is first expressed in mesenchymal pregranulosa cells and subsequently in granulosa cells (78). FOXL2 is suspected to contribute to granulosa cell differentiation and ovary maintenance because it is still strongly expressed in postnatal and adult follicular cells. However, there are only a few transcriptional targets described until now despite the significance of FOXL2 in ovarian development and maintenance (79). In the context of the pituitary, the expression of the gonadotropin-releasing hormone (GnRH) receptor appears to be stimulated by FOXL2 (79). Human blepharophimosis-ptosis-epicanthus inversus syndrome (BPES) is caused by a mutation in the FOXL2 gene. It has been proposed that in males, SRY (or SOX9 itself) would repress Z, a repressor of the male pathway. Without Z, SOX9 will be expressed, testis will develop and XX sex reversal will begin. (10, 80, 81)

**C.1. c. Müllerian ducts**

**AMH:** This hormone signals via two transmembrane receptors, type II (which is specific) and type I, (which is shared with the bone morphogenetic proteins). Produced by fetal Sertoli cells, AMH is responsible for regression of the Müllerian ducts, Mutations in AMH and AMH receptor type II (AMHR-II) genes will cause the uterus and Fallopian tubes to persist in males and are therefore involved in the Persistent Müllerian Duct Syndrome (82).
HOXA10: As a member of a family of conserved regulatory molecules, HOXA10 controls aspects of morphogenesis and cell differentiation in the development of the embryo. It is vital for the development of the Müllerian tract in the embryonic period, but is also expressed in the adult uterus. Hox gene expression is regulated by sex steroids during embryonic life and during endometrial development in the menstrual cycle. Emx2 and b3-integrin acting downstream of Hoxa10 are likely involved in both of these developmental processes (83).

Lim1/LHX1: Lim1/LHX1 encodes a LIM-class homeodomain transcription factor that is necessary for head and kidney development. In the developing urogenital system, Lim1 expression is detected in the Wolffian (mesonephric) duct, the mesonephros, metanephros and fetal gonads. Lim1 expression in the Müllerian duct is related to its formation and differentiation in females and its regression in males. Female Lim1-null neonates mice have ovaries; however, they lack a uterus and oviducts, indicating that Lim1 is required for Müllerian duct epithelium formation (84). The effect of Lim1 mutations in human have not yet been described. (85)

II. DISORDERS OF SEX DEVELOPMENT

A. Nomenclature and definition

The term Disorder of Sex Development (DSD) is used for any congenital condition associated with atypical chromosomal, gonadal or anatomical sex. In recent publications proposed subcategories are 46,XY DSD, 46,XX DSD and sex chromosome DSD. More specific terms are preferred over general terms but this depends on the availability of a further diagnostic classification, for instance based on a primary genetic defect (86).

As shown in figure 7, the primary root is based on the karyotype, the shaded row explains the disorders as the secondary root, and actual diagnoses are listed under each secondary root. The actual diagnosis is often based on the results of molecular, biochemical, or histological examination (87). Research in past decades has contributed a lot in explaining the physiology of sexual development and differentiation. This has made a significant input in understanding the mechanisms involved in gonadal maldevelopment as several genes have been discovered to be
vital in the development of male and female gonads. Mutation analysis of genes associated with these factors in patients with genital disorders has been shown to play an important role.

Figure 7. DSD classification

<table>
<thead>
<tr>
<th>Sex chromosome</th>
<th>46,XY DSD</th>
<th>46,XX DSD</th>
</tr>
</thead>
<tbody>
<tr>
<td>A: 45,X (Turner Syndrome and variants)</td>
<td>A: Disorders of gonadal (testicular) development</td>
<td>A: Disorders of gonadal (ovarian) development</td>
</tr>
<tr>
<td></td>
<td>1. Complete gonadal dysgenesis (Swyer syndrome)</td>
<td>1. Ovotesticular DSD</td>
</tr>
<tr>
<td>B: 47,XXY (Klinefelter Syndrome and variants)</td>
<td>2. Partial gonadal dysgenesis</td>
<td>2. Testicular DSD (e.g. SRY+, dup SOX9)</td>
</tr>
<tr>
<td></td>
<td>4. Ovotesticular DSD</td>
<td></td>
</tr>
<tr>
<td>C: 45,X/46,XY (mixed gonadal dysgenesis, ovotesticular DSD)</td>
<td>B: Disorders in androgen synthesis or action</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1. Androgen biosynthesis defect (e.g. 17-hydroxysteroid dehydrogenase deficiency, 5α reductase deficiency, StAR mutations)</td>
<td>2. Fetoplacental (aromatase deficiency, POR)</td>
</tr>
<tr>
<td>D: 46,XX/46,XY (chimeric, ovotesticular DSD)</td>
<td>2. Defect in androgen action (e.g. CAIS, PAIS)</td>
<td>3. Maternal (luteoma, exogenous, etc.)</td>
</tr>
<tr>
<td></td>
<td>3. LH receptor defects (e.g. Leydig cell hypoplasia, aplasia)</td>
<td>C: Other (e.g. cloacalextrophy, vaginal atresia, MURCS, other syndromes)</td>
</tr>
<tr>
<td></td>
<td>4. Disorders of AMH and AMH receptor (Persistent Mullerian Duct Syndrome)</td>
<td></td>
</tr>
</tbody>
</table>
A.1. 46,XY DSD

46,XY DSD patients are distinguished by ambiguous or undervirilized external genitalia due to incomplete intrauterine masculinization and the presence or absence of Mullerian structures. Patients with complete absence of virilization have normal female external genitalia, but due to the absence of breast development and/or to primary amenorrhea, these patients are often discovered only at a pubertal age (88).

46,XY DSD due to gonadal dysgenesis

As a genetically heterogeneous disorder with autosomal, X and Y-linked forms, gonadal dysgenesis occurs as the result of an impairment during formation of the primordia of the gonads related to the two major elements of the fetal testes, the Sertoli cells that secrete AMH and the Leydig cells that secrete testosterone. Gonadal dysgenesis covers clinical conditions with abnormal fetal gonad development which include both complete and partial forms. The characteristics of complete gonadal dysgenesis are displayed as female external and internal genitalia, lack of secondary sexual characteristics, normal or even tall stature with no Turner syndrome stigmata and bilateral dysgenetic (streak) gonads. The partial form includes conditions where external genitalia may be ambiguous with impaired testicular development also resulting in presence or absence of Mullerian structures. A similar phenotype can also result from a mosaic 45,X/46,XY karyotype (88). 46,XY gonadal dysgenesis is a heterogeneous disorder, which can be caused by SRY deletions or point mutations, dosage sensitive sex (DSS) locus duplication on the X chromosome or mutations in autosomal genes (88). Very often no gene mutation is found but candidate genes observed on the basis of knowledge of the phenotype of mouse knockout models include DAX1, SF1, WNT4, SOX3, LHX9 and FOG2 (89).

46,XY DSD due to Androgen synthesis or action defects

Aforementioned as disorders of androgen production, these conditions are caused by inability to produce testosterone due to defects in any of the enzymes required to synthesize testosterone from cholesterol. It could occur in all stages of testosterone biosynthesis and secretion carried out by the fetal Leydig cells, as well as in the conversion of testosterone into
5α-dihydrotestosterone (DHT) (90). Patients with 46,XY DSD secondary to defects in androgen production reveal a variable phenotype, which depends strongly on the specific mutated gene. Generally, these conditions are detected at birth because of the ambiguity of external genitalia. However, the diagnosis for patients with extremely undervirilised genitalia is often not made until late childhood or even adulthood (90).

The typical phenotype of 46,XY DSD due to impaired androgen synthesis varies from female external genitalia to male external genitalia in which specific characteristics are cause-dependent.

Table 2. Classification of 46,XY DSD caused by impaired androgen production (90)

- 46,XY DSD due to Impaired Leydig cell differentiation (LHCGR defects)
- 46,XY DSD due to Testosterone synthesis defects
  - 46,XY DSD due to Cholesterol synthesis defects
    - Smith-Lemli-Opitz syndrome
  - 46,XY DSD due to Enzymatic defects in adrenal and testicular steroidogenesis
    - StAR deficiency
    - P450scc deficiency
    - 3ß-hydroxysteroid dehydrogenase type II deficiency
    - 17-hydroxylase and 17,20 lyase deficiency
- 46,XY DSD due to enzymatic defects in testicular steroidogenesis
  - Isolated 17,20-lyase deficiency
  - 17β-hydroxysteroid dehydrogenase type III deficiency
- 46,XY DSD due to altered steroidogenesis due to disrupted electron transfer
  - P450 oxidoreductase defect
  - cytochrome b5 defect
- 46,XY DSD due to testosterone metabolism defects
  - 5α-reductase type 2 deficiency
The complete form of 46,XY due to impaired or inactivated Leydig cell differentiation features female external genitalia leading to female sex assignment, without any development of sexual characteristics at puberty, undescended testes, which are slightly smaller than normal with rather conserved seminiferous tubules and the absence of mature Leydig cells. Epidydimis and vas deferens are present but uterus and fallopian tubes are absent (90).

Partial inactivation of the hCG/LH receptor could cause a broad range of phenotypes. The majority of cases with this condition have predominantly male external genitalia with micropenis and/or hypospadias. Testes are undescended or in the scrotum (91). In contrast, activating mutations of this receptor will lead to familial male limited gonadotropin-independent precocious puberty (FMPP) or testotoxicosis (92).

The major androgens acting in the androgenic cascade are testosterone and DHT. The 5α-reductase type II (SRD5A2) deficiency is a defect in the conversion of T to DHT in (mostly) extratesticular target tissues, which is known as a part of the ‘androgen insensitivity syndromes’ (AISs). However, at present, 5α-reductase deficiency is classified as a special form of androgen-biosynthesis defect.

Predominantly female phenotype at birth followed by virilization at puberty is a characteristic of mutation of \textit{SRD5A2} gene (93). Ideally the diagnosis 5α-reductase type 2 deficiency should be made as early as possible in infancy using biochemical techniques and confirmed by molecular genetic analysis. Ratio of plasma testosterone:dihydrotestosterone (T:DHT) >8.5 has been indicated for identifying 5α-reductase type 2 deficiency, especially during the neonatal period (93, 94). The phenotypes of newborn 46,XY DSD with partial androgen insensitivity syndrome or 17-hydroxysteroid dehydrogenase deficiency may be indistinguishable from the phenotype of 5α-reductase type 2 deficiency (95).

As the main player in the translation of androgen action, the androgen receptor (AR) is a nuclear transcription factor that binds various androgenic steroids as ligands and acts through differential DNA targeting and genetic control afterward. The complete form of androgen
insensitivity syndrome (CAIS) is a condition of absolute absence of androgen action, whereas the partial form (PAIS) occurs as a result of variable degrees of androgen action impairment (88).

Since the description of the genetic structure of the AR, it is commonly acknowledged that most 46,XY patients with a presumed defect of androgen action carry mutations in the coding regions of the AR gene. This has been confirmed in the majority of patients with CAIS, but patients who were clinically assigned as PAIS or minimal AIS (MAIS) to a certain extent do not carry relevant mutations in the AR (96).

Patients with AIS will have a clinical phenotype that is consistent with the extent of remaining activity of the AR. However, because testicular function appears to be normal in AIS, the size and histology of the testes may be normal in childhood. Due to normal AMH synthesis and action, Müllerian structures are absent. Thus during clinical investigation, in childhood AIS cannot be differentiated from disorders of testicular androgen biosynthesis.

In CAIS, the external genitalia appear to be female. The gonads may be seen in the labia majora or in the inguinal region, but they may also be impalpable during clinical investigation as they may be located intra-abdominally. In infancy, a diagnosis is made on the fact that Müllerian structures (i.e., oviducts, uterus and the upper part of the vagina) are absent, in addition to phallic hypospadias or absence of androgen-dependent Wolffian structures, mainly the lack of epididymis as well as the prostate during either ultrasound investigation or surgical exploration.

The phenotype of PAIS is highly variable, ranging from minor signs of virilization, shown by an elongated ano-vaginal distance, through explicit signs of androgen action with rugation of labio-scrotal folds, urogenital sinus, phallic enlargement to a feature of predominantly male phenotype with appearance of normal male phallic size, despite moderate to severe hypospadias. However, in most of PAIS cases, reduction of phallic size is observed in conjunction with severe, mostly penoscrotal to perineal hypospadias. The specific clinical appearance of AIS becomes more visible during puberty when serum levels of testosterone, LH and estradiol are elevated. Due to dysfunction of androgen action, the negative feedback regulation of LH is impaired, resulting in elevated LH levels despite increased testosterone levels. Estradiol levels increase due to aromatisation of testosterone. This is the key feature of
pubertal development is the feminization that occurs in most of the patient with CAIS and PAIS with gonads in situ (96, 97).

Non-classified forms

Hypospadias *e causa ignota* is a rather common phenomenon, where 40% of the cases are related to other defects of the urogenital system. Generally, it is a sporadic phenomenon, but familial cases do exist. When hypospadias is present, it indicates that an alteration in testosterone secretion or action may have occurred during intra-uterine development. Fukami et al. explained this phenotype on basis of mutations in an X-linked gene, *CXorf6*, in three boys with penoscrotal hypospadias and micropenis (87). The presence of penoscrotal hypospadias along with decreased penis size requires assessment of testicular function in order to rule out causes such as defects in testosterone synthesis and action, which require not just surgical treatment, but also hormonal treatment and genetic counseling (88).

The time trends of prevalence of hypospadias in countries worldwide are not consistent. Some countries like Australia (98), Denmark (99), and the United Kingdom (100) have reported increasing trends of prevalence, whereas Japan (101), Scotland (102), and the U.S.A. states of New York (103), Washington (104), and California (105) have reported no significant increases.

Regional differences in hypospadias prevalence have also been reported. The prevalences of overall and isolated hypospadias in China were 9.03 and 7.64 per 10,000 male births, respectively, and lower than reported for other countries or regions (106). For example, the total prevalence of hypospadias was 34.9 per 10,000 live births in New York in 1992 to 2005 (Fisch et al., 2009), 29 per 10,000 male births in Bulgaria (Kumanov et al., 2007), 31 per 10,000 male births in northern England in 1993 to 2000 (Abdullah et al., 2007)

A.2. 46,XX DSD

46,XX DSD consists of disorders of ovarian development, disorders of androgen synthesis and other conditions affecting sex development (107). In rare cases, such as ovotesticular DSD, the developing ovary may contain some testicular tissue. The developing ovary may also lead to a functioning testis that secretes ample amounts of testosterone for
adequate virilization and AMH for regression of the Müllerian ducts, which is called testicular DSD (87).

46,XX ovotesticular or Testicular DSD

The developing ovary may contain testis tissue (ovotesticular) or may function as a testis that secretes amounts of testosterone and AMH which could make adequate virilization and müllerian regression possible (testicular DSD). Ambiguous genitalia are an initial manifestation in almost all cases of ovotesticular DSD with gradation of internal genitalia between male and female.

46,XX testicular DSD commonly results in a normal male phenotype or a relatively mild abnormality of the male genitalia, such as distal or mid-shaft hypospadias. In adulthood, testosterone synthesis is not affected even though spermatogenesis is usually severely affected (87).

Ovarian dysgenesis.

Ovarian dysgenesis is commonly associated with sex chromosome aneuploidy such as Turner syndrome and related variants. However, the condition does not cause physical abnormalities of sex development in infancy (87).

46,XX DSD due to disorders of androgen synthesis

A fetus with a 46,XX chromosomal complement and normal ovarian organogenesis could be exposed to excessive amounts of androgens originating either from the fetus itself or from the mother. The congenital adrenal hyperplasias (CAHs) are disorders of impaired cortisol biosynthesis and the most frequent cause of ambiguous genitalia of the newborn with 46,XX karyotype (89). Low levels of cortisol are causing reduction of feedback inhibition and therefore increased ACTH secretion, which results in hyperplasia of the adrenals and in disorder of steroidogenesis.

Clinical signs of these diseases are based on three conditions: the transformation of cortisol precursors to steroids normally produced in much lower amounts; the biological
activities of these cortisol precursors, which accumulate prior to the block and the deficiency of cortisol and other steroids normally produced by the adrenal and sometimes also the gonads (108). Most of the cases of CAH are caused by the 21-hydroxylase deficiency. A newborn girl with this disease may show virilization to a certain extent. High serum concentrations of 17-hydroxyprogesterone (>300 nmol/l) are present after the first 48 h of life and high androstenedione and testosterone in the early neonatal period are the biochemical characteristic of this condition. Due to a deficiency of mineralocorticoid synthesis, more than 75% of these infants will be salt-losers and the condition of salt-losing crisis will present in the second or third week of life (87).

The manifestation in each CAH patient varies depending on the severity of the enzyme deficiency, the other steroid pathways that are disrupted, the ethnic background, and additional genetic and environmental factors, which are correlated to the level of severity of the disease, many of which are unidentified (108).

Figure 8. Steroidogenesis scheme
Virilization in a female fetus can also be caused by a maternal source of elevated androgens. Ovarian tumours such as luteomas of pregnancy, arrhenoblastomas, hilar-cell tumours, masculinising ovarian stromal cell tumours and Krukenberg tumours are all androgen producing tumours. Even if the mother is overproducing androgens, the female offspring is exposed to relatively minimal androgenic effects. The less active virilization is due to placental aromatase activity, converting androgens into estrogens. Another factor inducing fetal virilization can be caused by the maternal ingestion of androgens, progestagens or other drugs.

Exogenous steroids consumed during pregnancy may result in posterior fusion of the labia, clitoral enlargement and even increased degrees of androgenization (87). Glucocorticoid resistance, although it is a rare case, leads to increased ACTH production, which in turn causes an increase in androgen production (109).

**46,XX DSD due to other conditions affecting sex development**

Complex urogenital abnormalities such as cloacal anomalies may occur in both sexes and require major reconstructive surgery. Disorders of müllerian development can be related to renal, cardiac or spinal abnormalities as part of the Mayer–Rokitansky–Kuster–Hauser (MRKH) syndrome or müllerian, renal, cervical spine syndrome (MURCS) (87, 110). In special cases, the absence of müllerian structures, and the presence of co-existing hyper-androgenaemia, has been associated with a mutation in the WNT4 gene (111).

**III. GENERAL PRINCIPLES OF DSD MANAGEMENT**

Either in the newborn baby or in the newly presenting adolescent, a comprehensive management is required once a patient with a disorder of sex development (DSD) is detected. The complexity of the treatment poses a difficult challenge for health-care professionals (86, 110, 112).
Based on consensus, the primary recommendations to manage the patient with DSD can be summarized as follows:

1. Sex assignment of all newborn infants with DSD should be based on consultation and diagnosis of a multidisciplinary team that includes an endocrinologist, urologist / surgeon, psychologist / psychiatrist, geneticist, neonatologist and gynecologist and, if possible, social workers, nursing and ethics specialists.

2. If the diagnosis is in doubt, a hasty decision about sex assignment must be avoided and expert evaluation should be sought.

3. When an infant with DSD is born, all specialists of the neonatal units are expected to manage the critically unwell newborn, while an experienced multidisciplinary team conducts a holistic evaluation and develops a long-term management strategy at a specialized center.

4. The specialized center is expected to complete first-line investigations sufficient for sex assignment and exclusion of immediate medical concerns; afterwards, the center should develop a plan for second-line investigations which will result in a long-term management plan for the child.

5. Implementing a holistic patient centered approach and individualized management, the team should make evidence based decisions as far as possible. Patient’s family should be informed of decisions that are not evidence based.

6. Patient and family concerns should be respected and addressed in strict confidence.

7. The relationship between team and family should include open communication, active involvement in decision making, attention to concerns and respect for privacy.

8. The multidisciplinary specialist team should be able to arrange or even provide a long-term care from infancy to adulthood for the patients.
A. Clinical evaluation of the infant with a suspected DSD

It is crucial that all professionals involved with the management of newborn babies (during labor and in the postnatal ward) are well-informed about the procedure of treating an infant with indeterminate sex. Health care professionals should regularly inform the family about the situation, taking into account the level of understanding as well as their religious and cultural beliefs (112).

An extensive investigation must be conducted, when the appearance of the external genitalia is sufficiently ambiguous to make sex assignment impossible; or when the phenotype is not consistent with prenatal genetic tests (107).

Gathering related information about the family is vital, such as consanguinity, stillbirths, multiple miscarriages, fertility problems, genital abnormalities, hernias, delayed puberty, genital surgery, unexplained deaths and the need for steroid replacement. In addition, maternal health and drug exposure during pregnancy and the pregnancy history should be collected, for it may hold important information. The patient is expected to have a general physical examination that focuses on any related dysmorphic features, and an assessment of the genital anatomy.

Information on the following points should be included at referral for further investigation by a specialist: overt genital ambiguity (cloacal exstrophy); female genitalia with an enlarged clitoris, posterior labial fusion, or an inguinal/labial mass; male genitalia with bilateral undescended testes, isolated micropenis, isolated perineal hypospadias, or mild hypospadias with undescended testes; any form of familial hypospadias and those who have a combination of genital anomalies with an External Masculinization Score (EMS) of <11 which is based upon the site of uretral opening, the severity of the micropenis, the degree of scrotal fusion, and the position of the gonads (figure 9), family history of DSD such as CAIS; a discordance between genital appearance and a prenatal karyotype (107).
Figure 9. External masculinization score (EMS) for assessing the degree of under androgenization in an individual with 46,XY DSD (87)

B. Surgical management

In this procedure, the surgeon (pediatric surgeon or pediatric urologist) will sketch the surgical sequence and its consequences from infancy to adulthood. Information obtained at early evaluation will accommodate the surgeon in envisaging an image of the genitalia at presentation, with regard to all the changes that may occur in the early months of life. Subsequently, the surgeon will decide on what investigations are the most appropriate for the diagnosis, as well as to guide decisions about the sex of rearing (cystoscopy, vaginoscopy, laparoscopy and so on).

Finally, the surgeon will consider about the type and the quantity of surgical procedures needed as well as the involvement of other surgical specialists (e.g., gynecologist) in order to create the desired outcome. The fundamental aim of delivering functional outcome should be taken into account, rather than a strictly cosmetic appearance. Additionally, it is recommended that the surgeons performing these procedures are only those who have an expertise in the care of children and specific training in the surgery of DSD (110, 112).
C. Psychosocial management

It is known that physical and psychological health for DSD patients are closely interrelated. Psychosocial care should not be separated from the management of the DSD patient, in order to promote positive adaptation and to allow parents to express and resolve their concern. Skill in psychosocial care is beneficial in facilitating team decisions about gender assignment/reassignment, timing of surgery, and sex hormone replacement (110, 112). Due to the degree of complexity and sensitivity of the disease, an experience of working with individuals and families with DSD is advantageous in dealing with the issues that commonly arise. Psychological input should be treated as a process instead of an event; therefore, the contact with a psychology team is implemented. Specific tasks may be required at different stages of development; therefore the family should be involved in planning from an early stage. Pacing and timing of disseminating the information and making decisions is specific to each individual circumstance.

Studies in other chronic medical disorders and of adoptees reveal that disclosure should be correlated with or is dependent on patient’s improving psychosocial adaptation (112, 113).
References


Chapter 3

Application of the New Classification on Patients with a Disorder of Sex Development (DSD) in Indonesia


PMID: 22253624
Abstract

Disorder of Sex Development (DSD) patients in Indonesia most often does not receive a proper diagnostic evaluation and treatment. This study intended to categorize 88 Indonesian patients in accordance with the new consensus DSD algorithm. Diagnostic evaluation including clinical, hormonal, genetic, imaging, surgical and histological parameters was performed. Fifty-three patients were raised as male and 34 as female. Of 22 patients with 46,XX DSD, 15 had congenital adrenal hyperplasia while in one patient an ovarian Leydig cell tumor was found. In all 58 46,XY DSD patients, 29 were suspected of a disorder of androgen action (12 with an androgen receptor mutation), in 9 gonadal dysgenesis was found and in 20 severe hypospadias e.c.i. Implementation of the current consensus statement in a resource–poor environment is very difficult. The aim of the diagnostic work up in developing countries should be to end up with an evidence based diagnosis. This is essential to improve treatment and thereby to improve the patients’ quality of life.
INTRODUCTION

The sequential expression of many genes is essential for gonadal development in the male as well as in the female (1, 2). In addition, timely secretion and action of hormones such as androgens and Anti-Müllerian Hormone (AMH) are crucial for normal male development (3). Mutation analysis of genes related to these factors in patients with genital disorders has substantiated their essential role (4-7). Therefore, in a number of cases a specific diagnosis can be made by mutation analysis. Disorders of sex development (DSD) are defined as congenital conditions in which development of chromosomal, gonadal, or anatomical sex is atypical (8). In patients categorized under the term 46,XY or 46,XX DSD with anomalies of gonadal development, often no specific etiology can be established (9). Yet, the establishment of a specific diagnosis is relevant with regard to proper gender assignment as well as regarding hormonal and surgical treatment. Moreover, patients with various forms of 46,XY DSD and Chromosomal DSD are at a substantially increased risk of developing gonadal germ cell tumors (10).

In Indonesia, patients presenting with DSD most often do not receive a diagnostic evaluation and there are limited options for medical and surgical treatment. In this study we performed a diagnostic evaluation in 88 patients with DSD referred to a major Centre in Semarang, Indonesia. The aim of this study was to categorize the patients in accordance with the nomenclature proposed in the new consensus statement (8). Therefore we performed a diagnostic evaluation including clinical and hormonal parameters. Furthermore results from imaging and surgery as well as genetic and histological parameters were evaluated.

SUBJECT AND METHODS

Subjects

Eighty-eight patients (from 84 index patients) with various forms and degrees of DSD were evaluated consecutively. They were referred for chromosomal analysis by clinicians of the departments of Urology, Pediatrics, Internal Medicine and Obstetrics of the Dr Kariadi Hospital, Semarang, Indonesia. Referral took place between 2004 and 2006 to the department of Human
Genetics Center for Biomedical Research, Faculty of Medicine Diponegoro University (FMDU), Semarang. Reason of referral was the presence of ambiguous genitalia or any anatomical abnormality of external or internal genitalia, including penoscrotal hypospadias, with or without descended testes. Patients with sex chromosome aberrations were included except patients with classical Klinefelter (47, XXY) and Turner syndromes (45, XO). In addition four patients with cloacal malformation were excluded.

All patients were recalled to the hospital for a physical examination, pedigree construction and collection of blood for hormonal and gene mutation analyses. The age at initial presentation was also the age of investigation and the start of follow up in 87 patients, one patient with presumptive CAH already received suppletion therapy for 9 months. The local medical ethics committee approved this study and informed consent was obtained from all participants, their parents or guardians.

Methods

A stepwise diagnostic approach (figure 1) was used in order to determine the diagnosis in each patient. First of all the patients were clinically evaluated, a detailed description of the external genitalia was obtained and the genitalia were staged according to Quigley (11). The assigned gender was also recorded. Subsequently chromosomal patterns were determined and based on the results the patients were categorized according to the primary root of the recent classification (8): 46,XY DSD, 46,XX DSD or chromosomal DSD. In all patients a blood sample was obtained for hormonal and gene analysis; in patients with 46,XY DSD or Y containing chromosomal DSD an additional blood sample was obtained 72 hr after the intramuscular injection of 1500 IU hCG (Pregnyl ®Organon,Oss, The Netherlands). The hCG test was not performed in 11 patients for the following reasons: the gonads had been removed (n=3), logistic reasons (n=7) and in one patient hCG therapy had been started by the referring doctor in order to enlarge the penis. Subsequently imaging was offered to all the patients as well as surgery in the form of a laparoscopy or cystoscopy whenever needed for diagnostic options or for gonadectomy in case of a high tumor risk. Based on the results, a differential diagnosis was made followed by
gene mutation analysis. Finally gonadal samples were analyzed when they were available in order to complete the classification.

**Chromosome analysis**

Karyotype was established using a G-banding technique in the Molecular and Cytogenetics Laboratory of the Center for Biomedical Research of FMDU (Semarang). G-banding was also performed for confirmation of the presence of the Y chromosome.

**Serum hormones**

Serum determinations of Inhibin B, AMH, LH and FSH in the basal serum samples were performed in the endocrine laboratory of Erasmus MC (Rotterdam) as described previously (12). Testosterone was determined in serum collected before and after injection of hCG using the Coat-a-Count radioimmunoassay purchased from Siemens (Los Angeles, CA). (12). Androstenedione, dehydroepiandrosterone sulphate and progesterone were also measured in these samples using the Immulite 2000 (Siemens). Finally, 17-hydroxyprogesterone levels were estimated using an in house method (13). Reference values were used as described earlier (12, 14).

**Gene analysis**

DNA was extracted from leucocytes of EDTA blood using the salting out method as described earlier (15). Based on the clinical and hormonal information, specific genes were analysed such as \( \text{CYP21A2} \), and \( \text{LHR} \) (6). \( \text{AR} \), \( \text{SRY} \) and \( \text{WNT4} \) were analysed by direct sequence analysis of the coding exons and exon-flanking intronic regions (reference sequence \( \text{AR} \): \text{nm}_000044 \) (numbering according to Gottlieb et al (18), \( \text{SRY} \): \text{X53772.1} \) and \( \text{WNT4} \): \text{nm}_030761 \). Primer sequences and locations are available upon request.

**Pathology:**

Histopathological assessments were performed by means of hematoxylin and eosin stainings and immunohistochemistry for various markers of germ cells, e.g. OCT3/4, TSPY,
VASA, SCF (including double staining for OCT3/4-TSPY or VASA); as well as SOX 9 and FOXL2 for supportive cells (19).

RESULTS

For a stepwise diagnostic approach the algorithm shown in figure 1 was followed.

1. Clinical evaluation and chromosome determination

All 88 patients were categorized according to their karyotype; there were 22 patients with 46,XX DSD, 58 patients with 46,XY DSD and eight patients with chromosomal DSD. Data on age, sex of rearing and Quigley stage (11) of the 88 patients are provided in table 1. The majority of patients were older than two years at the time of referral; only six patients were referred below the age of one year (figure 2). The group of 88 patients contains four families with one or more patients with DSD (a total of nine). There was no known consanguinity of the parents. Fifty-three patients were raised as male and 34 as female while one patient’s gender was undetermined due to early age; 16 patients (19%) were raised discordant with their genotype (two males with karyotype 46,XX and 14 females with karyotype 46,XY). Two 46,XY patients changed gender from female into male during the study and one patient with a 46,XX karyotype decided to live as a male. One patient with presumed androgen excess died one week after inclusion without gender assignment.
Table 1: Phenotype (Quigley stage) in correlation with the DSD classification, and sex of rearing. NA: not assigned, patient died after inclusion but before gender assignment

<table>
<thead>
<tr>
<th>Classification</th>
<th>Quigley stage</th>
<th>sex of rearing</th>
<th>NA</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>46, XX DSD</td>
<td>3</td>
<td>5</td>
<td>6</td>
</tr>
<tr>
<td>46 XY DSD</td>
<td>4</td>
<td>22</td>
<td>22</td>
</tr>
<tr>
<td>Chrom. DSD</td>
<td>1</td>
<td>3</td>
<td>0</td>
</tr>
</tbody>
</table>

Figure 1: Stepwise diagnostic approach. An algorithm used with the aim to classify the patients following the new classification system (8). Row number 1 represents the clinical evaluation of the patients and classification following the primary root; number 2 the hormonal analysis and imaging followed by the secondary root classification. Row number 4 shows the percentage mutations that were found and 5 the gonadal histology leading to the tertiary root and final classification of the patients. Explanation of abbreviations: GR: glucocorticoid receptor; MRS: Mayer – Rokitansky Syndrome; XX-M; XX male; OV-TU; ovotesticular DSD.
2. Hormonal Analysis, imaging and surgery

46,XX DSD

Hormonal analysis showed that out of the 22 46,XX patients, 15 patients (68%) had serum values of adrenal steroids suggesting CAH. Fourteen of these 15 patients showed marked elevation of levels of 17-hydroxyprogesterone, androstenedione and testosterone. In the remaining patient these values were in the normal range as she already received corticosteroid suppletion therapy before referral. No patients with the salt wasting form of CAH were found. As expected, AMH and inhibin B levels were all in normal range for females (data not shown). In one patient with no history of steroid medication, adrenal steroid levels including cortisol were suggestive of cortisol resistance. This could not be confirmed by sequencing the glucocorticoid receptor gene, however.

Extremely high testosterone levels (basal level of 59.9 nmol/l) and slightly increased values of gonadotrophins (LH: 12.3 IU/L, FSH: 8.1 IU/L) were identified in one 33 years-old patient with Quigley stage 4, phallus length 2.5 cm, and a low voice. Four patients had normal
ovarian and adrenal hormone levels and in view of the clinical presentation were suspected of having the Mayer – Rokitansky Syndrome (20).

One 11 years-old patient with the 46,XX male syndrome with palpable gonads in the scrotum had normal FSH and testosterone levels but low LH, AMH and Inhibin B levels for boys of this age. Testosterone rose from 0.3 to 3.4 nmol/l in response to hCG, suggesting that there were functional Leydig cells.

Only in 12 of the 22 patients that were eligible, a diagnostic ultrasound was performed. In seven patients surgery was advised, again only in two (28 %) patients diagnostic surgery in the form of a laparoscopy or cystoscopy was done. The remaining patients refused because of economic reasons.

46,XY DSD

In all 58 patients basal hormonal measurements were obtained. LH levels were elevated in nine patients, decreased in 35 patients and normal for age in 14. FSH levels were elevated in 18 patients and in the normal range in the remaining 40. Finally testosterone levels were elevated in 15 patients, decreased in 36 patients and normal in seven patients. Twelve patients showed elevated levels of AMH, 27 patients had levels in the normal range and 17 patients had decreased levels of AMH. In one patient, after gonadectomy, AMH was not determined.

Inhibin B levels were elevated in 17 patients, normal in 27 patients and decreased in 14 patients. An hCG test was performed in 47/58 patients (see methods), 45 patients showed a sufficient response of testosterone and its precursors. In two patients with a decreased response Leydig cell hypoplasia was suspected. Due to lack of material we could not test for DHT.

Diagnostic ultrasound was performed in 11 out of 58 (19%) patients and only in five (9 %) patients diagnostic procedures in the form of a cystoscopy were performed. In two (9 %) of the 21 eligible patients a gonadectomy was performed. The remaining patients refused because of economic and cultural reasons.
Chromosomal DSD

The karyotype of the eight patients is provided in table 2. The basal level of LH was increased for age in one patient. The level of FSH was elevated in two patients (age 2 and 33 years) with low levels of Inhibin B in comparison with male values, while AMH and Inhibin B were increased in comparison to normal female levels.

Ultrasound was performed in five out of eight (62.5 %) patients. In one (12.5%) patient a diagnostic procedure in the form of a cystoscopy was done. In only one (12.5%) of the eight eligible patients a gonadectomy was performed. The remaining patients refused because of economic and cultural reasons. Efforts to follow up on these patients have been performed.

<table>
<thead>
<tr>
<th>Karyotype</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>XXY/XY</td>
<td>2</td>
</tr>
<tr>
<td>XY/X</td>
<td>2</td>
</tr>
<tr>
<td>XX/XXq-</td>
<td>2</td>
</tr>
<tr>
<td>XY/XX</td>
<td>1</td>
</tr>
<tr>
<td>XX/XXY</td>
<td>1</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>8</strong></td>
</tr>
</tbody>
</table>

3. Secondary root classification

Based on the hormonal evaluation, imaging and diagnostic surgery, the following secondary root categorization was made.

46,XX DSD

Fifteen patients were suspected of congenital adrenal hyperplasia, one patient of a glucocorticoid receptor defect, four patients with Mayer – Rokitansky Syndrome, one patient with XX male syndrome and one patient with Ovotesticular DSD.

46,XY DSD

Twenty nine patients were suspected of a disorder of androgen action, nine with a disorder of gonadal development and 20 with severe hypospadias. We did not establish the
diagnosis testosterone synthesis disorders in any of the patients, but we cannot rule out the presence of 5-alpha-reductase deficiency in our patients without a definitive diagnosis and a normal response of 5α-dihydrotestosterone (DHT) levels to hCG.

**Chromosomal DSD**

All patients were categorized under the second root diagnosis disorders of gonadal development (Gonadal dysgenesis).

**4. Mutation analysis**

Based on these results mutation analysis was performed.

**46,XX DSD**

Based on their phenotype, hormonal and chromosomal analysis, CYP21A2 analysis was performed in 15 patients and indeed CYP 21 gene mutations were found in all of them (16). In four patients, clinically suspected of having Mayer – Rokitansky syndrome WNT4 gene analysis was negative. One patient was suspected of a glucocorticoid receptor defect, however, a mutation in the sequence of this receptor was not found.

**46,XY DSD**

Mutation analysis of the androgen receptor (AR) gene was performed in 29 patients who were suspected of having a disorder of androgen action and in 20 patients with severe hypospadias with a normal response to hCG. In two index patients (four patients) pathogenic AR mutations were found, R840H and 902insA. In an additional two patients the sequence variant V730M was found, of which it is unlikely that it is causing the phenotype; functional studies showed that this variant is an activating mutation. It has been described as a somatic variant in patients with prostate cancer (21, 22). In five index patients (six patients) unclassified variants were found, I603N, 2170T>A; P671S, 2373C>T; C175G, 885T>G and Q738R, 2575A>G; only one of these four variants (C175G) has been described at the nucleotide level. The three novel
sequence variants (I603N, P671S and Q738R) were functionally investigated (23). Further mutation analysis for the SRD5A2 should be performed for patients without AR gene mutation.

In the 20 patients with severe hypospadias no AR mutations were found. Two patients suspected of having Leydig cell hypoplasia were analyzed for a mutation in the LH receptor gene, but no mutation was found.

Chromosomal DSD

An SRY deletion was found in one patient with mosaic Klinefelter XX/XXY. In the remaining seven patients no SRY deletions were detected.

5. Gonadal Histology

Histology of the gonads was available in four patients as shown in table 3: one with 46,XX DSD (biopsy as mentioned earlier), two with 46,XY and one with chromosomal DSD (46,XY/46,XX).

One patient with 46,XX DSD had an ovarian Leydig cell tumor. In this patient, ultrasonography did not reveal abnormalities. However, a diagnostic laparoscopy showed normal adrenal glands and large ovaries. During laparoscopy a biopsy was obtained. In a 23-year-old 46,XY patient, the testis showed Leydig cell hyperplasia and atrophy of most seminiferous tubules but no evidence of CIS. A thirteen-year-old 46,XY boy was found to have Carcinoma in situ (CIS), the precursor lesion for malignant germ cell tumors, as reported recently (24). Ovarian tissue with multiple cysts including primordial follicles and granulosa cells was found without evidence of malignancy in one patient with mosaic XX/XY.

6. Final Classification

Based on the above mentioned steps in the diagnostic workup in patients with DSD syndromes a final classification was made following the current consensus statement (8). Data are shown in table 4. In sixteen 46,XX DSD patients (72%) a tertiary root classification was made, in patients with 46,XY DSD this was the case in 12 patients (21%) and in the group of patients with chromosomal DSD a tertiary root classification was made in one patient (12.5%).
Of course the last category is a special one because the chromosomal abnormalities itself are an explanation for the etiology. In the remaining patients without an identified genetic or pathologic cause of DSD, the tertiary root category had to be ‘other’.

The 6 patients aged less than one year were diagnosed as follows: androgen action disorder (2), excess androgen (2), and unknown male undermasculinization (2).

The two 46,XY patients who changed gender from female to male had the final diagnosis of androgen action disorder, while one 46,XX CYP21A2-deficient patient decided to live as a male.
### Table 3: Additional clinical data in patients with known histology results.

<table>
<thead>
<tr>
<th>Number</th>
<th>Age</th>
<th>Gender</th>
<th>Karyotype</th>
<th>Quigley Stage</th>
<th>Hormonal Analysis</th>
<th>Imaging</th>
<th>Surgery</th>
<th>Mutation</th>
<th>Histology</th>
<th>Diagnosis</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>33</td>
<td>Female</td>
<td>46 XY</td>
<td>4</td>
<td>very high testosterone</td>
<td>no abnormalities</td>
<td>laparoscopy</td>
<td>no</td>
<td>Leydig cell tumor</td>
<td>Disorder of Androgene excess</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>slightly increased values of gonadotrophines</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>23</td>
<td>Female</td>
<td>46 XY</td>
<td>6</td>
<td>high basal testosterone level</td>
<td>no abnormalities</td>
<td>gonadectomy</td>
<td>AR neg</td>
<td>Leydig cell hyperplasia and atrophy of most seminiferous tubules but no evidence of CIS</td>
<td>Disorder of Androgene action</td>
</tr>
<tr>
<td>3</td>
<td>13</td>
<td>Male</td>
<td>46 XY</td>
<td>3</td>
<td>high basal testosterone level</td>
<td>no abnormalities</td>
<td>gonadectomy</td>
<td>AR neg</td>
<td>CIS</td>
<td>PAIS</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>Male</td>
<td>46 XXXY</td>
<td>2</td>
<td>hCG test: good response to testosterone</td>
<td>no abnormalities</td>
<td>gonadectomy</td>
<td>SRY neg</td>
<td>ovarian tissue with multiple cysts including primordial follicles and granulosa cells</td>
<td>Gonadal Dysgenesis</td>
</tr>
</tbody>
</table>

*Gonads already removed before ultrasound*
DISCUSSION

Reports on presentation and age distribution of DSD patients in Asian countries are scarce and are mostly limited to CAH patients (25-27). The age of presentation of the DSD patients in our study differs greatly from the age of presentation in the western world. More than 75% of the patients were over two years old. In India 58% of the patients are referred within the first year of life (26). Reasons for this late clinical referral are a lack of awareness among primary care providers, limited diagnostic and therapeutic facilities as well as socio-economic problems. Moreover, parents are reluctant to discuss sexual issues, even with medical professionals (28). Thailand has started the multidisciplinary management of ambiguous genitalia in 1979 (27) while in Semarang, Indonesia a start was only made in 1999.

Out of 88 patients nine (10.2%) were related, spread over four families. There was no known consanguinity of the parents in any of the cases. Thus in only nine patients a familiar background suggestive of an inherited disease could be established. One family with 2 affected
children and their cousin from mother’s side had the same AR gene mutations (R840H). Identical mutations on CYP21A2 were found in 2 siblings in one family (IVS2-12A>G).

Based on physical examination, chromosomal analysis, and hormonal data and in a limited set of patients imaging and laparoscopy, the patients were categorized in accordance with the current consensus statement (8). A secondary root diagnosis was made in all patients, however, it should be noted that the secondary root includes male-under masculinization of unknown etiology, which was assigned in 20 patients (34%). However, we cannot rule out 5α-reductase deficiency in these patients.

In 15 out of 22 patients with 46,XX DSD the diagnosis CAH based on CYP21A2 mutations was made, including two familial cases. As a result of the diagnostic procedure 12 patients are presently under steroid treatment. Three patients remained untreated (parents’ request): two of them are sibs, and one of them showed a rather severe form of virilization. This patient was raised as a male and when the diagnosis of CAH was made at the age of 17 years he chose to continue to live as a male after full explanation was given. The parents decided to leave the 46,XX CAH sib (age 3 years) also untreated and are raising this child as a male. Parents of the third patient did not choose for hormonal treatment for economic reasons. One patient with presumed CAH died one week after inclusion. Because of lack of diagnostic and treatment options, it is suspected that patients with 46,XX DSD may have died from a crisis before coming to medical attention due to salt loosing CAH (29, 30).

Interestingly, one patient at first thought to have CAH turned out to have an androgen producing ovarian tumor with the histology of Leydig cell tumor. This demonstrates the value of histological examination of abdominal lesions in these patients.

One patient was categorised as 46,XX, gonadal dysgenesis. Gene mutation analysis was done in a patient suspected of a glucocorticoid receptor defect, but no mutant sequence was found (31), and in none of the four patients with the clinical diagnosis of Mayer –Rokitansky Syndrome a WNT4 mutation was detected (20).

Normal development and function of Sertoli cells and Leydig cells are essential for hormone – mediated sex differentiation of male internal and external genitalia.
In order to diagnose 46,XY DSD, determination of LH, FSH, gonadal steroids, AMH and Inhibin B levels are essential. Leydig cell activity is examined by hCG stimulation. In our patients measurement of testosterone precursors such as androstenedione, 17-OH progesterone, progesterone and DHEA did not give evidence of a testosterone synthesis disorder such as 17β-HSD or 17-20 Lyase deficiency (5, 7). Only in two patients no rise of testosterone and its precursors was observed after hCG stimulation, suggesting an LH receptor defect. However, no mutation of the LH receptor gene was found (32). In most of the patients with the clinical phenotype of Leydig cell hypoplasia no causative mutations are found (6).

In pre-pubertal patients, low AMH levels indicate malfunctioning Sertoli cells in the testis. The best marker to evaluate the presence of functional testis after puberty is inhibin B (33). Circulating concentrations of AMH remain high until puberty when they fall in response to the effect of testosterone. For this reason, we decided to categorize normal AMH values based on testosterone levels (34). We confirmed that increased AMH levels after puberty (testosterone level >6 nmol/l) are suggestive for a disorder of androgen action or synthesis. The combination of high LH and testosterone levels in undermasculinized patients also supports a defect in androgen action. However in only 12 (25 %) of the in total 48 patients with 46,XY DSD with clinical and hormonal features compatible with altered androgen sensitivity an AR mutation was found. Two of the mutations were pathogenic and four mutations were unclassified variants which in later investigation were found to be pathogenic (23). All of these patients showed the typical features of partial androgen insensitivity. It is noteworthy that 11 patients are being raised as males and only one as female. In none of the patients classified as severe (penoscrotal) hypospadias an AR mutation was found.

All patients with Chromosomal DSD had a chromosomal mozaicism. Three patients had a Klinefelter variant; all of them were raised as males.

Although imaging procedures are highly informative for the establishment of a second root diagnosis, sonography was only performed in 28/88 patients (31.8%) and a diagnostic laparoscopy or cystoscopy was done in only nine of the patients (10.2%). Limited facilities and economic problems are the main reason for these relatively low numbers. In 30/58 patients with
46,XY DSD (51.7%), genital surgery was performed such as hypospadias correction, gonadectomy and mastectomy. The rest of the patients (n=28) remained untreated mostly for economic reasons. Some patients or parents refused the advice of the gender team and just dropped out (n=9). One assumption is that the cultural reasons are of influence. Decision-making is not just based on what is recommended by the doctor, but is influenced by the family.

The risk of developing a malignant germ cell tumor is increased in patients with DSD containing Y chromosomal material, known as the Gonadoblastoma locus on the Y chromosome (GBY). This phenomenon is probably related to the expression of the TSPY gene on the Y chromosome (19). It is important to mention that a non-scrotal position of the gonad increases this risk. Pro-active clinical interference, like orchidopexy, biopsy or even gonadectomy, is recommended in patients with 46,XY DSD with maldevelopment of the testes (with or without known gene mutation such as WT1) and in addition, in patients with PAIS, especially when the gonads are in a non-palpable position (10). It is noteworthy that in our small sample of four gonadectomized patients already one patient with 46,XY DSD had developed carcinoma in situ (CIS). This is the known precursor of malignant germ cell tumors, which will progress to invasiveness in about 70% within seven years. A biopsy was not performed in all patients at risk because of the limited resources. This raises the question whether a prophylactic gonadectomy in all patients at risk for a malignancy should be performed. At the moment research is conducted focusing on the identification of factors to estimate the actual cancer risk in the individual patient to prevent unnecessary prophylactic gonadectomy (10).

A point of debate is the inclusion of the histology and the genetic analysis in a diagnostic workup. Of course mutation analysis provides confirmation, whereas the histology is also an important prognostic parameter as a base for further treatment. We used the tertiary root only if a mutation was found or if gonadal histology was known. This was the case in 29 out of 88 patients (32%).

In conclusion, in daily practice the implementation of the current consensus statement in a resource – poor environment is very difficult. Especially the tertiary root classification that is based on molecular genetic or histopathology diagnostics is in many cases not feasible.
Therefore we recommend the following stepwise approach: As a first step a careful clinical evaluation, karyotyping of peripheral blood and sonographic imaging of the internal genitalia should be performed in all patients.

Subsequently, in the 46 XX patients rapid determination of 17-hydroxyprogesterone in serum or saliva (35) are needed in the first week of life in order to recognize a salt-loosing CAH and prevent a life-threatening crisis. An increased level is highly suggestive of the diagnosis CAH and needs to be followed by immediate initiation of life-saving treatment. In patients with 46, XY or Y chromosome containing DSD, determination of gonadotropins, testosterone, DHT, inhibin B and AMH is to be performed. Dependent on age and stage of puberty, a second root working diagnosis can be made allowing gender assignment and planning for further diagnostic procedures and management in collaboration with global DSD centers of excellence.

This implies the need for education of primary health care workers on how to recognize DSD as a clinical feature that requires urgent assessment to prevent morbidity and mortality in some cases. Protocols on referral pathways should be implemented. Unfortunately, in Indonesia several factors such as patient’s and general society’s opinion on DSD problems, economic background of DSD patients and lack of access to health insurance can affect the complex management of DSD in a negative way.
References


Chapter 4

Clinical evaluation of 286 patients with a Disorder of Sex Development (DSD) from Indonesia in relation to phenotype and genotype


Submitted
Abstract

Objective: This study determined the etiological spectrum of DSD in a large cohort of patients and investigated which clinical, biochemical and genetic parameters are most useful in the diagnosis and management of patients with DSD in an underprivileged population.

Methods: Two hundred and eighty six patients with atypical external and/or internal genitalia from Semarang, Indonesia, previously undiagnosed and referred between 2004 and 2010 were included. The diagnostic evaluation included clinical, imaging, hormonal, molecular genetics, and histological parameters. Patients were categorized according to the recent consensus statement on DSD.

Results: The age at presentation was 0-0.5 years in 41 cases (14.3%), >0.5-12 years in 181 cases (63.3%), and >12 years in 64 cases (22.4%). 46,XY DSD was most common (68.2%, n=195), while 46,XX DSD was found in 23.4% of the patients (n=67) and sex chromosome DSD in 8.4% (n=24) of cases. In 61.2% of the 46,XX DSD patients, 17.9% of the 46,XY DSD patients and all sex chromosome DSD patients (27% in total) a final diagnosis was reached based on genetic (karyotype and/or gene mutation analysis) or histological evaluation. Familial DSD was reported in eleven cases from five families with 46,XX DSD, and in 11 cases from five families with 46,XY DSD.

No consanguinity of parents of any of the patients was reported. Serum determination of 17-hydroxyprogesterone and androstenedione were the most distinctive parameter in 46,XX DSD patients in whom congenital adrenal hyperplasia was the most common diagnosis (59.7%). Mutations in CYP21A2 or CYP11B1 were found in all of these. In the remaining 46,XX DSD patients determination of LH, FSH, testosterone and AMH were the subsequent parameters to establish gonadal function. In 46,XY DSD the following diagnostic groups were identified based on external masculinization score (EMS): androgen action disorder (AAD), unknown male undermasculinization (UMU) and gonadal dysgenesis (GD). Serum levels of LH, FSH and basal testosterone differed between AAD and UMU versus GD, particularly in post pubertal patients. hCG tests were of no additional value as no patients with androgen synthesis disorders were found. AR mutations were found in only 24.5% and 1.8% of patients with AAD and UMU,
respectively. In 16% of 46,XY GD patients causative copy number variants of several genes were found. The karyogram of 18 out of the 24 patients with sex chromosome DSD contained a Y-chromosome. Hormonal profiles of the patients with a Y-chromosome containing karyotype showed high levels of LH and FSH, and low levels of AMH, inhibin B, and testosterone.

Conclusion: A stepwise practical diagnostic approach in a large cohort of DSD patients in Indonesia led to a genetically or histologically proven final diagnosis in 27% of the patients. The most helpful parameters were serum levels of 17-hydroxyprogesterone and androstenedione in 46,XX DSD patients and LH, FSH and basal testosterone levels in 46,XY DSD patients. New Massively Parallel Sequencing techniques, which provide a higher resolution, are expected to improve the percentage of patients who can be given a molecular diagnosis.

INTRODUCTION

Sex determination and differentiation are regulated by a complex developmental network. Chromosomal sex determines gonadal sex, which in turn determines phenotypic sex (1). This has been referred to as the "central dogma" of sex differentiation (2). Sex determination results from the expression of genes that cause the bi-potential gonads to develop into either testes or ovaries.

Testicular differentiation occurs after the onset of the expression of sex-determining region Y (SRY) in a subset of somatic cells. This leads to their differentiation into Sertoli cells, which in turn produce anti-Müllerian hormone (AMH). These cells are the supportive cell lineage surrounding the developing germ cells. AMH inhibits the differentiation of the Müllerian ducts into a uterus and other Müllerian structures. Furthermore, the developing Leydig cells start secreting testosterone, which causes the stabilization of the Wolffian ducts. In females, there is no obvious single dominant gene that determines the sex of somatic and germ cells in the ovary (3-5).

Disorders of sex development (DSD) cover many different phenotypes of atypical sex anatomy, which result from faults in the underlying network that regulates gonadal development and differentiation. Many genes are involved in known pathways that lead to gonadal formation.
and differentiation. In addition, potentially novel and alternative pathways may play a role (3,4). Therefore, whereas the scope of molecular genetic analysis has markedly expanded, it is still not always possible to identify the molecular genetics causes of these disorders.

This paper describes the various steps in the diagnostic approach of a large cohort of Indonesian patients with DSD. Most of them had never received medical attention relating to DSD. The aim of our study was to determine the etiological spectrum of DSD. In addition, clinical and laboratory data were analyzed to determine which clinical, biochemical and molecular genetics parameters proved most useful to reach a final diagnosis relevant for further management.

**SUBJECTS AND METHODS**

**Patients**

For this study we evaluated 286 patients with various DSD phenotypes were evaluated. They were referred for chromosomal analysis by clinicians of the departments of Urology, Pediatrics, Internal Medicine and Obstetrics to the gender team of the Dr. Kariadi Hospital, Semarang, Indonesia. Referral and data collection took place between 2004 and 2010 at the division of Human Genetics, Center for Biomedical Research, Faculty of Medicine, Diponegoro University, Semarang, Indonesia. Reasons of referral were the presence of ambiguous genitalia or atypical external or internal genitalia, including severe hypospadias, with or without descended testes. Eighty eight of the patients included in this study have been described previously (6).

**Methods**

A detailed interview was performed at admission. Data concerning medical history, age of initial presentation, sex of rearing, family history (relatives with a genital disorder) and consanguinity were collected.

The patients were clinically evaluated. A detailed description of the external genitalia was obtained and the genitalia of 46,XY and sex chromosome DSD were staged according to Quigley (7), as well as using the External Masculinization Score (EMS) (8). The Prader stage
was used to determine the degree of virilization in patients with 46, XX DSD (9). Dysmorphic features were recorded.

A peripheral blood sample was obtained from all patients for karyotyping, hormonal analysis and DNA extraction for genetic analysis. Karyotypes were determined using a G-banding technique. In patients with 46, XY DSD or Y chromosome containing aneuploid DSD an additional blood sample was obtained 72 hr after the intramuscular injection of 1500 IU human chorionic gonadotropin (hCG;PregnylR, MSD, Oss, The Netherlands).

The medical ethics committee of Dr Kariadi Hospital approved this study and informed consent was obtained from all participants, their parents or guardians prior to their participation in this study.

**Diagnostic criteria**

Patients who were identified on the basis of genital ambiguity or atypical external and/or internal male or female genital development were categorized according to the primary root of the recent classification based on karyotype: 46,XX DSD, 46,XY DSD or sex chromosome DSD (10).

**Serum hormone measurements**

The measurements of inhibin B, AMH, LH and FSH in the basal serum samples were performed as described previously (11). Testosterone concentrations were determined in serum collected before and after injection of hCG using the Coat-a-Count radioimmunoassay (Siemens, Los Angeles, CA) (11). Androstenedione was also measured in these samples using the Immulite 2000 (Siemens). Finally, 17-hydroxyprogesterone and 11-desoxycortisol levels were estimated using in house methods (12). Age and sex dependent hormone levels in the normal population are given in supplementary Tables 1 and 2 (11, 13-15).

**Genetic analysis**

DNA was extracted from leucocytes of EDTA blood using the salting out method as described earlier (16). Based on the clinical and hormonal information, specific genes were
analysed such as *CYP11B1* (11β-hydroxylase; P450c11β reference sequence NM_000497.3 (17, 18), *CYP21A2* (21-hydroxylase; P450c21)(19), the *LHCGR* (LH receptor) (20) and the Glucocorticoid Receptor (*GR*) (21). The genes encoding the androgen receptor (*AR*), *SRY* and *WNT4* were analysed by Sanger sequencing of the coding exons and exon-flanking intronic regions (reference sequence *AR*: NM_000044.2 (22-24), *SRY*: X53772.1 and *WNT4*: NM_030761). Primer sequences and locations are available upon request.

Patient DNAs were also analysed for large genomic re-arrangements and copy number variations (CNVs), using genome wide SNP chip arrays (different versions of Illumina arrays) (25) and/or Multiplex Ligation-dependant Probe Amplification (MLPA) (26). MLPA was also used to confirm CNVs which were identified using arrays.

**Pathology**

Histo-pathological assessments of gonadal tissue following gonadal excision or biopsy were performed using hematoxylin and eosin staining and immuno-histo-chemistry for various germ cells markers, e.g. OCT3/4, TSPY, VASA, SCF (including double staining for OCT3/4-TSPY or VASA); as well as SOX9 and FOXL2 for supportive cells as described earlier (6, 27).

**Flow of the diagnostic process**

For the first diagnostic evaluation, patients were grouped based on their karyotype, and further assessment for the second stage of diagnosis was conducted based on clinical data, notably EMS with or without imaging (USG, MRI). The analysis of candidate genes was carried out based on the results of the two previous assessments and the results of the hormonal evaluation.

**Statistics**

Data was processed using the IBM SPSS statistics 20 software. To calculate the differences between hormonal values for each diagnosis, we used ANOVA followed by post hoc Tukey analysis. Pearson correlation coefficients were used to determine the relationship between the EMS score and the androgen sensitivity index. Mann-Whitney U tests and Independent T
tests were used to determine the difference of various variables among patients with an androgen action disorder with and without AR mutations. Data are presented as means ± s.e.m.

RESULTS

Amongst the 286 patients 46,XY DSD was most common accounting for 68.2% (195 patients), 46,XX DSD accounted for 23.4% (67 cases), and 8.4% (24 cases) had a sex chromosome DSD, as shown in Table 1 and Figure 1.

The age at presentation was 0-0.5 years in 41 cases (14.3%), >0.5-12 years in 181 cases (63.3%), and >12 years in 64 cases (22.4%). Familial DSD was reported in eleven cases from five families with 46, XX DSD, and in eleven cases from five families with 46, XY DSD. Consanguinity of parents of any of the patients was not reported.

46, XX DSD

Hormonal evaluation

From a total of 67 patients, 43 presented with varying degrees of virilization of the external genitalia. Forty of them showed hormonal levels characteristic for CAH while three had unclassified hyperandrogenism. 21-hydroxylase deficiency (CYP21A2) was suspected in 38 patients based on increased levels of 17-hydroxyprogesterone, androstenedione and testosterone, while in two cases 11β-hydroxylase dehydrogenase (CYP11B1) deficiency was suggested due to increased levels of 17-hydroxyprogesterone (Table 2) and 11-desoxycortisol (177 and 371 nmol/l, respectively). Clinically salt wasting was suspected in at least eleven cases based on intercurrent illnesses with hyponatremic episodes, but no confirmation by laboratory tests was available. Five of these patients died during the time this study was performed. One patient with a sex chromosome mosaic DSD, 46, XX (96%)/46, XY (4%) was also diagnosed with a 21-hydroxylase deficiency. As expected, LH, FSH, and inhibin B levels were normal with low levels of cortisol and AMH for age.
Table 1. Summary of patient diagnosis and characteristics

<table>
<thead>
<tr>
<th>Diagnosis</th>
<th>Total</th>
<th>median (range) age at presentation (years)</th>
<th>sex of rearing</th>
<th>Prader score</th>
<th>EMS score</th>
<th>number of family</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>male</td>
<td>NA</td>
<td>female</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Androgen excess</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>Fetal (CAH)</td>
<td>38</td>
<td>6.5 (0.01-33)</td>
<td>11 (6)</td>
<td>4</td>
<td>23 (28)</td>
<td>4 (1-7)</td>
</tr>
<tr>
<td>- mutation CYP21A2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>- mutation CYP11B1</td>
<td>2</td>
<td>11 (3-12)</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>(4-7)</td>
</tr>
<tr>
<td>Unclassified androgen excess</td>
<td>3</td>
<td>0.1 (1-29)</td>
<td>2</td>
<td>1</td>
<td></td>
<td>1 (1-4)</td>
</tr>
<tr>
<td>Other</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Defect of mullerian development (MRKH)</td>
<td>12</td>
<td>21 (2-27)</td>
<td>0</td>
<td>0</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>Unclassified</td>
<td>10</td>
<td>3 (0.2-15)</td>
<td>2</td>
<td>0</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td>Androgen action disorder (AAD)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AR mutation +</td>
<td>24</td>
<td>9(0.1-26)</td>
<td>20</td>
<td>0</td>
<td>4</td>
<td>3 (2-6)</td>
</tr>
<tr>
<td>AR mutation -</td>
<td>73</td>
<td>1.95 (0.02-23)</td>
<td>64</td>
<td>2</td>
<td>7</td>
<td>3 (2-6)</td>
</tr>
<tr>
<td>Disorders of gonadal development</td>
<td>31</td>
<td>14.5 (0-1-19.5)</td>
<td>15</td>
<td>2</td>
<td>14</td>
<td>3 (2-7)</td>
</tr>
<tr>
<td>Other</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Unknown male undermasculinisation (UMU)</td>
<td>55</td>
<td>7 (0.1-29)</td>
<td>55</td>
<td>0</td>
<td>0</td>
<td>2 (2-4)</td>
</tr>
<tr>
<td>Unclassified</td>
<td>12</td>
<td>1.2 (0.01-12)</td>
<td>10</td>
<td>1</td>
<td>1</td>
<td>4 (1-6)</td>
</tr>
<tr>
<td>Sex Chromosome DSD</td>
<td>24</td>
<td>10 (0.1-39)</td>
<td>13</td>
<td>1</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>KARYOTYPE</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Turner syndrome variants</td>
<td>4</td>
<td>XXX</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Klinefelter syndrome variants</td>
<td>3</td>
<td>XY/XXX</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mixed gonadal dysgenesis</td>
<td>8</td>
<td>X/XY</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chimeric ovotesticular DSD</td>
<td>6</td>
<td>XX/XY</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>286</td>
<td>192</td>
<td>11</td>
<td>83</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

NA*: Not available
Figure 1. Stepwise diagnostic evaluation in 286 patients with DSD in Semarang Indonesia

DSD patients
288 (F 83; M 192; NA 11)

Clinical Evaluation

46 XX DSD
N = 67 (F 48; M 15; NA 6)

Hormonal Assesment
(N=67)

Imaging
(N=41)

46 XY DSD
N=195 (F 76; M 119; NA 1)

Hormonal Assesment
(N=195)

Imaging
(N=52)

Surgery
(N=26)

laparoscopy
gonadal biopsy

Chromosomal DSD
N=24 (F 10; M 13; NA 1)

Hormonal Assesment
(N=24)

Imaging
(N=18)

Surgery
(N=16)
laparoscopy
gonadal biopsy

CAH
N = 40

androgen Excess
N = 8

MRKH
N = 12

Gon Dys
N = 2

unclassified
10

Androg Act
N = 97

UMU
N = 55

Gon Dys
N = 31

unclassified
12

AR
24.5% (N=24)

AR
1.6% (N=1)

Other Gene
18% (N=3)

SRY
8.7% (N=2)

CYP21A2/CYP11B
100% (N=40)

Antrogen Excess
33.3% (N=1)

WNT4
0%

Gonadal Histology
16 out of 288 (5.59%) (XX=11) (XY=7) (SexChr=8 available but just 5 analyzable)

Final Classification
77 out of 286 (27%)
Among the three patients with unclassified androgen excess, one patient was diagnosed with an ovarian Leydig cell tumor confirmed by histo-pathological analysis (28). In two patients high levels of cortisol and androgens were found (Table 2) and glucocorticoid resistance was suspected.

Gonadal dysgenesis was found in two patients, presenting with ambiguous genitalia. In one patient the serum level of FSH was high and of AMH low for age, whereas in the other both levels were normal in the presence of testes.

Mayer-Rokitansky-Kuster-Hauser syndrome (MRKH) was suspected in phenotypic females with normal gonadal function with hypoplasia of the vagina and absence of the uterus.

Eight out of ten patients in the “46,XX DSD other, unclassified” group had cloacal malformations with normal hormonal data for age whereas two showed clinically transient hypervirilization. Follow up revealed normal female genitalia (see Table 2).

Table 2. Hormonal values for 46,XX DSD

<table>
<thead>
<tr>
<th>AGE (yrs)</th>
<th>N</th>
<th>LH (IU/l)</th>
<th>FSH (IU/l)</th>
<th>Cortisol (nmol/l)</th>
<th>A'dione (nmol/l)</th>
<th>17-OHP (nmol/l)</th>
<th>Testosterone (ug/l)</th>
<th>AMH (ng/l)</th>
<th>Inhibin B (ng/l)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CYP 21</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;0-0.5</td>
<td>9</td>
<td>0.49±0.18</td>
<td>2.08±1.06</td>
<td>110±30</td>
<td>44±16.6</td>
<td>296±133</td>
<td>8.4±4.4</td>
<td>1.8±0.88</td>
<td>36.3±11.8</td>
</tr>
<tr>
<td>&gt;0.5-12</td>
<td>18</td>
<td>0.97±0.50</td>
<td>2.63±0.65</td>
<td>141±20</td>
<td>49.4±9.0</td>
<td>392±46</td>
<td>8.6±1.5</td>
<td>3.9±0.48</td>
<td>28.5±6.9</td>
</tr>
<tr>
<td>&gt;12</td>
<td>4</td>
<td>1.96±0.95</td>
<td>5.20±1.99</td>
<td>138±24</td>
<td>111±51.8</td>
<td>484±246</td>
<td>16.7±7.4</td>
<td>3.2±1.27</td>
<td>42</td>
</tr>
<tr>
<td>CYP11B1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&gt;0.5-12</td>
<td>2</td>
<td>&lt;0.1</td>
<td>0.22±0.12</td>
<td>&lt;35</td>
<td>13±2.5</td>
<td>15±5.3</td>
<td>12.0±4.0</td>
<td>2.20±0.60</td>
<td>25.5±7.5</td>
</tr>
<tr>
<td>Cortisol Resistance</td>
<td>12</td>
<td>12.3</td>
<td>8.11</td>
<td>191</td>
<td>18</td>
<td>9.9</td>
<td>59.5</td>
<td>2.76</td>
<td>NA</td>
</tr>
<tr>
<td>Transient virilization</td>
<td>0.5-12</td>
<td>2</td>
<td>0.2±0.06</td>
<td>3.4±2.66</td>
<td>134±172</td>
<td>63.8±16.9</td>
<td>14.5±0.8</td>
<td>4.05±1.35</td>
<td>0.25±0.19</td>
</tr>
<tr>
<td>Gonadal Dysgenesis</td>
<td>&gt;0.5-12</td>
<td>2</td>
<td>0.09±0.04</td>
<td>3.8±1.14</td>
<td>229±163</td>
<td>NA</td>
<td>15.2</td>
<td>&lt;0.1</td>
<td>6.2±3.88</td>
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<td>4.3±0.66</td>
<td>1.3±0.19</td>
<td>9.67±1.38</td>
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* we excluded seven patients who had been treated with glucocorticoid
Molecular genetics evaluation

The diagnosis of CAH was confirmed in all patients by *CYP11B1* (n=2) or *CYP21A2* (n=38) gene mutation analysis. As reported previously (19), gene sequencing revealed p.R356W, c.IVS2-12A>G and p.I172N as the most common *CYP21A2* mutations. In the MRKH patients *WNT4* gene mutation analysis was negative. In the two patients with suspected glucocorticoid resistance gene analysis did not show mutations in the *GR*.

46, XY DSD

We observed a preference of male sex of rearing in these patients: of 180 patients with a severe degree of ambiguity (Quigley stage 2-4), 159 were assigned to the male sex (Figure 2).

Hormonal evaluation

On the basis of an EMS score <9, ninety-seven patients were classified as suspected of Androgen Action Disorder (AAD). On the basis of an EMS score ≥9, 55 patients were classified as Unknown Male Undermasculinization (UMU) (29). Comparison between hormone levels in the AAD and UMU groups showed similar concentrations for LH, FSH and testosterone before and after hCG, AMH and inhibin B in all age groups, with the exception of increased levels of LH and basal testosterone in post-pubertal AAD patients (Figure 3). In none of the AAD or UMU cases the measured values of gonadal and adrenal steroids, as well as the T/DHT ratio, revealed an underlying diagnosis of an androgen synthesis defect or 5α-reductase deficiency (data not shown).
Gonadal dysgenesis was presumed in 31 patients. In this group of patients, external genitalia were often ambiguous, depending on the degree of impairment of gonadal function. Serum levels of LH and FSH were elevated compared to reference values, whereas AMH and inhibin B levels remained low for age in all age groups (Figure 3).

FSH levels were significantly higher in the group of gonadal dysgenesis compared to the groups of AAD and UMU patients at all ages. The same results were also shown for LH except in the age group over 12 years old, where LH levels were equally high in AAD and gonadal dysgenesis patients. AMH levels in patients with gonadal dysgenesis were decreased compared to the AAD and UMU groups but significant differences were only observed in the age groups >0.5-12 and >12 years. Inhibin B levels were significantly lower in the gonadal dysgenesis group, compared to the AAD group, except in newborn patients. In the post-pubertal age group (>12 years), inhibin B levels were significantly different between the UMU and gonadal dysgenesis patients.
Figure 3. Comparison of hormonal levels based on diagnosis and age
Basal testosterone levels in pre-pubertal boys (>0.5-12 yrs) with gonadal dysgenesis were higher compared to UMU but not different from AAD. These levels slightly increased after puberty but were then substantially lower than those in the other two groups (AAD & UMU). Post-hCG testosterone levels showed significantly different levels only in the age group of over 12 years old, and showed insufficient response to hCG in the group of gonadal dysgenesis (Figure 3).

The ratio of FSH over inhibin B was significantly higher in patients with gonadal dysgenesis (2.14±0.57) compared to UMU (0.02±0.004) and AAD(0.03±0.009). This was already apparent in the age group of >0.5-12 years and became very obvious in patients over 12 years of age.

Statistical analysis of the data on the androgen sensitivity index (ASI, the product of the serum concentrations of LH and testosterone) for post-pubertal patients with AAD and UMU revealed a significant correlation between ASI and EMS score (r = -0.615, p<0.01). Mean values of ASI in the AAD group were 516 ± 91U x nmol/l^2, and 43 ± 12U x nmol/l^2 in the UMU group (30).

Evaluation of the 12 unclassified cases revealed hormonal values within the normal range for the following cases: aphalia (n=2), cloacal anomalies (n=2), double penis (n=1), and severe hypospadias with multiple malformations (n=2). In the remaining five cases, results were compatible with hypogonadotropic-hypogonadism (n=2, low levels of LH, FSH and testosterone), Leydig Cell Hypoplasia (LCH, n=2, low testosterone after hCG test) and CYP11A1 deficiency (n=1, high gonadotropins and low levels of testosterone and adrenal steroids) (see supplement Table 3).

**Molecular Genetic Evaluation**

The AR gene was sequenced in all patients with AAD and UMU. We detected AR sequence variants in 24 out of 97 patients (24.5%) with AAD (23 pathogenic mutations and 1 unclassified variant). The phenotype was partial androgen insensitivity in 22 patients and complete androgen insensitivity in two. In one out of 55 patients with UMU, a pathogenic AR mutation was detected. We identified a total of 19 types of AR mutation, none of which was
found to be most prevalent. Four mutations had been unclassified so far, but we showed previously that three of these are pathogenic in nature (31). In the 2 patients with LCH analysis of the \textit{LHCGR} gene was negative.

As a final step, DNA of \textit{AR} mutation negative patients with AAD or UMU (n=73 and 54 respectively), or with gonadal dysgenesis (n= 31), was subjected to further analysis. In the group with \textit{AR} mutation negative AAD and UMU no CNVs were found. However, in five out of 31 gonadal dysgenesis cases CNVs were detected, which include the following DSD candidate genes: \textit{DAXI} duplication (n=2), deletions of \textit{DMRT1} (n=1), of \textit{WT1} (n=1), of \textit{WWOX} (n=1).

\textit{AR} mutation positive versus \textit{AR} mutation negative AAD patients

Multiple variables were analyzed to find out whether AAD patients having an \textit{AR} mutation (n= 24) differed from patients without detected \textit{AR} mutation (n= 73) (referred to as AAD (+) and AAD (-), respectively). Results are shown in Table 3.

\textbf{Table 3. Comparison of AR(+) and AR (-) AAD patients}

\begin{table}[h]
\centering
\begin{tabular}{|l|c|c|c|c|}
\hline
 & \textbf{Androgen Action Disorder} & & & \\
 & \textbf{Androgen Receptor Mutation (+)} & \textbf{Androgen Receptor Mutation (-)} & \textbf{P value} & \\
 & N=24 & N=73 & & Method \\
\hline
\textbf{EMS*} & 5.60 ± 0.34 & 5.34 ± 0.17 & 0.202 & Mann-Whitney U \\
Scrotal fusion (EMS) & 1.50 ± 0.31 & 0.78 ± 0.16 & 0.030 & Mann-Whitney U \\
Microphallus (EMS) & 2.12 ± 0.28 & 1.76 ± 0.17 & 0.299 & Mann-Whitney U \\
Urethral opening EMS) & 0.16 ± 0.08 & 0.11 ± 0.04 & 0.374 & Mann-Whitney U \\
Quigley Stage & 3.29 ± 0.23 & 3.15 ± 0.09 & 0.928 & Mann-Whitney U \\
\textbf{Delta testosterone**} & 6.95 ± 1.41 & 9.58 ± 0.77 & 0.095 & t- test \\
SDS*** AMH & -0.19 ± 0.65 & -0.63 ± 0.12 & 0.294 & t- test \\
SDS Inhibin B & -0.55 ± 0.35 & 0.19 ± 0.18 & 0.046 & t- test \\
\hline
\end{tabular}
\caption*{* EMS = External Masculisation Score ** difference between pre and post hCG test *** SDS = standard deviation score}
\end{table}
With regard to the clinical appearance such as total EMS, micropenis, location of the urethral opening and Quigley stage, there were no significant differences between AAD (+) and AAD (-) patients except for the scrotal fusion score. There were hardly any differences in hormone levels between the AAD (+) and AAD (-) patients except inhibin B. We did not find a significant difference in ASI between these groups of patients.

**Sex Chromosome DSD**

The karyogram of 18 out of the 24 patients with sex chromosome DSD contained a Y-chromosome; five of these patients and all patients who did not carry a Y chromosome were raised as females. SRY analysis were performed in 7 patients and 2 patients found to have Y deletion.

All patients without a Y-chromosome containing karyotype had an EMS score 1 and were adults at the time of referral.

Hormonal profiles of the patients with a Y-chromosome containing karyotype showed the same tendencies as found in patients with 46,XY gonadal dysgenesis particularly in the post-pubertal group (>12 years), i.e. high levels of LH and FSH, and low levels of AMH, inhibin B, and testosterone (Table 4).

**Histology**

In 16 patients, gonadal tissue was available for histology following gonadectomy or biopsy. Due to specimen quality issues, the analysis could be performed on tissue samples of 13 patients. One 46,XX patient had a Leydig cell tumor (28). Three out of seven patients with 46, XY DSD showed Leydig cell hyperplasia while the other four showed the following: carcinoma in situ (CIS), CIS with seminoma, streak gonad and gonadoblastoma. Five patients with sex chromosome DSD showed an ovary with multiple cysts (46,XY/46,XX), a normal ovary (46,XY/46,XX), Sertoli cells only phenotype (46,XY/45,X), Leydig cell hyperplasia (46,X,idicY) and seminoma (46,XY/45,X)(27).
Table 4. Sex Chromosome DSD

<table>
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<tr>
<th>Karyotype</th>
<th>AGE (years)</th>
<th>Number</th>
<th>TOTAL EMS (IU/l)</th>
<th>LH (IU/l)</th>
<th>FSH (IU/l)</th>
<th>Basal T* (nmol/l)</th>
<th>T+hCG (nmol/l)</th>
<th>AMH (ug/l)</th>
<th>Inhibin B (ng/l)</th>
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<td>0-0.5</td>
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<td>2.66 ± 0.88</td>
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<td>1 ± 0</td>
<td>10.3 ± 2.9</td>
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<td>0.65 ± 0.13</td>
<td>NA**</td>
<td>2.29 ± 0.99</td>
<td>47 ± 19</td>
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*T=Testosterone. **NA= Not available

DISCUSSION

We studied a large cohort of patients with a wide variety of genital anomalies referred to a single centre in Indonesia. The age distribution differs from what is observed in developed countries (32, 33). Patients referred after the age of one year and adults were dominant among our patients. Warne et al. pointed out that in many underprivileged Asian countries, a child born with ambiguous genitalia will grow up bearing the congenital anatomic sex features, which remain surgically untreated until adolescence or adulthood (33, 34). However, during the study period we noticed a trend in referral at an earlier age (data not shown).

The patients were grouped in accordance with the recommendations following a consensus meeting on DSD in 2005 (10). CAH was most common among 46,XX DSD patients. Following clinical and sonographic evaluation of these patients, the diagnosis of CAH was established with 17-hydroxyprogesterone and androgen measurements in serum and confirmed by gene mutation analysis. It should be noted that in 27/67 (40%) of the 46,XX DSD patients other causes of ambiguity or atypical genital development had to be considered. Among the three patients with unclassified androgen excess, in one patient an ovarian Leydig cell tumor was diagnosed. In two patients glucocorticoid resistance was suspected on the basis of the hormonal data but not confirmed by GR gene mutation analysis as described earlier (35).
We conclude that serum determinations of 17-hydroxyprogesterone and androstenedione are the most predictive parameters in determining the underlying cause in 46,XX DSD patients as CAH was the most common diagnosis whereas LH, FSH, testosterone and AMH levels are the subsequent parameters to determine the gonadal function in the non-CAH patients.

46,XY DSD was most prominent (68.2%) in our patient population. Various studies from non-Western countries have shown different results with respect to the proportion of 46,XY DSD: Joshi et al (India), Gollu et al (Turkey), Al-Jurayyan (Saudi Arabia) and Nimkarn et al (Thailand), showed that 46,XY DSD accounts for 31-52% of the DSD cases (36-39).

The diagnostic management of 46,XY DSD remains the greatest challenge. We made a distinction between patients with suspected AAD and UMU on the basis of the EMS score as suggested by Rodie et al (29). These authors studied 572 Scottish patients with DSD and found an EMS score < 9 in patients with disorders of androgen synthesis or androgen action. However in our AAD patient group we did not find any patients with androgen synthesis disorders and the AAD and UMU groups did not differ with respect to hormone levels before the age of 12 years, whereas in the post-pubertal patients both testosterone and LH levels were significantly higher in the AAD group compared to the UMU patients.

AR gene sequencing was performed in all patients with AAD and UMU and mutations were found in 25 of 152 patients, all but one being in the AAD group. The hormone levels of the 24 patients with androgen insensitivity, in whom indeed an AR mutation was found, did not differ from patients in whom no AR gene mutation was established. Apparently most of our patients classified as partial androgen insensitive, whereas in the recent study of Rodie et al, complete androgen insensitivity was most prominent (29). We could confirm the observation of Zuccarello et al. that the product of the levels of LH and testosterone forms an index for mild androgen insensitivity (30). There was a negative correlation between ASI and severity of virilization (EMS) in 46,XY DSD post-pubertal patients with AAD and UMU.

Subsequent CNV array and MLPA analysis in the AR mutation negative patients revealed no further diagnostic confirmation.
Levels of gonadotropins are clearly increased in patients with gonadal dysgenesis already at a young age. Our results suggest that there is no further discriminatory value of the determinations of AMH and inhibin B. Subsequent gene mutation analysis yielded the confirmation of a mutation of a gene involved in gonadal development and differentiation in 5 out of 31 patients. However, a definite diagnosis for this group is the pathological examination of the gonads, which is cumbersome for logistical, socioeconomic and cultural reasons (6). Importantly, in spite of the significantly lower risk of gonadal germ cell tumors in the general Asian population a preliminary study indicated that this risk is increased in Indonesian patients with DSD (27).

From our study we conclude that examination of LH, FSH and basal testosterone are the most important parameters to distinguish between groups of patients with 46,XY DSD, followed by AMH or inhibin B. The hCG test had limited value as in this large cohort of patients, we confirmed our previous observation that we could not establish the diagnosis of androgen synthesis disorder caused by e.g. deficiencies of 17β-hydroxysteroid dehydrogenase type 3 or 17-hydroxylase (6). We hypothesize that one of the reasons might be the absence of parents’ consanguinity in our population in contrast to other studies (36, 40).

On the basis of these data we conclude that it is not recommended to sequence the AR gene in patients with 46,XY DSD with an EMS score ≥9 because of the very low yield. The aetiology of male undervirilization, also confusingly termed PAIS-like phenotype remains unclear, raising questions whether additional factors may play a role such as unknown genetic variations (resulting from DNA methylation, histone modifications or other unknown related genes) or environmental factors (41-45).

Regarding sex chromosome DSD, karyotyping is the most important measure to establish aneuploidy. Hormonal data are largely depending on the degree of gonadal differentiation. Measurement of AMH and inhibin B at a pre-pubertal age and additionally post-pubertal FSH are most indicative for the quality of gonadal function.
Management in DSD varies greatly depending on many factors. Of utmost importance is the determination of an accurate and rapid diagnosis. After a thorough evaluation of clinical, karyotype, biochemical and if possible molecular data, treatments can be applied on basis of the results of these investigations. Evaluation is meant to determine sex of rearing, to detect life-threatening conditions, to plan the long-term management, to explain related issues such as fertility, risk of tumor genesis, sexual function and to counsel the parents and/or patients themselves on genetic aspects (46, 47). The final goal is to reach an optimal long-term outcome.

In conclusion, DSD is not infrequent in the Indonesian community. The etiological spectrum is broad, 46,XY DSD being most common phenotype, with a remarkable absence of androgen synthesis disorders. Among the 46,XY DSD patients the distinction of androgen action disorder and male undervirilization syndrome cannot be made on the basis of hormonal evaluation apart from the difference in LH and testosterone levels after the age of 12 years. The yield of AR gene mutation analysis in UMU is very low. In 46,XX DSD, the levels of 17-hydroxy progesterone and androstenedione are the most important hormones that should be examined and the yield of CYP21A2 or CYP11B1 mutation analysis are high. Using Sanger sequencing of candidate genes, CNV arrays, MLPA, and histology, a final diagnosis could be made in approximately 30 % of the patients. New Massively Parallel Sequencing techniques, which provide a higher resolution (down to the nucleotide level), compared to CNV arrays and MLPA, and which allow simultaneous sequencing of multiple genes, are expected to improve the percentage of patients who can be given a molecular diagnosis.
References


23. Androgen Receptor Gene Mutation Database.


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Chapter 5
Functional analysis of novel Androgen Receptor mutations in a unique cohort of Indonesian DSD patients

Abstract
Mutations in the androgen receptor (AR) gene, rendering the AR protein partially or completely inactive, cause androgen insensitivity syndrome (AIS), which is a form of 46,XY disorder of sex development (DSD). We present three novel AR variants found in a cohort of Indonesian DSD patients; p.I603N, p.P671S and p.Q738R. The aim of this study was to determine the possible pathogenic nature of these newly found unclassified variants. To investigate the effect of these variants on AR function, we studied their impact on: transcription activation, AR-LBD interaction with an FxxLF motif containing peptide, AR sub cellular localization and on AR nuclear dynamics and DNA binding. AR-I603N had completely lost its transcriptional activity due to disturbed DNA binding capacity and did not show the 114 kDa hyperphosphorylated AR protein band, normally detectable after hormone binding. The patient with AR-I603N displays a PAIS phenotype, which is explained by somatic mosaicism. A strongly reduced transcriptional activity was observed for AR-Q738R together with diminished interaction with an FxxLF motif containing peptide. AR-P671S also showed reduced transactivation ability, but no change in DNA or FXXLF binding capacity. AR-P671S interferes with transcriptional activity for as yet unclear reasons.
Introduction

Disorders of sex development (DSD) are defined as any congenital condition in which development of chromosomal, gonadal or anatomical sex is atypical (1). One of these disorders is caused by defects in androgen action. The androgen insensitivity syndrome (AIS) results from mutations in the X-linked androgen receptor (AR) gene. A great variety of mutations in the AR gene has been reported (www.mcgill.ca/androgendb) and resulted in a wide spectrum of clinical phenotypes (2).

The AR is a transcription factor that belongs to the super family of nuclear receptors and is composed of distinct domains characteristic for steroid hormone receptors. The variable NH2-terminal domain (NTD) is mainly involved in transcription activation (3). The DNA-binding domain (DBD) of the AR contains two zinc-clusters that specifically bind regulatory sequences in promoter/enhancer regions of androgen-regulated genes (4). A short flexible hinge region, containing highly positively charged amino acid residues links the DBD domain to the ligand-binding domain (LBD). The AR LBD consists of 10-12 α helices. Upon hormone binding, helix 12 functions as a lid and fixates the hormone in the ligand-binding pocket. As a result a hydrophobic coactivator-binding groove on the LBD-surface is created (5). The coactivator-binding groove functions as an interaction surface for LxxLL- and FxxLF-like motif containing coactivators (5-7) (where L is a leucine, F is a phenylalanine and X represents any amino acid) as well as for the FxxLF motif in the AR-NTD, important in the NH2/COOH terminal domain interaction (N/C-interaction) (8, 9).

Here we report three novel AR missense mutations found in a unique cohort of 101 Indonesian DSD patients. The aim of this study was to determine the possible pathogenic nature of these newly found unclassified variants. To investigate the effect of these mutations on AR function, we studied their impact on transcription activation, on AR-LBD interaction with an FxxLF motif containing peptide, on AR subcellular localization and on AR nuclear dynamics and DNA binding. Together these data provide a molecular explanation for the clinical presentation of these PAIS patients.
Patients, Materials and Methods

Patients

Patient A was referred to the Dr. Kariadi Hospital, Semarang, Indonesia at the age of 12 years because of genital ambiguity. He had a male gender and physical examination showed a bifid scrotum with palpable testes and perineal hypospadias, Quigley stage 5 (10) and breast development Tanner stage 3-4. His serum concentrations of LH (2.1 IU/l) and FSH (5.3 IU/l) were in the normal range for early puberty, and serum testosterone (basal 1.6 nmol/l) rose to 20.4 nmol/l at 3 days after the injection of 1500 IU of human chorionic gonadotrophin (hCG), indicating absence of disorders in testosterone biosynthesis. The serum level of AMH, which should decline under the influence of testosterone in early puberty, was relatively high (21 µg/l). He underwent surgical correction for his hypospadias and breast development. Sequencing analysis revealed a mosaic missense mutation in exon 3 of the AR gene (c.2170 T→A) at amino acid residue 603 (according to http://www.mcgill.ca/androgendb) leading to a substitution of isoleucine by asparagine. Both parents tested negative for this mutation.

Patient B was referred to the clinic at the age of 2.5 years because of hypospadias. He had a male gender. Testes were palpable in a bifid scrotum and there was scrotal hypospadias, Quigley stage 2. Serum LH (<0.1 IU/l) and FSH (0.55 IU/l) were normal for his age, as was serum testosterone (<0.1 nmol/l). The level of testosterone increased to 16.9 nmol/l after administration of hCG. Serum AMH was in the normal prepubertal range (68 µg/l). Hypospadias correction was performed at the age of 3.5 years. Using sequencing analysis a missense mutation was identified in exon 4 of the AR gene (c.2373 C→T ) leading to a substitution of proline 671 by serine. Sequencing analysis of the parents revealed that the mother was a carrier of the P671S mutation.

Patient C was seen at the clinic at the age of 4.5 years because of penoscrotal hypospadias. He presented with a bifid scrotum and a micropenis (2 cm), Quigley stage 4. Serum LH (0.26 IU/l) and FSH (0.68 IU/l) were normal for his age, as was serum testosterone (0.1 nmol/l). The level of testosterone increased to 20.5 nmol/l after administration of hCG. Serum AMH was in the normal prepubertal range (158 µg/l). He underwent a hypospadias correction.
Topical DHT treatment with DHT cream during 3 months resulted in an increase of penis length of 1.6 cm. Using sequencing analysis a missense mutation was identified in exon 5 of the AR gene (c.2575 A→G) leading to a substitution of glutamine 738 by arginine. Sequencing analysis of the parents DNA revealed that the mother was carrier of the Q738R mutation.

All these patients were of Javanese Indonesian origin, had a 46, XY karyotype and were diagnosed with partial androgen insensitivity syndrome (PAIS).

**Mutation analysis, site-directed mutagenesis and construction of AR expression vectors**

Numbering of the amino acid residues is according to the National Center for Biotechnology Information (NCBI) accession number AAA51729, which refers to the AR consisting of 919 amino acid residues (11). Extraction of DNA of peripheral blood cells was performed according to standard techniques. The coding exons and exon/intron boundaries of the AR gene were analysed by direct sequencing on a ABI3730XL automated sequencer. All variations except known neutral variants were confirmed by a second sequencing experiment on DNA of the patients.

The human wild type AR cDNA expression plasmid pSG5AR, a gift from Dr Andrew Cato, was used to generate constructs encoding the mutant AR’s using Quick Change site-directed mutagenesis (Stratagene, La Jolla CA). The following sense and antisense primers containing the mutated sequence (depicted in lowercase lettering) were used: for preparation of pSG5AR-I603N sense primer 5’-GTGCACCAGCAGAAATGATTGCACTAaTGATAAAATCC-3’ and antisense primer 5’-GGAATTTATCATATAGTGCAATCATTTCTGCTGGCAGC-3’; for pSG5AR-P671S sense primer 5’-CTATGAATGTCAGtCCATCTTTCTGATGTCATGAC-3’ and antisense primer 5’-GCTTCCAGGACATTGGAAGGATGGATCTGCATCATT-3’ and for pSG5AR-Q738R sense primer 5’-CCAGATGCGTCATCAAGAATGACAGCCATCTGG-3’ and antisense primer 5’-CATCCAGGAGTACcGAATGACAGCCATCTGG-3’. The introduction of the mutations was confirmed by sequence analysis. By digestion with restriction enzymes and subcloning, the mutant fragments were exchanged with wild type fragments of vector pSG5AR. For exchange of the I603N encoding fragment digestions with Asp718 and AspI were used. Digestions with AspI and BamHI were applied for the P671S and Q738R encoding fragments.
GFP-tagged mutant AR expression constructs were generated by subcloning of the mutated fragments into pEGFP-AR0 (Farla et al, 2004) by EcoRI and HindIII digestions. The cloning sites of all constructs were screened by direct sequencing. The Gal4-DBD-AR FxxLF expression construct has been described previously (5).

Measurements of hormone levels

Hormone levels were determined using a chemo luminescence-based immunometric method (Immulite 2000, Siemens-DPC, Los Angeles, CA) for LH and FSH, a coated tube radioimmunoassay (Coat-a-Count, Siemens-DPC) for testosterone and an enzyme immunometric assay (DPC, Webster, TN) for AMH.

Western blot analysis

For Western blot analysis COS-1 cells were seeded in 6-well plates (diameter 35 mm) at a density of 0.15 x 10^6 cells per well in DMEM:F12 supplemented with 100 U/ml penicillin, and 100 μg/ml streptomycin + Glutamax + 5% fetal calf serum (FCS) treated with dextran coated charcoal. The next day the cells were transfected with either pSG5AR, pSG5AR-I603N, pSG5AR-P671S and pSG5AR-Q738R or empty vector pSG5, respectively. For each well 0.25 μg DNA was mixed with 0.6 μl FuGENE reagent in MEM medium without FCS. After 24 hours 50 nM R1881 or vehicle (0.1% ethanol) was added to the wells. The next day the cells were washed with PBS. Per well 200 μl ice-cold SDS Laemmli sample buffer containing 10 mM dithiotreitol (DTT) was added and the cells were scraped with a policeman. The cell lysates were transferred to 1.5 ml eppendorf tubes and boiled for 2 min. After a short sonication step 7 μl of the lysate was loaded onto a 7% SDS-polyacrylamide gel. Proteins were separated and blotted to a nitrocellulose membrane (Schleicher & Schuell Dassel Germany). Immunoblotting was performed using polyclonal antibody SP197 (12) and proteins were visualized via the ECL method (Perkin Elmer NEL101 Shelton USA).
Luciferase (LUC) assays

For transcription activation studies Hep3B cells were cultured in αMEM medium (Lonza BioWhittaker) supplemented with 5% FCS (PerBio), 100 U/ml penicillin, and 100 μg/ml streptomycin. One day before transfection Hep3B cells were plated in 24-well plates (Greiner Bio) at a density of 5x10⁴ cells per well. After 24 hours αMEM medium supplemented with 5% FCS was replaced by αMEM medium with 5% charcoal treated FCS supplemented with either vehicle (0.1% ethanol) or a range of 10 pM – 10 nM synthetic androgen R1881. Four hours after addition of R1881 the cells were transfected with AR expression constructs using FuGENE reagent (Roche Diagnostics, Basel, Switzerland). The DNA mixture was composed of 50 ng AR expression construct, 100 ng ARE₂-TATA-Luc or MMTV-Luc reporter plasmid and 1 μl FuGENE reagent per well in 25 μl αMEM. The DNA mixture was pre-incubated for two hours at room temperature before addition to the cells.

For interaction assays the same procedure of cell culture was used as described above. All the interaction assays were performed with or without the addition of 1 nM R1881. A mixture of 50 ng AR expression construct, 50 ng Gal4-DBD-AR FxxLF expression construct and 150 ng UAS₄-TATA-luc reporter plasmid was applied per well. Twenty-four hours after DNA transfection the cells were lysed and Luciferase activity was measured in a Fluorescent Ascent FL (Labsystems Oy, Helsinki, Finland).

Subcellular localization and nuclear mobility of GFP tagged AR mutants

Two days before microscopic analysis, Hep3B cells were grown on glass cover slips in 6-well plates in α-MEM (Cambrex) supplemented with 5% FCS (Perbio), 2 mM Glutamine, 100 U/ml penicillin, and 100 μg/ml streptomycin. At least 4 hours before transfection, the medium was substituted by medium containing 5% dextran charcoal stripped FCS. Transfections were performed with 1 μg GFP-AR expression construct in FuGENE6 transfection medium (Roche). Four hours after transfection, the medium was replaced by medium with 5% dextran charcoal stripped FCS when indicated with 1 nM R1881.

Live-cell imaging and strip-FRAP analysis were performed using a confocal laser-scanning microscope (LSM510; Carl Zeiss MicroImaging, Inc.) equipped with a Plan-Neofluar
40X/1.3 NA oil objective (Carl Zeiss MicroImaging, Inc). Enhanced green fluorescent protein (EGFP) was excited using a 488 nm laser line of an argon laser at moderate laser power to obtain images. EGFP emission was detected using a 505-530 bandpass emission filter.

Strip-FRAP analysis was performed as described by (13). In short, fluorescence in a narrow strip (~700nm – corresponding to 10 pixels at zoom 6) spanning the entire nucleus is bleached and the recovery of fluorescence inside this strip is monitored in time with a 21 ms interval using a low laser power. Fluorescence intensity in the strip is expressed relative to prebleach intensities and the intensity directly after bleaching.

**Results**

To find a possible pathogenic effect for the clinical phenotypes of PAIS patients harbouring AR mutations p. I603N, p. P671S and p. Q738R, the corresponding mutant AR expression constructs were generated and the effect of the amino acid substitutions on AR function were studied in vitro. We investigated hyperphosphorylation, transcription activation, AR-LBD interaction with an FxxLF peptide motif, AR subcellular localization and nuclear mobility and DNA binding capacity of the distinct mutants.

*AR isoform pattern*

Previous experiments have shown that in the absence of hormone the AR protein displays a protein doublet of 110-112 kDa and an extra hyperphosphorylated 114-kDa band upon hormone binding during SDS-polyacrylamide gel electrophoresis (SDS-PAGE). Part of the hormone-induced phosphorylation occurs following DNA binding and during or following transcription regulation (14). To study the effect of the PAIS-associated AR mutations on phosphorylation, wild type AR and AR mutants I603N, P671S and Q738 were expressed in COS-1 cells by transient transfection of the distinct AR constructs and Western blot analysis was performed after SDS-PAGE. Figure 1 shows expression of the 110-112 kDa protein doublet by wild type AR and all mutant ARs. However, incubation with the synthetic androgen R1881
induced expression of the hyperphosphorylated 114-kDa protein band in case of wtAR, AR mutants P671S and Q738R, but not of the AR mutant I603N (Figure 1, lane 5).

**Fig 1:** Western Blot analysis of PAIS-associated AR mutants. Wild type AR (wt) and AR mutants I603N, P671S and Q738R were expressed in COS-1 cells in the absence (-) or presence (+) of 50nM R1881. After SDS-PAGE and immunoblotting AR protein was visualized by polyclonal antibody Sp197. ev= empty vector.

**Transcription activation**

Next we studied transcriptional activation by the different mutant AR’s. Hep3B cells were transiently transfected with one of the AR expression constructs described above and an ARE2-TATA-Luc luciferase reporter construct. Cells were incubated in the presence of increasing concentrations of R1881. The AR-I603N mutant completely lost its transactivation potential even at the highest hormone concentration tested (Figure 2). Both the Q738R and P671S mutant showed reduced maximal transactivation capacity of 56% and 78% of wild type AR activity, respectively, in the presence of 10^{-8} M R1881. In addition, higher R1881 concentrations were required for androgen induction as at 10^{-10} M R1881 their activities were only 10 % and 32 % of wild type AR, respectively. In CHO cells and with a MMTV-Luc reporter construct similarly reduced transcriptional activities were observed for the distinct mutants (data not shown).
**Fig 2:** Transcription activation assay in Hep3B cells. Dose-response curves of wild type AR, AR-P671S, AR-Q738R and AR-I603N, in the presence of increasing amounts of R1881. The activity of wild type AR at 10 nM R1881 was set at 100% and the other data points were calculated relative to that. Values represent the mean ± SEM of two independent experiments, performed in triplicate.

**Intracellular distribution in living cells**

To study the distribution of AR in living cells, wild type AR, a non-DNA binding AR mutant, AR-A573D as a positive control and the three AR mutants, were N-terminally tagged with green fluorescent protein (GFP). In the absence of hormone the proteins were mainly cytoplasmic (left panels in fig 3 a, b, c, e and g). After addition of 1 nM R1881 the GFP-AR translocated to the nucleus (right panels in fig 3 a, b, c, e and g). In the nucleus AR-P671S and AR-Q738R displayed a typical punctate distribution pattern similar to wild type AR (right panels in fig 3 a, e and g) (15, 16). Nuclei of cells transfected with AR-I603N however lacked this punctate pattern and showed a more homogeneous distribution (right panel in fig 3 c), similar to the non-DNA binding mutant AR-A573D (right panel in fig 3 b) (15).

FRAP was used to study the intranuclear mobility of the AR mutants. In concordance with their distribution pattern AR-P671S and AR-Q738R showed a transient immobilisation similar to wild type AR (fig 3 f and h), whereas the redistribution of AR-I603N was as fast as the non-DNA binding mutant AR-A573D (fig 3 d).
Fig 3: High-resolution confocal images and strip-FRAP analysis of cells expressing GFP-tagged AR mutants. (a, b, c, e and g) Confocal images of Hep3B cells expressing GFP tagged wild type AR (a) and mutant GFP constructs (b, c, e and g) in the absence (left panels) and presence (right panels) of 1 nM R1881. The nuclei in the hormone treated cells were represented at 1.6 x higher magnification as compared to the cells in the “minus hormone” situation in order to emphasize the differences in the speckled patterns in the nuclei. Bars represent 5 µm. (d, f and h) Strip-FRAP analysis of the indicated AR mutants in the presence of 1 nM R1881 (red curves). Redistribution of wild type AR (grey curve) and a non-DNA binding mutant (AR-A573D) (black curve) were plotted as references.
Interaction with an α-helical FxxLF peptide motif

Upon hormone binding a hydrophobic groove is formed in the AR LBD surface. This coactivator-binding groove is lined by 13 amino acid residues, which reside in helices H3, H4, H5 and H12 (Fig. 4), one of which is Q738 (7). The coactivator groove interacts with LxxLL- and FxxLF-like motifs present in AR cofactors and with the FxxLF motif in the AR-NTD. To investigate the effect of the AR mutations on LxxLL and FxxLF motif interaction, binding to the AR FxxLF motif was studied. For this purpose, Hep3B cells were transiently transfected with constructs expressing a Gal4-DBD-FxxLF fusion protein and full length ARs together with an UAS4-TATA luciferase reporter construct.

Experiments were done in the absence and presence of 1 nM R1881. Interaction of the AR FxxLF motif with AR-I603N and AR-P671S was strongly induced by hormone to similar levels as shown for wild type AR (Figure 5). However, AR FxxLF interaction with AR-Q738R was five-fold decreased compared to wild type AR. These data indicate that cofactor binding to the coactivator groove is hindered by Q738R substitution, but not by I603N and P671S substitutions.

Fig 4: Structure of the androgen receptor ligand-binding domain (LBD). (A) Ribbon representation of the androgen receptor LBD. In red the ligand is indicated positioned in the ligand-binding pocket. In dark blue helices 3, 4 and 5 are indicated, helix 12 is purple. In brown an FxxLF peptide motif is indicated interacting with the cofactor-binding groove in the LBD surface. The region in the red square is enlarged and rotated in (B). (B) Position of an FxxLF peptide (in brown) in the cofactor-binding groove of the LBD. Important amino acid residues are indicated in the LBD lining the cofactor-binding groove, in which missense mutations have a proven correlation with AIS. Colours are as shown in (A). The figures are generated in ViewerLite 5.0 (Accelrys) using the coordinates of Protein Data Bank entry 1XOW.
Fig 5: Interaction assay as measured in Hep3B cells transfected with wt AR and AR mutant constructs. The AR FxxLF-motif peptide construct and the UAS4-TATA-Luc reporter plasmid were used in this interaction assay. Interaction was measured in the absence (open bars) and presence of 1nM R1881 (closed bars). On top of the bars standard deviation is displayed plus the fold induction. DCC = dextran coated charcoal.

Fig 6: Sequencing analysis pattern of a part of exon 3 of the AR gene in control DNA and DNA of patient A (Sequencing analysis version 5.3.1). The arrow indicates base pair position 2170 of the Androgen receptor gene. F = Forward strand; R = Reversed strand. In the basecalling panel W represents an A or T nucleic acid. In DNA from patient A a mosaic pattern is seen at position 2170.
**Discussion**

In this study we report three novel mutations in the AR gene; p. I603N, p. P671S and p. Q738R, found in a cohort of 101 Indonesian DSD patients. All three patients presented with a PAIS phenotype. We performed extensive functional analyses of the mutant ARs to understand how these missense mutations correlate with the clinical phenotype of these patients. The results of these experiments are summarized in Table 1.

**Table 1. Summary of functional studies of AR mutants**

<table>
<thead>
<tr>
<th>Mutant</th>
<th>Hyperphosphorylation (114-kDa isoform)</th>
<th>Transactivation</th>
<th>Co-activator binding</th>
<th>Transient immobilization</th>
</tr>
</thead>
<tbody>
<tr>
<td>I603N</td>
<td>Absent</td>
<td>-</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>P671S</td>
<td>Present</td>
<td>±</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Q738R</td>
<td>Present</td>
<td>±</td>
<td>-</td>
<td>+</td>
</tr>
</tbody>
</table>

- : diminished, no activity; + : wild type activity; ± : 50-75% wild type activity

The AR-I603N mutation is located in the DBD region of the AR, close to the D box in the second zinc cluster. The D box is involved in AR dimerization and Hormone Responsive Element (17) half site recognition. Amino acid substitutions in the D box normally result in a PAIS phenotype (18). Our results show that the AR-I603N mutation leads to a defective hormone-induced hyperphosphorylation of the protein and absence of the 114 kDa phosphoprotein band probably due to a disturbed DNA binding. AR I603N displays a normal translocation to the nucleus upon hormone stimulation, but has completely lost its DNA binding capacity as shown by live cell imaging, which explains its total lack of transcriptional activity from two distinct promoters. Previously, we have shown that disrupted DNA binding underlies a complete androgen insensitivity syndrome (CAIS) phenotype of a patient harboring an A573D mutation in the first zinc cluster (19, 20). However, despite the presence of an inactivating AR I603N mutation the patient presented with a PAIS phenotype and partly suppressed AMH levels. Examination of the DNA sequence of exon 3 showed besides the mutant also a wild type nucleotide at position 2170 in DNA from blood cells of the patient (Fig. 6), indicative for
somatic mosaicism. A similar occurrence of a somatic mosaicism has previously been reported in a PAIS patient harboring a wild type AR and an AR with a premature stop codon in the NTD (21). Variable tissue distribution of wild type and mutant AR alleles may also underlie the PAIS phenotype of the AR-I603N patient.

The AR-P671S mutation is located in helix 1 of the LBD and encoded by exon 4 of the AR gene. This proline residue is highly conserved among human steroid receptors, underscoring an important role for this residue. AR P671S substitution results in a reduced transcription activity to 78% at physiological hormone concentrations, which could be partly overcome by increasing the level of androgen. The reason for this decreased activity is not yet understood, because in all other functional assays the AR-P671S mutation behaved like wild type AR. Hiort and colleagues reported a different mutation of the same amino acid residue, P671H, in a PAIS patient, although its effect on AR function has not been tested (22). Our data indicate that suboptimal AR functioning due to P671S mutation may be the underlying cause of the PAIS phenotype in this patient.

AR-Q738 is located in the hydrophobic coactivator groove in the surface of the AR LBD (see Fig.4) and (5, 17, 23). The coactivator groove is essential for both cofactor binding via LxxLL and FxxLF-like motifs and interaction with the FxxLF motif in the NTD. We have shown that AR-Q738R substitution does not affect the AR isoform pattern, intranuclear distribution and mobility, and DNA binding, but results in a two-fold decreased transcriptional activity at high hormone concentrations. The effect on transcription is even more pronounced at lower, more physiological hormone levels yielding only 10% of wild type activity. Most likely the underlying reason for loss of activity is the strongly diminished interaction with the AR FxxLF motif. Our data are in line with previous results showing that abrogation of N/C interaction via the coactivator groove reduced transcriptional activity (5, 8). According to crystal structures, residue Q738 makes hydrophobic contacts with the N-terminal F (F+1) of the AR FxxLF motif (Fig 4B) (17, 23). Substitution of the polar but uncharged glutamine residue by a charged arginine residue is probably not allowed because of interference with hydrophobic interactions with F+1, thus destabilizing FxxLF motif interaction. It is likely that binding of AR cofactors that largely depend on AR interaction via the coactivator groove in the LBD, is also negatively influenced by
the Q738R mutation (5, 6, 24). Altogether these data underscore the essential physiological role of AR-Q738 in FxxLF motif binding, including binding to the NTD, i.e. N/C interaction.

Several other amino acid substitutions in residues located in the hydrophobic coactivator groove are PAIS-associated. The F725L and I737T mutations disrupt the N/C terminal interaction (25). The L712F was found several times in PAIS patients and the Q733H mutation displayed a mosaic pattern (26).

In conclusion, we describe three novel PAIS-associated AR mutations present in the DBD (I603N), helix 1 of the LBD (P671S) and coactivator groove (Q738R) and provide insights in the clinical phenotypes of the patients harboring these mutations. AR-I603N entirely lost DNA binding capacity and transcriptional activity. Probably because of somatic mosaicism the patient displays a PAIS phenotype; AR-P671S mutation interferes with transcriptional activity for as yet unclear reasons; and AR-Q738R replacement strongly reduced transcriptional activity because of abrogated capability to perform N/C interaction and cofactor binding. Altogether, our functional analysis of these mutants further increases the molecular understanding of AR functioning.

Acknowledgements

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References


Chapter 6

Lack of correlation between phenotype and genotype in untreated 21-hydroxylase-deficient Indonesian patients

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Abstract

Background: Mutations in CYP21A2 lead to deficiency of 21-hydroxylase and have a severe effect on phenotype, which can be partly prevented by early treatment. We studied long-term effects of this deficiency on phenotype in patients who had not been treated for prolonged periods and correlated these phenotypes with the mutations found in our patients.

Objective: To assess the correlation between genotype and phenotype in untreated patients with 21-hydroxylase deficiency.

Design: Subjects with 21-hydroxylase deficiency were selected from a large population of Indonesian patients with disorders of sexual differentiation (DSD). CYP21A2 mutations in these patients were correlated with their phenotype in terms of genital development and steroid hormone levels.

Patients: Fifteen 46,XX patients with ages between 1 and 33 years, of whom 12 had never been treated before.

Measurements: Mutations in CYP21A2, genital phenotype according to Prader and steroid hormone levels.

Results: We found in all patients CYP21A2 mutations which affect enzyme activity, with a relatively high allele frequency of R356W (40%), I172N (20%) and IVS2-1A>G (13%). The phenotype was not always concordant with the genotype: different phenotypes (mild to severe virilization) were found in sibling pairs with the mutations IVS2-13A>G or I172N. The high frequency of homozygous mutants for R356W in patients aged from 1 to 11 years old is remarkable, since this mutation has been described only in salt wasting patients. In our study this mutation caused a Prader genital stage of III-IV with a urogenital sinus in 3 out of 7 cases, whereas in the remaining cases the labia were at least partially fused. This mutation caused severe virilization with remarkably high serum levels of renin. We found one novel mutation in intron 2 (IVS2-37A>G), containing the branch site, which is likely to affect the CYP21-enzyme. Two additional intron 2 mutations were discovered which are supposed to affect the 21-hydroxylase (i.e. IVS2+33A>C and IVS2+67C>T).
**Conclusion:** We conclude that a correlation exists between the concentration of androgens and the extent of virilization. However, there was no clear correlation between genotype and phenotype, except for the mutation R356W.

**INTRODUCTION**

Congenital adrenal hyperplasia (CAH) is an autosomal recessive disorder with impaired cortisol secretion (1,2). More than 90% of cases of CAH are caused by deficiency in the enzyme 21-hydroxylase (3).

21-hydroxylase deficiency impairs production of aldosterone and cortisol and as a result the secretion of the stimulating hormones renin and adrenocorticotrophic hormone (ACTH) is enhanced. The adrenal glands become hyperplastic and produce excess sex hormone precursors that do not require 21-hydroxylation for their synthesis. Therefore, levels of aldosterone and cortisol are decreased and production of adrenal androgens is increased, leading to sodium loss, Addisonian crisis and virilization (2,4).

Based on severity of symptoms, patients with 21-hydroxylase deficiency may belong to the classical or the non-classical form of the disease (1,2,5). The classical form encompasses the complete 21-hydroxylase deficiency, which leads to life-threatening salt-wasting crises during the neonatal phase in both sexes and prenatal virilization in females. Partial 21-hydroxylase deficiency leads to the simple virilizing form of CAH, and is characterized by prenatal virilization in females and pseudoprecocious puberty in males. An additional form is due to mild 21-hydroxylase deficiency. This so-called non-classical form is mostly asymptomatic or may be associated with signs of postnatal androgen excess consisting of pseudoprecocious puberty, acne, hirsutism and ovarian dysfunction (5). This makes it difficult to recognize the disease during the neonatal period and therefore these patients are mostly diagnosed in a later stadium of childhood (4).

In the Western world, a patient with CAH is most often diagnosed early in life on the basis of screening programs. Subsequent determination of serum hormone levels and investigation of gene mutations lead to a lifelong therapy with corticosteroids starting at a very
early age. Thus salt loss and Addisonian crises are prevented and postnatal progression of virilization will not occur. This situation differs from that in developing countries, where early diagnosis (new born screening) and treatment are not routinely available.

Within a large and heterogeneous group of patients with ambiguous genitalia followed by one of the authors (SMHF) 15 patients suspected of having CAH were identified.

This group of patients offers a unique opportunity to use modern methods to investigate the correlation between phenotype and genotype in untreated CAH patients.

**PATIENTS AND METHODS**

**Patients**

The local Medical Ethics Review Committee approved of this study, and informed consent was obtained from all participants, their parents or guardians. Out of a group of 130 patients with disorders of sexual differentiation (accumulated from 1991 until 2004) from the Dr. Kariadi University Hospital in Semarang, Central Java, Indonesia, 15 patients were provisionally diagnosed as suffering of CAH, based on the 46, XX karyotype in combination with hypervirilization. The ages of these patients varied from 1 to 33 years (Table 1). There were two pairs of siblings (pt 7-10 and pt 5-11). Twelve of the patients had never been treated; three of them (pt 13, 14 and 15) received glucocorticosteroids during a short period before the study.

**Methods**

Each patient underwent a physical examination and photographs were taken of the genital area. Blood was obtained for determination of hormone concentrations and isolation of DNA.
**Phenotype**

Most important characteristics were the length of the clitoris, presentation of a urogenital sinus and labial fusion (6). The photographs of the genital area were evaluated by an independent paediatric urologist (KPW).

**Serum hormones**

Levels of the following hormones were analysed in serum: 17-hydroxyprogesterone (17OHP), progesterone, androstenedione, dehydroepiandrosterone sulphate (DHEAS), testosterone, cortisol and renin. Cortisol, progesterone, androstenedione and DHEAS were analysed using luminescence-based immunoassays on the Immulite 2000 (Diagnostic Products Corporation, Los Angeles, CA). 17OHP was analysed using the \(^3\)H-radioimmuno-assay as described earlier (7). Testosterone was determined using the Coat-a-Count radioimmunoassay purchased from Diagnostic Products Corporation. Renin levels were estimated using an immunoradiometric assay purchased from CIS Bio international (Gif sur Yvette, France). Interassay coefficients of variation of those assays were all below 12%.

**CYP21A2 mutation analysis**

The CYP21A2 gene was amplified from DNA using the polymerase chain reaction and subsequently sequenced for detection of mutations. The CYP21A2 gene of each individual patient was sequenced from position –23 up to 90 bases downstream of the stop codon.

**PCR amplification of CYP21A2 gene fragments**

CYP21A2 gene specific amplification was performed using four sets of primers (Table 2) (8-10). Thirty cycles of PCR were carried out in a final volume of 50 µl containing 5 µl (10ng/µl) genomic DNA of each individual, PCR-buffer containing 1.5 mM MgCl₂ (Applied Biosystems, Foster City, USA), 250 µM dNTPs, 3.125 U AmpliTaq DNA Polymerase (Applied Biosystems), 400 nM forward-primer, 400 nM reverse-primer and 5% DMSO. Amplifications were performed using the GeneAmp PCR System 9700 (Applied Biosystems). The PCR-products were purified using the GFX-96 PCR Purification Kit (Amersham Biosciences, Little...
Sequencing the CYP21A2 PCR-products

The primers used for sequencing were described earlier (8-10). Sequencing was performed using a BigDye Terminator v1.1 Cycle Sequencing Kit (Applied Biosystems) to perform the sequence-reactions, a DyeEx 96 Purification Kit (Qiagen, Venlo, the Netherlands) or the Micro-Bio-Spin purification columns (Biorad, Veenendaal, the Netherlands) to purify the fragments, and an ABI PRISM 3100 Genetic Analyzer (Applied Biosystems) to read the sequences. To analyse the sequencing outcome the computer programme Sequencher 4.2 Ink for Windows (Gene Codes Corporation, Ann Arbor, USA) was used.

Restriction fragment length polymorphism (RFLP) and Deletion detection PCR (DDP)

DDP was used to detect whether apparent homozygous mutations were due the large deletions in one of the alleles, using DNA of homozygous patients and their parents. We used the techniques described by Asanuma et al (11) to detect hemizygosity in the 5’UTR and that of l’Allemand et al (12) for exon 3. To detect the CYP21-R356W mutation in the parents’ DNA, we used the RFLP method (13).

RESULTS

Phenotype

Clinical data of the patients are provided in Table 1. All patients had the female gender, except patient 11 who changed her female gender to male at the age of 20 years. Phenotype was based on genital characteristics. Most of the patients had no urogenital sinus and the labia were not or only partially fused. However, most patients had a large clitoris. This made it difficult to assign a Prader stage, because the Prader staging is based on the length of the clitoris (phallus) as well as on labial fusion and presentation of a urogenital sinus. We decided the clitoris length to be the decisive marker of the severity of virilization. As is indicated in Table 1, only one patient (pt 11) had completely fused labia.
Hormone levels

Hormone levels are also summarized in Table 1. In all patients levels of progesterone and 17OHP were elevated with the exception of patients 13, 14 and 15, who were treated irregularly with glucocorticosteroids. Cortisol levels were low to low-normal in all patients. Similarly, in all patients (except in the treated patients) levels of progesterone, androstenedione and testosterone were elevated.

In 10 out of the 15 patients renin levels were elevated, in some of them to more than 100 fold the upper level of normal. Only in 2 untreated patients (pt 7 and 12) renin levels were within the normal range. As expected in the 3 corticosteroid treated patients renin levels were normal.
Table 2. PCR-primers and conditions used in primary amplification

The levels of androstenedione and testosterone correlated significantly with the extent of virilization and clitoris length (see Fig. 1 for the correlation between testosterone and phallus length in non-treated patients), with one exception: patient 10 had high levels of androstenedione and testosterone but suffered from only slightly virilized features. Her younger sister (pt 7), was much more virilized with less elevated levels of androgens.

<table>
<thead>
<tr>
<th>primerset</th>
<th>annealing temperature</th>
<th>PCR primer*</th>
<th>position (bp)</th>
<th>sequence**</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>69°C</td>
<td>1</td>
<td>-57 to -31</td>
<td>5’-ATGGCTGGGGCTTTGAGCTATAAGT-3’</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2</td>
<td>1380 to 1405</td>
<td>5’-CCCTAGCTGCAATCTCCAGAATGTA-3’</td>
</tr>
<tr>
<td>B</td>
<td>68°C</td>
<td>3</td>
<td>-265 to -245</td>
<td>5’-AGCTGACTCTGGATGAGGA-3’</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4</td>
<td>706 to 727</td>
<td>5’-GAGACTGATGCTTCCAAG-3’</td>
</tr>
<tr>
<td>C</td>
<td>65°C</td>
<td>5</td>
<td>695 to 719</td>
<td>5’-CCGGACCTGTGCAATGACT-3’</td>
</tr>
<tr>
<td></td>
<td></td>
<td>6</td>
<td>2630 to 2656</td>
<td>5’-GAGACTGATGCTTCCAAG-3’</td>
</tr>
<tr>
<td>D</td>
<td>61°C</td>
<td>7</td>
<td>700 to 720</td>
<td>5’-TCTGCAATGACT-3’</td>
</tr>
<tr>
<td></td>
<td></td>
<td>8</td>
<td>2892 to 2912</td>
<td>5’-TCTGCAATGACT-3’</td>
</tr>
</tbody>
</table>

*reference NC_000006, A from ATG start site is 1
**specific nucleotides for the CYP21B gene are shown by bold letters and are underlined

Fig. 1 Relationship between serum testosterone levels and clitoris length in 12 non-treated patients with mutation of CYP21A2
It is well known that the conversion of 17-hydroxypregnenolone to dehydroepiandrosterone (DHEA) and 17OHP to androstenedione by the enzyme 17,20-lyase is facilitated by cytochromeB5 (CyB5) (14). Between the age of 1 and 7 years, CyB5 is hardly expressed in the adrenal glands (14) and therefore levels of DHEAS are low. Levels of this adrenal steroid increased after the age of 7 years, as did the ratios androstenedione - 17OHP (Fig. 2A), and testosterone - 17OHP (Fig. 2B). These ratios were significantly correlated with age.

![Graph showing age dependence of the ratio between serum androstenedione/17OHP concentrations (a) and serum testosterone/17OHP concentrations (b) in 21-hydroxylase deficient patients (N= 12).

Fig. 2 Age dependence of the ratio between serum androstenedione/17OHP concentrations (a) and serum testosterone/17 OHP concentrations (b) in 21-hydroxylase deficient patients (N= 12)

Levels of renin correlated with increased levels of 17OHP as explained by the severity of the 21-hydroxylase enzyme deficiency (Fig. 3).
Fig. 3 Relationship between serum levels of renin and 17 OHP in 21-hydroxylase-deficient patients

**CYP21A2 gene mutation analysis**

Table 3 summarizes the mutations in the CYP21A2 gene detected in each patient. Only mutations that are expected to affect the 21-hydroxylase activity are shown.

**Missense and nonsense mutations in exons**

In 13 patients a total of 4 missense mutations were discovered in exons, which resulted in an amino acid change. These mutations are known to affect the activity of the 21-hydroxylase enzyme and have been described in the literature: P30L, I172N, V281L, and R356W (see Table 3). No novel missense mutations were found. In addition, the nonsense mutation Q318X was detected. Patients 2 and 6 were hemizygous for the R356W mutation; both inherited the deleted gene from their mothers and the mutated gene from their fathers. Patients 7 and 10, who showed homozygosity for the I172N mutation, showed additional heterozygous single nucleotide polymorphisms close to the site of the mutation and were therefore assumed to be homozygous for this mutation.
Table 3. CYP21A2 mutations found in 15 Indonesian patients

<table>
<thead>
<tr>
<th>Patient</th>
<th>CYP21-mutation</th>
<th>Known mutations which cause a phenotype if homozygous</th>
<th>References</th>
<th>Cortisol/17OHP*</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>I172N/I172N</td>
<td>Simple virilizing</td>
<td>20–22</td>
<td>0.438</td>
</tr>
<tr>
<td>10</td>
<td>I172N/I172N</td>
<td>Simple virilizing</td>
<td>20–22</td>
<td>0.595</td>
</tr>
<tr>
<td>5</td>
<td>IVS2 - 13A &gt; G/IVS2 - 13A &gt; G</td>
<td>Salt-wasting/simple virilizing</td>
<td>17,18</td>
<td>0.215</td>
</tr>
<tr>
<td>11</td>
<td>IVS2 - 13A &gt; G/IVS2 - 13A &gt; G</td>
<td>Salt-wasting/simple virilizing</td>
<td>17,18</td>
<td>0.266</td>
</tr>
<tr>
<td>1</td>
<td>R356W/R356W</td>
<td>Salt-wasting</td>
<td>1,13,16,24</td>
<td>0.258</td>
</tr>
<tr>
<td>2</td>
<td>R356W/-</td>
<td>Salt-wasting</td>
<td>1,13,16,24</td>
<td>0.223</td>
</tr>
<tr>
<td>3</td>
<td>R356/W/R356W</td>
<td>Salt-wasting</td>
<td>1,13,16,24</td>
<td>0.435</td>
</tr>
<tr>
<td>6</td>
<td>R356W/-</td>
<td>Salt-wasting</td>
<td>1,13,16,24</td>
<td>0.122</td>
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<tr>
<td>8</td>
<td>R356W/R356W</td>
<td>Salt-wasting</td>
<td>1,13,16,24</td>
<td>0.268</td>
</tr>
<tr>
<td>9</td>
<td>R356W/R356W</td>
<td>Salt-wasting</td>
<td>1,13,16,24</td>
<td>2.258</td>
</tr>
<tr>
<td>15</td>
<td>I172N</td>
<td>Simple virilizing</td>
<td>20–22</td>
<td>Received therapy</td>
</tr>
<tr>
<td>12</td>
<td>I172N</td>
<td>Simple virilizing</td>
<td>20–22</td>
<td>0.870</td>
</tr>
<tr>
<td></td>
<td>R356W</td>
<td>Simple virilizing</td>
<td>1,13,16,24</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>-126C &gt; T</td>
<td>Salt-wasting</td>
<td>12,29,30</td>
<td></td>
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<tr>
<td></td>
<td>-113G &gt; A</td>
<td>Salt-wasting</td>
<td>12,29,30</td>
<td></td>
</tr>
<tr>
<td></td>
<td>-110T &gt; C</td>
<td>Salt-wasting</td>
<td>12,29,30</td>
<td></td>
</tr>
<tr>
<td></td>
<td>-103A &gt; G</td>
<td>Salt-wasting</td>
<td>12,29,30</td>
<td></td>
</tr>
<tr>
<td></td>
<td>-4C &gt; T</td>
<td>Salt-wasting</td>
<td>12,29,30</td>
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<tr>
<td>P30L</td>
<td></td>
<td>Salt-wasting/simple virilizing</td>
<td>12, 29, 30</td>
<td>0.301</td>
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<tr>
<td>13</td>
<td>Q318X</td>
<td>Salt-wasting</td>
<td>16,25,26</td>
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</tr>
<tr>
<td>14</td>
<td>Q318X</td>
<td>Salt-wasting</td>
<td>16,25,26</td>
<td>Received therapy</td>
</tr>
<tr>
<td></td>
<td>IVS2-37A &gt; G/IVS2-37A &gt; G</td>
<td>Salt-wasting</td>
<td>11</td>
<td>Received therapy</td>
</tr>
<tr>
<td>V281L</td>
<td>F306 + 1nt</td>
<td>Salt-wasting</td>
<td>16,25,26</td>
<td></td>
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<tr>
<td></td>
<td>Q318X</td>
<td>Salt-wasting</td>
<td>16,25,26</td>
<td></td>
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<tr>
<td></td>
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<td>Salt-wasting</td>
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<td>IVS2 + 67C &gt; T</td>
<td>Salt-wasting</td>
<td>16,25,26</td>
<td></td>
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</tbody>
</table>

*Reference value >40, see also Table 1 for age-dependent changes.
Intron and 3’UTR mutations

In all patients a total of 18 intron mutations were found: 12 mutations in intron 2, 1 mutation in intron 3, 3 mutations in intron 6 and 2 mutations in the 3’UTR. One of these (IVS2-13A>G) has been described in the literature as having an effect on enzyme activity. Both affected patients had 2 mutated alleles. The mutation IVS2-37A>G, which has not been described previously, contains the branch site in intron 2 and is likely to affect the formation of the lariat, which is involved in the RNA-splicing mechanism.

5’UTR mutations due to gene-conversion

In patient 4 we found 5 mutations in the 5’UTR region as a result of a small gene-conversion between the CYP21A2 gene and the CYP21A1 pseudogene.

DISCUSSION

In view of the age of the patients at the time of diagnosis, we assumed that the salt wasting type of CAH would not occur in our study population, since this is considered a life-threatening situation. For this reason, we were surprised to find only 2 patients without biochemical evidence of aldosterone deficiency. Some of the patients had marked elevation of renin levels and apparently have been able to compensate salt wasting by dietary means.

We could not determine the degree of virilization at birth because the patients did not visit a medical doctor shortly after birth, except for patient 1. This means that all patients have been exposed to high levels of androgens postnatally resulting in progressive virilization. Fusion of the labia and the presence of a urogenital sinus are prenatally determined and postnatal exposure to androgens will have no further effect. Remarkably all patients received the female gender at birth, suggesting that the patients had only slightly virilized genitals at that time. 17OHP levels were more elevated than progesterone in all untreated patients because of conversion of progesterone into 17OHP. The ratios androstenedione/17OHP and testosterone/17OHP were markedly age correlated, probably because of the age dependent expression of CyB5 (14).
We could not predict the severity of the 21-hydroxylase deficiency based on the renin values, since the values differed in equal genotypes even in siblings. This could be due to ‘mature onset’, which means that the adrenal glands fail during aging. Alternatively, this could be explained by variations in genotype / phenotype relationships. However, as expected, the renin levels rise with the increasing levels of 17OHP (Fig. 3).

**Most frequent CYP21A2 gene mutations in the Indonesian patients**

We have analysed the CYP21A2 gene of 15 Indonesian CAH patients. To our knowledge, there have been only few reports on CYP21A2 gene mutations in Asian patients. In 65 CAH families in Taiwan (15) and 28 families in Singapore (16) the most common mutation (40%) was the intron 2 mutation (IVS2-13A/C>G). I172N mutations occurred in ~22% and the R356W mutation in ~16%. In a study of 6 Japanese patients, IVS2-13A/C>G and I172N were responsible for 58% of the cases of 21-hydroxylase deficiency (8). Loke et al (16) suggested that the R356W mutation occurs more commonly in the Asian patients both in Singapore and in Taiwan (15-17%) and less in Caucasians (3-9%). The frequency of these mutations described in Caucasian patients is 11 to 30% for IVS2-13A/C>G, 1 to 30% for I172N and 2 to 10% for R365W (3). The mutation IVS2-13A>G in the splicing donor site is reported to be the most prevalent mutation appearing in the CYP21A2 gene among all ethnic groups (2). In our Indonesian patients there was a relatively high allele frequency of R356W (40%), I172N (20%) and IVS2-13A>G (13%).

**CYP21A2 gene mutation analysis; correlation with phenotype**

Two patients (a sibling pair) are homozygous for the intron 2 mutation IVS2-13A>G (pt 5 and 11). This mutation activates a cryptic splice site that results in aberrant splicing of the pre-mRNA with retention of 19 nucleotides normally spliced out of the pre-mRNA. As a result a shift in the reading frame occurs which generates a frame shift in the third exon, resulting in a stop codon and the production of a truncated protein (17,18). In cultured cells a small amount of normally spliced mRNA is detected. Therefore, a small amount of normal enzyme might be synthesized. Since this mutation is associated with the simple virilizing / salt wasting form we
can explain the phenotype of the two patients (19).

Four patients had the mutation I172N, of whom 2 were homozygous (pt 7 and 10, a sibling pair) and 2 were heterozygous (pt 12 and 15). The I172N mutation is associated with the simple virilizing form of CAH (20,21). In a study of Tusie-Luna et al (22), the mutation I172N showed 2% of wild-type activity for 17OHP and progesterone substrates. Km and Vmax values for both 17OHP and progesterone were determined in cellular lysates. When activities were expressed as first-order rate constants Vmax/Km, the activity of the I172N mutant was decreased 200-fold (0.5% activity). Therefore, the phenotype of the sibling pair, patients 7 and 10 can be fully explained. Nevertheless, patient 7 was more virilized than her sister.

Patients 12 and 15 have an additional heterozygous R356W mutation. Chiou et al (23) described a patient who was compound heterozygous for I172N/R356W, having the simple virilizing form of CAH. With the techniques we used, we were not able to determine whether the heterozygous mutations are located on the same allele. However, if the two mutations would have been present on the same allele, it is likely that the other, intact allele would yield sufficient enzyme to prevent the abnormalities detected in these patients.

Four patients were homozygous for the mutation R356W (pt 1, 3, 8 and 9) and two patients were hemizygous for this mutation (pt 2 and 6). This mutation has a dramatic effect on enzyme functioning (1,23), associated with the salt-wasting form. In 1990 it was assumed that the protein region involving R356W, constitutes a steroid-binding site (23). It was speculated that the replacement of Arg356 by Trp might be drastic enough to unfold the protein, which might destroy the steroid binding capacity of the enzyme leading to a 50-fold lower activity of the enzyme.

Recently it was discovered that in P450c21, Arg356 is probably located in a region that is involved in redox partner interaction (2). Stickelbroeck et al (3) as well as Loke et al (16) found that all CAH patients carrying the homozygous mutation R356W were salt wasters. However, all our six patients have survived 1 to 11 years in spite of the mutation. In all patients the Prader stage was III-IV. Furthermore, patients 1, 2 and 6 had a urogenital sinus. If we take the renin values into account, the four highest levels of renin (indicating a severe deficiency of 21-hydroxylase) are detected in patients with the homozygous R356Wmutation. We can conclude
that the mutation R356W in our patients caused a severe 21-hydroxylase deficiency resulting in
the severe virilizing form of CAH.

Patients 4, 13 and 14 are heterozygous for the mutation Q318X. This mutation is
predicted to result in a completely non-functional enzyme due to premature termination of
translation of the mRNA before the conserved heme-binding region of the P450 polypeptide
(24). When the mutated sequence was transfected into mouse Y1 adrenal cells, the resulting
mRNA levels were decreased. In the studies of Kharrat et al (25) and Loke et all (16) all patients
who were homozygous for the Q318X mutation had the salt wasting form. However Kharrat et
al also studied 2 patients with the simple virilizing form who were compound heterozygous for
this mutation, having the mutation R356W or I172N on the other allele.

Patient 14 is compound heterozygous for F306+1nt, V281L and Q318X. Wu et al (26)
demonstrated a fivefold reduced enzyme activity for the mutant V281L and Stikkelbroeck et al
(3) associated this homozygous mutation with the non-classical form of CAH. Besides that,
Stikkelbroeck et al (3) and Asanuma et al (11) reported a cluster mutation in exons 7 and 8 of
V281L -F306+1nt-Q318X: an extra T nucleotide is inserted in the allele which results in a 100%
reduced enzyme activity and consequently in a salt wasting phenotype. However, since this
patient is heterozygous for this cluster mutation, two additional intron 2 mutations in this patient
(IVS2+33A>C and IVS2+67C>T) could influence the enzyme activity. To prove this, these
mutations should be investigated in more detail.

Patient 4 had five additional mutations in the promoter region, 5’UTR and exon 1, which
are compatible with the sequence of the pseudogene CYP21A1 and can decrease the
transcriptional activity with 20% (12). It seems likely that a hybrid was formed between
CYP21A1 and CYP21A2, with a junction site just before intron 2. This hybrid would be formed
by unequal crossover, resulting in a deletion of the 5’end of the CYP21A2 gene, the C4B gene
and the 3’end of the CYP21A1 pseudogene (11,27). In addition, the mutation P30L causes an
enzymatic activity of 60% (28).

The heterozygous combination of the mutations together with Q318X in patient 4
explains the phenotype.

Besides the heterozygous Q318X mutation, we found in patient 13 the homozygous
mutation IVS2-37A>G, which contains the branch site in intron 2. This mutation has not been described previously and may affect the formation of the lariat during RNA splicing (29) which results in intron 2 retention or exon 2 skipping. This may have an important affect on the phenotype.

In conclusion, we found mutations in the CYP21A2 gene in all patients with a relatively high allele frequency of R356W (40%), I172N (20%) and IVS2-13A>G (13%). Most remarkable in this study is the high frequency of the mutation R356W, which is very often described as causing the life threatening salt-wasting form of CAH. Apparently patients having the R356W mutation were able to compensate salt waste by dietary means. The 21-hydroxylase deficiency resulted in postnatal progressive virilization and almost all patients had the female gender and a strong desire to have a female appearance. Therefore, a project has been initiated to offer medical and surgical treatment.

ACKNOWLEDGEMENTS

We thank the Gender team of the Medical Faculty and the Molecular and Cytogenetic Laboratory of the Diponegoro University / Dr. Kariadi Hospital for help in research of the patients and the karyotyping.

References


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Chapter 7
Correlation between Androstenedione and 17-hydroxyprogesterone Levels in Saliva and Plasma in Treated Patients with Congenital Adrenal Hyperplasia.

Achmad Zulfa Juniarto, Kristel Goossens, Bestari A Setyawati, SLS Drop, FH de Jong, Sultana MH Faradz.

Abstract

Background: Congenital adrenal hyperplasia (CAH) or adrenogenital syndrome (AGS) is the most common cause of female ambiguous genitalia. Management of these patients involves medical treatment using glucocorticoids such as hydrocortisone, prednisone or dexamethasone. Monitoring is done by measurement of 17-hydroxyprogesterone or androstenedione in serum, plasma or saliva.

Objective: To develop a monitoring system of steroid treatment in CAH patients using solely saliva.

Methods: We studied saliva of 24 CAH patients who received glucocorticoid replacement therapy. Patients were asked to collect saliva after awakening, and in the afternoon and evening. Levels of 17-hydroxyprogesterone and androstenedione were measured both in saliva and serum by immunoassay.

Results: There was a significant positive correlation between 17-OHP in serum and 17-OHP in saliva (R=0.929, p<0.01). A significant positive correlation between androstenedione level in saliva and serum was also found (R=0.611, P<0.01). This study also revealed a significant positive correlation between androstenedione and 17-OHP in serum (R=0.647; p<0.01) and in saliva (R=0.799; p<0.01). All patients showed increased level of 17-hydroxyprogesterone and androstenedione in the sample collected at awakening time.

Conclusions: Determination of salivary androstenedione and 17-hydroxyprogesterone in CAH patients can be a useful alternative to measurement of these hormones in serum.
Introduction

Sexual differentiation follows a specific complex sequence of events. The start of this process takes place between 6-14 weeks of gestation (1). During this period, developmental errors may occur and lead to sexual ambiguity or discordance between chromosomal sex and the appearance of external genitalia. Disorders of sexual development (DSDs) are now classified as 46,XY DSD, 46,XX DSD, and chromosomal DSD (2). Congenital adrenal hyperplasia (CAH), or adrenogenital syndrome (AGS) in older literature, is the most common cause of ambiguous genitalia in females (46,XX DSD) (2). This syndrome is due to a mutation in one of the genes encoding enzymes needed for the production of gluco- and/or mineralocorticoids in the adrenal cortex. About 90% of CAH is caused by 21-hydroxylase deficiency leading to a block in both cortisol and aldosterone production and resulting in an excessive adrenal androgen production causing masculinization of the genital and urinary structures. Lack of aldosterone and cortisol will lead to adrenal crisis which can cause severe illness and even lead to death. A milder, non-life-threatening form of CAH (non-classic form) in which salt loss does not occur becomes manifest in later childhood or even young adult life as a result of progressive virilization (3).

Management of CAH patients involves medical treatment in addition to surgery and psychological counselling. Glucocorticoids such as hydrocortisone, prednisone or dexamethasone are the drugs of choice in CAH patients (4). The synthetic mineralocorticoid fludrocortisone is needed for salt wasters to retain salt. Follow up of the treatment is important in order to prevent overtreatment causing growth inhibition and under treatment resulting in virilisation and increased height velocity (5). The effectiveness of treatment is traditionally monitored by measurements of 17-hydroxyprogesterone, androstenedione and testosterone in serum (6). This means the invasive procedure of phlebotomy every 3 to 6 months in patients, some of whom are babies or young children. Therefore we compared steroid hormone levels obtained simultaneously in plasma and saliva, with the purpose to develop a monitoring system of steroid treatment in CAH patients using solely saliva.
This paper aims to make a contribution in the area of CAH treatment by measuring the diurnal rhythm of salivary steroids during treatment with 3 daily doses of cortisol.

**Materials and methods**

*Samples*

For analysis of steroids in saliva we collected saliva of 24 patients with CAH with relatively high levels of 17-hydroxyprogesterone (17-OHP) in serum, which likely will result in high levels of salivary 17-OHP. The age range of the patients was from 1.4 to 16.3 years old. All of them received Hydrocortisone 12 mg/ metre body square /day in three divided doses. Patients with CAH were willing to participate in the study and consented to the procedures of saliva and blood collection. The diagnoses varied from the severe form of classical CAH to the non-classical form of CAH. All samples of saliva and blood were taken prior the glucocorticoid treatment. After a clear explanation of the procedure, saliva was collected with the Salivette of Sarstedt®©, Nümbrecht, Germany (figure 1) by chewing on the swab. Patients were asked to collect saliva at awakening, 30 minutes after awakening in the afternoon and in the evening before eating or brushing their teeth to prevent blood contamination. Patients were also instructed to keep the saliva in the refrigerator and to immediately hand the saliva during hospital visit at scheduled time. A duplicate saliva collection was performed during the patient’s hospital visit together with peripheral blood collection. After collection of saliva, the samples were centrifuged and stored frozen at -20°C until analysis.
This study has been approved by the Local Medical Ethics Committee.

![Salivette device](image)

**Figure 1.** Salivette device for the collection of saliva from left to right: stopper, cotton swab, cotton swab holder with hole in bottom, collection tube and complete device.

*Measurement of 17-hydroxyprogesterone and androstenedione*

Serum concentrations of 17-OHP were determined using a RIA technique as described before (7). Androstenedione levels in serum were determined using a commercially obtained chemoluminescence-based immunoassay (Immulite 2000, Siemens, Los Angeles, CA). Salivary concentrations of 17-OHP and androstenedione were determined using salivary ELISA Kits (DRG, Marburg, Germany). The procedure was as follows: 25 µl of saliva was pipetted into duplicate wells of a 96-well plate, coated with a specific antibody. 250 µl of enzyme-conjugate (17-OHP or androstenedione conjugated to horseradish peroxidase) was added. After 1-hour incubation at room temperature, the wells were washed 3 times with diluted wash solution and subsequently 200 µl substrate solution (tetramethylbenzidine) was added. After 15 minutes at room temperature the reaction was stopped with 100 µl stop solution (0.5 M H₂SO₄). The wells were read within 10 minutes in the Spectra Count (Packard Bioscience, Boston, USA) at 450 nm. Inter- and intra-coefficients of variation for salivary androstenedione; salivary 17 OHP; serum androstenedione and serum 17-OHP were <13.6% and <7.9%; 12.3% and <7.9%; <11% and <8%; and <10% and 6% respectively.
Statistics

Results are given as means ± s.e.m. Differences between hormone levels in samples collected at different times of the day were compared by paired Student’s t-test. Logarithmically transformed concentrations of saliva 17-OHP and androstenedione were correlated with serum values and the Pearson correlation coefficients were calculated using SPSS 11.0 for Windows. P-values < 0.05 were considered significant.

Results

1. Correlation between 17-OHP in serum and saliva

There was a significant positive correlation between 17-OHP in serum and 17-OHP in saliva collected from the same subject at one moment in time (R=0.929, p<0.01, figure 2).

2. Correlation between Androstenedione in serum and saliva

As we can see in figure 3, there was also a significant positive correlation between androstenedione levels in saliva and serum (R=0.611, P<0.01).
3. Correlation Androstenedione and 17-OHP in saliva and serum

Androstenedione levels in saliva showed a significant positive correlation with 17-OH level in saliva (R=0.641; p<0.01, figure 4). This study also revealed a significant positive correlation between androstenedione and 17-OHP in serum (R=0.647; p<0.01, data not shown).
4. *Diurnal rhythms of salivary 17-OHP and androstenedione*

A circadian variation of salivary 17OHP and androstenedione levels was found in this study (figure 5). Morning values of 17-OHP showed significantly higher levels than during the afternoon and evening. Furthermore, 17OHP levels in samples collected 30 minutes after awakening (3.00 ± 0.75 pmol/l) were significantly higher than those at the time of awakening (3.55 ± 0.87 pmol/l, P<0.05). Concentrations of androstenedione at awakening were greater than at other times during the day, but significance was only reached when morning and evening levels were compared.

![Figure 5. Diurnal rhythm of salivary 17-OH progesterone (black bar) and Androstenedione (hedged bar). means +/- SEM](image)

**Discussion**

Hormone levels are often measured in serum with the use of immunoassays. The result is most of the time based on the interpretation of hormone concentrations in a single sample. Single serum analysis is not ideal for the study of hormones that undergo circadian rhythms of secretion. Hormones such as cortisol and 17-hydroxyprogesterone can be quite different in concentration throughout the day depending on time of day and physical condition (8). Measurements of salivary 17OHP in healthy children revealed that values tended to be higher in the morning than during the afternoon and evening (9). Within the first minutes after
awakening, salivary cortisol levels rise by 50-60%. This response was not dependent on the
time of awakening, sleep quality, physical activity. After the morning peak, cortisol values will
decline during the day (10,11). A similar rise of 17OHP was found in treated CAH patients in
this study. Furthermore, all patients showed relatively high levels of 17OHP in samples
collected at awakening time probably because of the fact that the saliva was collected before
taking the morning dose of glucocorticoid. This observation suggests insufficient suppression
of adrenal steroid production during the early morning hours.

Salivary androstenedione values showed lower values than 17OHP and gradually fell
during the day to lowest values at evening time. There was a circadian rhythm in the
concentration of androstenedione in treated patients with CAH, but the level was lower than for
17OHP (12).

It was noted that 17 OHP is a better marker to make a treatment evaluation especially in
young patients because the level of androstenedione in these patients was rather low due to the
relatively inefficient adrenal conversion of 17OHP to androstenedione at this age.
We found a good correlation between serum and saliva levels of both 17-OHP and
androstenedione. These results indicate that the steroid levels in saliva describe steroid levels in
serum. Levels of androstenedione were also correlated with levels of 17-OHP. These findings
corrrelate well with earlier results of Young et al. (1988) who also found that there were high
correlations between plasma concentrations of androstenedione and testosterone as well as with
170HP (12). A strong correlation between the salivary androstenedione profiles and plasma
testosterone concentrations also found in the study (12). The same correlation was also found
between concentration of androstenedione in saliva and the unbound concentration in plasma in
the study of Baxendale et al. (13) Otten et al found significantly positive correlations between
salivary and plasma values of both Androstenedione and 17-OHP (14). Measurement of 17-OHP
concentrations was also performed by Hughes et al (15) in 19 patients with CAH who received
hydrocortisone treatment. This study found that serial measurement of 17-OHP in saliva
provided valuable information in the line of treatment. Arisaka et al (16) found good correlation
between 17-OHP concentrations in paired saliva and serum samples from the patients and the
control subjects. Salivary steroid profiles are now widely accepted and used to assess the quality
of substitution therapy, providing information on the efficacy of suppressive regimens in the
treatment of congenital adrenal hyperplasia patients. In addition to 17 OHP, salivary
androstenedione is also a direct marker of adrenal androgen secretion.

The advantages of the use of salivary steroid profiles include easy collection of sample
at home and dispatch to the laboratory between regular medical check-up for outpatient
monitoring (17-19).

**Conclusion**

As the measurements of levels of steroid hormone in saliva and serum showed good
correlations, we can conclude that determination of salivary androstenedione and 17-OHP are a
useful alternative to measurements of those hormones in serum for monitoring of CAH
treatment.

**Acknowledgments**

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Diponogoro University / Dr. Kariadi Hospital for their help in providing patients for this
research.
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Chapter 8
Salivary 17-hydroxyprogesterone (17-OHP) and Androstenedione in Monitoring Efficacy of Treatment Among Indonesian Congenital Adrenal Hyperplasia Patients

Achmad Zulfa Juniarto, Gerard Noppe, Nani Maharani, Erica van den Akker, Rudy Susanto, Sultana MH Faradz, Frank H. de Jong, Stenvert L.S. Drop

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Abstract

Objective: Early diagnosis of congenital adrenal hyperplasia (CAH) and the need for long term treatment are of great concern to the medical community. The aim of this study was to evaluate the effectiveness of glucocorticoid treatment-monitoring based on salivary 17-hydroxyprogesterone (17-OHP) and androstenedione measurements in CAH patients in Semarang, Indonesia in comparison to patients treated in Rotterdam, the Netherlands.

Methodology: 25 out of 43 patients with CAH from Semarang, Indonesia were included in the study. For comparison, twenty CAH patients from the Sophia Children’s Hospital/ Erasmus Medical Center Rotterdam, the Netherlands were included. The effects of treatment were monitored by estimations of the steroids 17-OHP and androstenedione in saliva. Auxology and bone age determination were recorded.

Result: 17-OHP and androstenedione levels were high in a substantial number of Indonesian patients under treatment but decreased after adjustment of dosage and timing. The steroid concentrations obtained after adjustment were similar to those found under comparable circumstances in patients in Rotterdam.

Conclusion: Optimal treatment of CAH patients in Semarang Indonesia can be reached by introducing hydrocortisone treatment and adjusting dosage and timing on the basis of salivary steroid monitoring. However, in Indonesia the management of these patients is still constrained by the lack of diagnostic and therapeutic means.
Introduction

Congenital Adrenal Hyperplasia (CAH) is classified as a Disorder of Sex Development (DSD) which is usually diagnosed on the basis of ambiguous genitalia in the female newborn or a salt losing crisis which may occur in both males and females (1,2). CAH infants with ambiguous genitalia are genetically female (46,XX) whereas 46,XY infants do not have a significant phenotype except for hyperpigmentation of the scrotum. This disorder occurs when one of the enzymes required for synthesis of cortisol and aldosterone in the adrenal glands is deficient. The condition results in hyperplasia of the adrenal glands and in increased secretion of steroid precursors, such as 17-hydroxyprogesterone (17-OHP) and androstenedione, leading also to elevated testosterone levels (3).

Based on its clinical appearance, CAH patients can be divided into two groups, those with the classical and those with the non-classical form. The classical form is characterized by congenital insufficiency of cortisol and aldosterone synthesis with a marked increase of androgen levels. This condition will lead to salt losing and virilisation of the female. The non-classical form is characterized by partial deficiency of cortisol and aldosterone synthesis resulting in late onset of mild clinical symptoms (4). The incidence of the classical form of CAH is approximately 1 in 14,000 births worldwide whereas that of the non-classical form is predicted to be much higher (5).

Early diagnosis and treatment of CAH patients is essential. The need for long term treatment especially of salt losing patient is of great concern to the medical community in view of the high risk of hyponatremia, hyperkalemia, dehydration and shock with a possibly fatal result.

Treatment of CAH patients aims to provide adequate adrenal hormone substitution in order to prevent adrenal crises and to suppress excess testosterone production. The goal of therapy is to optimize growth and pubertal development (6). Hormone replacement therapy using hydrocortisone (HC) is an option that allows control of the adrenal hormone balance. The effectiveness of therapy is measured by monitoring the adrenal precursor steroids (7). In a
previous study we confirmed that determination of salivary androstenedione and 17-OHP in CAH patients is a useful alternative to the measurement of these hormones in serum (8).

This is particularly relevant in Indonesia as the availability of treatment and monitoring of CAH is limited due to the scarcity of medicine, geographical distance and scattered area of patients’ dwelling, and financial issues.

Therefore, the aim of this study was to evaluate the effectiveness of glucocorticoid treatment-monitoring based on salivary 17-OHP and androstenedione measurements among Indonesian CAH patients in Semarang in comparison to CAH patients treated in Rotterdam, the Netherlands as reference. The Netherlands is a West-European country counting around 17 million inhabitants where newborns are screened within the first week of life for elevated 17-OHP levels to identify congenital adrenal hyperplasia. The prevalence of classic CAH in the Netherlands is about one in 10,000 to 18,000 newborns, of which 95% is caused by 21-hydroxylase deficiency.

**Patients & Methods**

**Patients Semarang**

This study is part of a stepwise diagnostic evaluation of a cohort of patients with DSD in Semarang Indonesia. Out of 286 patients diagnosed with disorders of sexual development between 2004 and 2010 from the Dr.Kariadi University Hospital in Semarang, Central Java, Indonesia, 43 patients were diagnosed as CAH based on phenotype and hormonal analysis. This diagnosis was confirmed by chromosomal and gene mutation analysis. Patients’ age at the time of referral ranged from 3 days to 33 years with a median of 6 years. Among the 43 CAH patients, 40 had 46,XX karyotype; two had 46,XY and one had 46, XX (99%) / 46, XY (1%) karyotype.

The latter patient presented at age 0.2 years with undescended testis and severe hypospadias. All patients with a Y chromosome were raised as males, while of the 40 CAH patients with 46, XX karyotype, 5 were raised as males and 35 as females. Thirteen patients were diagnosed at an early age (<2 months), 23 with ages between 1.5 and 13 years while 7 were detected after 12 years of age. Five patients died during the study period because of a salt losing
crisis, 10 were not treated for the following reasons: 5 patients were living as males and another five refused the treatment.

Twenty-eight out of 43 patients were treated and 25 patients were regularly followed up in our outpatient clinic, while 3 patients were followed up in another centre. The effect of glucocorticoid treatment was studied in these 25 CAH patients: 2 patients received prednisone while 23 patients received HC. Patients age at treatment ranged between 0.7 - 18.7 years (see Table 1).

Patients were treated with HC at a dose of 12-15 mg/m2/day given in 3 divided doses. In 2 adult patients age 18.7 and 17.5 years old, prednisone was given at a dose of 5 mg twice a day.

Six patients were suspected of the salt wasting type of CAH. This diagnosis was based on a history of intercurrent illnesses during therapy. We could not establish the diagnosis as no data on urinary salt loss and on renin levels were available. These patients were treated additionally with 0.05-0.2 mg/day of 9α-fludrocortisone, a synthetic mineralocorticoid.

The regular follow up every 3 months included physical examinations and measurements of blood pressure, height and weight. Instructions were given to parents and patients which included dosing schedules for medication and check of compliance. Auxological parameters, such as growth velocity and weight were also recorded. The effect of treatment was regularly monitored by assessment of salivary levels of 17-OHP and androstenedione. As much as
possible an X-ray of the left hand for bone age determination was obtained once a year in prepubertal and pubertal children. In addition, we obtained auxological data in prepubertal children.

**Patients Rotterdam**

The Dutch patients were included in the study to provide a reference of salivary steroid precursor concentrations in well-controlled congenital adrenal hyperplasia patients treated in a tertiary reference outpatient-clinic in a country with one of the best health-care systems worldwide. As there are no reference values available for salivary adrenal steroid precursor concentrations, this population provides the next best reference.

Twenty CAH patients from the outpatient clinic of the Sophia Children’s Hospital/Erasmus MC, Rotterdam, the Netherlands were included in this study. The age of the patients ranged between 5-16 years, 13 were males and 7 females; 12 patients had a salt wasting type of CAH. All patients in this study were treated with HC, 8.8 to 17.5 mg/24h per square meter body surface area, divided in three doses per day. An additional treatment with 9α-fludrocortisone at a dose of 0.05-0.2 mg/day was given to the salt wasting patients.

**Methodology**

*Measurement of salivary 17-hydroxyprogesterone and androstenedione*

Salivary concentrations of 17-OHP and androstenedione were determined using salivary ELISA Kits (DRG, Amersfoort, the Netherlands).

*Saliva Sample collection for day profile investigation*

After a clear explanation of the procedure, the patients were asked to collect saliva by passive drooling into Sarstedt® (Nümbrecht, Germany) polypropylene tubes or, for babies, by pipetting with a minimum volume of 1 ml before eating or tooth brushing in order to prevent blood contamination. Contamination with food debris was avoided by rinsing the mouth with water. Collection times were as follows: the first sample before the morning tablet of medication at 06.00-07.00 h, the next three samples at 12.00-13.00, 16.00-17.00 and 21.00-22.00 for two
successive days. Saliva was stored frozen at -20°C until measurement in order to avoid microbial decomposition of the steroids.

**Auxology measurements**

Height standard deviation scores (SDS) were calculated with a growth calculator using Growth Analyser version 2 (www.growthanalyser.org). Growth data of the Chinese population in the programme were used as reference as no data are available for the Indonesian population. Body mass index (BMI) was calculated as weight (kilograms)/height (meters)$^2$.

Bone age was assessed by x-ray of the left hand using the Greulich and Pyle method (9). The patients or their parents gave informed consent to participate in this study, which was approved by the ethics committee of both institutions.

**Results**

After a period of steroid treatment varying between 1 - 46 months (median of 34 months), 17-OHP and androstenedione levels in saliva were measured four times a day prior to HC administration for two consecutive days for each patient to obtain the diurnal rhythm. Results are shown in figure 1, indicating high levels in a substantial number of patients. Therefore the dosage of HC and particularly the timing were adjusted. Based on these results, additional saliva samples were obtained after 1 month of adjusted treatment and just prior to the administration of HC for one day. Saliva steroid precursor concentrations decreased after treatment was adjusted (Figure 1). A clear correlation between saliva levels of 17-OHP and androstenedione was confirmed ($r = 0.88$). The morning saliva steroid concentrations of the patients in Semarang obtained after adjustment of dosage and timing were compared to steroid concentrations in saliva of CAH patients in Rotterdam obtained under comparable circumstances. As shown in Figure 2, the concentrations were comparable for most patients.
Figure 1: Salivary 17-hydroxyprogesterone and androstenedione diurnal rhythms
Circadian rhythms of 17-hydroxyprogesterone and androstenedione of 25 CAH patients on two subsequent days (full lines). Their levels were significantly correlated. In the morning, the concentrations of these steroids were high and then decreased gradually until the lowest values were found in the evening. A significant decline of hormone levels occurred after adjustment of dosage and time of administration of the medication (P = 0.01 and 0.04 respectively for 17-OHP and androstenedione) (broken lines). Figure shows means and SEM. Reference ranges for 17-hydroxyprogesterone and androstenedione are below 225 and 250 pmol/l, respectively.

Figure 2: Salivary steroid levels in CAH patients in Semarang and Rotterdam
Comparison of the levels of 17-hydroxyprogesterone and androstenedione in saliva samples collected from CAH patient in Semarang (after treatment adjustment) and Rotterdam showing similar concentrations both in prepubertal and pubertal patients. (Pre-pubertal age: <12 years, pubertal age: ≥12 years) Reference ranges for 17-hydroxyprogesterone and androstenedione are below 225 and 250 pmol/l, respectively.
Auxological data

With regard to bone age examinations, 11 patients already stopped growing before start of therapy, 5 patients were examined only once, and in five patients no data were available. In 4 patients, the progression of bone maturation could be analyzed and all were found to have advanced bone age; The progression of maturation decreased in 3 patients after 45, 45, 35 months of therapy respectively.

Of the 16 patients who were still experiencing growth, 8 had improvement in height SDS during therapy, 3 experienced a decrease, 2 were unchanged and the other 3 could not be assessed because no data were available (Table 2).

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*dos: date of study, **NA: Not available

Discussion

Lifelong use of glucocorticoids is the therapy of choice in patients with CAH. Dose adjustments to avoid the adverse consequences of inadequate treatment and overtreatment are based on rigorous assessment of biochemical parameters.

This study shows that the result of treatment of CAH patients in Semarang, Indonesia is comparable to that in a Dutch endocrine centre. Both centres utilized salivary steroid measurements to monitor and adjust HC treatment.
The purpose of early treatment of CAH is to suppress the excessive adrenal androgen secretion without disrupting growth and the development of puberty. To achieve this, the glucocorticoid dosage should not exceed the physiological secretion of cortisol (6 mg/m2/day) which is equivalent to a HC intake of 8-10 mg/m2/day.

The deficiency of the adrenal enzyme 21-hydroxylase leads to markedly increased concentrations of steroid precursors from the adrenal gland. Thus dosing glucocorticoids at slightly supra-physiological levels will suppress the increased adrenal androgen production (10). This can be achieved with an intake of HC 10-15 mg/m2/day.

While our results indicate that suppression can be achieved, adjustment of dosage as well as time of dosing was necessary to reach an acceptable degree of suppression that was comparable to results in another clinic. When the medication was taken at defined hours (07-13-18 hr), the profile of hormones showed a steep increase in the morning and a gradual decline in the evening. This is because intake of HC in the early evening (18 hr) is insufficient to cover the corticosteroid requirement until the next morning. Therefore, we advised to administer the medication regularly every 8 hours at 06-14-22 hr to improve the hormonal profile.

HC is preferred over prednisone or dexamethasone in infants and children for the treatment of CAH because it is well tolerated, leads to less side-effects because of its shorter half-life and it is inexpensive (6). Most importantly, it will not inhibit linear growth provided it is given in the correct dosage. In pre-pubertal and pubertal children, treatment with long acting glucocorticoids such as prednisone or dexamethasone is no longer used because of the side effects of suppressing linear growth. Slow release preparations of HC accommodating the circadian rhythm of cortisol in the body are not yet available (11). Thus, specifically in infants and young children, HC in a dosage adapted to body surface is the drug of choice.

Whereas the short half-life of about 8 hours may allow a dosing schedule of 3 times a day, this dosing schedule may be insufficient especially in infants and young children to cover their overnight requirement. As a result, the HC does not last until the morning explaining high levels of 17-OHP and androstenedione in the morning samples of our patients, whereas the levels of both hormones decline appropriately during the day following morning and noon.
administration of HC. In contrast, in patients with compliance problems levels remain high throughout the day.

Monitoring HC therapy of patients with CAH, using saliva to measure steroid hormones is used extensively (7,10). The main advantage of using saliva is the non-invasive way of collecting samples. In fact, steroid levels in saliva reflect the physiologically active fraction of steroid hormones (6,12). Moreover, saliva collection is very patient friendly as it may be done at home at designated times. Steroids in saliva are stable at room temperature allowing to send samples by regular mail to the laboratory for measurement.

Because single sample monitoring provides a picture of adrenal hormonal production at only one point in time and does not take into account the circadian rhythm of steroid secretion, some experts favour checking the hormonal profile during 24 hours by collecting blood or saliva samples several times during the day. Drawing a blood sample is bothersome to the patient, and is often logistically not feasible (10). In several studies, steroid levels in saliva and serum have been found to have a high correlation (10,13).

During periods of rapid growth such as during infancy and puberty the extent to which one should relax standards for 17-OHP, androstenedione and testosterone levels are not fully determined (14). Many of our patients (12 out of 25) were in the age range of 8-15 yr and were in (early) puberty. During this age period, it is difficult to maintain androgen suppression with HC treatment because of compliance problems as a result of pubertal behaviour and the changing endocrine milieu during puberty (15). Growth hormone and IGF 1 levels which are elevated during this period stimulate the activity of 17-hydroxylase/17,20-lyase resulting in increased adrenal androgen biosynthesis (16). Similarly in 7 out of 25 patients who started therapy during infancy HC dosing was notably difficult because of the rapid change of bodily proportions. Therapeutic efficacy was difficult to evaluate because most of our Indonesian patients were diagnosed and started therapy at a late age with advanced bone age which was not compatible with their chronological age. Due to premature epiphyseal closure, many of them did not achieve the optimal height: their average height amounted to -2.42 (±1.39) SDS.

Among the patients who were still experiencing growth, data are insufficient to draw firm conclusions. Education of patients and parents and regular monitoring of auxological parameters
and saliva steroid levels will lead to further improvement of height potential. It is well recognized that the age of diagnosis, the type of CYP21 mutation and the response to a certain dose of HC in view of individual variation of drug metabolism all are relevant factors contributing to the final outcome of HC treatment.

Many patients on treatment live in remote areas. To anticipate the situation when a patient is suffering from inter-current illness during which there is a need to increase HC dose, we offer them a reference letter that serves as information for the local doctor.

Availability of HC is very urgent because it is life-saving and it reduces morbidity not only in CAH patients but also in patients with congenital or acquired ACTH deficiency. It is believed that there are many under reported or unrecognized cases in Indonesia.

**Conclusion**

The diagnosis of CAH can be established in most of the patients with great certainty. However in Indonesia the management is still constrained by the lack of diagnostic and therapeutic means. The drug of choice in infants, young children and adolescents is HC, which is lifesaving. HC, declared an essential drug by the WHO, should be made widely available throughout Indonesia. With regular follow up HC treatment will enable a favourable outcome of patients with CAH. As saliva can be collected at home and sent by regular mail to the laboratory a major practical problem can be overcome. Collaboration with the local health provider for auxology measurements and monitoring of the health status of patients should be well promoted and will be a major step forward to optimize treatment.

**Acknowledgements**

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References

Chapter 9

Virilization due to Androgen Hypersecretion in a Patient with an Ovarian Leydig Cell Tumor: Diagnostic and Psychosocial Implications


Abstract

Background: Virilization due to hyperandrogenism in women causes male signs and symptoms such as swelling of the clitoris, deepening of the voice, facial hair and increase in body hair. Virilization is caused by less than 0.5% of all ovarian tumors. Here we report a case of virilizing Leydig cell tumor of the left ovary in a 36 years old woman. Misinterpretation of symptoms, conflicting medical information and advices from previous doctors had confused of the patient.

Design: We performed a diagnostic evaluation including clinical, hormonal parameters, imaging, surgery, histological parameters and psychological assessment.

Results: Blood analysis showed a testosterone level in the high male range. The presence of an ovarian tumor was confirmed by laparoscopy. Since the patient refused ovariectomy, a biopsy of the left ovary was performed. Pathology showed a Leydig cell tumor without histological signs of malignancy. Inspite of extensive explanation and psychological counseling, cultural barriers prevented appropriate treatment.

Conclusion: An ovarian Leydig cell tumor should always be considered in a woman in the reproductive age with symptoms of virilization. The diagnosis is suspected on the basis of an ovarian mass on examination and further investigation and should be proven by biopsy. This is important before giving advice and carrying out treatment to the patient.
INTRODUCTION

Androgen excess is the most common endocrine disorder in reproductive-aged women, affecting approximately 7% of this population (1). This results in ovulatory dysfunction and the development of androgenic features such as hirsutism, androgenic alopecia, acne, and, if extreme and prolonged, virilization of the genitalia.

Hyperandrogenism comprises a heterogeneous group of disorders that exhibit a common phenotype. The most common causes include Poly Cystic Ovary Syndrome (PCOS), defects of adrenal or ovarian steroidogenic enzymes, ovarian hyperthecosis and theca cell hyperplasia. Another reason is the presence of an androgen producing ovarian neoplasm, although these are rare and account for less than 0.5% of all ovarian tumors. These tumors are composed entirely or predominantly of Leydig cells. A previous investigation showed that SRY-independent SOX9 expression can be found in ovarian Sertoli-Leydig cell tumors although the exact mechanisms still remain obscure (2). Finally, spontaneous testosterone production might be caused by an activating mutation in the LH receptor (LHR).

Here we report a case illustrating an androgen producing ovarian tumor in an adult woman. In addition, we describe the psychosocial and cultural barriers that prevented appropriate treatment.

CASE ILLUSTRATION

History of patient

A 36-year-old unmarried woman presented at our outpatient clinic with complaints of fatigue, hirsutism and signs of marked virilization (Figure 1). Menarche occurred at the age of 12 and she had regular cycles until the age of 28. After a period of 5 months of amenorrhea, she visited a gynecologist. Presuming the clinical diagnosis of PCOS, progestagen treatment was prescribed, which induced withdrawal bleedings. Since then, her periods under progestagen therapy. She reported that during the following 3 years there she experienced progressive masculinization such as virilization, facial hair growth, deepening of her voice, and a prominent Adam’s apple. Her family history was negative for endocrinopathies.
Subsequently, she was referred to our center. Upon physical examination she was 152 cm tall and weighed 56 kg (BMI: 24.2). She had excessive pubic and abdominal hair (Ferriman-Gallwey score 15). A male type beard was present; there was no acne. The breasts were atrophied (Tanner stage 3). The blood pressure varied between 110/70 and 200/110 mm Hg and pulse rate was 80 per minute. External genital examination showed an enlarged clitoris (2.5 cm) and a normal female opening of the urethra, absent of fusion of labia majora and minora (Figure 1).

Hormonal analyses were performed, of which the results are shown in Table 1. Pelvic and abdominal ultrasonographic examination showed normal ovaries on both sides and a normally sized uterus. The adrenal glands and kidneys were also normal.

Hormonal results suggested an androgen producing tumor originating from the ovary although this was not confirmed by ultrasound. Therefore, abdominal laparoscopy was undertaken. A biopsy was taken of the left ovary, which contained a structure with the

![Figure 1. Enlargement clitoris and excessive pubic hair](image-url)
appearance of a polycystic tumor (lesion size 4x3.2x3.4cm). The right ovary did not show macroscopic abnormalities (size:3.3x2.8x1.5 cm).

Table 1. Results of hormonal evaluation of the patient

<table>
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<th>Hormone*</th>
<th>unit</th>
<th>patient</th>
<th>Reference ranges women**</th>
</tr>
</thead>
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<td>1.5 - 8.0</td>
</tr>
<tr>
<td>FSH</td>
<td>IU/l</td>
<td>8.1</td>
<td>1.0 - 8.0</td>
</tr>
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<td>&lt;0.5 - 3.0</td>
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<td>nmol/l</td>
<td>9.9</td>
<td>&lt;0.5 - 2.0</td>
</tr>
<tr>
<td>Androstenedione</td>
<td>nmol/l</td>
<td>18.0</td>
<td>2.0 - 10.0</td>
</tr>
<tr>
<td>Testosterone</td>
<td>nmol/l</td>
<td>59.5</td>
<td>0.5 - 3.0</td>
</tr>
<tr>
<td>DHEA sulfate</td>
<td>µmol/l</td>
<td>3.8</td>
<td>1.0 - 10.0</td>
</tr>
<tr>
<td>Cortisol</td>
<td>nmol/l</td>
<td>191</td>
<td>200 - 800</td>
</tr>
<tr>
<td>AMH</td>
<td>µg/l</td>
<td>0.9</td>
<td>0.5 - 7.0</td>
</tr>
</tbody>
</table>

*DHEA: dehydroepiandrosterone; AMH: anti-Müllerian Hormone; LH: Luteinizing Hormone; FSH: Follicle Stimulating Hormone

** Values during the first week of the menstrual cycle

Histopathological examination

Histopathological examination demonstrated the presence of an ovarian tumor. The tissue consisted of small epithelioid cells with a pale eosinophilic, well-demarcated cytoplasm and small nuclei with dark chromatin. No atypical cells or mitotic figures were noticed. Reinke crystals were not found in the specimen. The tumor cells stained positive for the inhibin α-subunit and LHR, markers for Leydig cells, and negative for SOX9, a marker for Sertoli cells (Figure 2). These findings are consistent with a gonadal stromal tumor, and specifically for a
Leydig cell tumor. No histological signs of malignancy were identified. Analysis of the hot spot region in exon 11 of the LHR gene, mutations of which can lead to constitutive activation of the LHR, did not show a mutation. In conclusion the left ovary contained a gonadal stromal tumor compatible with a Leydig cell tumor lacking histological signs of malignancy.

Figure 2. Ovary with a Leydig cell tumor. H&E staining revealed ovarian structures with gonadal stromal tumor compatible with Leydig cells (A1-2) (black arrow). Positive inhibin α-subunit was staining (B1-2); Negative for SOX 9 staining (C1-2). Magnification: left panel x 100, right panel x 400. Luteinizing hormone receptor (LHR) presence was detected by immunohistochemistry. Brown staining in cytoplasm shown in cord-stromal of the ovary. Magnifications were x 100 (D1) and x 400 (D2)
Luteinizing hormone receptor analysis

Analysis of the hot spot region in exon 11 of the LHR gene, mutations of which can lead to constitutive activation of the LHR, did not show a mutation (Figure 3)

![Sequence of Luteinizing Hormone Receptor gene on exon 11 from Leydig cell tumor coding for Phe576, Thr577, Asp578 and Phe 579 showing a wild type receptor.](image)

**Psychosocial aspects**

The patient came from a middle class Javanese family and obtained a university degree. The virilization of her body caused her a lot of distress. She consulted several medical doctors and beauticians who gave her conflicting advice. All treatments she underwent had been unsuccessful as she virilized progressively. After we found the cause of her virilization, we informed her about her condition and the nature of the ovarian tumor and proposed ovariectomy. She refused treatment, as she feared to become infertile after treatment. She particularly feared the social consequences of being an infertile woman. As an alternative, hormonal replacement therapy was proposed, but she refused. In the past she had already experienced that progestagen therapy could not stop virilisation. One of the doctors she had consulted before had informed her that a pregnancy would cure her disease and she preferred to follow this advice. She kept looking for a partner, but remained unsuccessful. Psychological counselling was offered to allow her to
express her worries and to help her understand her condition, its consequences, the necessity for treatment and the rationale behind the proposed treatments. She discussed the pressure she felt to marry and have children. She had already turned 36, whereas most Javanese women will marry and have their first child between age 20 and 30. It was expected that family support could take away some of the experienced shame and distress and proposed to establish such support by informing the family about her condition. However, this was unsuccessful. She told that she had already informed her family and disliked subsequent discussions. No signs of mental disorder and symptoms of depression were present. Her openness to discuss the impact of her condition on her life and her maintained confidence in cure by getting pregnant clarified her resistant attitude.

**DISCUSSION**

Systematic investigations in adult women with virilization are necessary to get to the right diagnosis. According to the literature, clinical signs of virilizationshould be confirmed by hormonal and ultrasound examination (3). Laparoscopy followed by biopsy is necessary to obtain a hystopathological description and diagnosis

In this patient, symptoms of hyperandrogenism were the main initial clinical features. The signs of hirsutism and amenorrhea appeared at the age of 28 years within a 5 months period. Before she had regular menses and pubertal development had also been normal. Initially a diagnosis of PCOS was considered and indeed hormonal treatment resulted in regular bleedings, which may have convinced the patient that she was fertile. However the progressive virilization even under hormonal treatment had raised suspicion for an androgen-secreting tumor. The hormonal data suggested an androgen-producing tumor of the ovary since serum hormone assay showed increased levels of 17-hydroxyprogesterone and androstenedione and extremely high levels of testosterone with normal levels of the adrenal steroids cortisol, and dehydroepiandrosterone sulfate. Her bodily changes such as signs of virilization, including severe hirsutism, frontal balding, clitoromegaly, increased libido, altered body fat, increased muscle mass, breast atrophy, deepening of voice, and pustular acne were in accordance with
hormonal data are common symptoms in Leydig cell ovarian tumors (4). Estrogenic
manifestations, such as irregular menses have also been reported. Symptoms and signs may
present gradually with the onset of symptoms ranging from 5 to 7 years prior the diagnosis (5).
Leydig cell tumors are usually benign histo-pathologically, these tumors can behave in a
clinically malignant fashion (6). About 20% of patients develop metastatic lesions usually within
the peritoneal cavity, and rarely at distant sites (7). Therefore, early treatment is necessary to
prevent tumor to get worse.

The appearance of a virilizing tumor on radiological imaging depends on the type of
tumor. Characteristic of steroid cell tumors are typically small nodules less than 3 cm and
unilateral (8). These tumors show a heterogeneous solid mass with internal areas of intracellular
lipid and may be difficult to identify on radiological imaging, in part because they are isoechoic
to the uterus on ultrasound. This may be the reason why no abnormality of the ovaries was
found during ultrasound examination of our patient. CT or MRI was not done because of
financial limitations.

In view of patient’s age and nulliparity, unilateral oophorectomy was offered as the first
therapeutic option. Her refusal worsened her medical condition. Her decision to decline the
given advice was related to the psychological mechanisms that will be triggered in case the
offered cure is not congruent with the patient’s beliefs and also includes unfavorable social
consequences (9,10). For young adult females, loss of fertility involves a social disadvantage. It
may become difficult to get married, but if she is married, she may get divorced or may have to
accept that her husband will seek a second spouse. The patient made clear that she considered
her ovaries as the only female part of her body that had been left and removal of even one ovary
would mean taking away her femininity and everything that made her life worth to live. Her
refusal for further discussion about treatment created a dilemma based on the respect for the
patient’s right on the one hand, but the risk of further progression of the tumor on the other. In
spite of efforts for additional appointments to discuss the possibility of ovariectomy, no changes
in her opinion occurred. Therefore it is expected that over the years, virilization and weight gain
will become more prominent. Androgen excess in women may lead to shame and social
withdrawal or even social phobia which will normalize after treatment (5,11). However, in our patient, no signs of anxiety or depression were found.

This case report confirms that virilization in women should be investigated systematically and comprehensively. The diagnosis of Leydig cell tumor is made using clinical parameters such as amenorrhea, signs of virilization, and high serum testosterone levels and subsequently the finding of an ovarian mass on imaging. A diagnostic laparoscopy is indicated to confirm the diagnosis. Androgen secreting tumors, especially Leydig cell tumors of the ovary, should be considered amongst disorders causing virilization in women at reproductive age. What can be learned from this case? Even after extensive explanation and counseling psychosocial and cultural barriers prevented appropriate treatment. Social and community support is essential to help individuals to cope with shame and the prospect of infertility.
References


Chapter 10

Gonadal malignancy in 13 Consecutive Collected Patients with Disorders of Sex Development (DSD) from Semarang (Indonesia)


Abstract

Aims: Caucasian patients with Disorders of Sex Development (DSD) have increased risk for Germ Cell Cancer (GCC). GCC are prominent in young adults in Western countries, while the incidence is significantly lower in Asia. So far it is unknown what the risk of GCC in Asian DSD patients is.

Methods and Results: A detailed gonadal histology study was undertaken on 16 Indonesian DSD patients using morphologically and immunohistochemistry (OCT3/4, TSPY, VASA, SCF/KITLG, SOX9, FOXL2). 13 cases could be analyzed, including ovarian tissue (n=3); streak gonad (n=1); undifferentiated gonad (n=1) and testicular tissue (n=8), diagnosed as 46,XX (n=1), 46,XY (n=7) and sex chromosome DSD (n=5). The precursor lesion gonadoblastoma or carcinoma in situ, or a GCC was diagnosed in four cases (30.8%; three 46,XY and one sex chromosomal DSD). A hormone producing ovarian Leydig cell tumor was identified in a 46,XX patient, supposed to be a late onset congenital adrenal hyperplasia. Conclusions: In spite of the significant lower risk of GCC in the general Asian population, DSD is a dominant risk factor. The study demonstrates the power of immunohistochemical markers for (early) diagnosis. This knowledge deepen understanding of the patho-biology of GCC and clinical handling of patients with DSD globally.
INTRODUCTION

Testicular Germ Cell Cancer (GCC) are the most frequent malignancy found in Caucasian males aged 20-45 years and has increased over the last decades (1, 2). The highest incidence exists in Nordic countries (11.5 per 100,000 men), although also heterogeneously, while it accounts for the lowest rates (1 to 2 per 100,000) among the black and Asian population. The rates are notably lower in East Asia (0.7-1.6 per 100,000) compared to West Asian (4.1 per 100,000) (3). Among the known risk factors for GCC are a previous GCC, cryptorchidism, infertility (suggested to be part of the Testicular Dysgenesis Syndrome, TDS) and Disorder of Sex Development (DSD) (4,5). DSD patients are currently classified based on a three root system, in which the first step divides the patients into 46,XX DSD, 46,XY DSD, and sex chromosomal DSD (6,7,8). Certain DSD subgroups are prone to develop a GCC, even up to 60% of the patients (9). This risk is related to the presence of a specific region of the Y chromosome, referred to as gonadoblastoma locus on the Y chromosome (GBY), for which the Testis Specific Protein-Y encoded (TSPY) is the main candidate (10,11). High risk is shared among gonadal dysgenesis (GD) patients who have the GBY region in their genome combined with intra-abdominal gonads (15-35%); non-scrotal gonads specifically in partial androgen insensitivity syndrome patients (PAIS) (50%). Intermediate risk includes variants of Turner syndrome variant (Y+) (12%) as well as 17β-hydroxysteroid dehydrogenase deficiency patients (28%). These forementioned DSD variants are all part of the 46,XY DSD entity (7,8). At low risk are patients with complete androgen insensitivity syndrome (CAIS), ovo-testicular DSD and Turner syndrome without Y-chromosomal material, with 2%, 3% and 1% respectively. Patients with GD and mosaic GD (45X/46, XY) show a prevalence of 30% and 15-40%, respectively, while the risk in cases of 5α-reductase deficiency and Leydig cell hypoplasia are still unknown (12).

Development of an invasive GCC is preceded by CIS (carcinoma in situ)/IGCNU (intratubular germ cell neoplasia unclassified) of the testis or gonadoblastoma (GB) of the dysgenetic gonad (13). The formation of these precursors is dependent on the level of testicularization of the gonad, directly related to the presence of SOX9 as marker for Sertoli cells and FOXL2 as marker for Granulosa cells (14). Long term effects on quality of life, including
fatigue, metabolic syndrome, heart and vascular diseases, as well as secondary cancers, have been identified related to application of irradiation and chemotherapy at relative young age (15). Therefore, identification of the GCC as early as possible is of relevance for optimal treatment with long term effect (16).

Here we present results of the first series ever of histopathological characterization of consecutively collected gonadal tissues of Indonesian DSD patients. Various germ cell and stromal markers were applied, informative for the identification of GCC at the earliest possible pathogenetic stage.

MATERIAL AND METHODS

Patient selection and tissue samples

Indonesian DSD patients with the presence of ambiguous genitalia or any anatomical abnormality of external or internal genitalia, including penoscrotal hypospadias, with or without descended testes were examined in the Center for Biomedical Research, Diponegoro University (CEBIOR)/Dr. Kariadi Hospital from 2004-2011 and diagnosed in accordance with the recent consensus on DSD (7). Chromosome analysis was conducted using a G-banding technique in CEBIOR as described (17). Hormonal and mutation analysis was performed at the Departments of Endocrinology and Clinical Genetics Laboratories (Erasmus MC), respectively. Supposed gonadal tissue samples of 16 patients with androgen action disorders (n=2), androgen excess (n=1), and gonadal dysgenesis (n=13) aged from 0.9 to 30.9 yr (median age at time of operation was: 19.9 yr) were obtained after biopsy or gonadectomy. Bilateral specimens were available from five (31.2%), while the others were from unilateral biopsy or gonadectomy. Only 13 patients were included in the final examination. Characteristics of patients are summarized in Table 1. All gonadal samples were acquired for prophylactic and diagnostic purposes with written informed consent. Histological and immunohistochemical analysis (OCT3/4, TSPY, VASA, SCF, SOX9, FOXL2 and INHα subunit) were done at the Department of Pathology Diponegoro University Indonesia and Erasmus MC, Josephine Nefkens Institute, Rotterdam (the Netherlands).
**Histological analysis**

Specimens were first examined using routine H&E staining. Gonadal differentiation was determined per sample (testis/ovary/streak/undifferentiated gonad) as described previously (18). General morphology and maturity of seminiferous tubules and germ cells, presence of supporting cells, e.g. Sertoli cells, Leydig cells, and granulosa cells, adnexal structures e.g. fallopian tube or uterus were assayed. A Johnson score was attributed to each sample containing seminiferous tubules.

Diagnosis of the precursor lesion (CIS and GB) and their invasive GCC counterpart was made according to the World Health Organization Classification by an experienced pathologist (JWO). On the basis of morphology, germ cells were classified as immature or mature (1).

**RESULTS**

**General histology**

Histological examination of the available gonadal samples demonstrated the following pattern: ovarian structures (n=3); testicular structures (n=8); streak gonad (n=1) and undifferentiated gonads (n=1) (Table 2). Overall, the anatomical localization of the gonads was 50% abdominal, 46.2% inguinal, and 3.8% scrotal (one out of 26). However, within the group of 46,XY DSD the anatomical localization was mainly inguinal (78.6%) (Table 1). In case of the presence of testicular tissue (n=8), atrophic seminiferous tubules (based on Johnson score) were found in nearly all cases (n=7) (Table 2). Maturation of spermatogenesis was variable, however elongated spermatids were never found. The Johnson score ranged from 1 to 6 with the mean of 2.5. Two patients with sex chromosome DSD had a Johnson scored of 2 and 2.5, respectively.
Table 1. Summary of clinical data and cytogenetic result for each patient

<table>
<thead>
<tr>
<th>CASE</th>
<th>AGE *</th>
<th>GENDER</th>
<th>KARYOTYPE</th>
<th>DIAGNOSIS</th>
<th>GENETIC ANALYSIS</th>
<th>PHALLUS (cm)**</th>
<th>RIGHT GONAD</th>
<th>LEFT GONAD</th>
<th>QUIGLEY</th>
<th>POSITION OF URETHRAE</th>
</tr>
</thead>
<tbody>
<tr>
<td>46,XX DSD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>30.9</td>
<td>F</td>
<td>46,XX</td>
<td>Hypervirilization e. Androgen producing tumor</td>
<td>2.5</td>
<td>NA</td>
<td>abdominal</td>
<td>NA</td>
<td>abdominal</td>
<td>4</td>
</tr>
<tr>
<td>46,XY DSD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>13.8</td>
<td>F</td>
<td>46,XY</td>
<td>Gonadal dysgenesis</td>
<td>No SRY mutation</td>
<td>4.1</td>
<td>NA</td>
<td>inguinal</td>
<td>NA</td>
<td>inguinal</td>
</tr>
<tr>
<td>3</td>
<td>23.3</td>
<td>F</td>
<td>46,XY</td>
<td>Gonadal dysgenesis</td>
<td>No SRY mutation</td>
<td>normal clitoris</td>
<td>&lt;1</td>
<td>inguinal</td>
<td>&lt;1</td>
<td>inguinal</td>
</tr>
<tr>
<td>4</td>
<td>1.9</td>
<td>M</td>
<td>46,XY</td>
<td>Androgen action disorder</td>
<td>NoAR Mutation</td>
<td>3.5</td>
<td>1</td>
<td>inguinal</td>
<td>NA</td>
<td>abdominal</td>
</tr>
<tr>
<td>5</td>
<td>16</td>
<td>F</td>
<td>46,XY</td>
<td>Androgen action disorder</td>
<td>859delG</td>
<td>normal clitoris</td>
<td>NA</td>
<td>abdominal</td>
<td>NA</td>
<td>abdominal</td>
</tr>
<tr>
<td>6</td>
<td>1.8</td>
<td>M</td>
<td>46,XY</td>
<td>Gonadal dysgenesis</td>
<td>No SRY mutation</td>
<td>2.5</td>
<td>&lt;1</td>
<td>inguinal</td>
<td>NA</td>
<td>inguinal</td>
</tr>
<tr>
<td>7</td>
<td>18.2</td>
<td>F</td>
<td>46,XY</td>
<td>Gonadal dysgenesis</td>
<td>DAX-1 duplication</td>
<td>5.0</td>
<td>NA</td>
<td>inguinal</td>
<td>NA</td>
<td>inguinal</td>
</tr>
<tr>
<td>8</td>
<td>27</td>
<td>F</td>
<td>46,XY</td>
<td>Gonadal dysgenesis</td>
<td>No SRY mutation</td>
<td>5.0</td>
<td>NA</td>
<td>inguinal</td>
<td>1</td>
<td>inguinal</td>
</tr>
<tr>
<td>CHROMOSOMAL DSD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>3.8</td>
<td>M</td>
<td>46,XY/46,XX</td>
<td>Gonadal dysgenesis</td>
<td>No SRY mutation</td>
<td>3.5</td>
<td>NA</td>
<td>abdominal</td>
<td>1</td>
<td>inguinal</td>
</tr>
<tr>
<td>10</td>
<td>22</td>
<td>F</td>
<td>46,XY/46,XX</td>
<td>Gonadal dysgenesis</td>
<td>No SRY mutation</td>
<td>normal clitoris</td>
<td>NA</td>
<td>abdominal</td>
<td>NA</td>
<td>abdominal</td>
</tr>
<tr>
<td>11</td>
<td>13</td>
<td>M</td>
<td>45,X/46,XY</td>
<td>Gonadal dysgenesis</td>
<td>4.0</td>
<td>NA</td>
<td>abdominal</td>
<td>8</td>
<td>scrotal</td>
<td>2</td>
</tr>
<tr>
<td>12</td>
<td>20.8</td>
<td>F</td>
<td>46X,idicY</td>
<td>Gonadal dysgenesis</td>
<td>6.0</td>
<td>NA</td>
<td>abdominal</td>
<td>NA</td>
<td>abdominal</td>
<td>3</td>
</tr>
<tr>
<td>13</td>
<td>19.8</td>
<td>F</td>
<td>45,XY/46,XY</td>
<td>Gonadal dysgenesis</td>
<td>5.5</td>
<td>NA</td>
<td>abdominal</td>
<td>NA</td>
<td>abdominal</td>
<td>3</td>
</tr>
</tbody>
</table>

*Age: Age when gonadectomized or biopsed; ** According to Judith G Hall, et.al. [Handbook of Normal Physical Measurements. Oxford University Press, 2003]; NA = not available; *** No gonadal histology
### Table 2. Summary of patient’s characteristic, histological finding and immunohistochemistry staining

<table>
<thead>
<tr>
<th>CASE</th>
<th>AGE *</th>
<th>SIDE GONAD</th>
<th>LOCATION OF GONAD</th>
<th>MATERI AL FROM</th>
<th>MORPHOLOGY (JOHNSON SCORE)</th>
<th>OCT3/4</th>
<th>TSPY</th>
<th>VASA</th>
<th>SCF</th>
<th>SOX9</th>
<th>FOXL2</th>
<th>DOUBLE STAINING</th>
<th>OTHERS</th>
<th>HISTOLOGY</th>
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<tbody>
<tr>
<td>46, XX DSD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>30.9</td>
<td>L</td>
<td>Abdominal</td>
<td>B</td>
<td>Ovary with gonadal stromal tumor compatible with a Leydig cell tumor lacking histological signs of malignancy. The histology does not reliably predict the clinical behavior of the tumor (NP)</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>Inh (+); LH-R (-)</td>
<td>Ovary with Leydig cell tumour</td>
</tr>
<tr>
<td>2</td>
<td>13.8</td>
<td>L</td>
<td>Inguinal</td>
<td>G</td>
<td>Testicular tissue with many germ cells at different stages of maturation (6)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>NP</td>
<td>OCT/VASA (+)</td>
<td>c-KIT (+); PLAP (+)</td>
<td>CIS</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>R</td>
<td>Inguinal</td>
<td></td>
<td></td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>23.3</td>
<td>L</td>
<td>Inguinal</td>
<td>G</td>
<td>Testis with Leydig cell hyperplasia. Most seminiferous tubules are atrophic (2-3)</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>NP</td>
<td>-</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>R</td>
<td>Inguinal</td>
<td></td>
<td></td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>1.9</td>
<td>R</td>
<td>Inguinal</td>
<td>G</td>
<td>Dysgenetic gonad, no germ cells</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Streak gonad, remnant sex cords, adjacent fallopian tube</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>16</td>
<td>L</td>
<td>Abdominal</td>
<td>G</td>
<td>Atrophic testis (1)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>R</td>
<td>Abdominal</td>
<td></td>
<td></td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>1.8</td>
<td>L</td>
<td>Inguinal</td>
<td>G</td>
<td>UGT (NP)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>OCT/TSPY (+)</td>
<td>NP</td>
<td>Gonadoblastoma</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>18.2</td>
<td>L</td>
<td>Inguinal</td>
<td>G</td>
<td>Testis with Leydig cell hyperplasia. Most seminiferous tubules are atrophic (1-2)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>R</td>
<td>Inguinal</td>
<td></td>
<td></td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>27</td>
<td>L</td>
<td>Inguinal</td>
<td>G</td>
<td>Atrophic testis with seminoma and carcinoma in situ on both sides (1-2)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>OCT/TSPY (+)</td>
<td>NP</td>
<td>CIS and seminoma</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>R</td>
<td>Inguinal</td>
<td></td>
<td></td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>CIS and seminoma</td>
<td>NP</td>
<td>CIS and seminoma</td>
<td></td>
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<tr>
<td>CHROMOSOMAL DSD</td>
<td></td>
<td></td>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>9</td>
<td>3.8</td>
<td>R (L in situ)</td>
<td>Abdominal</td>
<td>G</td>
<td>Ovary with multiple cysts, follicles and granulosa cells, including primordial follicles (NP)</td>
<td>-</td>
<td>-</td>
<td>+ (in cysts/ follicles)</td>
<td>NP</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>c-KIT (+); PLAP (+)</td>
<td>Ovary with multiple cysts, follicles and granulosa cells</td>
</tr>
<tr>
<td>10</td>
<td>22</td>
<td>R (L in situ)</td>
<td>Abdominal</td>
<td>G</td>
<td>Normal ovary (NP)</td>
<td>-</td>
<td>-</td>
<td>+ (in follicles)</td>
<td>NP</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>Normal ovary</td>
</tr>
<tr>
<td>11</td>
<td>13</td>
<td>R (L in situ)</td>
<td>Abdominal</td>
<td>G</td>
<td>Atrophic testis, Johnson 1, Leydig cell hyperplasia, no CIS (2)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Sertoli cells only</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>20.8</td>
<td>L (R in situ)</td>
<td>Abdominal</td>
<td>B</td>
<td>No germ cells; no malignancy; diffuse Leydig cell hyperplasia (2-3)</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>Leydig cell hyperplasia</td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>19.8</td>
<td>L (R in situ)</td>
<td>Abdominal</td>
<td>B</td>
<td>Testicular (NP)</td>
<td>+</td>
<td>+</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>NP</td>
<td>PLAP (+)</td>
<td>Seminoma</td>
</tr>
</tbody>
</table>

* Age: Age when gonadectomized or biopsied; L: left; R: right; B: Biopsy; G: Gonadectomy; NA: not available; NP: not performed; UGT: undifferentiated gonadal tissue
GCC, *in situ* and invasive

The presence of germ cells was recognized by cytoplasmic staining for VASA and TSPY. In total, a GCC was identified in four cases (30.7%), predominantly in the 46,XY DSD group (42.9%), and one in the sex chromosomal DSD group (20%). All contained the Y chromosome in their karyotype, in agreement with the results of TSPY staining (see below). The presence of malignant cells was visualized using the OCT3/4 staining, showing a nuclear localization in all cases. In the 46,XY DSD patients, all GCC containing gonads were located at an inguinal position, while the sex chromosomal DSD patient with the GCC affected an abdominal gonad.

CIS was identified in two patients with high level of LH and FSH, low testosterone and no response for hCG test. One presented unilaterally (case 2, Figure 1), while the other was bilaterally, adjacent to an invasive seminoma (case 8, Figure 2), all at an inguinal position. Another pattern observed in a single patient (46, XY DSD) was the previously described undifferentiated gonadal tissue (UGT), consisting gonadal tissue with germ cells without seminiferous tubule structures or follicles, mixed with Sertoli cells or granulosa cells in cord like structures, supposed to be the precursor of GB (case 6, Figure 3) (18). Indeed, a combined expression of SOX9 and FOXL2 in GB derived from UGT has been reported previously (18).

No OCT3/4 positive germ cells were found in fully matured ovarian structures. SCF as marker for early malignant germ cells was consistently expressed in both invasive and precursor lesions (19). OCT3/4 –TSPY or VASA coexpression was encountered in CIS as well as GB as seen in our double staining experiments (Figure 4).
Figure 1. Case 2: 46, XY female with androgen action disorder. Breast development was present. After gonadectomy the patient received estrogen hormonal therapy. H&E staining (A1-2), morphology of the gonad showing testicular tissue with germ cells at different stages of maturation. Presence of carcinoma in situ (black arrow) confirmed by morphology and immunohistochemical staining for OCT3/4 (B1-2), TSPY (C1-2), VASA (D1-2), SCF (E1-2) and SOX9 (F1-2). Magnifications are as indicated in each pictures.
Figure 2. Case 8: 46, XY female with androgen action disorder. No breast development. After gonadectomy the patient received estrogen hormonal therapy. Carcinoma in situ (CIS) (A,C,E) was found adjacent to seminoma (B,D). H&E staining (A) showing almost complete atrophy of the seminiferous tubules containing extensive carcinoma in situ (CIS) (black arrow), which also expressed TSPY (C) and SCF (E). Seminoma (black arrow head) found in the same sample expressed OCT3/4 (B) and VASA (D). Sertoli cells (white arrow head) identified by SOX9 (F). Magnifications are 200x.
Figure 3. Case 6: 46, XY male with severe hypospadias and cryptorchidism staining depicting undifferentiated gonad with gonadoblastoma nest (black arrow) in H&E staining (A). Presence of immature germ cells confirmed by immunohistochemistry staining: OCT3/4 (B), TSPY (C), VASA (D), SCF (E). Supportive cells (F) are stained both for SOX9 (white arrow) and FOXL2 (black arrow) indicative for Sertoli cells and granulose cells, respectively. Magnifications are 200x.
Figure 4. Representative examples of double staining experiments. Shown are TSPY (blue cytoplasmic signal) and OCT3/4 (red nuclear signal) in case gonadoblastoma in undifferentiated gonad (case 6) (A-B); VASA (red cytoplasmic signal) and OCT3/4 (blue nuclear signal) in case of carcinoma in situ (case 2) (C-D). Note the double positive cells are indicated by a black arrow. Magnifications are 100x (left panel) and 400x (right panel).

An unexpected Leydig cell tumor is a supposed late onset CAH patient

Within the series of patients investigated, a 46,XX virilized female presented with virilization and secondary amenorrhea. The testosterone value was tremendously increased (59.5 nmol/L, normal level 3.3 nmol/L) despite a normal level of LH and FSH (12.3 IU/L, and 8.1 IU/L, respectively). Abdominal laparoscopy revealed a right normal ovary and a tumor lesion of the left, subsequently demonstrated to be a Leydig cell tumor confirmed by immunohistochemical detection of inhibin and LH receptor (LHr) (data not shown). No mutation within exon 11 of the LHr was identified (20).
DISCUSSION

We performed a detailed investigation based on histology and immunohistochemistry of a unique series of gonadal tissues from 13 DSD patients from the Indonesian population. To our knowledge, this represents the first of such a series and shows the high incidence of GCC and its precursor. Three malignancies were found in patients belonging to the category of 46,XY DSD and one case from sex chromosome DSD (46,XY/45,X). Indeed, these have been reported to show the highest risk for malignant transformation of germ cells leading to a GCC (9,21,22). It is important to consider the presence of gonadal malignancy (ovarian Leydig cell tumor) in case of adult women with virilization, which is a rare finding (21).

Despite varying histopathology features, the general morphology of the DSD gonads and germ cells did not differ from previous findings in Caucasian populations (22,23). The majority of the gonads had a non-scrotal localization. Most GCC or precursors were identified in gonads localized in the inguinal region and one in the abdominal. This highlights the potent malignancy of partially descended testes, as compared to abdominal testes. In the latter position the germ cells are probably undergoing apoptotic cell death before they can give rise to malignancy (23). Regarding age, 75% of GCC and their precursor lesions were at pre-pubertal and pubertal age ranges. The only two invasive GCC (seminomas) were found in two postpubertal patients (aged 19.8 and 27 years). This demonstrated the timing of progression from an in situ lesion to invasive growth happening after puberty.

Infertility is a well-established feature of cryptorchid testis, also confirmed by this study based on the low Johnson score in inguinal and abdominal gonads, although increased proliferation of fetal gonocytes has been reported in case of testicular feminization (24, 25). In general germ cells express markers like TSPY and VASA (26, 27), while OCT3/4 and SCF depends on the maturity of the germ cells, and their transformed phenotype. All GCC and the precursors, including dysgenetic and fetal gonads show presence of OCT3/4, which is absent on fully matured (non-embryonic) germ cells (11). OCT3/4 is reported to prevent apoptosis in embryonic germ cells, while in embryonic stem cells it mainly regulates pluripotency (28). Again demonstrated in this study, CIS, seminoma and GB can be diagnosed based on OCT3/4
staining, also in the undervirilised gonad (11). Similar to previous findings abundant and abnormal expression of TSPY, which proposed to accelerate proliferation and promote tumorigenicity, was identified in all our cases (11,25,29). However, TSPY can be lost upon progression to invasiveness (11). This situation also applies to germ cells in an unfavorable environment in DSD situations as nicely illustrated in case 8 displayed a CIS adjacent to seminoma. TSPY was abundantly expressed in CIS component but strongly reduced in seminoma as it gained its invasive capability. All gonads with high risk for malignant transformation also expressed SCF/KITLG, confirming the use of this marker for detection of early malignant characteristics of a GCC (19).

Taken together, it is obvious that the use of specific immunohistochemical markers is highly informative for detection of GCC and its precursors; which is rarely applied in Indonesia. However, OCT3/4 alone, which could be done in Indonesia, is sufficient to detect early malignancy.

Incidence of GCC is low in most Asian countries like Indonesia (2,3,30). However, and highly relevant, within the group of DSD patients, the incidence is as high as found in the Caucasian DSD population (1). This indicates that the combination of genetic and environmental factors, we refer to as “GENVIRONMENT”, which supposedly contribute to the high incidence of GCC in the Caucasian population, and which are less prominent in the Indonesian population, are compensated for in specific variants of DSD independent of ethnic background. Two recent studies indicate an association between specific genetic variants of the KITLG (as well as others) and the risk for GCC in the general population (29,31). It is an intriguing hypothesis that the effects of environmental factors are likely modulated by genomic variation (polymorphisms), thus explaining the individual susceptibility and population-level differences in the incidence of GCC. It might be of interest to study the distribution of high risk alleles both in the general - as well as in Asian DSD population. Based on the first description of gonadal histology of Indonesian DSD patients, it can be concluded that DSD is a dominant determinant for development of GCC. This insight opens relevant new perspectives in the diagnosis and investigation of the pathogenesis of this type of cancer.
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Chapter 11

General Discussion and Future Organization of the Management of Disorders of Sex Development in Indonesia
Introduction

The term Disorder of Sex Development is presently used as an umbrella term including previous terms such as hermaphrodite, intersex, ambiguous genitalia. The history of the nomenclature is reflecting the confusion not only of experts but also for sure, for lay people.

Although the older terms are still included in this thesis for reference, they have been replaced by most experts (and patients and families) because they are misleading, confusing, and insensitive. Increasingly this group of conditions is being called disorders of sex development (DSD) in order to avoid conflicting anatomy with identity. Members of The Lawson Wilkins Pediatric Endocrine Society and the European Society for Pediatric Endocrinology accepted the term "disorders of sex development" in their "Consensus statement on management of intersex disorders" published in the Archives of Disease in Children and in Pediatrics in 2006. The term is defined by congenital conditions in which development of chromosomal, gonadal, or anatomical sex is atypical. However, this has been met with criticism from activists who question a disease/disability model and advocate no legal definition of sexes, no formal gender assignments, no legal sex on birth certificates, and no official sexual orientation categories. Alternatives to labelling these as "disorders" have also been suggested, including "variations of sex development".

Genital anomalies are estimated to occur in 1 in 4500 births (1). Where in 46,XY individual the ratio is 1: 16,000 in every life birth. In 46 XX individuals the most common form of DSD is congenital adrenal hyperplasia (CAH) with an occurrence of 1 : 9000-16000 in every life birth.

The subjects of this research are 286 patients referred to the Kariadi Hospital/Diponegoro University Semarang, Indonesia during the period 2004-2010. A number of patients with mild genital anomalies such as isolated mild hypospadia and other mild sexual disorders, amounting to 347 subjects, were excluded from the main research.

Among these 286 patients of RSDK, the occurrence of 46,XY DSD was 68.2%, 46, XX DSD was 23.4% and the rest is accounted for by Sex Chromosome DSD.
The DSD treatment in RSDK did not cover all of the patients. Only 50.7% of patients were treated with hypospadia correction in boys and CAH therapy in girls being the most common. It became clear that most of the reasons for patients not to undergo the therapy were problems such as lacking financial resources, a too large distance to the center, hesitance for the surgery process, while some of the patients obtained too little information.

This research is novel in Indonesia, and as far as we know, the multidisciplinary treatment of DSD as in this research has never been performed before.

1. The development of Management of DSD in Indonesia

The management of DSD has been set up to guide the medical community in treating DSD patients; however, the implementation and the outcome is variable and depends on many factors such as type of the disorder, the patient’s general health and the financial condition of the patient or his family, and patient’s and family’s reaction and understanding towards DSD.

In Indonesia, the Ministry of Health (or government) did not pay much attention to the management of DSD since infectious diseases are still a priority, being the major cause of morbidity and death. Actually, six major hospitals in Indonesia were recommended to have a gender team since the year of 1989; however due to lack of expertise and laboratory equipment as well as financial constraints development has been slow. Moreover, awareness of medical personnel and of the community for the particular problems related to DSD remained limited. In order to improve the management of DSD in Indonesia, understanding of this last issue is important. At the same time, extensive research of the etiology of DSD of Indonesian patients and identification of the structure of the ethnic and cultural background is necessary.

The general guidelines of DSD management should be set and standardized nationally and be accountable. Hence it will provide adjustable implementation for the various conditions of the patients and their families. Therefore, DSD management should be employed differently depending on the diversity of cultural and demographic background.
1.1 Conditions of the DSD Patients in Indonesia

As mentioned above, the background of the patient is an important factor contributing to the intensity (length and depth) of the care provided, including the decision making process. Several factors such are affecting the management of DSD.

First, the general community, of which the patient and family are part in daily social life is still considering DSD as a taboo. Sexual related problems such as DSD are not well understood and just ignored. Most of the parents and adult patients are reluctant to seek medical attention. The majority of the parents are embarrassed of having children with a sexual abnormality. Thus they consider it as a disgrace which should be concealed from the others. This is one of the reasons why there are still undetected DSD patients. The clinical condition of DSD in Indonesia is mostly identified because patients or parents seek medical attention due to urgent matters, such as severe dehydration (salt loosing crisis in CAH), hernia inguinalis incarcerata, delay or absence of puberty, gender related problems such as desire to get married, or getting an identity card. For some people in Indonesian society the term DSD is misleading. A lot of people confuse a DSD patient with a transgender or transsexual individual or with a homosexual (gay, lesbian) or bisexual person. In the Indonesian population these forms of sexuality are considered to be against nature and individuals are often labelled as condemned persons and discriminated in the community.

The Bugis tribe in South Sulawesi, Indonesia is one community that acknowledge three sexes, which is male, female and hermaphrodite. There are four genders; the makunrai (female women), oroane (male-men), calalai (biological females who serve the roles and functions expected from men), calabai (men who behave close to what is expected of women) and in addition the bissu (the meta gender). The bissu are assumed to be hermaphrodites by embodying both female and male elements, and usually fit as a specific group acting as priests. The Bugis believe that a bissu who appears externally as a male internally is a female, and vice versa. This combination of sexes leads to communal acceptance of ‘meta-gender’ as the third sex among them (2-4).
Second, most of the patients who are seen by our sex adjustment team in Semarang are from middle and lower economic classes. Therefore their financial situation limits their access to health care. In addition their often limited educational level influences their capability to receive new information and to communicate on further procedures. These limits affect the implementation of diagnostic procedures, particularly as procedures are often rather expensive.

Third, most patients do not have health insurance; and even if they have health insurance it often does not cover genetic testing. This situation is adding to the complexities of the problem.

1.2 Current Management of DSD in Indonesia

A guideline for DSD diagnostic implementation has been created and published by ESPE in 2006, which is continuously improved (1). In principle, there are several stages in the diagnostic process of a DSD patient (1,5,6), which are listed below:

1. General physical examination
2. Chromosomal analysis
3. Hormonal analysis
4. Determination of electrolyte levels in serum and urine essential for the urgent management of CAH
5. Hormonal stimulation tests (HCG, ACTH) as a second line of investigation specifically to determine disorders of steroidogenesis.
6. Additional investigations such as ultrasound, MRI, and endoscopy to check the anatomy of the internal genitalia
7. Specific molecular genetic analysis such as gene mutation analysis to confirm a genetic diagnosis.

However, despite recent developments, there are several factors that are slowing the pace of the further development of structured management of DSD patients in Indonesia:

1. The term DSD is unknown and even considered unpopular among health care professionals in Indonesia
2. DSD management in Indonesia is not yet integrated in centers other than Semarang
3. There is a lack of specialised diagnostic facilities in medical centres.
4. It is still unclear whether the final decision regarding gender choice and genital surgery is decided by the patient/parent or by the doctor (medical team).
5. There are no certain rules or ethical guidelines regarding surgical management of DSD patients; it is unclear whether definitive surgery should be performed at an earlier age with informed consent (mostly by the parent) or should be postponed until the patient has the age to decide for her/himself.

These potentially inhibiting factors will be explained here in more detail:

First, for health care professionals, the terminology of DSD as well as the clinical diagnosis is still not widely understood and relevant information is available only in the major cities. Most medical personnel is familiar with the term ambiguous genitalia or “double sex” (kelamin ganda) or hermaphroditism rather than DSD. The referral centre/hospital for proper diagnosis and multidisciplinary management is unknown to them. Thus this indicates a need for education regarding the recognition of clinical signs and early treatment as well as of the referral system relating to DSD.

Second, the mechanism of DSD management is not yet integrated in the Indonesian health care system. A multidisciplinary team approach to treat DSD cases is exceptional in Indonesia. However in Semarang a multidisciplinary approach by the gender team called Tim Penyesuaian Kelamin is in use since 1989. DSD patients are usually extensively treated in only one department with limited collaboration assistance from the other departments. Moreover extensive hormonal and genetic analysis is rarely performed because of limited laboratory facilities and financial constraints. This situation needs to be improved so that management of DSD patients can be implemented comprehensively.

Third, not every medical centre has adequate facilities. Taking into consideration the diagnostic complexities, this gap in medical centres’ facilities is likely to affect the accuracy of diagnosis and treatment.

Fourth, in the case of gender assignment or gender alteration especially in very young age patients, it is still unclear whether the final decision is taken by the team of medical professionals, or by the parents. The treatment of patients needs to be initiated immediately after
diagnostic tests are conducted. Problems usually occur when diagnostic tests are conflicting or in mismatch with patient’s current gender or with parent’s wish. Extensive explanation and instruction with subsequent adaptation is then required. In typical situations like this, the medical team is not supposed to force the decision making respecting the feeling of the patient and family. The opinion and the needs of the patients and family are to be listened to. Most importantly, the decision for surgical therapy, often a key part of therapy, should be taken only following thorough consideration and without rushing.

In conditions where consensus is not reached, treatment relating to gender assignment can be delayed until consensus is reached between patient and family (parents) and the medical team. When elective surgery and hormonal treatment is considered there is consensus that the preferred option in typical DSD is to delay treatment until the patient can actively participate in the decision-making about how his or her own body will look, feel, and function.

Fifth, taking into consideration that the clinical spectrum of DSD is very broad and varied, the individual management of each patient is important since it cannot be generalized. Even when the clinical appearance is quite similar, there may be a situation where a different decision regarding outcome is taken. There are no general recommendations for each case except comprehensive management procedures, and the rule of thumb to prioritize on longevity and quality of life of the patient. This requires not only a profound and specialized medical knowledge of the medical team, but also experience.

2. **Recommendations for Management of DSD Patients in Indonesia:**

2.1 **Treatment**

Ideally, a professional team of DSD experts should collaborate to treat DSD patients in a comprehensive and understanding manner, including genetic and psychosocial counselling of both patients and his or her family.

Parents must be able to grasp the controversies in management of DSD patients. Gender assignment that is decided too early based just on the anatomy of the external genitalia could harness further problems on the child. The phenotype does not always depict the actual conditions due to intrauterine mal-development. Gender assignment in a hasty way will directly
impact on the child’s rearing. If a mismatch occurs between sex of rearing and the biological condition of the child in the future life then the solution to these problems will become more complicated.

Chromosomal (genetic), hormonal, neurological, psychological and behavioural factors all affect one’s gender. Presently, the majority of experts prefers to delay the surgical interventions for gender assignment as long as the patient is in healthy condition, in order to involve the individual him/herself in the decision making process. However, our experiences with Indonesian parents indicate that they are very dominant to decide gender assignment and surgical treatment as soon as possible. They will push the medical gender team to initiate treatment directly for their own wish and to hide their shame.

2.2 Follow up
After the diagnostic procedures and when treatment is initiated, a regular follow up is beneficial to record the development of patient’s health; any required action could be taken whenever related problems occur during or after hormonal treatment or surgical therapy. Maintaining quality of life of a patient is a doctor’s main priority. Many of the patients are living in small villages and far from the medical centre. Sometimes their compliance is limited and thus the team should actively contact them for medical follow up; it is not rare that their cost of transportation has to be provided.

2.3 Prognosis
Prognosis of DSD is heavily dependent on the specific cause. A correct understanding of the etiology, effective medication and comprehensive support from every involved party will result in the best possible prognosis. In Indonesia the prognosis is difficult to predict because comprehensive management cannot be provided to the whole archipelago and not even to the major cities.
2.4 Support Group

The existence of a support group will provide an essential prop up for patients. They will feel that they are not alone in facing their problems. There are others who are dealing with the same issues. It will ease the psychological burden of the patients. It is not very common in Indonesia as most of the patients do not want to be disclosing their anomaly, however in Semarang we established a patient support group named “Forkis” with initial funding from the Central Java governor. This support group is comprised of patients and volunteers who will accompany a new patient to alleviate the psychological burden by sharing their experiences. Creating a website that contains information related to DSD and to common concerns of patients, should be seriously considered for implementation.

2.5 Support from the Government (Policy Maker)

DSD is not the main priority of the health sector in a developing country such as Indonesia. However, supportive action from the government is expected. Efforts in providing health insurance for poor people are on-going for several years and have been proven to be advantageous in treating the DSD patients. Budget allocation for research and treatment of general medical problems also including DSD should be taken into consideration for overall health improvement of all Indonesian people. Pharmaceutical preparations such as hydrocortisone and fludrocortisone, presently on the WHO list of essential drugs are not available in Indonesia. Efforts are underway to request the Ministry of Health and National agency for food and drug control (NAFDC) to make these drugs available. Awareness of the medical personnel and pharmacists to the need of these medication should be encouraged.
2.6 The need for an MDT (multidiscipline team) organization

In order to manage DSD patients the organization of a multidisciplinary team should have adequate manpower (7):

- **Team Leader** as the formal institutional head of the team. He or she assembles the team and oversees and steers the work of the team.

- **Team Coordinator** will keep team members connected (including organizing consultations, case discussions, and team meetings) and ensure timelines and continuity in case management.

- **Team Liaison** will serve as the contact person for the patients and family, ensuring that parents and or patients are kept informed of all care and treatment options and linking them with resources and support services. In addition, a religious figure needs to be included in the MDT in Indonesia. As a religious society, spiritual perspectives weigh heavily in every decision of daily life. The role of a religious expert is vital, especially in the final decision of assigning gender prior to surgical therapy.

2.7 The need to establish a network of medical centres

In view of the current situation of a substantial gap of facilities between medical centres in major cities, it is recommended to establish a network of collaborations regarding certain diagnostic examinations and procedures. This may mean that a patient who requires a certain test needs to be referred to another medical centre for a specific examination. This is important to improve the treatment quality and the accuracy of diagnosis based on the current protocol (1).

2.8 Cooperating with medical centre in other countries

Another important action is to cooperate with medical centres from other countries, preferably those who are more advanced in the competency of health care professionals as well as research and diagnostic facilities. It is expected that health care professionals in Indonesia could be assisted in performing the management of DSD patients, as well as receiving assistance in the form of expert opinion on DSD cases. The development of websites or networking through internet either jointly with Asia Pacific countries or with European countries will greatly facilitate further improvement of care and will be of great benefit of DSD patients in Indonesia (8).
References


Chapter 12
Summary
This thesis elaborates the stepwise diagnostic procedure in DSD patients using a multidiscipline approach to obtain the diagnosis of these patients which includes clinical assessment, hormonal, genetic, and pathological investigations, so that it is beneficial as the background for decisions on the required therapy.

Most of the patients in this research had a 46,XY karyotype where Androgen Action Disorder was found to affect the majority of the cases. In the majority of the 46,XX DSD cases, CAH required immediate comprehensive treatment because its nature often leads to a life threatening situation.

In a developing country such as Indonesia, it is rare to have a complete diagnostic procedure where a molecular evaluation is needed for DSD confirmation. A health care center providing molecular analyses as its service is considered very rare, if not nonexistent. Such luxury is limited to a research center in a capital town. Early diagnosis and integrated treatment is vital for DSD patients, in order to obtain the proper outcome in terms of medical, psychological and social aspects.

DSD management in Indonesia is still striving to reach the ideal state, which is explicable by the country’s priority on epidemic health diseases such as infectious or degenerative diseases which affects the nation to a large extent. However, by taking into account the long term effect on the patient, increasing concern over this matter is inevitable.

In order to put the results in proper international perspective, in chapter 2 normal sexual differentiation and development as well as concepts, definitions and classifications of DSD were discussed in detail.

Results of the research is reported in 4 sections

A. Stepwise diagnostic evaluation of DSD

In chapter 3 and 4 the results of a stepwise diagnostic evaluation are given. Patients with various forms and degrees of DSD were evaluated. They were referred to the department of Human Genetics Center for Biomedical Research, Faculty of Medicine Diponegoro University, Semarang, Indonesia for chromosomal analysis by clinicians of the departments of urology, pediatrics, internal medicine and obstetrics of the Dr Kariadi Hospital, Semarang between 2004 and 2010. Reason for referral was the presence of ambiguous genitalia or any anatomical
abnormality of external or internal genitalia including penoscrotal hypospadias with or without descended testes.

In chapter 4 data pertaining to 88 patients are reported. In chapter 5 the number of patients is expanded to 286 and additional data on gene mutations are included. Mutations in the androgen receptor (AR) gene, rendering the AR protein partially or completely inactive, cause androgen insensitivity syndrome, which is a form of a 46,XY disorder of sex development (DSD). In chapter 5, three novel AR variants found in Indonesian DSD patients are presented. The aim of this study was to determine the possible pathogenic nature of these newly found unclassified variants. Indeed reduced functionality of the mutated androgen receptors was demonstrated.

B. Congenital Adrenal Hyperplasia, diagnosis and management

In chapter 6, the long-term effects of 21-hydroxylase deficiency on phenotype in 15 patients with ages between 1 and 33 years who had not been treated for prolonged periods were studied to assess the correlation between genotype and phenotype. Results suggest that a correlation does exist between the concentration of androgens and the extent of virilization. However, no clear correlation between genotype and phenotype could be established.

In chapter 7, saliva of 24 CAH patients who received glucocorticoid replacement therapy was studied. The question was whether determination of salivary androstenedione and 17-hydroxyprogesterone in CAH patients would be a useful alternative to the measurement of these hormones in serum. The results suggest that this is indeed the case.

Chapter 8, describes the result of hydrocortisone therapy in CAH patients especially by taking their saliva for hormonal analysis during various periods of treatment. Among 43 CAH patients, clinical aspects, mutations found, therapy as well as the follow up which was carried out in 25 patients were described.
C. Gonadal tumor risk

Chapter 9 consist of a case report describing the diagnostic evaluation of a 32 yr old women presenting with severe virilization including clinical, hormonal, imaging and histological parameters and psychological assessment. Blood analysis showed a testosterone level in the high-normal male range. The presence of an ovarian tumor was confirmed by laparoscopy followed by biopsy of the left ovary since patient refused ovariectomy. Pathology showed a Leydig cell tumor without histological signs of malignancy. In spite of extensive explanation and psychological counselling, psychosocial and cultural barriers prevented appropriate treatment.

Caucasian patients with Disorders of Sex Development (DSD) have increased risk for Germ Cell Cancer (GCC). GCC are prominent in young adults in Western countries, while the incidence is significantly lower in Asia. So far it is unknown what the risk of GCC in Asian DSD patients is.

In chapter 10, a detailed gonadal histology study was undertaken on 16 Indonesian DSD patients using morphological studies and immunohistochemistry (OCT3/4, TSPY, VASA, SCF/KITLG, SOX9, FOXL2). 13 cases could be analyzed, including ovarian tissue (n=3); streak gonad (n=1); undifferentiated gonad (n=1) and testicular tissue (n=8), from patients diagnosed as 46,XX (n= 1), 46,XY (n=7) and sex chromosome DSD (n=5). The precursor lesions gonadoblastoma, carcinoma in situ, or GCC were diagnosed in four cases (30.8%; three 46,XY and one sex chromosomal DSD). A hormone producing ovarian Leydig cell tumor was identified in a 46,XX patient.

In spite of the significantly lower risk of GCC in the general Asian population, DSD is a dominant risk factor. This study demonstrates the power of immunohistochemical markers for (early) diagnosis. This knowledge deepens understanding of the pathobiology of GCC and clinical handling of patients with DSD globally.
General Discussion and Future Organization of Management on Disorder of Sex Development in Indonesia

In chapter 11, the implementation of comprehensive management of DSD in Indonesia is discussed in more general. The outcome varies and depends on many factors such as the level and type of the disorders, general health of patients, financial conditions, patient’s and family’s reaction and understanding towards DSD. Medical, psychosexual, social and economic factors are discussed that are influencing management of DSD in Indonesia. Based on the studies described in the present thesis, subsequently recommendations for future improvements are formulated.
Summary (in Bahasa Indonesia)

Thesis ini membahas tahapan secara multi disiplin untuk mencari dan mendapatkan diagnosis pada pasien DSD yang meliputi pemeriksaan klinik, hormon, genetik, pathologi sehingga bisa digunakan sebagai pijakan dalam menentukan macam terapi yang diperlukan.

Pada riset ini, sebagian besar pasien mempunyai karyotype 46 XY dimana androgen action disorder menempati diagnosa terbanyak dari kelompok ini. CAH yang merupakan bagian terbesar dari 46 XX DSD, juga merupakan suatu keadaan yang harus diperhatikan mengingat kedaruratan yang bisa ditimulkannya yang tidak jarang menimbulkan kematian.

Di negara yang sedang berkembang seperti Indonesia, masih sangat susah untuk bisa mendiagnosis sampai tahapan akhir prosedur dimana diperlukan pemeriksaan molekuler untuk konfirmasi penyakit. Sangat jarang, kalau tidak bisa dikatakan tidak ada, pusat pelayanan kesehatan di Indonesia yang menyediakan pemeriksaan molekuler sebagai bagian dari produk pelayanannya. Pemeriksan molekuler ini masih terbatas pada pusat pusat riset yang hanya ada di kota kota besar di tanah air. Diagnosis dini dan penanganan secara terpadu sangat diperlukan pada pasien DSD ini, sehingga permasalahan medis, psikologis dan sosial dapat segera diantisipasi.

Penanganan kasus DSD di Indonesia masih membutuhkan perjuangan untuk bisa dikatakan ideal, hal ini dapat dimaklumi oleh karena DSD bukanlah merupakan prioritas kesehatan seperti halnya penyakit infeksi atau degenerasi yang memang mengenai banyak orang. Walaupun demikian, perhatian pada masalah ini tetap harus ditingkatkan mengingat efek jangka panjangnya yang sangat mengganggu penderita.
Hasil dari penelitian ini dilaporkan dalam 4 bagian.

A. Evaluasi diagnostik DSD secara bertahap


Dalam bab 4 dilaporkan hasil penelitian terhadap 88 pasien DSD. Dalam bab 5 jumlah pasien diperluas menjadi 286 dan dilengkapi tambahan data pada mutasi gen. Mutasi pada reseptor androgen (AR) gen, memberikan perubahan protein pada AR sehingga menyebabkan sebagian atau seluruhnya tidak aktif sehingga mengakibatkan sindrom insensitivitas androgen, yang merupakan bentuk dari 46, XY DSD. Dalam bab 5, ditemukan tiga varian baru mutasi pada gen AR yang ternyata terbukti memberikan efek terjadinya gangguan perkembangan kelamin.

B. Diagnosis dan managemen Congenital Adrenal Hyperplasia,

Dalam bab 6, dilakukan penelitian untuk menilai korelasi antara genotipe dan fenotipe terhadap efek jangka panjang defisiensi 21 - hidroksilase pada 15 pasien dengan usia antara 1 dan 33 tahun yang tidak pernah diobati. Hasil menunjukkan bahwa terdapat korelasi antara konsentrasi androgen dan tingkat virilisasi. Namun, tidak ditemukan adanya korelasi yang signifikan antara genotipe dan fenotipe.

Dalam bab 7, diteliti air liur dari 24 pasien CAH yang menerima terapi glukokortikoid. Pertanyaannya adalah apakah penentuan androstenedion saliva dan 17 – hydroxyprogesterone pada pasien CAH akan menjadi alternatif yang berguna untuk pengukuran hormon-hormon dalam serum. Hasil penelitian menunjukkan bahwa hal ini memang dapat dibuktikan kebenarannya.
Bab 8, menjelaskan hasil terapi hidrokortison pada pasien CAH terutama dengan mengambil air liur mereka untuk analisis hormon selama berbagai periode pengobatan. Dari 43 pasien CAH yang ada, hanya 25 pasien yang bisa dilakukan penelitian lebih lanjut mengenai aspek klinis, terapi serta tindak lanjut yang dilakukan.

C. Risiko Tumor Gonad


Pasien DSD pada bangsa Kaukasia mempunyai risiko peningkatan terjadinya kanker dari germ cel. Jenis kanker ini sangat menonjol terjadi pada dewasa muda di negara barat dimana hal tersebut tidak terjadi di Asia. Sejauh ini tidak diketahui apa risiko apa yang membuat fenomena ini diantara pasien DSD di Asia.

Didalam bab 10, penelitian secara detil gambaran histology gonad pada 16 pasien DSD di Indonesia dengan menggunakan study morfologi dan imunohistokimia (OCT3/4, TSPY, VASA, SCF/KITLG, SOX9, FOXL2). Terdapat 13 jaringan yang dapat dianalisis, didapatkan jaringan ovarium (n=3), streak gonad (n=1), gonad tak berdiferensiasi (n=1) dan jaringan testis (n=8) dari pasien dengan 46,XX (n= 1), 46,XY (n=7) dan sex kromosom DSD (n=5). Lesi precursor gonadoblastoma, karsinoma in situ, atau karsinoma germ sel didapatkan pada 4 kasus (30.8%; tiga 46,XY and satu sex kromosom DSD). Terdapat satu pasien dengan tumor sel Leydig yang memproduksi androgen ditemukan pada pasien dengan 46,XX.

Terlepas dari risiko yang rendah pada populasi Asia secara umum, DSD merupakan faktor risiko yang dominan terjadinya karsinoma germ sel. Studi ini menunjukkan kegunaan penanda imunohistokimia untuk diagnosis(awal). Pengetahuan ini memperdalam pemahaman tentang pathobiologi dari karsinoma germ sel dan penanganan klinis pasien dengan DSD secara global.
Diskusi Umum dan Organisasi Manajemen masa depan dari Gangguan perkembangan Kelamin di Indonesia

Di dalam bab 11, pelaksanaan pengelolaan DSD secara komprehensif di Indonesia dibicarakan secara lebih umum. Hasilnya bervariasi dan tergantung pada banyak faktor seperti tingkat dan jenis gangguan, kesehatan umum pasien, kondisi keuangan, pasien dan keluarga reaksi dan pemahaman terhadap DSD

Chapter 13
ACKNOWLEDGEMENT

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I would like to express my thanks to the member of sexual adjustment team Faculty of Medicine Diponegoro University-Kariadi Hospital Semarang Indonesia.

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To my parents Moecharom Aziz, Nanik Sri Mulyani and mother in law Roehati, thank you for caring my family during my stay in Rotterdam and your relentless pray for us.

To the parents and children who have suffered this disease, I hope this work can give a little contribution in addressing the DSD better and relief your hardship.

I owe special thanks to my dearest family since without their encouragement, love and understanding it would have been impossible for me to finish my work. My beloved wife Krisma Irmajanti, for unrelenting support and love helped me a lot to pass many tides during this assignment. I count myself truly blessed to have you by my side on our journey through life.

To my wonderful children: Zadit, Hasna and Aing. I am blessed to have you. I am indebted a lot of things for not accompanying you during which time the desperately need my presence.
This research project would not have been possible without the support of many people. Lastly I offer my regards and blessings to all of those who supported me in any respect during the completion of the project. I salute and thank all of you who have provided me with inspiration, information and useful suggestions.

To be a good doctor one has to be a good listener first.

Achmad Zulfa Juniarto
Curriculum Vitae

Achmad Zulfa Juniarto was born in Semarang Indonesia, 8 June 1970. Living in Semarang Indonesia, he graduated at SMA 3 (high school) in 1989 and entered medical school in Diponegoro University in the same city.

After graduating from the Faculty of medicine in 1995, he became a lecturer at the medical biology and continued his master programme in the field of reproductive medicine at the same university until 2004. In 2006, he became an andrologyst and have additional position at the Kariad hospital. Between the period of 2007-2010, he became The head department of Medical Biology Diponegoro University/ Dr.Kariadi Hospital, Semarang, Indonesia.

He joined Center for Biomedical Research Faculty of Medicine Diponegoro University and Sexual Adjustment Team Faculty of Medicine Diponegoro University - Kariadi Hospital Semarang Indonesia in 1999 till present.

Since then, together with Prof Sultana MH Faradz, he was active in the clinical care of patients with ambiguous genitalia and developed researches in disorder of sexual development at Kariadi hospital Semarang in which in 2004, research collaboration with Erasmus Medical Center Rotterdam The Netherlands (headed by Prof Stenvert L.S Drop) were initiated.

He is a member of Indonesian Medical Doctor Association, Indonesian Andrology Association, Indonesian Sexology Assosiation.
List of Publications


# PhD Portfolio

**Name PhD student:** Achmad Zulfa Juniarto  
**PhD period:** September 2010 – January 2014  
**Promotors:**  
- Prof.dr. S.L.S Drop  
- Prof.dr. S.M.H. Faradz  
- Prof. Frank H de Jong

## PhD Training

<table>
<thead>
<tr>
<th>General Academic Skills</th>
<th>Year</th>
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<tbody>
<tr>
<td>Basic SPSS</td>
<td>2011</td>
</tr>
<tr>
<td>The Ensemble Workshop</td>
<td>2011</td>
</tr>
<tr>
<td>Systematic Literature Retrieval using PubMed (by Medical Library)</td>
<td>2012</td>
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<tr>
<td>Systematic Literature Retrieval using Medline/PsycInfo (by Medical Library)</td>
<td>2012</td>
</tr>
</tbody>
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In-depth courses (e.g. Research School, Medical Training).  
| - The Course on Basic and Translational Endocrinology | 2011 |
| - The Course on Molecular Medicine | 2011 |

## Seminars and workshop

| - PhD day of the Erasmus-MC | 2011 |

## Presentations

| - Indonesian Student Association (PPI) Rotterdam (Oral) | 2012 |
| - DSD symposium, Erasmus-MC (Oral) | 2012 |
| - 2\textsuperscript{nd} International seminar and workshop on DSD, Semarang, Indonesia (Oral) | 2012 |

## Grant/reward

| - DIKTI scholarship from the Directorate of Higher Education, Ministry of Education and Culture, Indonesia | 2010 |
Abbreviations

AR : Androgen Receptor
AAD : Androgen Action Disorder
CIS : Carcinoma in Situ
CNVs : Copy Number Variations
CAH : Congenital Adrenal Hyperplasia
DSD : Disorder of Sex Development
DBD : DNA binding Domain
FOXL2 : Forkhead box L2
GB : Gonadoblastoma
GCC : Germ Cell Cancer
GR : Glucocorticoid Receptor
IGCNU : Intratubuler Germ Cell Neoplasia Unclassified
LCH : Leydig Cell Hypoplasia
LHCG : Luteinizing Hormone/Chorio Gonadotropin Receptor
LBD : Ligand Binding Domain
MRKH : Mayer-Rokitansky-Küster-Hauser syndrome
NTD : NH2-Terminal Domain
OCT3/4 : Octamer-binding transcription factor 4
SCF : Stem cell factor, also known as KITLG
SOX9 : SRY-related HMG-box, gene 9
TSPY : Testis-specific Y-encoded protein 1
UMU : Unknown Male Undermasculinization
UGT : Undifferentiated Gonadal Tissue
WNT4 : Wingless-type MMTV integration site family, member 4
Ngudia Dalan Sing Bener
Aja Mingar Minger
Yen Minger
Mundhak Kehlinger

( Find the right path in order not to get lost)