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**Liquid Chromatography Tandem
Mass Spectrometry Measurements of
Steroids in Biological Samples for
Clinical Research Studies:
Methodology and Application**

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The University of Sydney

PhD

March 2015

Declaration

This thesis is submitted to the University of Sydney in fulfilment of the requirement for the Degree of Doctor of Philosophy.

I declare that this thesis is my own work and effort and that has not been submitted for any other award. Where other sources of information have been used, they have been duly acknowledged.

Ethical approval from Human Research Ethics Committee, University of Sydney (HREC 13094) and Sydney Local Health District Human Ethics Committee within National Health and Medical Research Council Guidelines for Human Experimentation (NHMRC) were granted for the studies presented herein.

A handwritten signature in black ink, appearing to read 'J. G. ...', is positioned above the signature line.

Signature:.....

Date: 27/03/2015

Dedication

I would like to dedicate my thesis to my dear father. Daddy, you are always in my thoughts. I still remember the last hug you gave me. I wish you were here to see my success.

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Publications

Peer-reviewed journals

Singh GKS, Turner L, Desai R, Jimenez M, Handelsman DJ 2014 Pharmacokinetic-pharmacodynamic study of subcutaneous injection of depot nandrolone decanoate using dried blood spots sampling coupled with ultrahigh pressure liquid chromatography tandem mass spectrometry assays. *J. Clin. Endocrinol. Metab.* 99:2592-2598

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Abbreviations

ACAT	acyl-coenzyme A:cholesterol acyltransferase
ACTH	adrenocorticotropin
AKR	aldo-keto reductase
APCI	atmospheric pressure chemical ionization
API	atmospheric pressure ionization
APPI	atmospheric pressure photo ionization
APS	adenosine 5'-phosphosulfate
AR	androgen receptor
Asn	asparagine
BMI	body mass index
CBG	corticosteroid binding globulin
CDC	Centres for Disease Control
CTP	carboxyl terminal peptide
CV	coefficient of variation
CYP	cytochrome P450
DBS	dried blood spot
DELFI	dissociation-enhanced lanthanide fluorescence immunoassay
DHEA	dehydroepiandrosterone
DHEAG	dehydroepiandrosterone glucuronide
DHEAS	dehydroepiandrosterone sulphate
DHT	dihydrotestosterone
DHTG	dihydrotestosterone glucuronide
E ₂	estradiol
E ₂ G	estradiol glucuronide
ECD	electron-capture detector
EMA	European Medicines Agency
ER	estrogen receptor
ESI	electrospray ionization
FDA	Food and Drug Administration
FID	flame ionization detector
FSH	follicle stimulating hormone
FT ICR	Fourier transform ion cyclotron resonance
GAB	granulosa cell aromatase bioassay

GABA	γ -aminobutyric acid type A
GC	gas chromatography
GC-MS	gas chromatography-mass spectrometry
GH	growth hormone
GlcNAc	N-acetylglucosamine
GnRH	gonadotropin-releasing hormone
hCG	human chorionic hormone
HPG	hypothalamic-pituitary-gonadal
HSD	hydroxysteroid dehydrogenase
<i>hν</i>	photons energy
ICL	immunochemiluminometric
IE	ionization energy
IF	immunofluorometric
IGF-1	insulin-like growth factor 1
im	intramuscular
IRMA	immunoradiometric assays
LC-MS	liquid chromatography-mass spectrometry
LC-MS/MS	liquid chromatography tandem mass spectrometry
LDL	low density lipoprotein
LH	luteinizing hormone
LLE	liquid-liquid extraction
LLOQ	lower limit of quantification
<i>m/z</i>	mass-to-charge ratio
MICT	mouse interstitial cell testosterone assay
MKRN	makorin ring finger 3
MO-TMS	methyloxime-trimethylsilyl ether
MRM	multiple-reaction-monitoring
MS	mass spectrometer
MTBE	methyl tert-butyl ether
N	nandrolone
NADPH	nicotinamide adenine dinucleotide phosphate
ND	nandrolone decanoate
P450 _{scc}	cytochrome P450 side-chain cleavage enzyme
PAPS	3' phosphoadenosine-5'-phosphosulfate
PP	protein precipitation

Q	quadrupole
QC	quality control
r	correlation coefficient
R ²	correlation of determination
rhCG	recombinant human chorionic hormone
RIA	radioimmunoassay
RICT	rat interstitial cell testosterone assay
S/N	signal to noise ratio
sc	subcutaneous
SD	standard deviation
SDR	short-chain dehydrogenase/reductase
SEM	standard error of mean
SG	specific gravity
SHBG	sex hormone binding globulin
SIM	selected-ion-monitoring
SPE	solid phase extraction
SRM	selected-reaction-monitoring
StAR	steroidogenic acute regulatory protein
SULT	sulphotransferases
T	testosterone
TG	testosterone glucuronide
TOF	time-of-flight
TSH	thyroid stimulating hormone
UDP	uridine diphosphate
UDPGA	uridine diphosphate-glucuronic acid
UGT	uridine diphosphate glucuronosyltransferases
UV	ultraviolet
WHO	World Health Organization
17-OHP	17-hydroxyprogesterone
3 α -diol	5 α androstan-3 α -17 β -diol
3 β -diol	5 α androstan-3 β -17 β -diol

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ABSTRACT

Steroids are endogenous compounds derived from cholesterol which can be divided into five families comprising of estrogens, androgens, progestins, mineralocorticoids and glucocorticoids. Most circulating steroids are conjugated to a hydrophilic moiety (e.g. glucuronide and sulfate) or bound to carrier proteins (e.g. sex hormone binding globulin and albumin) with a small proportion in a non-protein bound form. The production of steroids is regulated by the pituitary gonadotropins i.e. luteinizing hormone (LH) and follicle stimulating hormone (FSH) that mediate their bioactivity by binding to cognate G protein-coupled receptors expressed on the surface of specific target cells in the gonads – Leydig cells for LH and Sertoli cells for FSH. Steroids exert biological activities by binding to their specific intracellular receptors in both reproductive and non-reproductive target tissues. Accurate measurement of reproductive hormones is vital to evaluate neonatal disorders of sexual differentiation, pubertal status, gonadal function, and hormonal doping in sports. Steroids from biological fluids, notably serum and urine, can be measured using immunoassays and gas chromatography mass spectrometry (GC-MS); however, these traditional assays have significant limitations. The advent of liquid chromatography tandem mass spectrometry (LC-MS/MS) coupled with soft ionization (e.g. atmospheric pressure photo ionization: APPI) method has expanded the scope for measurement of small molecules from biological matrices with higher accuracy, specificity, sensitivity and requires less sample preparation. The overall aim of this study is to develop and validate LC-MS/MS methods to measure steroids from biological samples for clinical research studies.

The first part of this thesis was to develop methodologies and analysis of androgens i.e. testosterone (T) and nandrolone (N) from dried blood spot (DBS) samples using LC-MS/MS. Conventionally T esters are used as replacement therapy for T deficient men and is usually

administered by intramuscular (im) injections to produce long-acting depots which is more convenient in sustaining T release for weeks to months and thereby assists in maintaining long-term adherence to treatment. However, administration of androgen esters via deep im injections into the gluteal muscle requires medical personnel (to give the injection at the right site) and yet the injectate is often deposited into subcutaneous (sc) fat due to the thick sc fat layer in most men. IM injections are also associated with local pain and discomfort, injection site infection or bleeding and may not be suitable for patients with bleeding disorders or using anti-coagulants. Thus, the aim of this clinical study was to investigate the feasibility and pharmacology of sc injection (at a single abdominal site) of nandrolone decanoate (ND), as a typical androgen ester in an oil vehicle, in healthy men and to collect whole blood samples from finger pricks onto filter cards at home for 21 days to investigate the pharmacokinetics of single sc injection of ND and its pharmacodynamic effects on endogenous T. A LC-MS/MS method was developed to enable measurement of serum T and N from the whole blood spot. This bypassed using a subsample to avoid non-homogenous distribution of blood and hematocrit effect on the filter paper. The assay had lower limits of quantitation of 50 (T) and 156 (N) pg/mL, respectively using 50 μ L of blood. In the clinical study, daily serum N peaked 2.50 ± 0.25 (SEM) ng/mL at a median (range) of 6 (4-13) days causing a reduction in serum T from 3.50 ± 0.57 ng/mL at baseline to a nadir of 0.38 ± 0.13 (SEM) ng/mL ($89 \pm 3\%$ suppression) at a median (range) of 8 (5-16) days. This study demonstrates that (a) DBS sampling with LC-MS/MS steroid assays achieves frequent time sampling in the community without requiring clinic visits, venesection or frozen serum storage and (b) an androgen ester in oil vehicle can be delivered effectively by sc injection avoiding the need for medically supervised deep im injections.

The second part of this thesis evaluated the measurement of urinary LH immunoreactivity using immunofluorometric (IF) and immunochemiluminometric (ICL) LH assays after

prolonged frozen storage. These commercially available LH immunoassays are developed and validated for human blood samples but not urine thus LH assays intended for use with urine samples needs thorough validation. LH was measured in serial urine samples following administration of a single injection of one of two doses of recombinant human chorionic hormone (rhCG) with assays run at the end of study (2008) and again after 4 years of frozen (-20 °C) storage where samples were stored without adding preservatives. The ICL assay showed quantitatively reproducible LH measurements after prolonged -20 °C storage. However, the IF immunoassay gave consistently lower LH levels relative to ICL (2008) with a further proportionate reduction after 4 years of sample storage (2012). Yet, both the assays displayed similar patterns of the time-course of urine LH measurement both before and after 4 years of frozen storage. We found that both immunoassays are suitable for urinary LH measurements with ICL assay being more robust for quantitative urinary LH measurement such as for anti-doping purpose whereas the IF could be applicable for research studies where urine LH levels are compared within-study but not in absolute terms.

Urinary hormone concentrations are often adjusted to correct for hydration status. The third part of this thesis investigated whether first morning void urine hormones in growing adolescents require adjustments for urine dilution/concentration and, if so, whether urinary creatinine or specific gravity (SG) are better adjustments. The study population was adolescents aged 10.1 to 14.3 years initially who provided fasting morning blood samples at 0 and 12 months (n=343) and first morning urine every three months (n=644). LC-MS/MS method was developed and validated to measure unconjugated T, estradiol (E₂), dihydrotestosterone (DHT) and dehydroepiandrosterone (DHEA) in human urine. In addition, urine LH was measured using the previously validated ICL assay. Unadjusted, creatinine and SG-adjusted hormonal concentrations were compared by Deming regression and Bland-Altman analysis and grouped according to self-rated Tanner stage or chronological

age. Correlations of paired serum and urinary hormonal concentration of unadjusted and creatinine and SG adjusted were also compared. Fasting first morning void hormone concentrations correlated well and were unbiased between unadjusted or adjusted by either creatinine or SG. Urine creatinine concentration increases with Tanner stages, age and male gender whereas, urine SG was not influenced by Tanner stage, age or gender. Adjustment by creatinine or SG of urinary LH, E₂, T, DHT and DHEA concentrations did not improve correlation with paired serum concentrations. The study demonstrates that urine steroid and LH concentrations in first morning void samples of adolescents are not significantly influenced by hydration status and may not require adjustments; however, if desired, both creatinine and SG adjustments are equally suitable.

The final part of this thesis aimed to describe the longitudinal relationships of within-individual hormone and anthropometric changes during puberty. Temporal changes in urine and serum hormones over 12 months to standard measures of pubertal development were assessed. A community sample of 104 adolescents (57 female) was studied over 12 months with annual anthropometric assessment, blood sampling and self-rated Tanner staging and urine collected every 3 months. Serum and urine sex steroids (T, E₂) were measured by the developed and validated LC-MS/MS method and LH by ICL assay. A high proportion (92%) of scheduled samples were obtained with low attrition rate of 6.7% over the 12 months. The study demonstrated that the urine hormone measurements correlated cross-sectionally and longitudinally with age, anthropometry and Tanner stage. This study successfully developed a feasible and valid sampling methodology and measurements for puberty hormones in urine, which allows a sufficiently intensive sampling frequency to monitor individual pubertal progression in adolescents.

Chapter 1 Literature Review

1.1 Steroid hormones

1.1.1 Structure and classification

Steroids can be classified into five families depending on its structural and biological basis. These comprise estrogens, androgens, progestins, mineralocorticoids and glucocorticoids. Vitamin D, bile acids and thyroid hormones also have close structural resemblance to the steroid family of molecules. Steroids are lipophilic compounds derived from cholesterol, a sterol which is made up of three hexagonal carbon rings (A, B and C) and a pentagonal carbon ring (D) to which a side chain is attached (Figure 1.1). This four-membered hydrocarbon core has two important methyl groups are attached at position 18 (attached to C13) and 19 (attached to C10). The carbon rings fused in a *trans* orientation to form a planar structure. The orientation of the substituent groups on the steroid skeleton is either above (β) or below (α) the plane. According to the chemical structure, steroids are divided into cholane, cholestane, androstane, estrane and pregnane. Cholanes (bile acids) and cholestanes (vitamin D and cholesterol) are known as sterols with long and branched hydrocarbon side chains attached to D ring. Partial cleavage of the cholestane, C27 sterol side chain (ring-D) produces pregnane C21 series steroids (progestins and corticosteroids), whereas the total cleavage of the side chain yields androstane C19 series steroids (androgens). Finally, removal of the methyl group between the A- and B-rings results in production of estrane C18 series steroids (estrogens). The structures of the three classes of steroids are shown in Figure 1.2. Various functional groups such as hydroxy, keto and methyl-groups are located at different positions of the carbon backbone in all series depending on the compound.

Each steroid has common alike structure and stereochemistry. However, each class of steroids displays distinct physiologic activities depending on the family of nuclear transcription factors the molecules activate via its cognate (steroid hormone receptor)

(Strauss 2014). Progestagens, androgens and estrogens are classified as sex steroids whereas corticosteroids and mineralocorticoids are adrenal steroids (Figure 1.2). The ovary, testis, adrenal cortex and placenta are the endocrine organs that specialize in steroid hormone production. The ovaries secrete estrogens and progestagens, the testis produces mainly androgens and the adrenal produces both corticosteroids (mineralo- and glucocorticoids) and sex steroid precursors. During pregnancy, the placenta produces progestagens and estrogens.

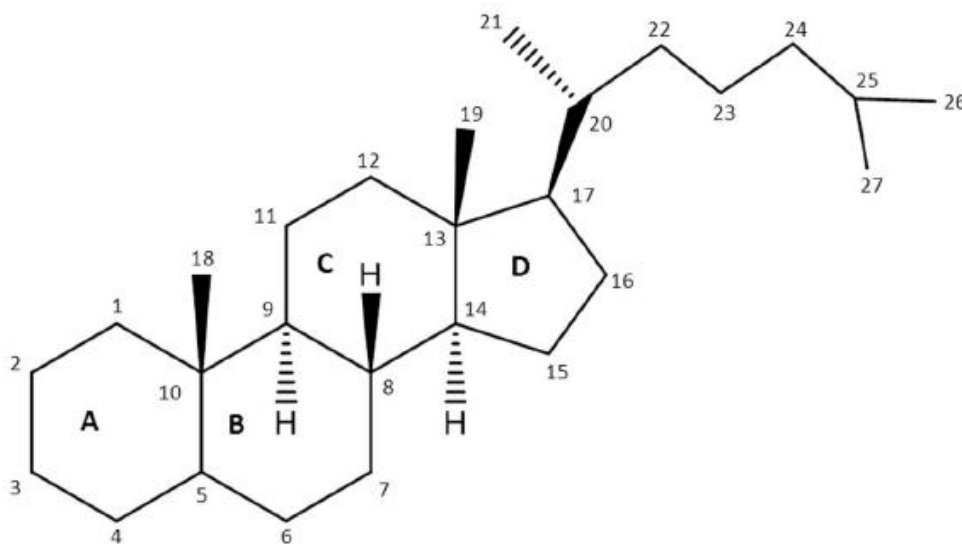


Figure 1.1 Cholesterol structure

The rings are identified with capital letters and carbon atoms are numbered. The bold and cross-hatched wedges represents the bonds extending above and below the plane, respectively.

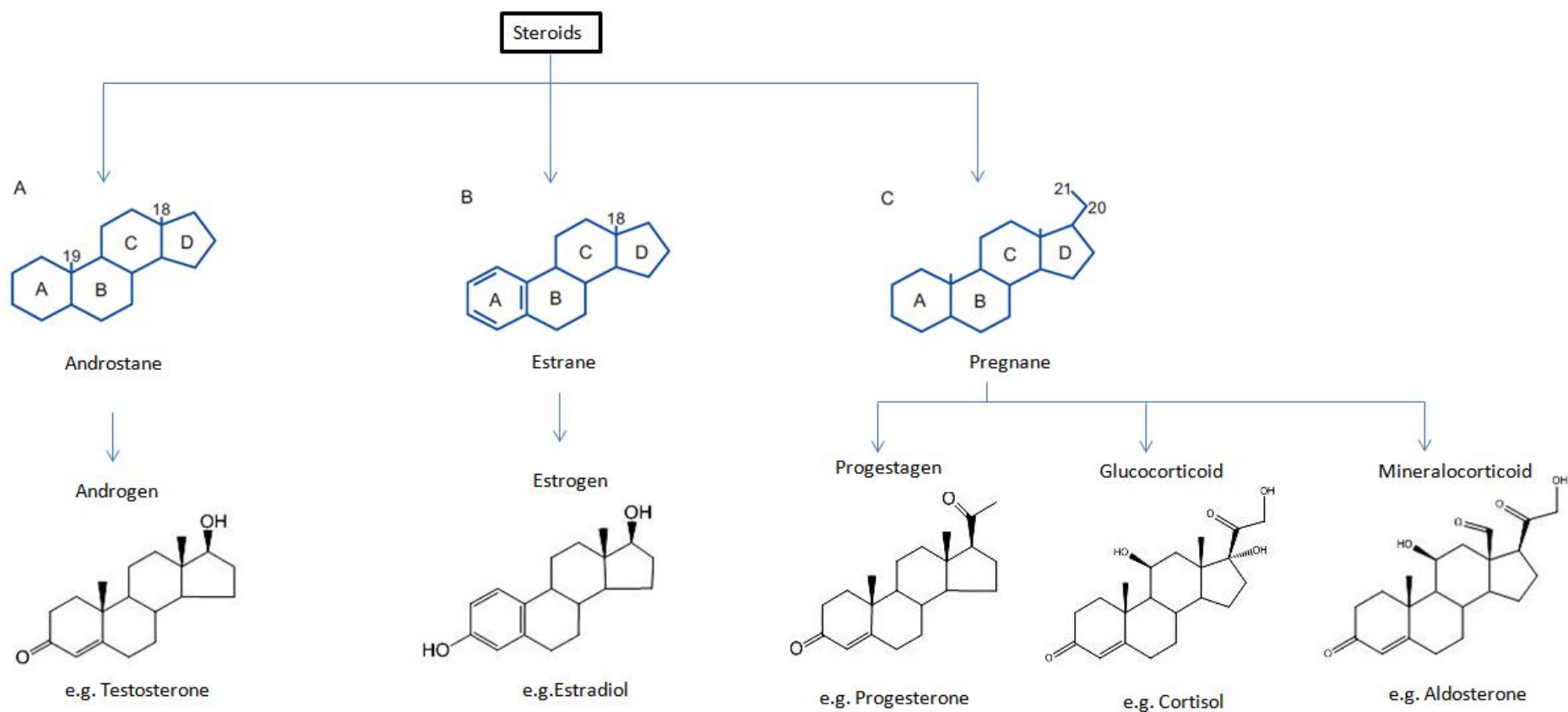


Figure 1.2 Classification of steroids according to basic backbone structure (androstane, estrane and pregnane) and example of steroid classes: sex steroids (androgen, estradiol and progesterone), corticosteroids and mineralocorticoid.

1.1.2 *Physiological action*

The production of steroids occurs in the mitochondria and smooth endoplasmic reticulum of cells in the adrenal cortex, the gonads or the placenta. Steroids are hydrophobic molecules that can penetrate biological membrane of lipophilic cells and are not stored in intracellular vesicles like peptide hormones. They are then transported rapidly in the bloodstream to reach targeted cells where the steroids bind to its specific receptor, which acts as transcriptional activators of steroid-responsive genes. Besides genomic response which may take between a few hours to days to manifest, steroids also regulate non-genomic responses (or ‘rapid actions’) that occurs within seconds to an hour (Norman et al. 2004). The pathway of steroid hormone biological responses is shown in the schematic diagram below (Figure 1.3).

In biological fluid, small proportion of steroids circulate in unbound form (2-3%) and the remaining are in conjugated form with a hydrophilic moiety such as glucuronide or sulfate or they are bound to 50-60 kd carrier protein glycoproteins, such as sex hormone binding globulin (SHBG), corticosteroid binding globulin (CBG) as well as albumin (Dunn et al. 1981). Albeit the steroid binding proteins circulate at low concentration compared to albumin, they have higher binding affinity to certain steroids. SHBG and CBG have high binding affinity towards sex steroids (testosterone and estradiol) and corticosteroids, respectively (Kicman 2010). The binding of steroids to the circulating binding proteins serves as a reservoir of the hormone, protects the steroids from rapid inactivation or urinary/biliary excretion and ensures ubiquitous distribution of the steroids (Kronenberg et al. 2011). According to the free hormone hypothesis, the free steroids are physiologically available to bind to their target cell, whereas the steroids bound to the carrier proteins are believed to have different and limited physiological activity (Mendel 1989). Contrary to this latter concept, recent studies have found that the cell membrane endocytic receptors, also known as the megalin receptor, expressed in the reproductive tissues mediates cellular uptake of circulating

protein-bound sex steroids. Once transported into the cells, lysosomes degrades the carrier protein bound and releases the steroids allowing it to bind to its receptor that further induces steroid responsive-genes (Hammes et al. 2005). SHBG bound androgens and estrogens are involved in the development and maturation of reproductive organs (Hammes et al. 2005, Kahn et al. 2008).

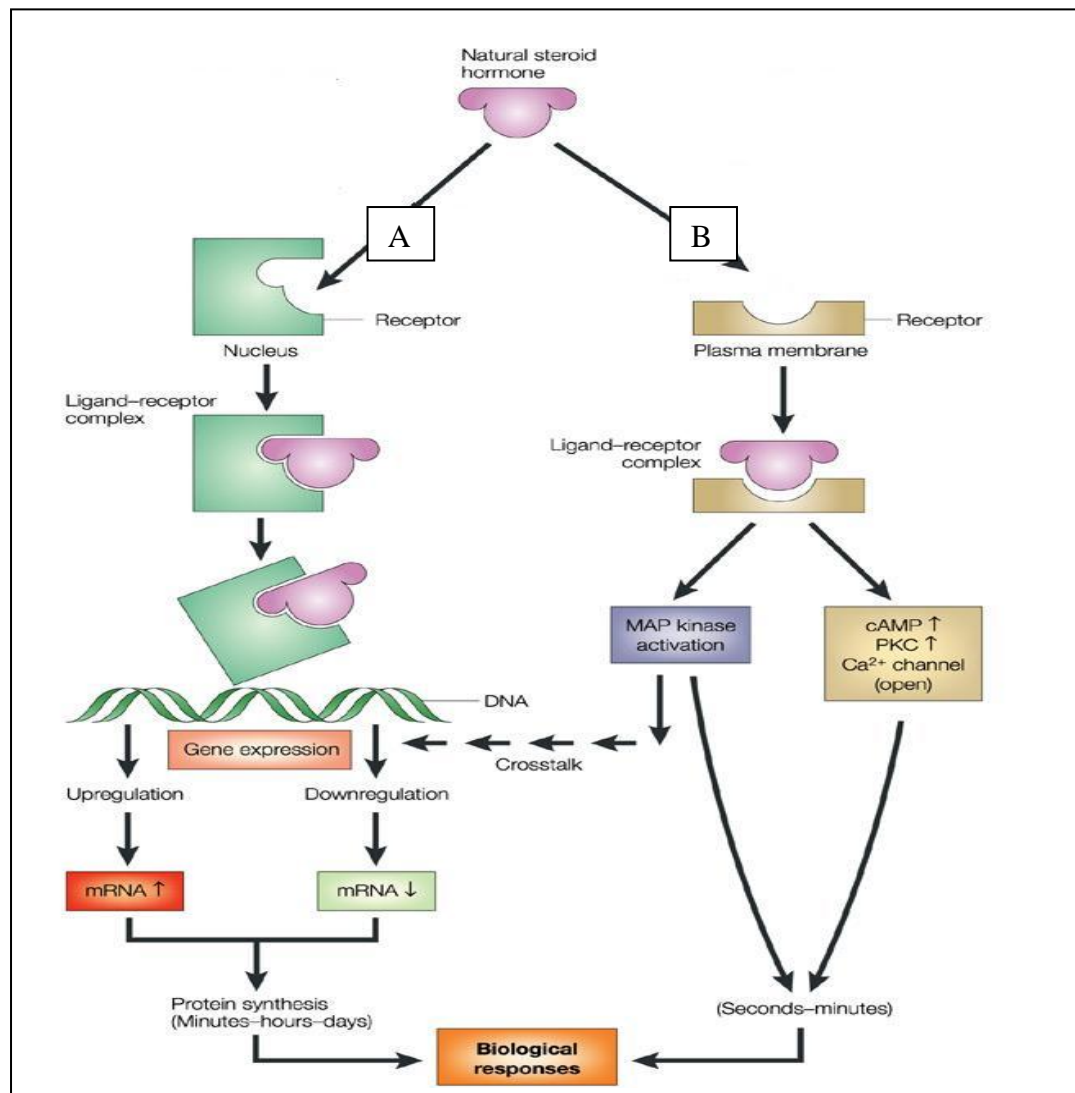


Figure 1.3 Genomic (A) and non-genomic (B) pathways of steroid hormones

A. In the genomic pathway, binding of steroids to the nuclear receptors (present either in the nucleus, in the cytoplasm complexed to chaperones or in between the cytoplasm and nucleus) leads to up- or down regulation of gene transcriptional responses regulating protein synthesis within minutes to days. **B.** Non-genomic biological responses of steroid involves occupancy of steroids to the plasma membrane of the cell, which in turn activates direct biological responses by intracellular signaling molecules such as mitogen activated protein (MAP) kinase, protein kinase A (PKA), cyclic adenosine monophosphate (cAMP), and opening of calcium channels or indirect biological responses through genomic pathway [adapted from (Norman et al. 2004, Vogeser and Parhofer 2007)].

1.2 Steroid metabolism

1.2.1 Steroidogenesis (Biosynthesis of steroids)

The synthesis of steroids specifically takes place in the adrenal cortex (zona fasciculata, reticularis and glomerulosa), testicular Leydig cells, ovarian granulosa and theca cells and the placental syncytiotrophoblast cells (Miller and Bose 2011). Cholesterol is a starting point for biosynthesis of all steroid hormones, bile acids and vitamin D. The three sources of cholesterol are from dietary low density lipoprotein (LDL)-uptake, stored cholesterol and *de novo* synthesis. LDL is taken up by the steroidogenic cell via specific receptor-mediated endocytosis. Within the cell, stored lipoprotein cholesterol esters are then converted by the lysosomal acid lipase into free cholesterol which is the substrate for steroidogenesis (Brown et al. 1978, Gwynne and Strauss 1982). Excessive cholesterol uptake by the cell is either transferred out as an external lipoprotein or stored within the cell cytoplasm as lipid droplets upon cholesterol esterification catalyzed by the acyl-coenzyme A:cholesterol acyltransferase (ACAT). As required, the stored lipid droplets are hydrolyzed by acid lipase to release free cholesterol (Miller and Bose 2011). Cholesterol is also synthesized *de novo* by the smooth endoplasmic reticulum of the steroidogenic cells catalyzed by at least 17 enzymes. The cellular cholesterol synthesis and lipoprotein uptake by the steroidogenic cells is stimulated by the tropic peptide hormones (Miller and Bose 2011).

The conversion of cholesterol to steroids is regulated by a series of enzyme reactions. The two main classes of enzymes involved in the steroid conversion pathway are the cytochrome P450 (CYPs) heme containing proteins and hydroxysteroid dehydrogenases (HSDs) (Miller and Auchus 2011, Payne and Hales 2004). The CYP enzymes include type I or type II which is located in the mitochondria and endoplasmic reticulum, respectively. Whereas the HSD enzymes can be classified into aldo-keto reductase (AKR) and short-chain dehydrogenase/reductase (SDR) families (Miller and Auchus 2011). CYP enzymes mediate

hydroxylation, aromatization and carbon-carbon bond cleavage using molecular oxygen and nicotinamide adenine dinucleotide phosphate (NADPH) as a cofactor which irreversibly oxidize steroids (Miller 2005). *In vitro*, the HSD reactions are reversible directing reactions to either oxidation of hydroxysteroids or reduction of ketosteroids depending on conditions, for example, pH, cofactor and substrate availability. However *in vivo*, HSD enzymes catalyze unidirectional reactions and are classified as dehydrogenases or reductases where pyridine nucleotide acts as cofactors (Agarwal and Auchus 2005).

Steroidogenesis is first initiated from the conversion of cholesterol (C₂₇) to the first steroid pregnenolone (C₂₁) via the action of CYP11A (cytochrome P450 side-chain cleavage enzyme: P450_{scc}) (removes six carbon units) (Waterman and Simpson 1985) and steroidogenic acute regulatory protein (StAR) (Lin et al. 1995). CYP11A is expressed in all steroidogenic cells as a rate-limiting step at the start of steroidogenesis (Ishimura and Fujita 1997, Oonk et al. 1990, Payne and Youngblood 1995, Pelletier et al. 2001, Strauss et al. 1996). The StAR protein is responsible for transporting the hydrophobic cholesterol substrate from the outer to the inner mitochondrial membrane where this reaction takes place (Miller and Auchus 2011, Miller and Bose 2011). The CYP11A enzyme reaction introduces hydroxyl groups at C₂₀ and C₂₂ and cleaves the cholesterol side chain between these carbons (Payne and Hales 2004). After this rate limiting step, pregnenolone is transported out of the mitochondria into the endoplasmic reticulum where the remainder of steroidogenesis takes place. Pregnenolone further undergoes 17 α -hydroxylation to produce 17 α -hydroxypregnenolone in a reaction catalyzed by CYP17 (P450_{c17}). In the adrenal zona reticularis, ovarian theca cells and Leydig cells, the CYP17 enzyme also catalyzes cleavage of C₁₇ and C₂₀ (lyase) bond to produce dehydroepiandrosterone (DHEA, C₁₉ steroid) (Payne and Hales 2004). The 3 β -HSD type 2 converts 5-ene-3 β -hydroxylated steroids (Δ^5) to 4-ene-3-oxo steroids (Δ^4), resulting in conversion of DHEA to androstenedione in the gonad

and adrenal (Payne and Hales 2004). The 17β -HSD type 3 which is expressed exclusively in the testicular Leydig cells converts androstenedione to testosterone (Geissler et al. 1994). Whereas, the 17β -HSD type 5 which is the only form of 17β -HSD found in the ovarian theca cells catalyzes the production of testosterone from androstenedione (Pelletier et al. 1999). Testosterone is converted to dihydrotestosterone (DHT) by the irreversible 5α -reductase type 2 enzyme reaction in the prostate and external genitalia (Thigpen et al. 1993). Additionally, DHT can also be generated through the “backdoor pathway” bypassing DHEA, androstenedione and testosterone, as intermediates. This pathway involves the conversion of 17-hydroxyprogesterone (17-OHP) to produce androstanediol which is an immediate precursor of DHT. The conversion involves 3α and 5α -reduction activity followed by sequential CYP17 and 17β -HSD type 3 enzyme activity. Finally, androstanediol can be back-converted to DHT by 3α -oxidation reaction (Auchus 2004). Figure 1.4 outlines the classic and backdoor pathways involved in DHT biosynthesis. In humans, DHT generated by both pathways plays an indispensable role in male fetal sexual development but the role of the backdoor pathway in mature individuals remains unclear (Flück et al. 2011, Greaves et al. 2014).

In the ovary, the androstenedione produced by the theca cells is later diffused into the granulosa cells, where the aromatase enzymes, CYP19 (P450arom) catalyses hydroxylations of androstenedione to produce estrone (C18 steroid with phenolic A ring). Estrone is later converted to estradiol by the 17β -HSD type 1 (Miller and Auchus 2011). The aromatase enzyme also converts testosterone to estradiol in brain, bone and adipose tissues but not liver (Perel and Killinger 1979, Sasano et al. 1997). In the adrenal zona fasciculata, the enzyme 3β -HSD converts 17-hydroxypregnenolone to 17-OHP (Payne and Hales 2004). Consequently, CYP11B1 (P450c11 β 1) and CYP21 (P450c21) enzymes convert 17-OHP to 11-deoxycortisol and cortisol. The biosynthesis pathway of androgens, estrogens,

corticosteroids (mineralocorticoid and glucocorticoid) and progestogen metabolites are outlined in Figure 1.5.

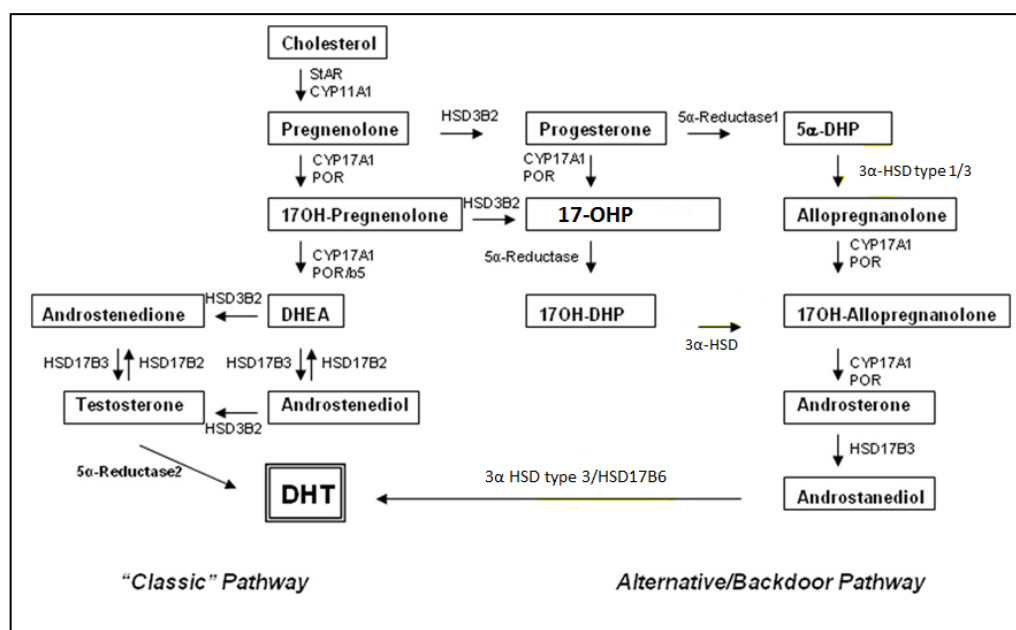


Figure 1.4 Classic and backdoor pathways of DHT synthesis.

The classic and backdoor pathways involved in DHT biosynthesis are shown on the left and right, respectively. Adapted from (Flück et al. 2011, Holčapek et al. 2010).

The classic pathway requires the following protein and enzymes: StAR (steroidogenic acute regulatory protein), CYP11A (cytochrome P450 side-chain cleavage enzyme, P450_{sc}), CYP17A1 (17 α -hydroxylase/17,20-lyase, P450_{c17}), HSD3B2 (3 β -hydroxysteroid dehydrogenase, type 2), HSD3B2 (3 β -hydroxysteroid dehydrogenase, type 2), HSD17B3 (17 β -hydroxysteroid dehydrogenase, type 3) and 5 α reductase, type 2.

Additional enzymes involved in the backdoor pathway includes: 5 α -reductase, type 1 (5 α -reductase 1, 3 α -reductase, type 3 and possibly 3 α -reductase, type 1 and HSD17B6 (17 β -hydroxysteroid dehydrogenase, type 6).

Steroid abbreviations: 17-OHP: 17-hydroxyprogesterone; 17OH-DHP: 17-hydroxy-dihydroprogesterone (or 5 α -pregnane-17 α -ol-3,20-dione); 17OH-allo: 17-hydroxy-allopregnanolone (or 5 α -pregnan-3 α ,17 α -diol-20-one); 5 α -DHP: 5 α -dihydroprogesterone (or 5 α -pregnane-3,20-dione), and 3 α -OH-DHP: allopregnanolone (or 3 α -hydroxy-dihydroprogesterone or 5 α -pregnane-3 α -ol-20-one).

1.2.2 Phase I metabolism

Phase I metabolism involves converting active steroids into inactive metabolites that are substrates for phase II conjugation for eventual excretion in the urine and bile. The inactivation primarily occurs in the liver although there are also metabolic enzymes present in the steroid target tissues (Strauss 2014). The enzymes that are involved in the phase I steroid metabolism include $3\alpha/3\beta$ -HSDs, 5β -reductase, 11β -HSDs, 17β -HSDs and 20α -HSDs that acts on C3, C5, C11, C17 and C20 positions of steroid, respectively (Rižner and Penning 2014). However, most of the target tissues also express HSD isoforms that are capable of converting the inactive steroids metabolites back into active form (Bélanger et al. 2003). Thus, these enzymes acts as ‘switches’ that tightly regulate the receptor occupancy by the steroids and balance the synthesis and metabolism of the steroids (Penning 2011). In the liver, 5α and 5β reductase converts circulating testosterone to form 5α -DHT and 5β -DHT, respectively. In the prostate and androgen target tissues, DHT is reduced by 3α -HSD, 3β -HSD and 17β -HSD forming androsterone, 5α androstan- 3α - 17β -diol (3α -diol), 5α androstan- 3β - 17β -diol (3β -diol), androstanedione and epiandrosterone (Bélanger et al. 2003, Dufort et al. 2001). Basically steroids with 3-keto- $\Delta^{4,5}$ structure may first be 5α -reduced and subsequently 3α -reduced to form stereoisomeric tetrahydrosteroids which are later conjugated in phase II metabolism and finally excreted in the urine (Jin and Penning 2001). However, the 17β -HSD type 6 can catalyze oxidation of 3α -diol back to form 5α -DHT in the prostate (Penning 2011). In the kidney, the 11β -HSD type 2 catalyzes the oxidation of potent glucocorticoid, cortisol into its inactive counterpart cortisone to enable the less abundant aldosterone to occupy the mineralocorticoid receptors (Strauss 2014). Conversely in the liver, adipose tissue and skeletal muscle, the inactive cortisone is reduced back to the inactive moiety cortisol by 11β -HSD type 1 (Strauss 2014). In breast tissues, 17β -HSD type 1 converts estrone to estradiol whereas 17β -HSD type 2 and type 4 inactivates estradiol by

catalyzing the reverse reaction. Progesterone is converted by $20\alpha(3\alpha)$ -HSD to a weaker progestin metabolite, 20α -hydroxyprogesterone whereas 17β -HSD type 2 directs the reverse reaction (Rižner and Penning 2014). Figure 1.6 illustrates the HSD enzymes involved in the activation and inactivation of androgens, glucocorticoid, estrogens and progestins.

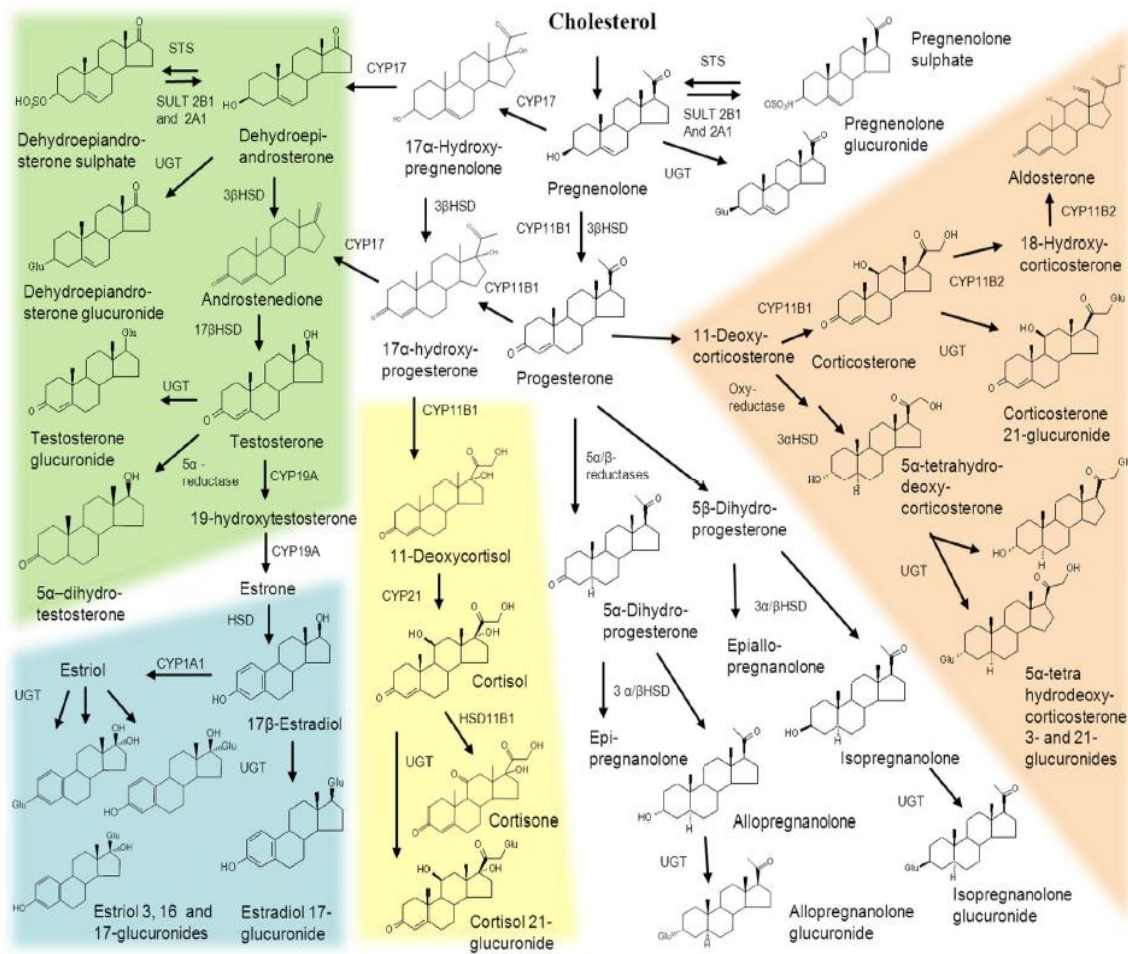


Figure 1.5 Biosynthetic pathway and steroidogenic enzymes involved in the pathway.

The pathway is divided into colour zones to depict the different classes of steroids; androgen (green), estrogen (blue), glucocorticoid (yellow), mineralocorticoid (orange) and progestogens metabolites (white) [adapted from (Jäntti et al. 2010)].

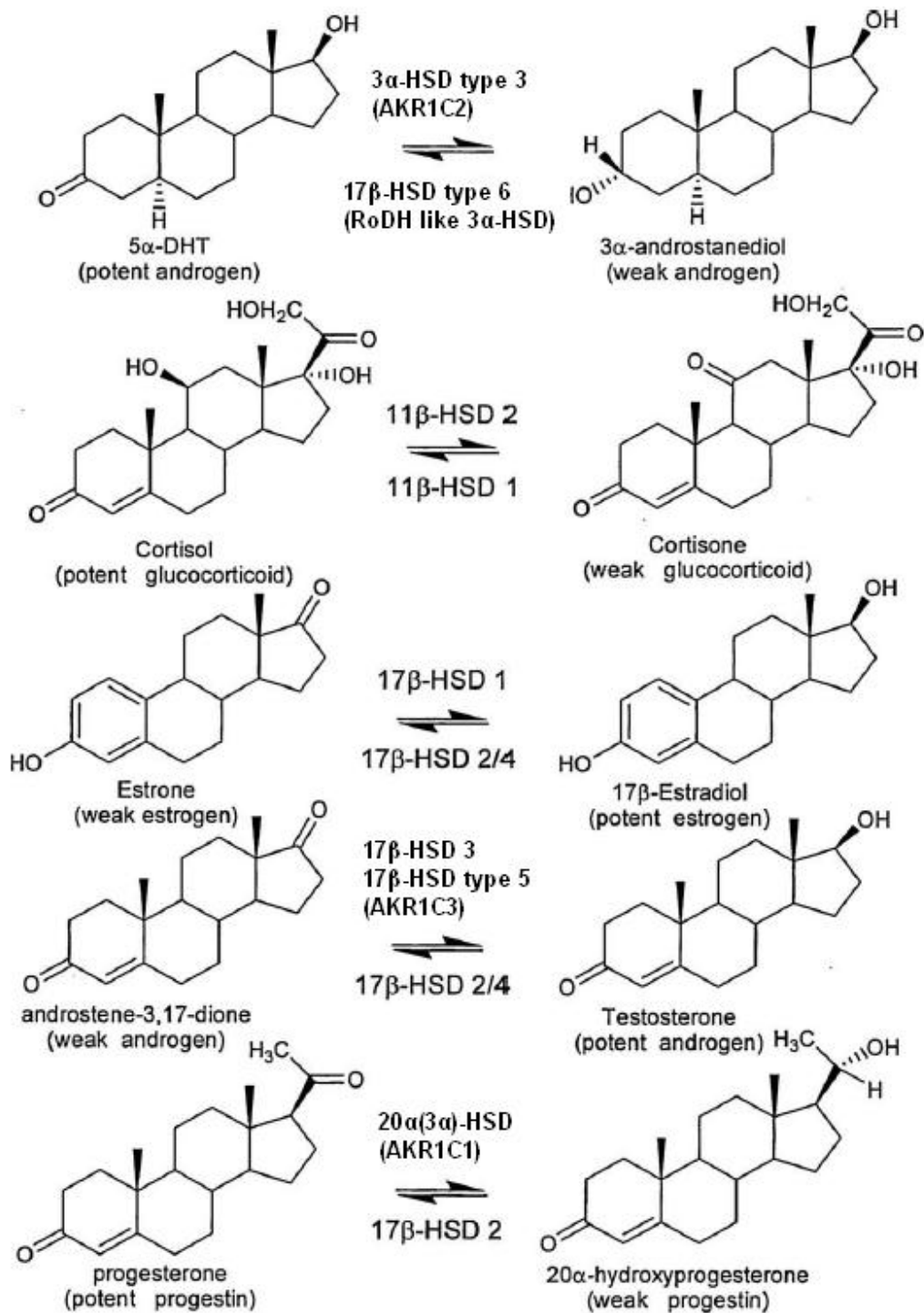


Figure 1.6 Androgens (5 α -DHT and testosterone), glucocorticoid (cortisol), estradiol (estrogen) and progestin (progesterone) phase I metabolism by hydroxysteroid dehydrogenase enzyme (aldo-keto reductase; AKRs and short-chain dehydrogenase; SDRs).

The enzymes act in pairs to regulate the steroid occupancy towards the specific receptor at target tissues. The steroids are activated and deactivated by the specific enzymes to form potent steroids weak steroids, respectively which the latter is readily available for phase II metabolism. Adapted from (Penning 2011).

1.2.3 Phase II metabolism (conjugate formation)

Steroid hydroxyl metabolites from phase I metabolism further undergo conjugation reactions to form hydrophilic conjugates with lower affinity for cognate receptor and plasma proteins compared to their parent steroid (Andrew 2001, Tukey and Strassburg 2000). This metabolic pathway is catalyzed by enzymes which inactivate steroidal biological activity and increases the polarity of the steroids to aid their excretion (urine and bile). Phase II metabolism involves conjugation of steroids with glucuronides or sulfates which are the most abundant conjugated derivatives. Other cholesterol metabolite conjugates involved in phase II metabolism includes N-acetylglucosamine (GlcNAc), amino acids, glucose and galactose (Goto et al. 2005, Marschall et al. 1989, Vessey 1978, Wietholtz et al. 1991). Only small amount of steroids are excreted in unconjugated form in urine (e.g. less than 3% of urinary androgens secreted in free form) (Dehennin and Matsumoto 1993). Generally steroid conjugates are regarded inactive, however there are conjugated steroids that remain in circulation (e.g. DHEA sulfate) or stored locally in tissues (e.g. estrone sulfate) serving as a reservoir for back conversion to its active hormones or as steroid hormone precursor, reactions catalyzed by sulfatase enzyme (Andrew 2001, Hobkirk 1985, Reed et al. 1996, Zhu and Conney 1998).

Glucuronidation: This is a major route of steroid elimination. This reaction involves covalent linkage (conjugation) of glucuronic acid moiety (glycosyl group) derived from uridine diphosphate-glucuronic acid (UDPGA) co-substrate to lipophilic substrates that commonly contains hydroxyl, carboxyl or nitrogen group. This mechanism is catalyzed by an endoplasmic reticulum membrane enzyme, uridine diphosphate (UDP)-glucuronosyltransferases (UGTs) (Figure 1.7) (Court 2014, King et al. 2000, Tukey and Strassburg 2000). The co-substrate UDPGA is formed in the cytosol from the oxidation of UDP-glucose catalyzed by the UDP-glucose dehydrogenase (Zamek-Gliszczyński et al.

2006). The human genome encodes 19 UGT enzymes which are most abundant in the liver, although some are also expressed in other tissues such as the intestine, kidney, mammary gland and prostate (Gaganis et al. 2007, Mackenzie et al. 2005, Ohno and Nakajin 2009). The distribution of the enzyme varies in tissues according to age, gender, hormonal status, genetic factors and environmental exposure (Ritter 2000). Based on the homology of primary structure, UGTs can be divided into four families: UGT1, UGT2, UGT3 and UGT8 (Mackenzie et al. 1997). UGT1 and UGT2 are the two main enzyme families involved in steroid glucuronidation comprising of three subfamilies: UGT1A, UGT2A and UGT2B (Barbier and Bélanger 2003, Hum et al. 1999, Mackenzie et al. 1992). The UGT1 isoforms have specificity for bilirubin, amines and phenolic compounds as substrate, whereas the UGT2 targets the elimination of steroids, bile acids and opioids (You 2004). Metabolism of most estrogens and androgens are catalysed by subfamily UGT1A and UGT2B, respectively. All of the UGT1A isoforms members specificity (with exception to UGT1A6) are mainly directed towards C18 steroid substrates such as estradiol, estrone (UGT1A1; UGT1A10), 2-hydroxyestrone (UGT1A3) and 4-hydroxyestrone (UGT1A9) (Albert et al. 1999, Basu et al. 2004, Cheng et al. 1998, Mojarrabi et al. 1996, Strassburg et al. 1998). In humans, there are seven UGT2B isoforms isolated namely UGT2B4, UGT2B7, UGT2B10, UGT2B11, UGT2B15, UGT2B17 and UGT2B28 with broad overlapping substrate specificities (Girard et al. 2003, Riedy et al. 2000). All of the UGT2B isoforms are involved in the glucuronidation of steroids with exception to UGT2B10 and UGT2B11 (Turgeon et al. 2001). The UGTB4 catalyzes the conjugation of 3 α -diol, estriol and hydroxyestrone (Lévesque et al. 1999). Whereas, UGT2B7 is involved in conjugation of different classes of steroids which includes the 5 α -reduced metabolites of cortisol, progestins and androgens (Girard et al. 2003). UGT2B7, UGT2B15 and UGT2B17 enzymes catalyzes glucuronidation of major circulating C19 steroid metabolites at 17 β -hydroxy position (e.g. DHT, testosterone and 3 α -

diol). The UGT2B7 and UGT2B17 enzymes (but not UGT2B15) also catalyzes the C19 steroid metabolites at 3 α hydroxy position (e.g. androsterone) (Beaulieu et al. 1996, Chen et al. 1993, Turgeon et al. 2001). The UGT2B28 type 1 catalyzes the conjugation of 3 α -diol, estradiol, androstane and testosterone (Lévesque et al. 2001). Androsterone glucuronide circulates 20 times higher compared to 3 α -diol glucuronide concentration in the circulation and both the glucuronide forms are indicators of androgen metabolism in peripheral tissues (Bélanger et al. 1986, Horton and Lobo 1986). Table 1.1 summarizes glucuronidation of various steroids by UGT conjugating enzymes.

Table 1.1 List of steroid substrates metabolized by UGT enzymes.

UGT isoform	Steroid substrate
1A1	Estradiol, estrone
1A3	2-hydroxyestrone, estrone
1A4	16 α -OHP
1A7	Estriol, 2-hydroxyestradiol
1A8	2-methoxyestradiol, 4-hydroxyestrone, 16,17-epiestriol
1A9	4-hydroxyestrone, 11 α -OHP
1A10	Estradiol, estrone, estriol, 2-hydroxyestradiol, 4-hydroxyestrone, androsterone
2B4	3 α -diol, estriol, hydroxyestrone
2B7	Cortisol, progestins, DHT, testosterone, androsterone, 3 α -diol, estradiol, estriol, 11 α -OHP
2B15	DHT, testosterone, 3 α -diol, 16 α -OHP
2B17	DHT, testosterone, androsterone, 3 α -diol, 16 α -OHP
2B28	Estradiol, androsterone, testosterone, 3 α -diol

Abbreviations: OHP: hydroxyprogesterone; 3 α -diol: 5 α androstan-3 α -17 β -diol; DHT: dihydrotestosterone

References are given in text.

Sulfation: Sulfate conjugation (also called sulphonation) is another important conjugation reaction that modulate the pharmacological activity of steroids. This reaction is catalysed by cytosolic sulphotransferases (SULTs) that attaches a sulfonate group (SO_3^-) from an enzyme cofactor, 3' phosphoadenosine-5'-phosphosulfate (PAPS) to an acceptor group (O-, N- or S-) (Figure 1.7) (Mulder et al. 1990). The formation of PAPS involves two reactions: first the conjugation of the cytosolic inorganic sulphate with adenosine monophosphate catalyzed by ATP sulfurylase to form adenosine 5'-phosphosulfate (APS) followed by the phosphorylation of APS by the APS kinase to form PAPS (Zamek-Gliszczyński et al. 2006). The sulfation and glucuronidation reaction have overlapping substrates, with the sulfation reaction occurring at low substrate concentration due to its high affinity, whereas at high substrate concentration, the activation of the glucuronidation reaction occurs as the SULT enzymes saturates or its cofactor PAPS are exhausted (Pang et al. 1994, Zamek-Gliszczyński et al. 2006). The SULT enzymes display unique tissue distribution with varying degree of activity. SULT enzymes for steroid metabolism are located in the cytosol, mainly in cells of the liver and gastrointestinal tract, although they are also found in the brain, kidney, lung, prostate and placenta (Coughtrie 2002). Four families of SULTs namely, SULT1, SULT2, SULT4 and SULT6 have been identified in human with at least 13 distinct members (Gamage et al. 2006, Li et al. 2008). The SULT1 members (or known as phenol SULT), are involved in sulfation of various estrogens such as estrone and 17β -estradiol (SULT1A1 and SULT1E1) (Falany 1997, Falany et al. 1994, Pasqualini 2009). Whereas SULT2 members (or known as hydroxysteroid SULT) are divided into SULT2A1, SULT2B1a and SULT2B1b. SULT2A1 also referred as DHEA sulfotransferase catalyses a broad range of steroids including the 3α , 3β , and 17β -hydroxyl groups as well as 3-phenolic hydroxyl estrogens (Falany 1997, Falany et al. 1994). SULT2B1a and SULT2B1b sulfonates pregnenolone, DHT and DHEA. However, SULT2B1b has higher cholesterol sulfation activity compared to

pregnenolone (Meloche and Falany 2001, Strauss 2014). Table 1.2 listed the sulfate isoforms involved in steroid metabolism.

Table 1.2 List of steroid substrates metabolized by sulfate isoforms.

SULT isoform	Steroid substrate
1A1	Estradiol, estrone, 2-hydroxyestradiol, 4-hydroxyestradiol, 4-hydroxyestrone
1E1	Estradiol, estrone, DHEA, pregnenolone and androstenediol
2A1	DHEA, testosterone, androsterone, epiandrosterone, androstenediol, pregnenolone, etiocholanolone, estrone and estradiol
2B1a	Pregnenolone, DHT, epiandrosterone, DHEA, androstenediol
2B1b	Pregnenolone, DHT and DHEA

Abbreviations: DHT: dihydrotestosterone; DHEA: dehydroepiandrosterone
References are given in text.

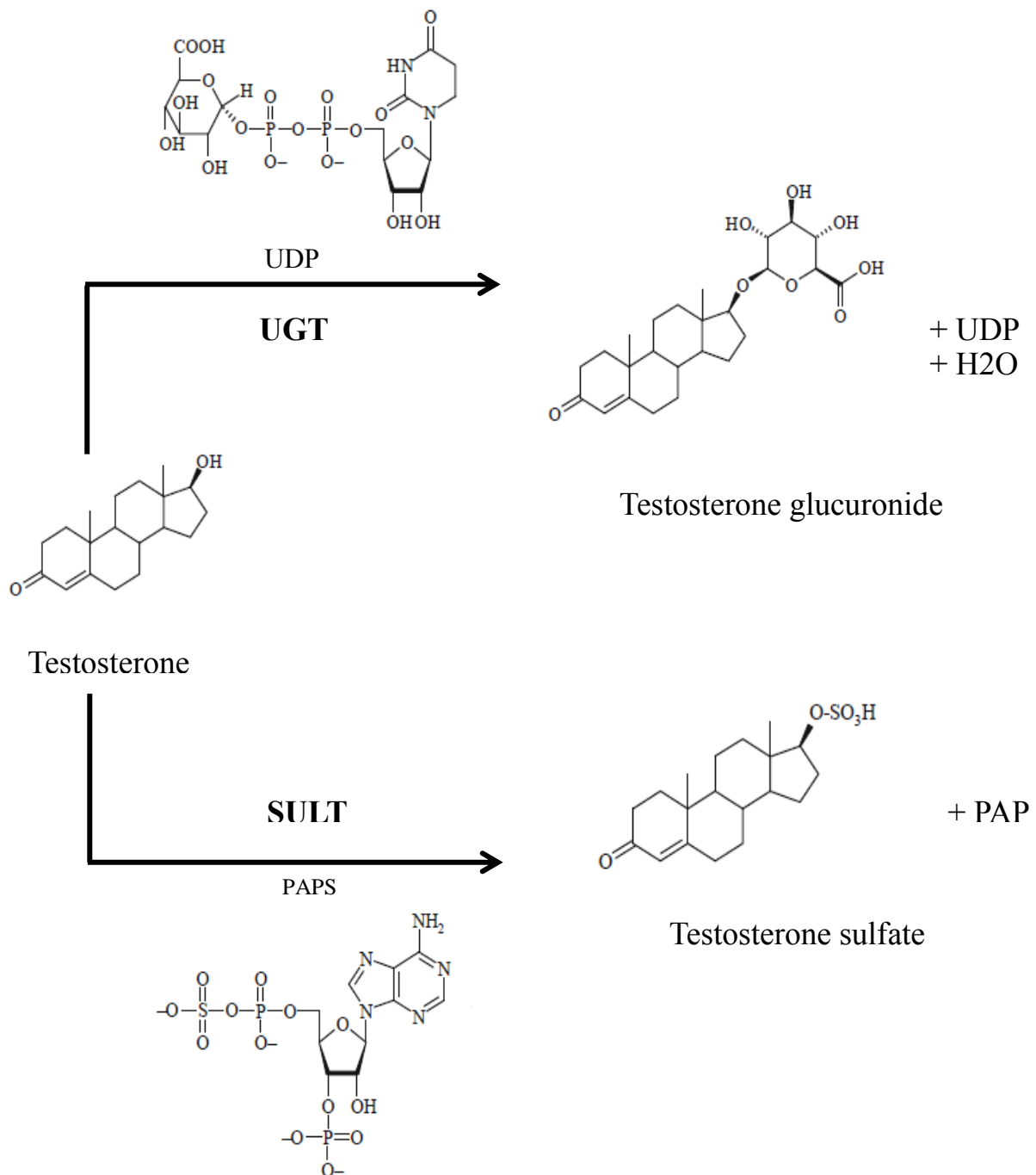


Figure 1.7 Phase II metabolism of testosterone.

Glucuronidation and sulfation reactions catalyzed by UDP-glucuronosyltransferases (UGTs) and sulphotransferases (SULTs).

1.3 Gonadotropin structure and regulation

The pituitary luteinizing hormone (LH), follicle-stimulating hormone (FSH) and placental human chorionic hormone (hCG) are gonadotropins that, together with thyroid stimulating hormone (TSH), comprise the glycoprotein hormone family (Pierce and Parsons 1981). The glycoprotein hormones are large proteins with a molecular mass of 30 – 40 kDa. They are heterodimers featuring a common α -subunit with a specific β -subunit that confers biological specificity by binding to their specific G protein-coupled receptors. Although the subunits (mainly α) exist in “free” form in the pituitary or circulation, they are biologically inactive. Thus, both subunits must be combined as α/β heterodimers and form a strong and specific noncovalent interaction complex that enables hormonal activation (Pierce and Parsons 1981). The α -subunit contains 92 amino acid residues whereas the LH β , FSH β and hCG β have 121, 110 and 145 amino acids residues respectively (Stenman et al. 1997, Themmen and Huhtaniemi 2000). Each glycoprotein has specific oligosaccharide structure bound on the β -subunit that determines its physiological specificity and differentiates the members of the glycoprotein hormones (Robinson et al. 2007, Ulloa-Aguirre et al. 2001). However, more than 85% of the first 114 amino acids sequence of LH and hCG β -subunit are significantly similar which is potentially responsible for the similar biologic activity of their respective dimers (Garcia-Campayo et al. 1997). Figure 1.8 illustrates the specific location of the oligosaccharide glycosylation of the four glycoprotein hormones. The α -subunit consists of two N-linked oligosaccharides, positioned at asparagine (Asn)-52 and Asn-78. Study on the mutagenesis of hCG α oligosaccharides revealed that they have distinct functions; the Asn-52 is involved in the formation of intact glycoprotein dimer whereas the Asn-78 is important for the protein stability (Fares 2006, Matzuk and Boime 1988). Studies have also reported disruption in the glycoprotein secretion with the absence of the β -subunit N-linked oligosaccharides (Lash et al. 1992, Matzuk and Boime 1988). The carbohydrate portion is

also involved in the folding, assembly and clearance of the gonadotropin (Thotakura and Blithe 1995).

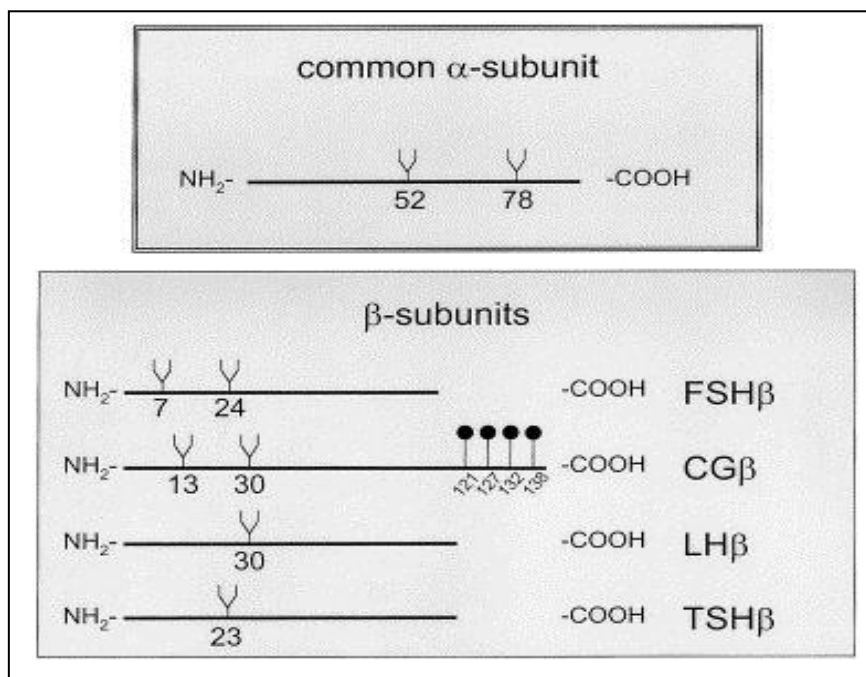


Figure 1.8 Location of glycosylation sites in the human glycoprotein hormone α and β -subunits.

The horizontal bar and the branched-like structures represent the amino acids and the N-linked oligosaccharides, respectively. The subunits contains one (LH β and TSH β) or two (the common α -subunit, FSH β and hCG β) N-glycosidically linked oligosaccharides attached to the amino acids residues (locations of the oligosaccharides attachment to the amino acids are indicated with the numbers). Additionally, the hCG β -subunit consists of four O-glycosidically linked oligosaccharides in the carboxyl terminal extension (adapted from (Ulloa-Aguirre et al. 2001).

The hCG is distinct from the other glycoprotein due to the O-linked glycosylation to a carboxyl terminal peptide (CTP) extension of the hCG β subunit (Figure 1.8) which prolong the half-life and enhance the *in vivo* bioactivity of the hormone (Fares 2006, Kalyan and Bahl 1983, Matzuk et al. 1990). Studies have shown insertion of CTP domain of the hCG β subunit into other glycoproteins β -subunit (e.g. FSH and TSH) resulting in increase of the CTP-

modified hormones' half-life which proved to be beneficial for therapeutic purposes (Bouloux et al. 2001, Fares et al. 1992, Joshi et al. 1995). For *in vitro* fertilization, CTP-modified FSH is used to induce the development of ovarian follicle maturation with only a single dose due to its long half-life in contrast to multiple doses using recombinant human FSH analog (Balen et al. 2004).

The oligosaccharide contains side chains that terminate with sialic acid, galactose, fucose as well as sulfated N-acetylgalactosamine (only in LH). These complex carbohydrate side chains influences the glycoprotein hormones' bioactivity and clearance rates by the liver and kidney (Ulloa-Aguirre et al. 2001). The glycoprotein hormones with highly sialylated or more acidic oligosaccharides (e.g. FSH and hCG) have longer plasma half-life but reduced in potency and lower receptor binding activity *in vitro* compared to the galactose and sulfated or more basic oligosaccharides (e.g. LH) which are cleared rapidly from the plasma by specific hepatic receptors (Fiete and Baenziger 1997, Fiete et al. 1991, Ulloa-Aguirre and Timossi 2000). The glycosylation patterns of the glycoprotein hormones are variable depending on various physiological changes that occur according to age and sex (Ulloa-Aguirre et al. 2001). Studies have shown that the secretion of gonadotropin glycosylated variants with low sialic acid or sulfate content during the preovulatory phase of the menstrual cycle compared to the early, mid-follicular and luteal phases which are believed to be influenced by high estrogen secretion (Birken et al. 2007, Padmanabhan et al. 1988, Wide and Bakos 1993). In males and postmenopausal women, the gonadotropins circulate in more acidic/sialylated isoforms (Veldhuis et al. 1989, Wide 1985, Wide 1989). Other examples include the release of the less sialyted FSH isoforms which are more biologically active during the mid-puberty in boys compared to other stages of puberty (Campo et al. 2007). Due to the heterogeneity of the gonadotropin carbohydrate side-chains (microheterogeneity), many assays fail to either detect or differentiate between these isoforms. For example, throughout pregnancy the hCG

isoforms changes and a common hCG immunoassay employing monoclonal antibodies was unable to detect certain hCG isoforms produced during the early stages of pregnancy (Birken et al. 2001, Kovalevskaya et al. 1999).

The cross-linked disulfide bond existing between the subunits stabilizes the glycoprotein structure and is responsible in maintaining the three-dimensional structure to the subunits which is important in maintaining the biological activity of the dimeric structure (Ulloa-Aguirre and Timossi 2000). Figure 1.9 illustrates the known crystal structures of hCG and human FSH.

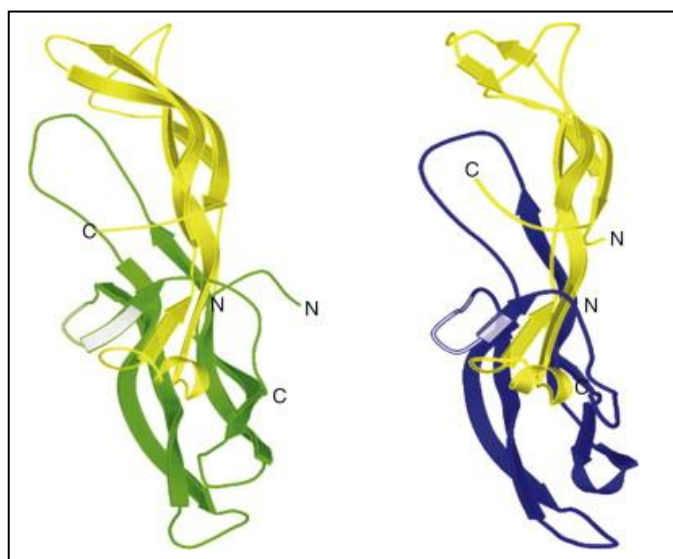


Figure 1.9 Crystal structure of human chorionic gonadotropin (hCG; left) and human follicle-stimulating hormone (hFSH; right).

The α -subunit (yellow) and the β -subunit (hCG in green; hFSH in blue) have similar folding forming highly elongated molecules. Both the subunits intertwined with a 20 amino acid residue region of the β -subunit known as seatbelt (white region) wraps around and latched a portion of the α -subunit. The two gonadotropins exhibit differences in the conformation at the C-terminal portions of the seatbelt. As for the LH and TSH, no structures are yet available. However, it is believed that the conformation of LH and TSH are closely related to the known structures. Adapted from (Ascoli and Narayan 2014)

The gonadotropin-releasing hormone (GnRH) (previously known as luteinizing releasing hormone), regulates the release of LH and FSH. GnRH is a decapeptide hormone synthesized by the cell body of the hypothalamic neurons that projects axon to the median

eminence of the brain. Regardless of the developmental stage, the secretion of GnRH from their terminals into the pituitary-portal blood supply is in a pulsatile or episodic manner. This pattern of release is absolutely critical as continuous release of GnRH causes desensitization of the GnRH receptors which further suppresses the release of LH and FSH by the gonadotrope cells (Belchetz et al. 1978). Additionally the ratios of the LH and FSH released are also influenced by the GnRH pulse frequency. High GnRH frequencies leads to higher LH secretion but lower FSH secretion, thus the LH/FSH ratio is high. However, the ratio decreases with the lowering of GnRH frequencies, due to increase in FSH and lower LH secretion (Wildt et al. 1981). Thus the GnRH pulse frequency and amplitude plays a pivotal role in the regulation of episodic release of LH and FSH into the general circulatory system. These gonadotropins binds to the glycoprotein hormone receptors to regulate hormonal and reproductive function of the gonads. The gonadotropin receptors are characterized by the large N-terminal extracellular domain that determines the recognition and binding affinity of their appropriate hormones (Braun et al. 1991). Both LH and hCG mediates their bioactivity through a single LH/CG receptor which is expressed in Leydig, theca, granulosa and luteal cells whereas FSH binds to its specific follicle stimulating hormone receptors expressed in the granulosa and Sertoli cells (Caltabiano et al. 2008, Pierce and Parsons 1981).

In males, the placental hCG plays an important role to stimulate fetal steroidogenesis and Leydig cell growth and differentiation after the initial gonadotropin-independent phase (Huhtaniemi et al. 1977). hCG also circulates at very low concentrations in men (produced by testes) and nonpregnant women which increases around menopause (produced by the ovaries) (Handelsman 2006, Stenman et al. 1997). Meanwhile, the circulating concentration of LH stimulates the activity of steroidogenic enzymes including CYP11A and CYP17 α -hydroxylase in the testicular Leydig cells for the production of testosterone (Wu et al. 2007). LH is also responsible in maintaining high intratesticular testosterone levels required for

spermatogenesis. Testosterone binds to the androgen receptors (ARs) expressed in the somatic cell in the testes (Sertoli, Leydig and peritubular) but not germ cells to initiate spermatogenesis (Verhoeven et al. 2010). The FSH is also involved in the initiation and maintenance of spermatogenesis but is not essential to spermatogenesis (Singh et al. 1995). Studies on transgenic FSH mice revealed that both the FSH and testosterone binds to their specific receptors expressed in Sertoli cells in order to initiate and maintain spermatogenesis (Allan and Handelsman 2005).

In females, LH regulates ovarian steroid synthesis. LH stimulates the thecal cells and the luteinized granulosa cells of the corpus luteum to produce androgen and precursors as well as progesterone, respectively. The androgen precursors then move to the neighboring granulosa cells where they are aromatized into corresponding estrogens under the control of FSH (Themmen and Huhtaniemi 2000). LH is also involved in regulating cholesterol availability for steroidogenesis and stimulates the activity of CYP11A to catalyze formation of pregnenolone from cholesterol. LH stimulates the gene expression and production of enzymes involved in steroidogenesis (Kaiser 2011). Mid-cycle peak of LH terminates preovulatory follicle growth and triggers ovulation and stimulates the corpus luteum to synthesize progesterone in the second half of the ovulatory cycle (Themmen and Huhtaniemi 2000). In the ovary, granulosa cells express FSH receptors and are the only target cells of the FSH action. FSH is required for granulosa cell differentiation, modulates LH receptor expression in granulosa cells and regulates the estrogen production (Richards and Pangas 2010). FSH is also important for follicular recruitment, selection and growth (Zelevnik and Pohl 2006).

Taken together, the regulation of gonadotropins secretion is under positive control of the hypothalamic GnRH. The gonadotropins in turn regulate the gonadal secretion of androgen, estrogen and progesterone that exert their effects by binding to their specific

receptors. These are expressed in both reproductive and nonreproductive target tissues including the reproductive tract and genitalia, breast, fat, bone, muscle, liver and kidney. The sex steroid hormone receptors are also expressed in the central nervous system and pituitary gland to enable steroid feedback regulatory mechanisms by the hypothalamic-pituitary-gonadal (HPG) axis. The gonadal steroids and peptide (inhibin) exert negative and stimulatory (positive) effects on the gonadotropin regulation and release, either directly at the level of pituitary gonadotrophs by the modulating the genes encoding LH β and FSH β or indirectly at the hypothalamus level to modulate patterned GnRH secretion.

1.4 Steroid hormone production and action

1.4.1 Androgens

Androgens are produced by the gonads and androgen precursors by the adrenal glands in response to LH and adrenocorticotropin (ACTH), respectively, in both sexes. Testosterone and DHT are the two major and most potent androgens, both of which have a 17 β -hydroxyl group and 3-oxo group (Figure 1.10). DHEA, dehydroepiandrosterone sulphate (DHEAS) and androstenedione are steroids with minimal androgenic activities but are pro-androgens (Mo et al. 2006). Testosterone is the most abundant androgen in mammalian males whereas the other weaker androgen precursors circulate at the same concentration in male and female. Testosterone is primarily produced by the testicular Leydig cells in men (approximately 95%), the thecal and stroma cells of the ovaries in women (25% through direct secretion and 25% through peripheral conversion of androgen precursors) and at a lesser amount in the adrenal zona reticularis and peripheral tissues (liver, skin and adipose) from conversion of androstenedione (Kicman 2008, Palacios 2007). Daily production of testosterone in eugonadal men is approximately 3-7 mg per day whereas only 0.1-0.3 mg is produced in women (Burger 2002, Kicman 2010). Approximately half of the circulating testosterone in women is produced peripherally by androstenedione conversion (Bardin and Lipsett 1967).

As described previously, circulating testosterone also acts as a pro-hormone at the target tissues when converted into DHT by 5 α -reductase and into estradiol by aromatase (Figure 1.5) (Kicman 2008). Approximately 50% of the DHT production in men originates from this peripheral conversion and the remaining is secreted by the testes (Hammond et al. 1977, Saez et al. 1972). Although testosterone circulates at 10-fold higher concentration than DHT, the potency of DHT is approximately 3-10 fold greater than testosterone (Barbier and Bélanger 2008, Wright et al. 1996). Testosterone and DHT binds to the same AR under physiological conditions. However, DHT binds with a higher affinity than testosterone resulting in activation of target genes even at lower concentrations compared to testosterone (Kicman 2008, Wright et al. 1996). Despite binding to the same AR, testosterone and DHT have different physiological roles in males. During sexual differentiation, testosterone stimulates the urogenital sinus and Wolfian duct development that leads to formation of internal male genitalia (epididymis, seminal vesicle and vas deferens) (Themmen and Huhtaniemi 2000). Postnatally, testosterone maintains spermatogenesis, maturation of sexual characteristics, and plays a role in masculinization and libido. During embryogenesis, DHT is responsible for development of urogenital sinus (the male external genitalia, urethra and prostate) (Marchetti and Barth 2013). During puberty, DHT is involved in the development of phallus and prostate, and the appearance of virilizing features such as body and facial hair. In adults, DHT is also associated with modulation of prostatic function, and is believed together with other androgens to be involved in the homeostasis between cell proliferation and cell apoptosis (Carson III and Rittmaster 2003, Isaacs 1984).

Androstenedione and DHEA are major androgen precursors. The adrenal glands and gonads produces large amount of androstenedione. DHEA and its sulfated analog (DHEAS) are primarily produced by the adrenal cortex and lesser amount by the gonadal tissues (Labrie et al. 1995). DHEA and DHEAS are also known as neurosteroids, whereby

the production of these steroids occurs locally by the neurons and glia of the brain (Lazaridis et al. 2011). These steroids are postulated to regulate brain function. For example, the DHEA acts on γ -aminobutyric acid type A (GABA) receptors as an agonist whereas DHEAS acts on the same receptor as an antagonist (Park-Chung et al. 1999). DHEAS circulates in the bloodstream at a higher concentration (250-500 times) compared to its unconjugated form and is the most abundant androgen in human circulating 20 times higher than other steroid hormone (Ebeling and Koivisto 1994, Kroboth et al. 1999, Labrie et al. 1997). The enzyme steroid sulfatase acts on DHEAS to produce DHEA and further converted into other androgenic and estrogenic compounds in reproductive (endometrium, ovary, prostate, testis) and non-reproductive tissues (bone, breast, skin and brain) (Reed et al. 2005). During gestation, the sulfatase enzyme is highly expressed in the placental syncytiotrophoblast regulating the production of estrogen in the placenta from the sulfated DHEA produced by the fetal adrenal (Salido et al. 1990).

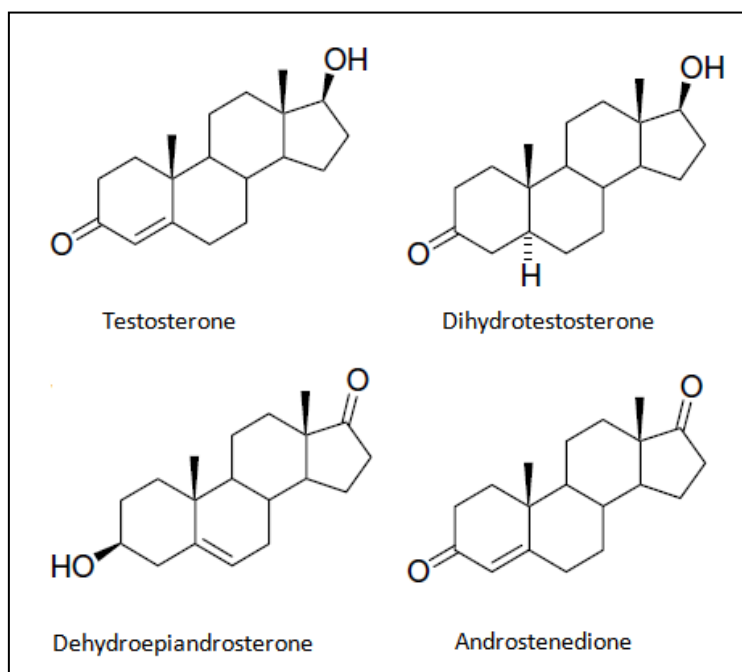


Figure 1.10 Chemical structure of four main androgenic steroids: testosterone, dihydrotestosterone, dehydroepiandrosterone and androstenedione.

1.4.2 Estrogens

The only naturally occurring estrogen is estradiol (or 17β estradiol) with one pro-estrogen (estrone) and phase I metabolite estriol (Figure 1.11). Typically estradiol and estrone circulate at higher concentration compared to estriol (Wiren 2007). Aromatase is expressed primarily in the ovarian granulosa cells (premenopausal women) and placental syncytiotrophoblast (pregnant women) to catalyze the synthesis of estrogen from androgens. Testosterone is aromatized into the potent estrogen, estradiol whereas the adrenal precursor androstenedione and DHEA are converted into the weaker pro-estrogen, estrone (Nawata et al. 1995). The aromatase enzyme is also expressed in the peripheral tissues (adipose and skin) which are the primary site for estrogen formation from C19 steroids precursor in both men and postmenopausal women (Simpson and Davis 2001, Simpson et al. 1994). The aromatase enzyme is also expressed in the muscle, brain, testicular Sertoli and Leydig cells and the osteoblast (Frieden et al. 1968, Longcope et al. 1978, Roselli et al. 1987, Saez et al. 1972, Sasano et al. 1997). Approximately 80% of the daily estradiol production in eugonadal men is produced peripherally from testosterone and the remainder is secreted directly by the testes (Baird et al. 1965). Estradiol has high affinity for estrogen receptors (ER) compared to the other pro-estrogens, hence known as the only potent bioactive estrogen (Jones 1992). In premenopausal women, the circulating level of estradiol is between 68 and 107 pg/mL across the menstrual cycle with higher levels during ovulation and is reduced in postmenopausal women to less than 5 pg/mL (Rothman et al. 2011). Although the levels of estradiol decrease dramatically in postmenopausal women, its metabolite estrone produced from the conversion of androstenedione in the adipose tissue remains unchanged (Ruggiero and Likis 2002). In men, the mean concentration of estradiol is about 20-30 pg/mL and its daily blood production rate is approximately 30-40 μ g (Vermeulen et al. 2002).

Although throughout adulthood, men have plasma estradiol levels equivalent to postmenopausal women, estrogen action plays a pivotal role in the regulation of LH feedback. Recent studies have shown that testosterone and estradiol act independently on the LH regulation presumably via AR and ER α (Pitteloud et al. 2008). Studies have reported that estrogens act in the regulation of LH through the aromatization of testosterone at the pituitary level but testosterone does not require aromatization at the hypothalamic level to regulate LH secretion (Hayes et al. 2000, Pitteloud et al. 2008, Rochira et al. 2005). The role of estradiol on negative feedback regulation was demonstrated through studies conducted in normal or GnRH-deficient men where administration of aromatase inhibitor resulted in elevated of LH (Finkelstein et al. 1991, Marynick et al. 1979). In female, during the menstrual cycle, the concentration of estradiol regulates the negative or positive feedback action on gonadotropins. The serum estradiol levels gradually increase with the progression of follicular phase which resulted in inhibition of the gonadotropins secretion via the negative feedback. As the serum estradiol begins to rise rapidly during the late follicular phase, the positive feedback action leads to a preovulatory surge of LH and FSH. Thus estrogens play an important role in the gonadotropin regulation for ovulation (Ulloa-Aguirre and Timossi 2000). Estrogens are also involved in the bone maturation, mineralization, prevention of osteoporosis and maintenance of cardiovascular health in both men and women (De Ronde et al. 2003, Grumbach and Auchus 1999). During puberty, estrogens are responsible in the development of secondary sex characteristics in females which includes breast development by stimulating alveolar growth, subcutaneous adipose tissue distribution, typical female body proportion and estrogen dependent changes of the genital tract (external genitalia, uterus, vagina, fallopian tubes and ovaries) (Dösch et al. 2001).

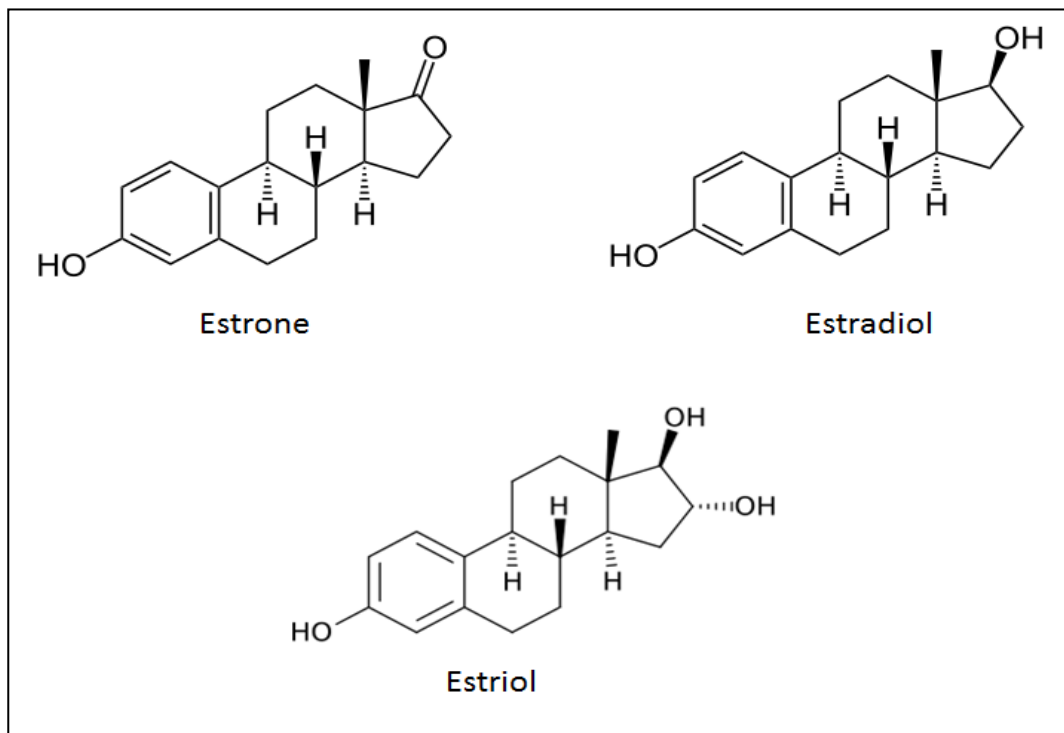


Figure 1.11 Structures of estrone, estradiol and estriol.

Estradiol is the most potent estradiol in non-pregnant women predominately produced by the granulosa cells from androgens. Estrone is produced via conversion of androstenedione in the adipose tissue. Estriol, a phase 1 metabolite of estradiol is produced peripherally and by the placenta during pregnancy.

1.5 Puberty

1.5.1 *Hormonal changes in puberty*

Puberty is a biological event that results in physical and reproductive maturity. This process is coordinated by a complex cascade of neuroendocrine changes which initiates secondary sexual characteristics, maturation of the genitalia, increase in growth velocity and ends with the acquisition of reproductive capability and attainment of adult body habitus and height (Plant and Barker-Gibb 2004, Styne and Grumbach 2011). The pubertal transition involves two independent but temporarily overlapping physiological processes namely, adrenarche and gonadarche.

Adrenarche refers to substantial increase of adrenal androgens, firstly DHEAS followed by DHEA and androstenedione, in response to ACTH (Styne and Grumbach 2011). The stimulus for this adrenal androgen steroidogenesis is unclear. The event of adrenarche only occurs in human and higher primates (chimpanzee, gorilla). Thus studies on its development in lower animals model are regarded as uninformative (Dorn and Biro 2011). The maturation of the adrenal cortex occurs from the age of about 6 to 7 years onwards in girls and 7 to 8 years onwards in boys (Ducharme et al. 1976, Korth-Schutz et al. 1976). The increase of adrenal androgens production occurs between 1 to 2 years before the changes of other pubertal hormones (Rogol et al. 2002) with higher levels reported in girls than in boys (Apter et al. 1979, Courant et al. 2010). The rise of adrenal androgens continues during gonadarche, with higher DHEAS levels in males compared to females after the age of 15 (de Peretti and Forest 1978). Adrenal androgen continues to increase on until the third decade of life and thereafter DHEAS levels gradually decline in both sexes (Ibáñez et al. 2000). Adrenarche is associated with the appearance of sexual hair (pubarche), axillary hair, adult apocrine odor and appearance of acne in some individuals (Rogol et al. 2002).

Gonadarche refer to the reactivation of the HPG axis at the end of the prepubertal phase resulting in dramatic surge in gonadal steroid production and initiation of folliculogenesis and ovulation in female and spermatogenesis in male (Witchel and Plant 2014). Gonadarche also leads to the final maturation of primary sex organs (ovaries and testis) and external signs of puberty. The stages of sexual development have been well defined by Tanner and Marshall as a predictable and ordered sequence of event (Marshall and Tanner 1969, Marshall and Tanner 1970). This clinical assessment of pubertal maturation known as Tanner staging remains the primary system used as the descriptive standards for assessing pubertal development. Other measures of puberty status includes Petersen Pubertal Development Scale (PDS) which is a self-report that focuses on physical changes in growth and development (Petersen et al. 1988). Morris and Udry (Morris and Udry 1980) also introduced self-report method along with line drawings of external physical changes. Other groups combined method of physical examinations for pubertal staging and pubertal hormone concentrations to define pubertal status. Tanner stages are divided into five anatomically defined stages which include pubic hair growth, development of breast in females and the development of phallus in male (Carel and Leger 2008). Figure 1.12 illustrates the Tanner stages of both girls and boys. Overall, girls usually enter and complete each stages of puberty before boys. The timing (onset) and tempo (rate) is affected by many factors including genetic factors although it even varies among individual from the same ethnicity and gender (Clark and Rogol 1996, Euling et al. 2008).

In girls, the appearance of breast buds (thelarche) underneath the areola is the initial sign of gonadarche (Tanner stage 2) which occurs between the age of 8 and 13 years indicating increased ovarian estrogen production (Jenner et al. 1972). As puberty progresses, the areola size, erectility and colour changes. Estrogen action is also demonstrated by the production of vaginal secretion and the enlargement of labia minora and majora. The adrenal

and ovarian androgen secretion leads to the development of pubic hair. Approximately 2.5 years after the appearance of breast buds, the first menstrual cycle (menarche) takes place (Marshall and Tanner 1969). The duration of pubertal development in girls and boys normally takes between 3-3.5 years to complete or in some cases occur earlier (within 2 years) or later (5 years) (Dorn et al. 2006).

In boys, the first sign of gonadarche is associated with the enlargement of the testes and a thinning and reddening of scrotum which occurs between the age of 9 and 13 years (Rogol 2002). The volume of testes increases from 1-2 mL (prepubertal) to 4 mL at the onset of puberty (Tanner stage 2) coincides with the increase of testicular androgen production (August et al. 1972). The testicular volume dramatically increases to about 10-fold by the end of pubertal development with the initiation of spermatogenesis and proliferation and differentiation of the Sertoli cells (Marshall 1975). Adrenal and testicular androgen secretion reflects the manifestation of pubic and axillary hair and development of acne (Greiner and Kerrigan 2006). As stated above, the two main hormones that mediate the biological manifestations of puberty are estradiol and testosterone, in girls and boys, respectively. However, most studies in the past have utilized assay methodologies that are considered inaccurate to measure low levels of these hormones in early and mid-puberty (Ankarberg-Lindgren and Norjavaara 2008, Moal et al. 2007, Taieb et al. 2003).

Adrenarche and gonadarche are two separate maturational events (Sklar et al. 1980). This is evident as the increase in adrenal androgens occurs when HPG axis is still inactive before the initiation of gonadarche. However, absence of adrenarche does not prevent gonadarche and vice versa. Girls with Turner's syndrome, despite the absence of functioning ovaries, have normal adrenarche (Saenger 1996) but does not result in reproductive maturation. This was also noted in patients with hypogonadotropic hypogonadism (Counts et

al. 1987). Additionally normal onset of gonadarche was noted in boys with primary adrenal insufficiency condition (Urban et al. 1980).

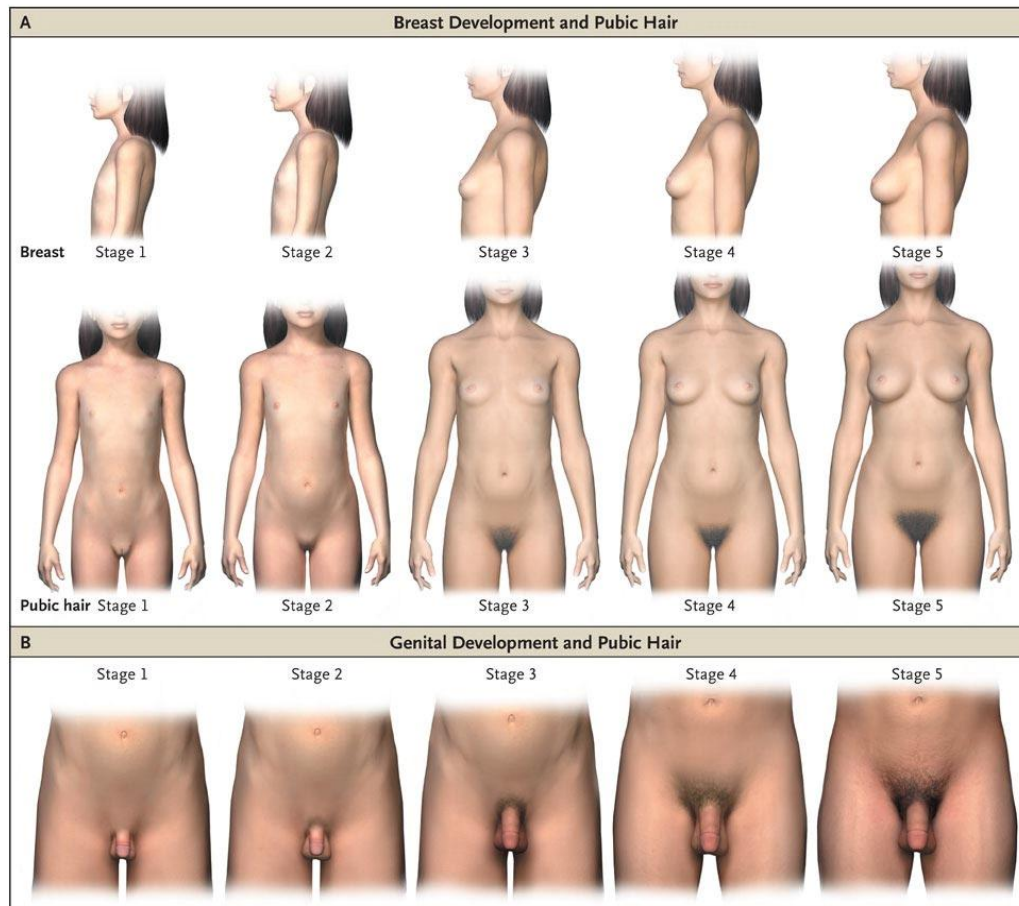


Figure 1.12 Pubertal rating according to Tanner stages.

Panel A demonstrates the development of breast and pubic hair in girls rated from stage 1 (preadolescent) to 5 (mature). The development of breast buds (stage 2) marks the onset of gonadarche. Adrenarche begins at stage 2.

Panel B illustrates the genital development and pubic hair development in boys rating from stage 1 (preadolescent) to 5 (adult). Stage 2 genital development marks the onset of gonadarche, which is characterized by enlargement of the testis and scrotum accompanied by changes in scrotal skin texture and color (reddening). The onset of pubic hair growth begins in stage 2.

Here the pubic hair and genital/breast development is illustrated simultaneously; however it should be scored separately as they do not necessarily take place at the same time. Adapted from (Carel and Leger 2008).

1.5.2 *Activation of hypothalamus-pituitary-gonadal axis during development*

In humans, the activation of the HPG axis first occurs *in utero*. The diffusely distributed network of hypothalamic neurons expressing gonadotropin releasing hormone-I (GnRH-I) gene known as GnRH pulse generator activates the release of fetal pituitary LH and FSH. The fetal pituitary contains detectable levels of gonadotropins at the 10th week of gestation and the gonadotropins are detectable in fetal circulation by 12-14th week of gestation in response to the decreasing placental estrogen (Seminara et al. 1998, Styne and Grumbach 2011, Witchel and Plant 2014). The fetal testes expresses LH/hCG receptors that activates the Leydig cell to synthesize testosterone important for male gonadal maturation *in utero* (Biro and Dorn 2005) whereas at this stage the ovary development of female fetuses remains quiescent (Witchel and Plant 2014). The fetal ovary apparently does not express gonadotropin receptors and appears to be independent of gonadotropins and gonadal function (Huhtaniemi et al. 1987, Themmen and Huhtaniemi 2000). The circulating gonadotropins concentrations are much higher in female compared to male fetus. It is postulated that the male fetus have early development of negative feedback by testosterone (Grumbach and Gluckman 1994). At the end of pregnancy, the fetal LH and FSH levels decline progressively and the GnRH pulses are inhibited with the increase of maternal and fetal estrogen levels and the development of negative feedback mechanism (Grumbach 2004, Nagata et al. 2006).

In male neonates, within a couple of minutes after birth, LH secretion surges approximately 10 times greater than the cord blood concentration resulting in secretion of testosterone which lasts for about 12 hours (Corbier et al. 1990, De Zegher et al. 1992). However, this LH surge is absent in female neonates (Grumbach 2005). After the first few days of birth, as the placental sex steroids inhibition is removed, the HPG axis activity commences. The circulating levels of LH and FSH rise intermittently to adult values or even occasionally higher at 2-3 months age and then declines to prepubertal levels between 6 to 9

months of age in boys and 2 to 3 years of age in girls (Andersson et al. 1998, Kuiri-Hänninen et al. 2011, Wright et al. 1996). This period is known as the neonatal surge or minipuberty. After this period of postnatal gonadotropin surge, the GnRH pulse generator becomes quiescent until its reactivation before onset of puberty. However, studies utilizing sensitive assays have shown that gonadotropins are released at low levels in pulsatile pattern primarily at night in prepubertal children with greater amplitude of FSH than LH pulses (Albertsson-Wikland et al. 1997, Apter et al. 1989, Wu et al. 1991). Low levels of gonadal steroids circulate during this childhood period (Rogol 2010).

Puberty represents the final step in the maturational process of the HPG axis. The onset of puberty is referred as (re)activation of the previously quiescent neuroendocrine reproductive axis which is reflected by increase in GnRH secretion (Ojeda and Skinner 2006, Plant and Skinner 2006). During this period, the reactivation of GnRH secretion transforms from low-level irregular pattern to a regular and pulsatile pattern which is detectable even prior to the exhibition of pubertal external signs (Harris and Levine 2003, Watanabe and Terasawa 1989). Marked increase in the amplitude and frequency of GnRH secretion enhanced the release of gonadotropin. At early progression of puberty, the pulses occur predominantly at night resulting in augmented LH secretion which in turn stimulates early morning release of gonadal steroids. Once again the gonadal steroid is able to inhibit GnRH secretion that cause decline in the gonadotropin and gonadal steroid levels throughout the day. As puberty progresses the gonadotropin pulses occurs both during the night and day as the negative feedback sensitivity of the hypothalamus decreases resulting in a more stable elevation of gonadal steroids hormones (Grumbach 2004, Grumbach 2005). At each pubertal stage, overnight LH values are approximately the same in both the genders but girls have higher FSH values (Manasco et al. 1997).

The specific neural and molecular mechanism that regulates the activation of the GnRH neuron during the initiation of puberty is not fully understood. However, previous studies have associated neurotransmitter and neuropeptide such as glutamate (Plant et al. 1989), γ -amino butyric acid (GABA) (Keen et al. 1999), neurokinin B (Topaloglu et al. 2008), leptin (Cheung et al. 2001), neuropeptide Y (El Majdoubi et al. 2000) and glial cell regulatory system (Grumbach 2004) with activation of GnRH neurons at puberty. In the last decade, neuropeptide kisspeptin has emerged as an important regulator of GnRH neurons in a number of mammalian species which led to the perception that kisspeptin signaling controls the timing of puberty (Terasawa et al. 2013). The involvement of kisspeptin in regulating reproductive axis was first reported by two independent groups in 2003. Their studies have shown that mutation or deletion of kisspeptin receptor, Gpr54 (G-protein receptor 54) recently renamed as Kiss1 receptor (Kiss1R) in humans and mice resulted in striking deficits in reproductive function, including failure to initiate puberty and infertility (de Roux et al. 2003, Seminara et al. 2003). In the following years, many studies have emerged unraveling the role of kisspeptin in regulation of puberty and fertility. Exogenous treatment of kisspeptin accelerates the age of puberty in prepubertal rats by early activation of gonadotropic axis (Matsui et al. 2004). Studies also demonstrated increase in LH and FSH levels in adult rodents and primates (including human) with administration of kisspeptin (Dhillon et al. 2005, Kinoshita et al. 2005). This suggests that the secretion of kisspeptin is necessary not only for puberty to occur, but required for the maintenance of reproductive function. The increase in kisspeptin expression in the hypothalamic region immediately before the onset of puberty further elucidates the role of this neuropeptide in the maturation of the reproductive axis (Navarro et al. 2004, Silveira et al. 2010). Kisspeptin plays a critical role in the control of reproductive axis at different stages of life including postnatal, pubertal development and

adulthood. Figure 1.13 illustrates a model demonstrating the role of kisspeptin signaling in controlling the timing of puberty in primates.

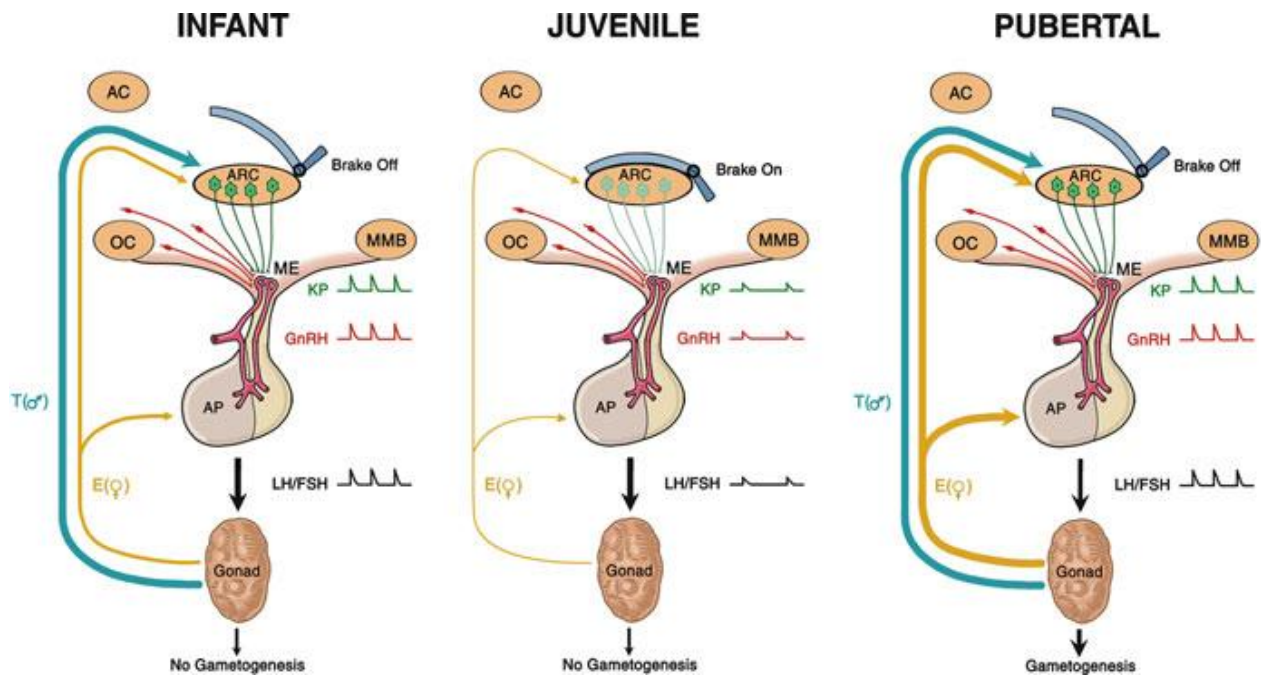


Figure 1.13 A proposed model for the control of the timing of puberty in primates.

During infancy (left panel), the robust activity of GnRH pulse generator leads to the intermittent release of kisspeptin in the ME, that causes corresponding pattern of GnRH release in the portal circulation. This further leads to the secretion of LH and FSH by the AP.

During the developmental progression from infancy to juvenile stage, a neurobiological brake results in inhibition of pulse generation by GnRH (reduce production of GnRH) and reduces the pulsatile release of kisspeptin into the ME (middle panel).

Puberty is initiated when this neurological brake is release which then triggers reactivation of GnRH pulse generator and release of kisspeptin in the ME (right panel). However, the nature of the neurobiological brake during infancy and its release at the end of juvenile developmental phase is not well understood.

The thickness of the arrows marked in blue (T, male) and gold (E₂, female) indicates the degree of negative feedback by the gonadal steroids produced by the gonads (testis and ovaries) on LH secretion at the different developmental stages. Adapted from (Hu et al. 2005, Terasawa et al. 2013)

Abbreviations: T: testosterone; E₂: estradiol; AC: anterior commissure; AP: anterior pituitary gland; ARC: arcuate nucleus; OC: optic chiasm; ME: median eminence; MMB: mamillary body.

More recent genetic studies of familial central precocious puberty have linked another possible gene known as makorin ring finger 3 (MKRN3) with initiation of puberty (Abreu et al. 2013, Settas et al. 2014). MKRN3 is a maternally imprinted gene that contains no introns and is located on chromosome 15q11.2 in Prader-Willi syndrome critical region. Mutations in MKRN3 gene has been associated with acceleration of puberty initiation leading to development of pubertal signs in both sexes which supports MKRN 3 role as a physiological inhibitor of hypothalamic activity during childhood (Abreu et al. 2013, Macedo et al. 2014, Schreiner et al. 2014). Studies have suggested that the MKRN 3 might function as a silencer of downstream genes that controls the activation of puberty such as kisspeptin (Hagen et al. 2015, Ojeda and Lomniczi 2014).

1.5.3 *Growth and skeletal maturation during puberty*

Puberty is accompanied by rapid sexually dimorphic changes in body composition, size and shape. Growth spurt is a major physical change that occurs during puberty which encompass 15-20% of the final adult height (Juul 2001). During childhood, growth is relatively stable primarily depending on the dietary intake, hormonal balance (growth and thyroid hormone), general health and adequate psychosocial environment (Rogol 2010). Generally, in the first year of life, a child grows 25 cm and 12 to 13 cm the following year. After this age, the child growth is stable about 5 to 6 cm until puberty (Rogol et al. 2002). The stable growth rate slows to a nadir (preadolescent dip) just before the onset of puberty and thereafter accelerates during mid-puberty. Although pubertal development in both genders takes about 4.5 years to complete, there is a marked difference in the timing of pubertal growth spurt between males and female. In girls, growth spurt occurs earlier compared to boys. However the growth spurt in girls does not reach the same magnitude of that in boys (Clark and Rogol 1996).

In girls, the growth spurt is commonly detected with the first sign of puberty (breast development and pubic hair) (Pinyerd and Zipf 2005). Peak height velocity occurs between

Tanner stage 2 and 3 (breast stage 2 [B2] and breast stage 3 [B3]) at about 11 to 12 years of age that averages about 9 cm annually with about 25 cm of total height gained (Marshall and Tanner 1969). However, peak height velocity varies between individual around this median pattern; 40% occurring at B2, 30% at B3, 20% at B4 and 10% at B1 (Coste et al. 2002). As the peak height velocity is about a year before menarche, the growth slows down to about 2.5 cm in height until completion of growth although it varies among individuals (Styne and Grumbach 2011). In males, peak growth velocity is observed at the Tanner genital stage 3 to 4 between the age of 13 and 14 years with an average of 10.3 cm per year, gaining about 28 cm of height during the pubertal growth period (Marshall and Tanner 1970). In boys, peak height velocity also varies between individuals with 60% occurring at genital stage 3 (G3), 28% at G4 and less than 8% at G2 and G5 (Coste et al. 2002). 95% of boys complete height velocity by Tanner genital stage 5 (Styne and Grumbach 2011). The pubertal growth rate decreases rapidly after the gender-specific peak in height velocity with increase of 1 cm per year or less in height after the age of 14.5 and 17 years in girls and boys, respectively (Veldhuis et al. 2005). In boys, the combination of higher peak velocity and for a longer duration of growth compared to girls results in an average height difference of 13 cm between men and women (Greiner and Kerrigan 2006). Peak height velocity is also greater in youths who mature earlier (Veldhuis et al. 2005).

Pubertal growth spurt is marked by the significant increase of growth hormone (GH), insulin-like growth factor 1 (IGF-1), estrogens and androgens. During childhood, the GH hormone secretion rates are stable and secretion pattern is similar in both genders with striking day-night rhythm (Martha et al. 1989). The secretion of GH is highest at early hours of sleep followed by small episodic bursts throughout the night/day (Finkelstein et al. 1972). The GH pulses are also released during the day, however at low levels (Miller et al. 1982).

During puberty, the activation of GH/IGF-1 axis and gonadal sex steroids not only demonstrates independent effects on growth, but the synergistic effect between them alters linear growth and body composition. Normal growth is attained with the presence of both GH and gonadal sex steroids. The growth spurt is impaired in conditions when either hormone is absent (Rogol et al. 2002). The increase in GH/IGF-1 axis during puberty is influenced by sex steroids. Elevated concentration of sex steroids especially estrogens stimulate 24-hours GH levels in a maximal pulse amplitude and increase in mass of GH released per burst which subsequently stimulate the hepatic IGF-1 production (Mauras 2001). Pulsatile secretion of GH increases between 1.5 and 3 fold which is accompanied by more than 3 fold serum IGF-1 concentration increase during puberty (Juul et al. 1994). The secretion of GH differs between genders that are parallel with the pattern of height velocity. In girls, the GH/IGF-1 levels rise significantly at Tanner B2 and peaks at Tanner B3-B4. Meanwhile in boys the increase of GH/IGF-1 occurs later during the pubertal development, peaking at Tanner G4 (Albertsson-Wikland et al. 1994). At the end of pubertal stage and adulthood, the levels of GH and IGF-1 reduces significantly even though the gonadal steroids levels are high (Martha et al. 1989).

The growth plate of bones undergoes functional and structural changes during growth. The growth plate contains chondrocytes and is divided into three zones; resting (containing immature cells close to the epiphyseal bone), proliferative (containing replicating and mature chondrocytes) and hypertropic (containing large chondrocytes). In both boys and girls, estrogens play an important role to modulate the secretion of GH and act directly on the growth plate maturation and fusion that leads to termination of longitudinal growth rates (Nilsson et al. 2005). During early puberty, low circulating levels of estradiol increases GH secretion followed by IGF-1 synthesis that stimulate chondrocyte growth in the proliferation zone of the growth plate and initiates pubertal growth spurt. As puberty progresses, augmentation of estradiol leads to apoptosis of hypertropic chondrocytes and stimulates

invasion of the growth plate by osteoblast. The completion of growth depends on estrogen action via ER α that induces exhaustion of chondrocytes proliferation that leads to fusion of the epiphyseal plate (Lazar and Phillip 2012, Weise et al. 2001). In conditions such as precocious puberty when premature exposure of estrogen occurs, skeletal growth accelerates leading to early epiphyseal fusion and decreased in final height (Carel et al. 2004). On the contrary, conditions featuring lack of estrogens (e.g. hypogonadism) causes delay in epiphyseal fusion and tall stature (Sedlmeyer and Palmert 2002).

Testosterone requires aromatization to estradiol in order to influence the GH/IGF-1 axis. This is evident in patients with aromatase deficiency where lack of estradiol lead to reduced epiphyseal closure, lack of pubertal growth spurt and the linear growth continues even after reaching adulthood (Morishima et al. 1995). Other studies have also shown administration of a non-aromatized androgen (DHT) in pre- and peripubertal boys does not increase GH secretion (Eakman et al. 1996, Veldhuis et al. 1997). Testosterone exerts its effect indirectly by enhancing the abundance and responsive of IGF-1 receptors in the growth plate chondrocytes (Lazar and Phillip 2012). Although non-aromatized androgens do not alter the GH/IGF-1 axis, they may have direct effects on bone growth independent of estrogens as AR expression is present within the growth plate cartilage (Nilsson et al. 2003).

1.5.4 *Body composition during puberty*

Dramatic changes in body composition occur *in utero*, across infancy, childhood and puberty. Endocrine factors play a key role in these dimorphic changes regulating the increase in bone density, fat free mass (lean mass) and the distribution and amount of adipose tissue. In early development, infant boys are heavier than girls due to greater lean mass whereas the fat mass are unchanged between the sexes (De Bruin et al. 1996). Thus proportionally newborn female have more subcutaneous fat than males with slightly higher mean skin-fold thickness (Rodriguez et al. 2005, Rodríguez et al. 2004). During prepubertal years, the differences in

body composition in both sexes are modest compared to postpubertal. Boys and girls weigh approximately 23 kg and 22 kg respectively by the age of 7 years (Veldhuis et al. 2005).

As puberty progresses, the body composition markedly changes. In girls, the total body fat increases steadily with the mean of approximately 5.5 kg at the age of 8 years to about 15 kg at 16 years. The increase beyond this stage is considerably slow. In boys, the total body fat increases from 5.5 kg to 11 kg between the age of 8 and 14 years and falls beyond this stage to approximately 9 kg at the age of 16 years and reaches a plateau (Siervogel et al. 2000). The fat free mass increases in girls by the age of 6 years and attain stability by the age of 15 to 16 years. Boys acquire fat free mass more quickly and for longer duration than girls during puberty with a steady increase between the age of 8 and 18 years (Siervogel et al. 2000, Veldhuis et al. 2005). The pattern of higher fat distribution and lower fat free mass in girls is not only hormonally driven but is also related to lower energy expenditure during puberty (Goran et al. 1998). Body mass index (BMI) calculated as weight (kg) divided with the square of stature (m^2) provides useful information to define over-weight and obesity (Siervogel et al. 2000).

1.6 Analytical measurements of LH and FSH.

The importance of gonadotropin measurement as biochemical indicator of endocrinological status and for therapy monitoring has led to development of various specific and sensitive assays. The measurement of LH and FSH can be divided into two assay systems. The first type of measurement is the immunoassays that quantitate the mass of immunoreactive hormone molecules of the sample. This assay includes the radioimmunoassay (RIA), immunofluorometric assay (IF) and immunochemiluminometric assay (ICL). The second type of assay measures the biological activity of the gonadotropin such as receptor binding assay and bioassays that quantitate functional aspects of gonadotropins. The bioactive to immunoactive ratio provides a useful index to assess qualitative changes in the gonadotropin for clinical diagnostics (Jaakkola et al. 1990).

RIA: The first immunoassay was developed by Yalow and Benson for peptide hormones measurements in the late 1950s, for which their work was awarded a Nobel Prize in Medicine to Yalow in 1972 (Yalow and Berson 1959). The development of RIA proved to be beneficial in studying gonadotropin regulation in health and disease conditions (Jaffe and Midgley Jr 1969). The RIA technique is based on competitive binding of unlabeled gonadotropin in biologic fluid and radiolabelled gonadotropin to a limited number of binding sites on a specific antibody. As the amount of unlabeled hormone increases, the binding of radioactive labeled hormone binding to the antibody decreases. Immunoradiometric assays (IRMA) on the other hand are a variation of RIA in which the antibody is labeled instead of antigen. For LH RIA, antisera from hCG were initially used based on the resemblance in structure and immunologic properties (Wide et al. 1961). However, the hCG antisera were replaced with the availability of highly purified human LH and its antibodies (Odell et al. 1967, Odell et al. 1966). Although this assay for gonadotropin measurement is known to be robust and is extensively employed for endocrine research, there are a number of limitations associated

with it. This includes considerable cross-reactivity of the free α -subunit of LH in some RIAs system (Dahl and Sarkissian 1993). RIA is also limited in sensitivity to measure low levels of gonadotropins. This hampers the assay application for measurement of low or suppressed gonadotropin levels for physiological or clinical assessment. Some IRMA and RIA were unable to measure LH pulses in prepubertal children (Clark et al. 1997). Studies have also shown discrepancy in the gonadotropin values measured by polyclonal antibodies in RIA compared to monoclonal antibodies immunoassays (enzyme linked immunoassay) possibly due to the differences in the antibody specificity (Olivares et al. 2000). Other disadvantages such as radiation hazard associated with, short half-life of the iodine tracer and costly gamma counter gradually lead to the replacement of RIA methods with new non-radioactive immunoassays such as IF and ICL (Munro et al. 1991).

IF and ICL assays: These immunometric assays make use of two antibodies forming a sandwich. The first antibody bound to solid phase is used to capture the antigen. Whereas the second antibody labeled to signal transducer, commonly fluorescence (IF assay) or luminescence (ICL assay) is used to measure the concentration of the analyte. No radioactivity is involved in these assays. The gonadotropin molecules present in the sample will be enclosed (“sandwiched”) between the antibodies. The development of commercially available two-site-directed assays has overcome the limitation of gonadotropin RIAs associated with sensitivity and cross-reactivity of the α -subunit. IF assays are able to measure low serum LH and FSH during early puberty development that was difficult to obtain with the RIA assays (Apter et al. 1989).

The dissociation-enhanced lanthanide fluorescence immunoassay (DELFLIA) is a commercially available IF assay that utilizes europium as a label and time-resolved fluorescents as the detection method. This solid-phase assay is based on two site sandwich technique with high affinity monoclonal antibody. The monoclonal capture antibody is

immobilized on the plate which is directed against the specific β subunit of the glycoprotein hormone. The europium labeled detector monoclonal antibody is directed against the common α subunit (Lövgren et al. 1984). The long fluorescent decay time of the europium label enhances the sensitivity of the assay (Hemmilä et al. 1984).

Immulite is another widely used automated immunoassay technology which utilizes the enzyme-amplified chemiluminescent technology. The solid phase of the system consists of a polystyrene bead sealed in the test unit and coated with a capture monoclonal antibody against LH or FSH. The gonadotropin standard or sample binds to the monoclonal antibody coating the bead. A detector polyclonal antibody which is conjugated to alkaline phosphatase enzyme binds to the gonadotropin bound to the monoclonal antibody forming a sandwich. Finally, the chemiluminescent substrate added to the complex undergoes hydrolysis through the action of the alkaline phosphatase enzyme creating unstable anion that emits sustained light which is then measured using a luminometer (Reimers et al. 1996).

FSH Bioassay: The Steelman-Pohley was the earlier *in vivo* assay to assess FSH. For this assay, immature female rats are pretreated with hCG to increase sensitivity to exogenous FSH. This is detected by measuring its response to exogenous FSH which results in a linear dose-response increase in mean ovarian weight (Steelman and Pohley 1953). The problems associated with this ovarian augmentation assay includes that it is too susceptible to serum interference, lacks sensitivity and is cumbersome for routine clinical studies (Wang 1988).

The granulosa cell aromatase bioassay (GAB) and Sertoli cell aromatase assay are *in vitro* FSH bioassays that provide sufficient sensitivity for measurement of serum FSH. This non-species-specific assay is based on stimulation of estrogens production by the rat ovarian granulosa cell primary culture to measure biologically active FSH. Serum samples are pretreated with polyethylene glycol to remove inhibitory substances prior to assay (Dahl et al.

1988, Jia and Hsueh 1986). Meanwhile, the Sertoli cell bioassay is based on measurement of estradiol production from exogenous testosterone in the presence of FSH (Van Damme et al. 1979).

LH/hCG Bioassays: The mouse interstitial cell testosterone assay (MICT) or the rat interstitial cell testosterone assay (RICT) are *in vitro* bioassays commonly used by laboratories for LH and hCG bioactivity measurements. These assays are based on the stimulation of testosterone from dispersed Leydig cells and the assays measure all LH/hCG like bioactivity but do not cross-react with the biologically inactive free subunits of the gonadotropins (Dufau et al. 1976).

Receptor-binding assays: These assays are competitive protein binding assays similar to RIA but using a binding protein other than antibody, typically a receptor that utilizes radioligand gonadotropin (^{125}I -hCG/ ^{125}I -LH or ^{125}I -FSH) as a ligand and crude rat homogenate from rat testes or corpora lutea which is rich in LH/CG and FSH receptors, respectively (Catt et al. 1972, Leidenberger and Reichert Jr 1972, Sanzo and Reichert 1982).

1.7 Analytical techniques of steroid measurement

Steroid hormone analysis plays an indispensable role for the diagnosis of endocrinological disorder or gonadal function in clinical laboratories. Steroid hormones and their metabolites can be measured in various biological fluids such as plasma, serum, urine, amniotic fluid, saliva and tissue extracts (Table 1.3). Generally, binding assays or chromatographic methods are used for steroid quantitation. Quantitation of steroids using gas chromatography-mass spectrometry (GC-MS) and liquid chromatography-mass spectrometry (LC-MS) are superior to immunoassays with regards to specificity and sensitivity (Krone et al. 2010). Rapid growth in the mass spectrometry (MS) technology has enabled routine analyses of steroids in clinical and research laboratories (Stanczyk and Clarke 2010). Table 1.4 shows comparison studies between immunoassays and GC/LC-MS for testosterone and estradiol measurements.

1.7.1 Immunoassay

RIA to measure steroid was first developed in 1969 for estradiol analysis in serum/plasma (Abraham 1969). The 'indirect' RIA method involves extraction of steroid with organic solvent (to remove conjugated steroids and denature the SHBG or CBG protein bound to the steroids) and Celite or Sephadex column chromatography separation (to remove possible interfering structurally related precursor or metabolites) prior to RIA quantitation that increases the specificity of the assay (Abraham et al. 1972, Giton et al. 2009). Since steroid molecules are too small to be antigenic, they are covalently attached to carrier protein such as bovine serum albumin forming hapten (Abraham 1974). The specificity of the assay antibody increases when the binding of protein to the steroid is distant from the functional groups (Honour 2010).

The antibodies used for RIAs are available commercially for many but not all steroids. Tritiated steroid were used in earlier RIA methods which was then replaced with

iodinated derivatives that increased the assay sensitivity (Stanczyk 2004). The assay involves displacement of radioactively labelled steroid from the antibody binding site by steroid in the assay sample. Then the antibody-bound and the unbound steroid are separated either by activated charcoal where the unbound steroids is adsorbed (Wu and Lundy 1971) or by precipitation of the antibody-bound steroid complex forming a pellet upon centrifugation (Honour 2010). The liquid scintillant fluid is then added to the radioactive sample (only for the tritiated label) that produces light which is then measured using a photomultiplier (beta counter).

The RIA has high throughput of samples. Pre-assay purification method removes interfering metabolites so as to provide accurate and reliable steroid measurements. However, RIAs are cumbersome, requires prolonged incubation and time-consuming purification steps. Large sample volume is also required especially when quantifying samples with low steroid concentrations (Stanczyk and Clarke 2010). Due to all these disadvantages, direct (non-extracted) immunoassay such as IF, ICL or enzymatic assays were developed. These assays do not require radioactive ligands and steroid purification prior to steroid analysis. Additionally the direct immunoassays are simple, rapid and more affordable. However, steroid immunoassays generally lack in specificity because the antibodies cross-react with steroids having or sharing structural similarities, especially when present at higher concentration than the steroid of interest. For example in women and children, high DHEAS concentration may cross-react with testosterone measurements and in such condition there will be an overestimation of testosterone steroid concentrations (Heald et al. 2006, Moal et al. 2007). Cross-reactivity also occurs due to conjugated metabolites of the steroid of interest resulting in erroneous steroid measurement (Yarrow et al. 2013). Other inherent problem of using immunoassays includes inaccuracy and limited sensitivity to measure steroids at low concentrations. These immunoassays are unsuitable for steroids quantitation below the assay

validated range for example quantitation of estradiol in children, postmenopausal women and men (Stanczyk et al. 2010, Taieb et al. 2002) and testosterone measurement in children and women (Moal et al. 2007, Rothman et al. 2011, Taieb et al. 2003). Assay comparison studies demonstrated large inter-assay variability for testosterone and estradiol measurements (Table 1.4) (Handelsman et al. 2014, Sikaris et al. 2005).

The presence of heterophilic and auto-antibodies that form complexes with the reagent antibodies may also interfere with the immunoassays giving false negative or positive measurements (Boscato and Stuart 1988, Boscato and Stuart 1986). Additionally, direct immunoassays utilizing samples without extraction, chromatographic separation or authentic tracers (H^3 , C^{14}) are susceptible to matrix and SHBG interference (Handelsman et al. 2014, Sikaris et al. 2005, Taieb et al. 2003). Removing the pre-immunoassay purification step was reported to falsely underestimate or overestimate analyte measurements (Marks 2002). Immunoassay performance was improved with extraction method prior to assay for samples with low estradiol in children (Ankarberg-Lindgren and Norjavaara 2008). However, studies have also reported positive bias in assays involving extraction and chromatographic separation methodologies compared to reference methods (Cawood et al. 2005, Wang et al. 2004). Furthermore, the presence of endogenous compounds such hydrophobic and amphiphatic lipids in serum samples has been reported to interfere with the RIA assays by interacting with the steroids or the antigen-antibody reaction (Rash et al. 1980).

1.7.2 Gas chromatography- mass spectrometry

The first gas chromatography (GC) to measure steroids was developed in 1960 which preceded the use of immunoassay in endocrine studies (Sweeley and Horning 1960, Vanden Heuvel et al. 1960). The coupling of GC and MS to measure sterols was first carried out in 1964 (Eneroth et al. 1964) followed by the GC-MS steroids analysis in the late 1960s in biological matrices (Sjövall and Vihko 1968).

GC-MS is a robust and widely used method for detection and analysis of major steroids and their metabolites in complex matrices such as urine (Weykamp et al. 1989). The GC consists of flexible silica-based column (approximately 30 m in length) that utilizes large gas volumes (normally helium) with high pressure as mobile phase and for chromatographic separation. Samples injected into the column are vaporized upon reaching the analyte boiling point which is about 300°C for steroids. The volatile analytes then move into the vacuum detector such as flame ionization detector (FID), electron-capture detector (ECD) or the mass spectrometer (MS). The MS detector is preferred for steroid analysis as it provides highly sensitive and selective detection.

The GC-MS is capable of providing baseline separation of steroids with structural similarities or α/β stereoisomers (Krone et al. 2010). However, prior to GC-MS analysis, non-volatile and thermolabile analytes have to be chemically derivatized, for example, using methyloxime-trimethylsilyl ether (MO-TMS) to enhance volatility and to withstand the GC high temperature during vaporization. Derivatization with suitable reagents increases the ionization efficiency by changing the steroid physical and chemical property by forming covalent linkage to the specific functional group of the analyte. Common concerns with derivatization includes incomplete derivatization, nonspecific derivatization and production of multiple products (Liberato et al. 1987). Steroids in conjugated form have to be enzymatically or chemically hydrolyzed before analysis as steroid conjugates have low volatility and degrade at high temperature (Caulfield et al. 2002). There are two types of enzyme solutions normally used for steroid deconjugation which includes *Escherichia coli* and *Helix pomatia*. β -glucuronidase extracted from *E.coli* deconjugates the glucuronide moiety from steroids whereas the β -glucuronidase/arylsulfatase extracted from *H. pomatia* hydrolyses both the glucuronide and sulfate conjugates. However, the use of *H. pomatia* yields unwanted steroid by-product (e.g. conversion of DHEA to androst-4-ene-3,17-dione)

and incomplete deconjugation (e.g. androsterone-3-sulfate and testosterone-17-sulfate) (Messeri et al. 1984, Vanluchene et al. 1982, Venturelli et al. 1995). This is not a problem with the enzymatic hydrolysis using the enzyme from *E.coli*. The GC-MS run time for multiple steroid profile analysis is also commonly very long thereby limiting the sample throughput. Although only small volume of sample is required for GC-MS analysis (1-5 μ L), it requires extensive sample cleanup before analysis.

1.7.3 Liquid chromatography-mass spectrometry

In the 1980s, the development of liquid chromatography (LC) technology coupled with MS provided a much simpler and faster analysis of steroid compared to the GCMS (Liberato et al. 1987). To date, LC-MS/MS is now considered the most accurate method to measure small molecules from variety of biological matrices (Xu et al. 2007). The LC consists of pumps that delivers mobile phase under high pressure to maintain a constant flow rate thereby ensuring reproducible chromatography. Mobile phase for steroids separation consist of a mixture of organic solvents (e.g. methanol and acetonitrile) and water with modifiers (e.g. formic acid, ammonium acetate, ammonium formate). Samples injected into the column (stationary phase) separates the steroids and the effluent is then transferred into the MS. The LC separation is dependent on the physical or chemical characteristics of the analytes such as molecular size and presence of functional groups.

LC-MS analysis is highly sensitive and specific for steroid quantitations. A robust LC-MS method to quantitate steroids requires high quality chromatography to separate the steroid of interest from isobaric compounds (i.e. identical nominal mass to charge ratios) (Keevil 2013). Examples of isobaric compound pairs include cortisone/prednisolone, testosterone/DHEA and 11-deoxycortisol/corticosterone. However, separating these isobaric or interfering compounds may increase the assay runtime and requires more mobile phase. Multiple analytes can be measured with lesser sample preparation compared to GC-MS.

Additionally LC-MS steroid profile provides more useful data than single steroid measurement such as from using immunoassay. With the LC-MS system, the analysis operates at low temperature which is beneficial for measurement of unstable analytes such as conjugated steroids and thermolabile steroids (Borts and Bowers 2000, Bowers 1996). Derivatization step is added to increase the sensitivity of LC-MS methods for certain steroids analysis especially for analytes that are not effectively ionized such as estradiol and DHEA (Kushnir et al. 2008) (Table 1.3). Derivatization reagent reacts with a functional group (eg hydroxyl) to improve column retention and ionization efficiency (Xu et al. 2011). Dansyl chloride is commonly used for hydroxyl group to esterify estrogens (Nelson et al. 2004, Xu et al. 2005). However, derivatization for LC-MS adds complexity to the method, possibility of artifact formation and requires certain functional groups (Jääntti et al. 2010, Xu et al. 2010). Unlike GC-MS, the LC-MS has generally shorter run time and is not limited to measurement of volatile compounds and is able to measure heat-labile steroidal compounds.

The LC is combined with ionization source that ionizes compounds delivered by the LC in liquid droplet. The atmospheric pressure ionization (API) which was introduced in the 1980s facilitates ionization for MS analysis. Ionization techniques commonly used for steroids LC-MS/MS analysis includes electrospray ionization (ESI), atmospheric pressure chemical ionization (APCI) and atmospheric pressure photo ionization (APPI) (refer section 1.8.2 for details on ionization interface). The ESI, APCI and APPI are considered as “soft” ionization technique as they form protonated or de-protonated molecules without fragmentation (Souverain et al. 2004). This type of ionization is achieved by transferring minimum internal energy to the analytes during ionization (El-Aneed et al. 2009). However, conjugated steroids could be fragmented by the ion source (Field 2013).

The ionization technique selected for LC-MS method is dependent on the molecular weight and the polarity of the analytes (Figure 1.14). APCI and APPI are known to be less

susceptible to ion suppression or enhancement due to matrix effect as the ionization occurs in gas phase compared to ESI (liquid phase ionization) (Elviri et al. 2010, Holčapek et al. 2010). However, ionization with APCI is not completely free from ion suppression for certain compounds and the analyst should perform through investigation on ionization technique selection during method development (Sangster et al. 2004). Table 1.3 shows different ionization techniques used in previous studies to determine free and conjugated steroids measurement using MS.

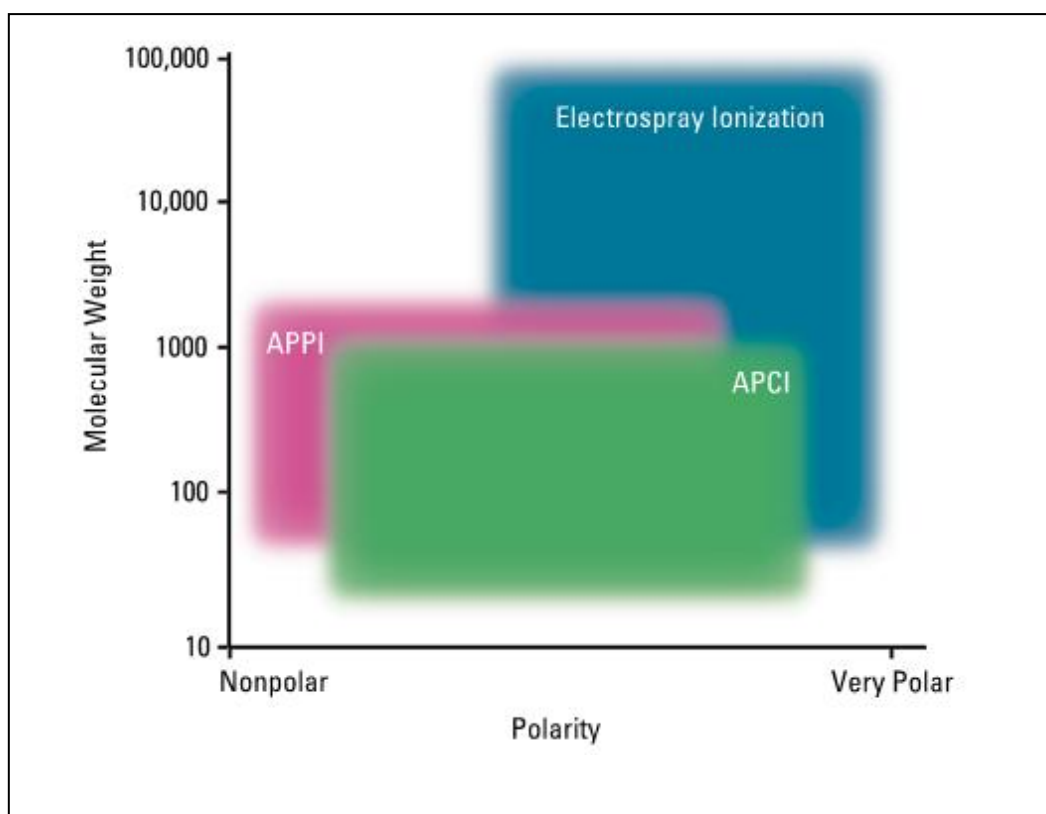


Figure 1.14 Ionization capabilities of ESI, APPI and APCI according to the molecular weight and polarity of the analytes (Holčapek et al. 2010).

Table 1.3 Examples of endogenous steroids analysis by GC/LC-MS.

Analyte	Analytical method	Biological Matrix	Sample preparation	Derivatization	Deconjugation	Assay validation	LOD/LOQ	Reference
T, ET, A, Etio, DHEA (Sulfates and glucuronides)	LC-ESI-MS/MS (- mode)	Urine (human)	SPE (Oasis WAX)	No	No	Yes	Not reported	(Strahm et al. 2008)
T, E, DHEA, DHT, 5 α 3 α 17 β , 5 β 3 α 17 β , 5A3 β 17 α , 5A3 β 17 β , EpiA, A, Etio	GC-MS	Urine (human)	SPE (C18)	ITMS/MSTFA	Chemical and Enzymatic (<i>E.coli</i>)	Partial	Not reported	(Dehennin et al. 1996)
ADT, CORT, E1, E2, E3, T, 5AD, ALD, 17OHPreg, DHEA, 5 α DHT, 5 β DHT, P5, THS, DOC, 5 α -THB, HC, S, M, 2-OH E1; 16 α -OH E1, 17-OHP, A4	LC-ESI-MS/MS (+ mode)	Urine (human)	SPE (Oasis HLB)	DMAB (all steroids except for P5, 17-OHP, A4)	No	No	LOD: 5-500 pg/mL	(Dai et al. 2012)
15 estrogen and estrogen metabolites	LC-ESI-MS/MS (+ mode)	Urine (human)	LLE (dichloromethane)	Dansyl chloride	Enzymatic (<i>H. pomatia</i>)	Partial	LOQ: 0.04 ng/mL	(Xu et al. 2005)
23 estrogens, androgens and pregnanes (free/glucuronide conjugated)	LC-ESI-MS/MS (+ mode for all steroids except pregnandiol)	Urine (primate)	LLE (MTBE)	No	Chemical and Enzymatic (<i>E.coli</i>)	Yes	LOQ: 0.3-3 ng/mL	(Hauser et al. 2008)

E1, E2, E3, P4, P5	LC-ESI-MS/MS (+ mode for P4 and P5, - mode for estrogens)	Urine (human)	Online SPE (C18)	No	Enzymatic (<i>E.coli</i>)	Partial	6-61 pg on column	(Alvarez Sanchez et al. 2008)
T, ET, DHEA, A, Etio (free, sulfates and glucuronides)	LC-MS/MS (+ mode for free steroids and - mode for sulfates and glucuronide steroids)	Urine (bovine and human)	SPE (Strata X)	No	No	No	LOD: 80-100 ng/mL	(Buiarelli et al. 2004)
TG, ETG, AG, EtioG	LC-ESI-MS/MS	Urine (human)	Filtration or LLE (ethyl acetate)	No	No	Yes	Filtration method: 0.25-1 ng/mL LLE method: 0.05-0.25 ng/mL	(Pozo et al. 2008)
AG, TG, E23G, E2-17G, E2-3G,17diG, DHEAS, TS, E1S, E2S, E2-3G17S, E2-3S17G, CRLG, CRLS, CRNS	LC-ESI-MS/MS (-mode)	Urine (human)	SPE	No	No	No	Not reported	(Antignac et al. 2005)
E1, E2	LC-APPI-MS/MS (- mode)	Tissues, serum (human)	Tissue homogenization (water), LLE (hexane:ethylacetate)	No	No	Yes	LOQ: 2.5-5.0 pg/mL	(Huhtinen et al. 2012)

T, DHT, 3 α -diol, 3 β -diol, E2, E1	LC-APPI-MS/MS (- mode: estrogens; + mode: androgens)	Tissues (Mouse testis, prostate, ovary, uterus)	Tissue homogenization (EDTA in PBS), LLE (hexane:ethyl acetate)	No	No	Yes	LOQ: 0.3-40 pg	(McNamara et al. 2010)
E1, E2, E3, 17 β T, 17 α T, 5 β DHT, 5 α DHT, A, Etio	GC-MS/MS (- mode: estrogens; + mode: androgens)	Serum (human)	LLE (ether), SPE (ChromP), SiOH SPE column, HPLC	MSTFA-TNIS-DTT mixture	Enzymatic (<i>H.pomatia</i>)	Yes	LOD: 0.03-1.8 pmol/L LOQ: 0.07-3.7 pmol/L	(Courant et al. 2010)
DHEAS, A, F, CORT, S A4, E2, T, 17 α -OHP, DHEA, P4	LC-APPI-MS/MS (- mode: A; + mode: all other steroids studied)	Serum (human)	PP (ACN)	No	No	Yes	LOD: 1.5-10 pg/mL	(Guo et al. 2006)
Seven C-21 adrenal steroids	LC-APCI-MS/MS (+ mode)	Serum (human)	PP (ZnSO ₄ /MeOH) Online extraction C18 silica monolithic pre-column	No	No	Yes	LOD: 0.10-2.75 nmol/L LOQ: 0.30-12.40 nmol/L	(Carvalho et al. 2008)
DHEAS, F, A4, E3, P4, DHEA, S, 17 α -OHP, E2	LC-APPI-MS/MS (+ mode)	Serum (human)	PP (ACN)	No	No	Yes	Not reported	(Guo et al. 2004)
E1, E1S, E2, E13G, E2, 2MeOE1, 2MeOE2	TS-LC-MS/MS (- mode)	Serum (human)	LLE and SPE (Strata X)	No	No	Partial	Not reported	(Caron et al. 2009)

17OHP, T, A4	LC-APCI-MS/MS (+ mode)	Plasma/Serum (human)	Online SPE (Oasis HLB)	No	No	Yes	LOD: 0.14-0.17nmol/L LOQ: 0.30-0.35 nmol/L	(Rauh et al. 2006)
A4, T, DHT	LC-ESI-MS/MS (+ mode)	Plasma	SPE (Oasis MAX)	No	No	Yes	LOQ: 0.29 ng/dL	(Kulle et al. 2010)
A4, T, DHT	LC-ESI-MS/MS (+ mode)	Cultured human cell lines	Online SPE (C4-alkyl-diol silica)	No	No	Yes	Not reported	(Chang et al. 2003)
T, DHEA	LC-ESI-MS/MS (+ mode)	Saliva (human)	SPE (Strata-X)	HMP	No	Yes	LOQ: 10 pg/mL	(Shibayama et al. 2009)
17OHPreg, 17OHP	LC-ESI-MS/MS (+ mode)	DBS (human)	SPE (Strata-X)	HP	No	Yes	LOQ: 0.5-1 ng/mL	(Higashi et al. 2008)
CORT, DOC, P4, 17 α -OHP, F, DF, A4, T, DHT, F	LC-ESI-MS/MS (+ mode)	DBS (human)	LLE (acetone/ACN)	No	No	Yes	LOQ: 0.75-6.3 nmol/L	(Janzen et al. 2008)

Abbreviations: HMP: 2-hydrazino-1-methylpyridine; HP: 2-hydrazinopyridine; DMAB: 4-Dimethylamino-benzoic acid; ACN: acetonitrile; MTBE: methyl tert-butyl ether; MSTFA-TNIS-DTT: N-methyl-N-(trimethylsilyl)-trifluoroacetamide/trimethyliodosilane/dithiothreitol; T: testosterone; ET: epitestosterone; A: androsterone; M: mesterolone; Etio: etiocholanolone; DHEA: dehydroepiandrosterone; E1: estrone; E2: Estradiol; E3: estriol; 2-OH E1: 2-hydroxyestrone; 16 α -OH E1: 16 α -hydroxyestrone ; E1S: Estrone sulfate; E13G: Estrone glucuronide; 2MeOE1: 2-methoxy estrone; 2MeOE2: 2-methoxy estradiol; CORT: corticosterone; A4: Androstenedione; ADT: Androsterone; ALD: Aldosterone; P5: pregnenolone; 17 α -OHP: 17 α -hydroxyprogesterone; 17OHPreg: 17 α -hydroxypregnenolone; P4: progesterone; S: 11-Deoxycortisol; 21-Deoxycortisol; DF ; deoxycorticosterone; DOC; F:Cortisol; THS: tetrahydrodeoxycortisol; 5 α -THB: 5 α -tetrahydrocorticosterone; HC: Hydrocortisone; 17 α -OHP: 17 α -hydroxyprogesterone; E: epitestosterone; 5AD: 5-androstenediol; 5 α 3 α 17 β : 5 α -androstane-3 α ,17 β -diol; 5 β 3 α 17 β : 5 β -androstane-3 α ,17 β -diol ; 5A3 β 17 α : 5androstane-3 β ;17 α -diol; 5A3 β 17 β : 5androstane-3 β ,17 β -diol; EpiA: epiandrosterone; AG: 5-androstane-17-glucuronide; TG: testosterone-17-glucuronide; E2-3G: 17-estradiol-3-glucuronide; E2-17G: estradiol-17-glucuronide; E23,17diG: estradiol-3,17-diglucuronide; DHEAS: dehydroepiandrosterone sulfate; TS: testosterone-17-sulfate; E2-3S: 17-estradiol-3-sulfate; E2-3G17S: estradiol-3-glucuronide,17-sulfate; E2-3S17G: estradiol-3-sulfate,17-glucuronide; CRLG: cortisol 21-glucuronide; CRLS: cortisol 21-sulfate; CRNS: cortisone 21-sulfate; TS: Turbo IonSpray; ESI: electrospray ionization; APCI: atmospheric pressure chemical ionization; APPI: atmospheric pressure photoionization; LC: liquid chromatography; GC: gas chromatography; MS: mass spectrometry; SPE: solid phase extraction; LLE: liquid-liquid extraction; PP: protein precipitation; LOD: lower limit of detection; LOQ: lower limit of quantitation; HPLC: High performance liquid chromatography; DBS: dried blood spot

Table 1.4 Examples of immunoassay and GC/LC-MS comparative studies for quantitation of testosterone (T) and estradiol (E₂).

Analyte	Analysis technique comparisons	Samples (number)	Findings	Reference
T	GC-MS versus 10 immunoassay (8 direct non-isotopic immunoassays and 2 direct RIAs)	Serum from normal 50 men, 55 women and 11 children	<ul style="list-style-type: none"> Men: Immunoassays underestimate T with 12% below GC-MS measurement. Women: Degree of bias significantly higher in women with 46% above GC-MS concentration. Children: Immunoassays measured higher T concentration for undetectable GC-MS levels (< 4.3 ng/dL). 	(Taieb et al. 2003)
T	LC-API- MS/MS versus 6 immunoassays (4 automated and 2 RIAs)	Serum from 62 normal and 60 hypogonadal male.	<ul style="list-style-type: none"> Deming regression demonstrated variability (underestimation or overestimation) of T measurements with most of the immunoassays studied compared to LC-MS/MS. 90% of the samples measured with immunoassays demonstrated T concentrations of more than 20% from LC-MS/MS measurements. 	(Wang et al. 2004)
T	LC-ESI- MS/MS versus 5 immunoassays (2 automated non-isotopic and 3 RIAs)	Serum from 28 children and 31 women	<ul style="list-style-type: none"> Immunoassays overestimated T concentration and unreliable for T below 100 ng/dL. 	(Moal et al. 2007)
T	LC-APCI- MS/MS versus one automated immunoassay	Serum/plasma from 107 children	<ul style="list-style-type: none"> Immunoassay underestimated T for samples with concentrations >5 nmol/L. High variability samples with T <5 nmol/L determined by immunoassay. 	(Rauh et al. 2006)
T	GC-MS versus 7 automated immunoassays	Serum from 124 healthy men	<ul style="list-style-type: none"> Deming and Passing-Bablok regression demonstrated variability in six immunoassays with significant difference in slope and intercept when compared to GC-MS measurements. Reported wide variability in immunoassay performance against valid healthy young men reference population. 	(Sikaris et al. 2005)
E ₂	LC-APPI-MS/MS versus 5 direct non-isotopic immunoassays	Serum from 101 healthy older men	<ul style="list-style-type: none"> Only three immunoassays were able to measure E₂ concentrations in all the samples. Upward bias ranging between 6 and 74% for E₂ measured with immunoassays compared LC-MS/MS (method certified with 3 certified reference materials). 	(Handelsman et al. 2014)
E ₂	GC-MS/MS versus 7 immunoassays (3 indirect and 4 direct assays)	Serum from 40 postmenopausal women	<ul style="list-style-type: none"> The three indirect assays that involve extraction prior to assays demonstrated better correlation (0.94, 0.91 and 0.88) with GC-MS/MS measurements compared to the 4 direct assays (without extraction). 	(Lee et al. 2006)

1.8 Mass spectrometry

All MS comprise of four basic components - the inlet, ion source, mass analyzer and detector (Figure 1.15). Six basic types of mass analyzers are currently available. These includes quadrupole, ion trap, time-of-flight (TOF), Orbitrap, double focusing magnetic analyzer and Fourier transform ion cyclotron resonance (FT ICR) (Holčapek et al. 2010). Each has different mass accuracy, mass resolution parameters and capability to measure different of mass-to-charge (m/z) range (Holčapek et al. 2010). Recent advancement to the MS with higher mass resolution allowed separation of co-eluting isobaric compounds that have the same nominal masses but different exact masses (Xian et al. 2012). The mass analyzer measures gas phase ions according to their m/z ratio, where the charge is produced by addition or loss of proton(s), cation(s), anion(s) or electron(s). Utilizing electrical fields, these charged molecules are separated according to their m/z that further allows its mass measurements. Table 1.5 lists the basic principles of the six mass analyzers in use today. The most common mass analyzer for quantitative steroid analysis is the triple quadrupole instrumentation which is also known as tandem MS (Keevil 2013, Rauh 2010).

1.8.1 Triple quadrupole mass spectrometer

The triple quadrupole MS consists of two resolving quadrupoles (Q1 and Q3) and a collision cell positioned in between the quadrupole (Q2) (Kushnir et al. 2011). Sample steroids separated by the LC are first ionized by the ion source before further transfer into the mass spectrometer where the first quadrupole monitors the precursor ions. The analyte(s) of interest (precursor ion) is selected at Q1 according to the m/z ratio and all other compounds are filtered out. Then, the second quadrupole (collision cell) performs the collision between the collision gas (e.g. argon, helium and nitrogen) and the introduced steroids producing fragmented or product ions. Finally, the third quadrupole monitors the product ions of the

steroids according to the radiofrequency set and removes the unwanted fragment ion. The targeted precursor and product ion finally reaches the ion detector (Figure 1.15).

New LC-MS/MS method development requires infusion of the standard steroid reference and its isotope labeled internal standard separately using a syringe pump and a 'tee mixer' to introduce the analyte into the LC mobile phase and the ion source. Analyte quantitation can be carried out by two common techniques, selected-ion-monitoring (SIM) or multiple-reaction-monitoring (MRM), which are commonly used for a single or triple quadrupole mass spectrometer, respectively. MRM (also known as selected-reaction-monitoring; SRM) mode provides high selectivity and sensitivity compared to SIM. High background chemical noise in SIM mode caused by isobaric compounds and impurities leads to lower signal to noise ratio (S/N) for the target analyte (Bakhtiar and Majumdar 2007). The analyte of interest should be tested in positive or negative ion modes to determine the most suitable and efficient ionization conditions with highest S/N ratio. For MRM, the specific ion transition for each analyte is selected based on precursor ion and product ions pairs, which is then used for quantitation of steroids from the biological samples (Shibata et al. 2014). During the method development, other MS parameters such as ion source voltage and temperature, collision cell energy, declustering potential, entrance potential, collision cell exit potential and dwell time are optimized. Biological samples have to be pretreated prior to sample quantitation by MS and the method has to be validated for limit of quantitation (lower and upper), accuracy and precision, recovery, reproducibility, stability and matrix effect according to the appropriate guidelines such as US Food and Drug Administration guidance (FDA 2001) or European Medicines Agency (EMA 2011).

Table 1.5 Basic principles of different types of mass analyzers

(Barrow et al. 2005, El-Aneed et al. 2009, Glish and Vachet 2003, Ho et al. 2003, Hu et al. 2005, Moens and Jakubowski 1998, Nikolaev et al. 2014, Vogeser and Parhofer 2007).

Mass analyzer	Main principles
Quadrupole	<ul style="list-style-type: none"> • Consist of four metal rods installed in parallel orientation • RF and DC voltages applied to rods guide the ions with desired m/z ratios to pass through and move towards the detector while other molecules are guided out and neutralized • Mass range: <4000 Da; Resolution: <4000
Ion trap	<ul style="list-style-type: none"> • Consist of three hyperbolic electrodes: ring, entrance and exit end cap electrode • RF and DC potential applied to the ring electrode produces 3-dimensional quadrupolar potential field • The ions losses kinetic energy and are trapped forming an ion “cloud” • Ions are ejected according to their m/z ratios into the detector • Mass range: <4000 Da; Resolution: <4000
Time-of-flight (TOF)	<ul style="list-style-type: none"> • Ion generated by ion source is accelerated into flight-tube • Smaller ions travel faster compared to molecules with higher mass • Molecules with different m/z travel at different time intervals into the detector • Mass range: >1 MDa; Resolution: 4000
Orbitrap	<ul style="list-style-type: none"> • Consist of two electrodes: outer electrode (barrel shape) and inner electrode (spindle shape) • DC voltage applied • Ions are pulsed into the orbitrap, rotates around the central electrode and oscillate along the horizontal line • m/z of different ions are determined from different frequencies of the oscillation by Fourier transform • Mass range: <6000 Da; Resolution: 150,000
Double focusing magnetic analyzer	<ul style="list-style-type: none"> • Involves two sectors: electrostatic and magnetic • Ions with same kinetic energy are directed from electrostatic sector (act as a kinetic energy selector) to the magnetic sector before ion separation and detection • Mass range: 10,000 Da; Resolution: 60,000
Fourier transform ion cyclotron resonance (FT ICR)	<ul style="list-style-type: none"> • Consist of an analyzer cell (or known as Penning trap) with two excitation, detection and trapping plates each • Analyzer cell is located within strong magnetic field • Ions generated by ion source moves into the analyzer cell and RF applied to the excitation plates causes excitation of the ions • Ions starts to precess in center of magnetic field resulting it to orbit (known as cyclotron motion) • Ions with lower m/z have higher cyclotron frequencies compared to ions with higher m/z • Ion packets frequencies are detected by the detection plates and the frequency analysis is performed using Fourier transformation • Frequencies are converted to m/z to give a mass spectrum. • Mass range: 10,000 Da; Resolution: >500,000

Abbreviations: RF: radiofrequency; DC: direct current; m/z : mass/charge

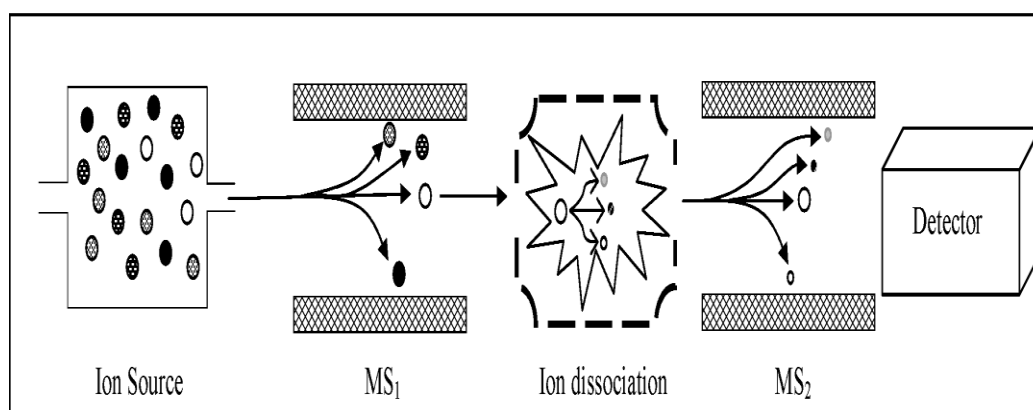


Figure 1.15 Representation of precursor ion and product ion selection of MS₁ and MS₂, respectively in the tandem mass spectrometer (El-Aneed et al. 2009).

1.8.2 Ionization interfaces

The eluent from the LC column must be effectively converted into gaseous phase before being measured by the MS. Since the introduction of electrospray ionization (ESI), atmospheric pressure chemical ionization (APCI) and atmospheric pressure photoionization (APPI), LC-MS/MS has become widely used for steroid analysis with superior sensitivity and specificity (Table 1.3).

1.8.2.1 Electrospray ionization (ESI)

This ionization method, developed by Fenn and co-workers in 1988 (Fenn et al. 1989), led to award of a Nobel Prize in Chemistry to Fenn in 2002. ESI technique is based on the production of ions from liquid phase into gas phase by the dispersal of highly charged droplets at near atmospheric pressure followed by the formation of evaporated droplet. The LC mobile phase is sprayed from the tip of the metal capillary. The needle is applied with high voltage typically between 3-5 kV that leads to the formation of Taylor cone (Taylor 1964) (Figure 1.16). A fine spray of highly charged droplets is generated which then undergoes rapid evaporation due to heat and dry nitrogen (desolvation gas). The ion polarity is controlled by adjusting the capillary voltage that forms either positive or negative charged

ions. Evaporation of the solvent further reduces the droplet diameter and increases the droplet surface charge density. The parent droplets undergoes “Coulomb explosion” or “Coulomb fission” when the electrostatic forces overcome the surface tension of the droplets (Rayleigh limit is reached) forming smaller offspring droplets. This process continues until the charged analyte molecules escapes the droplets by field desorption and these analyte ions are guided into the mass analyzer by the electric field gradient (Banerjee and Mazumdar 2012, Gomez and Tang 1994) (Figure 1.16). To facilitate ionization, the presence of ionic solution is important. Mobile phase consisting of methanol/water or acetonitrile/water containing weak acids such as formic or acetic facilitate protonation (for positive mode ionization), whereas diluted ammonium hydroxide in aqueous solution or diluted volatile buffers (ammonium acetate or formate) facilitates deprotonation (for negative mode ionization) (Cech and Enke 2001). ESI is a soft ionization technique (i.e. non-disintegrating) suitable for polar compounds such as labile conjugates (glucuronides and sulfates) (Figure 1.14) (Kostiainen et al. 2003) or compound that forms charged adduct with ammonium or alkali cations (Himmelsbach 2012). The LC-ESI-MS/MS method is able to measure steroids in free and conjugated forms simultaneously (Moeller and Stanley 2012). However, steroids are commonly measured after hydrolysis, which is enzymatic or chemical deconjugation. Steroids with high proton affinity such as androgens, glucocorticoids and mineralocorticoids are easily ionized with ESI source due to the 3-oxo-4-ene structure (Shibata et al. 2014). Derivatization is commonly carried out to improve ESI ionization efficiency and sensitivity for trace steroids or steroids with low ionization potential. Although derivatization may increase the sensitivity of steroids measurement for LC-ESI-MS methods (1-10,000 fold) (Dai et al. 2012) (Table 1.3), the derivatization step increases sample preparation time, causes loss or degradation of target steroids and increases “noise” (Higashi and Shimada 2004, Mao et al. 2004, Santa 2011).

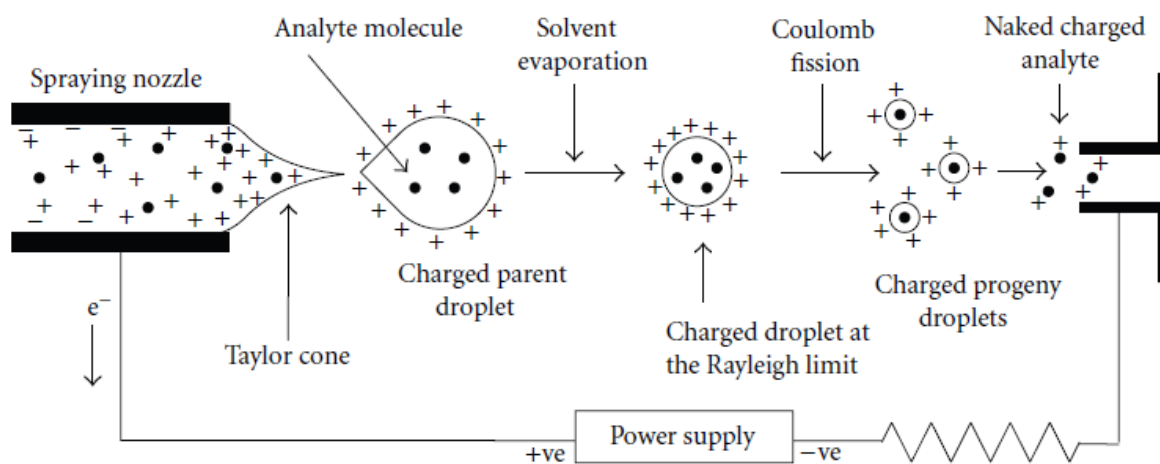


Figure 1.16 Schematic diagram of ESI source.

The highly charged capillary releases charged droplets. Size of the droplets decreases with the desolvation process and further droplet fission produces the gas phase analyte ions (Banerjee and Mazumdar 2012, Robb and Blades 2008).

1.8.2.2 Atmospheric pressure chemical ionization (APCI)

This is a chemical ionization process that ionizes analytes in gas phase. Mobile phase and analytes are first vapourized in the ion source with heat (from the nebulizer probe) and nebulizing gas flow. A sharp needle is positioned directly in the forming gas cloud and this needle generates electron from corona discharge which bombards the vapour. Solvent molecules become charged and the electrical charge is transferred to the analyte molecules (Figure 1.17). The LC mobile phase commonly used is a mixture of water and organic solvent (e.g. methanol and acetonitrile) which forms either protonated or deprotonated ions of these solvents that transfers their charge to ionizable analytes. APCI is preferred over ESI for steroid analysis as it is capable of ionizing non-polar or poorly ionized compounds (Kushnir et al. 2010) (Figure 1.14).

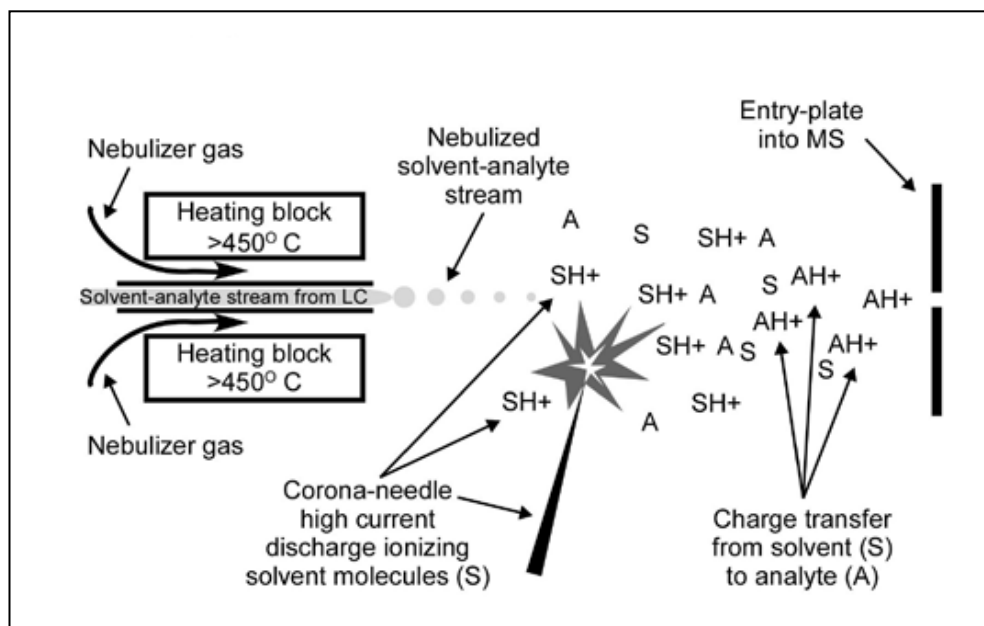


Figure 1.17 Schematic diagram of APCI source (Grebe and Singh 2011).

1.8.2.3 Atmospheric pressure photoionization (APPI)

This is a newer API source for LC-MS that also operates by chemical ionization in gas phase. Similarly to APCI, the solvent first undergoes vaporization as it passes the heated nebulizer. Instead of the corona discharge needle used in APCI source, krypton lamp produces ultraviolet (UV) light that induces ionization via emission of photons in vacuum (Figure 1.18). The analyte ionization in this system is enhanced with the addition of dopant such as toluene and acetone that is involved in the chemical ionization (Robb and Blades 2006). Krypton lamp delivers photon energy ($h\nu$) of 10.0 and 10.6 eV and only ionizes ions with lower ionization energy (IE) including the dopant (e.g. toluene IE: 8.82 eV). Common LC mobile phase such as water (12.61 eV), methanol (10.85 eV) and acetonitrile (12.19 eV) with IE above the lamp photon $h\nu$ are not ionized therefore do not aid analyte ionization (Robb and Blades 2008). APPI produces charged ions via two mechanisms: (1) direct photoionization of analyte by absorbing a photon of light from Krypton emission, (2) the dopant ionized by the UV lamp forms free radicals followed by the reaction with the analyte by charge exchange (non-polar compounds) or proton transfer (polar compounds) (Robb and Blades 2006) (Figure 1.19). APPI ionization is more suitable for compounds with mid to low-polarity that

cannot be ionized by ESI and APCI (Figure 1.14). The sensitivity of APPI for steroid measurement in biological matrices is 3-5 fold higher than APCI (Alary 2001). Table 1.6 summarizes the properties of ESI, APCI and APPI.

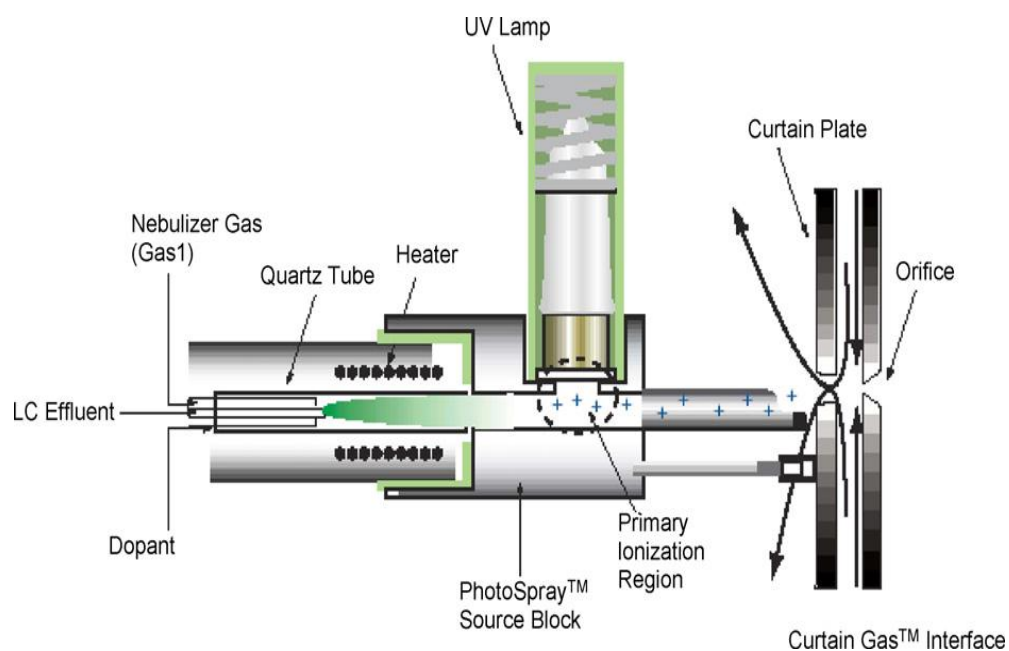


Figure 1.18 Schematic diagram of APPI source (Robb and Blades 2008).

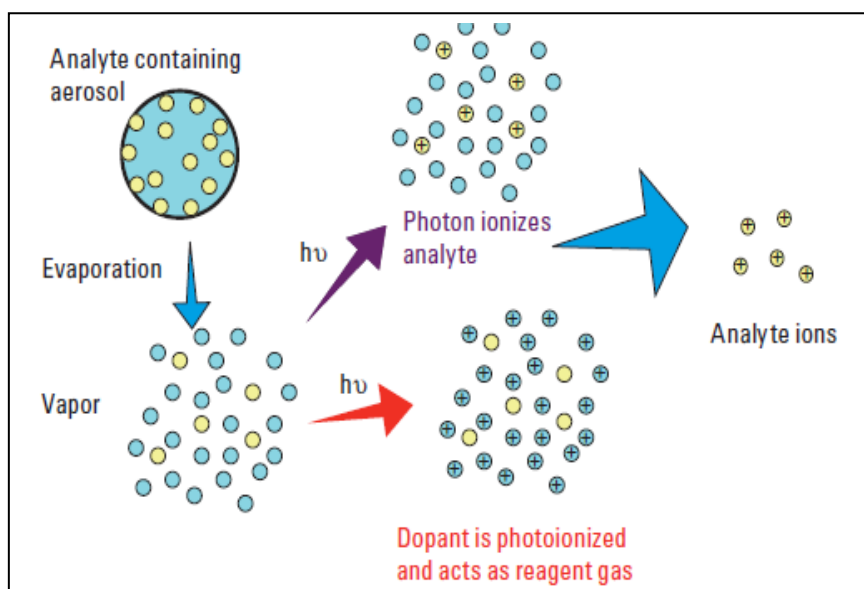


Figure 1.19 Schematic diagram of APPI ionization mechanism.

Adapted from <http://www.chem.agilent.com/Library/technicaloverviews/Public/5990--7413EN.pdf>

Table 1.6 Summary of ionization techniques (ESI, APCI and APPI) commonly used for steroid LC-MS/MS analysis

(Bakhtiar et al. 2002, Bos et al. 2006, Cech and Enke 2001, Kostianen and Kauppila 2009).

	ESI	APCI	APPI
Ionization reaction phase	Liquid	Gas	Gas
Compound suitability (common mass range)	Polar and ionic compound (less than 100,000 Da)	Neutral or less polar (less than 1500 Da)	Mid to low polarity (less than 1500 Da)
Ideal compounds	non-volatile chargeable large molecules e.g. protein, peptide, polysaccharide, bile acids, steroid conjugates	Volatile, thermally stable and small molecules e.g. non-polar lipids, pesticides, drugs, steroids with conjugated double bond or keto group	Volatile, thermally stable and small molecules e.g. polycyclic aromatic hydrocarbons, drugs, non-polar lipids, pesticides, steroids with conjugated double bond and low polarity (pregnanes)
Matrix interference	More prevalent compared to APCI and APPI	Less prevalent compared to ESI	Less prevalent compared to ESI and APCI
Suitable flow rate	Few $\mu\text{L}/\text{min}$ (operates at very low flow rate)	Up to 2 mL/min	Suitable for both low and high flow rates
Suitable solvents	Polar and medium polar	Polar and non-polar	Polar and non-polar

Abbreviations: ESI: electrospray ionization; APCI: atmospheric pressure chemical ionization and APPI: atmospheric pressure photoionization

1.8.3 *Matrix effect*

Urine, whole blood, serum, plasma and saliva are matrices commonly used for bioanalytical analysis. These matrices contain endogenous (e.g. phospholipids, salts, urea, amines and metabolites) and exogenous substances (e.g. buffers, anticoagulants, polymers from collection tubes, drugs and chemicals) that may co-elute with the compound of interest that may lead to ion suppression or enhancement (Antignac et al. 2005, Matuszewski et al. 1998, Mei et al. 2003). This phenomenon, known as matrix effect is defined as “The direct or indirect alteration or interference in response due to the presence of unintended analytes (for analysis) or other interfering substances in the samples” (Shah et al. 2000). It is important to identify and eliminate matrix effect using adequate validation procedure for bioanalytical method development as matrix effect dramatically affects the LC-MS method performance (especially for quantitative analysis) in terms of detection capabilities, reproducibility, linearity, selectivity, accuracy and limit of quantitation, leading to erroneous results (Gosetti et al. 2010, Trufelli et al. 2011).

For LC-MS analysis, matrix effects can be assessed either by post-column infusion (qualitative), post-extraction spike method (quantitative) or assessment of “relative” matrix effect (also known as standard line-slope method). The post-column infusion assessment involves simultaneous injection of sample extract and continuous infusion of analyte into the LC-MS/MS system. This assessment allows identification of the chromatographic region that could possibly be affected by matrix effects and appropriate changes should be made to the elution condition to shift the analyte of interest retention time away from the area affected in the chromatogram (Bonfiglio et al. 1999). However, this assessment does not provide the degree of matrix effect that is affecting the analyte quantitatively and is time consuming especially for optimizing a method with multiple analytes.

Post-extraction spike method is based on the response of analyte spiked after sample preparation against neat standard solution and is expressed as a percentage, with values above or below 100% indicates ion enhancement or suppression, respectively (Matuszewski et al. 2003). This method allows quantitative assessment for ion suppression or enhancement of multiple analytes simultaneously. The presence of matrix effect can also be determined by “relative” matrix effect assessment by directly comparing standard line slopes (made from five different lots of a biofluid) constructed using identical compound, IS, sample preparation and chromatographic conditions. The standard line slopes and precision of the slopes were calculated to determine the absence or presence of “relative” matrix effect on the quantification of the analytes assessed. For a method to be acceptable (free from matrix effect), the precision value of the standard line slopes should not exceed a cut-off value of 3-4% (Matuszewski 2006). Figure 1.20 illustrates the block diagram and MS chromatogram for the two most commonly used matrix effect assessments: post-column infusion and post-extraction spike.

The degree of interference caused by matrix effect in LC-MS analysis does not only depend on the sample matrix. Selection of sample preparation, mobile phase, reagents, chromatographic separation and ionization interface used for the LC-MS method developed also influences the extent of matrix effect (Annesley 2007, Chambers et al. 2007). There are steps that can be taken to overcome matrix effects such as appropriate modification to a cleaner sample preparation technique, sample dilution (limited by the method sensitivity and not suitable for monitoring trace compound), use of smaller sample volume (also limited by the method sensitivity) and utilization of stable labelled internal standard. Matrix effect can also be minimized by using lower LC flow rate, so that the ion source is exposed to lesser amount of contaminants. Other strategies include to separate the interfering compound from target analyte(s) by changing the chromatographic conditions and if possible, use other

ionization technique that minimizes matrix effects (Chambers et al. 2007, Van Eeckhaut et al. 2009). Selection of appropriate MS ionization source (ESI, APPI, APCI) and mode (positive or negative) may also eliminate matrix effects (Hsieh et al. 2001, Janzen et al. 2008, Matuszewski et al. 1998, Mei et al. 2003).

Ion sources are prone to different degree of signal suppression or enhancement mainly because of difference in the ionization mechanisms (Himmelsbach 2012). A comparative study of LC-MS/MS method using three different ion sources, ESI, APCI and APPI for estradiol analysis in human serum and endometrial tissue demonstrated that ESI efficiently ionizes estradiol in negative polarity but estradiol is highly susceptible to ion suppression compared to the latter two ion sources (Keski-Rahkonen et al. 2013). APCI is also susceptible to signal suppression due to matrix effect but at a lower degree compared to ESI especially in the presence of hydrophobic interferences (Dams et al. 2003, Matuszewski 2006). For ESI, it is postulated that the signal suppression occurs when the analyte of interest competes for charge with co-eluting analyte. The co-analyte that has higher gas-phase proton affinity will be protonated first therefore reducing the intensity of the target analyte (Matuszewski et al. 2003). This is not the case for APPI, where its ionization mechanism is not based on charge affinity, therefore is less susceptible to ion suppression compared to ESI and APCI (Chen et al. 2009, Chu and Letcher 2008). The presence of high concentration non-volatile compounds (e.g. salts, ion-pairing agents, drugs) in the extracted sample matrix also lead to ion suppression by decreasing the ESI efficiency to form droplet and prevent evaporation (King et al. 2000). Furthermore, ESI is more susceptible to ion suppression in the presence of more polar analytes and the presence of molecules with higher mass that suppresses the signal of smaller molecules (Bonfiglio et al. 1999, Sterner et al. 2000). On the contrary, ion enhancement is caused by overlap of ions with specific m/z ratios, thus proper fragment ions selection with different combination of m/z may resolve the problem (Trufelli et al. 2011).

The degree of ion suppression differs between sample, compound and sample preparation (Bonfiglio et al. 1999).

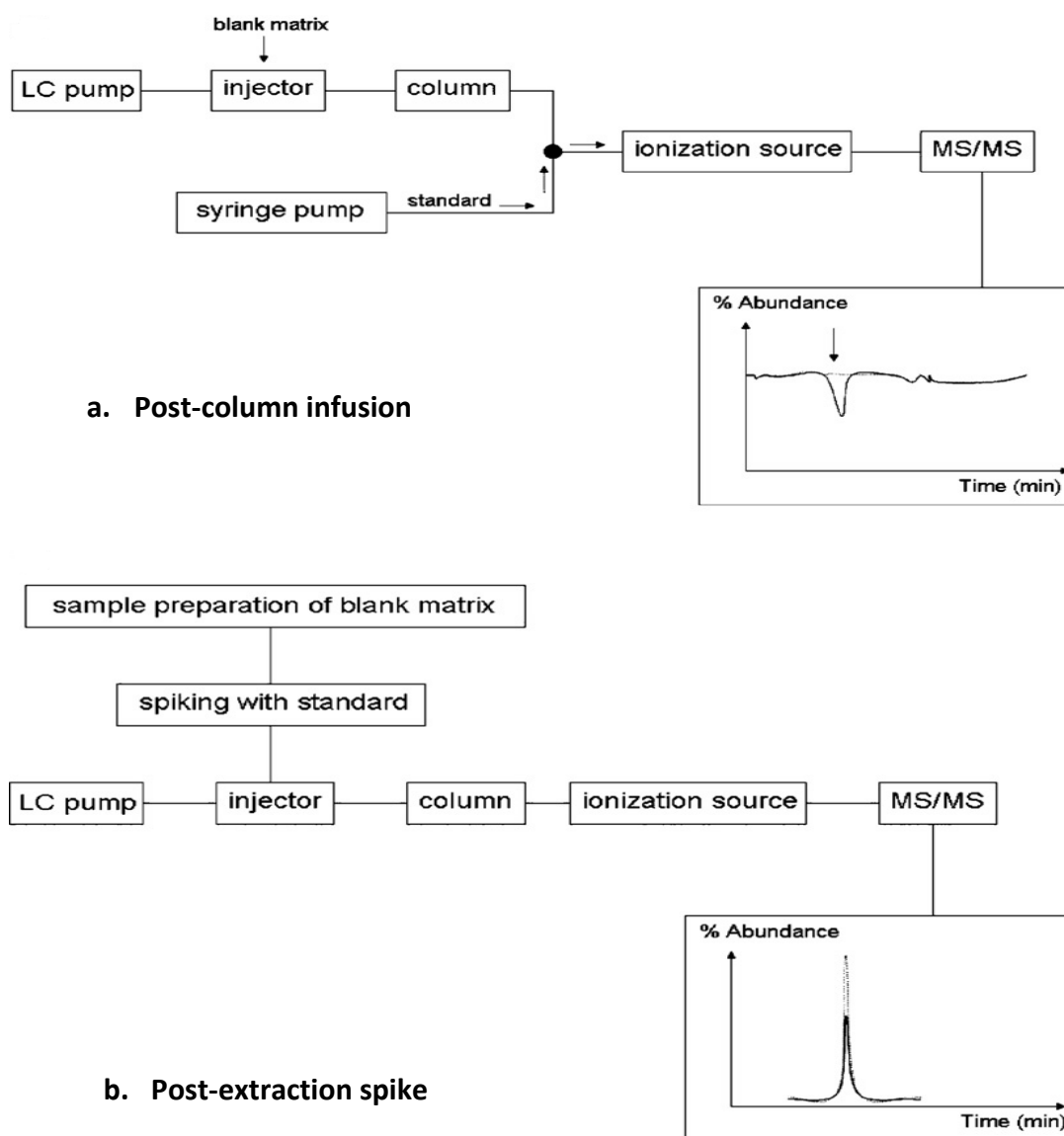


Figure 1.20 Matrix effects evaluation (a) post-column infusion and (b) post-extraction

- a)** For the post-column infusion, the analyte is infused into the LC stream using a ‘tee-mixer’ at a stable and constant flow to the MS ion source using an infusion pump. Sample extract (blank matrix) is injected via autosampler after extraction into the LC column. Elution of endogenous compound that interferes with the infused analyte will result in negative or positive peaks in the MS response due to ion suppression or enhancement, respectively. The arrow in the example above indicates ion suppression.
- b)** In the post-extraction spike method, comparison is made between the signal response of standard in sample extract (indicated as full peak in the chromatogram above) against the response obtained from standards in neat solution (dashed line). A reduction or increase in the response indicates ion suppression or enhancement, respectively. Adapted from (El-Aneed et al. 2009, Van Eeckhaut et al. 2009)

1.8.4 *Sample preparation*

Sample pretreatment prior to LC-MS is required to reduce the complexity of the sample. Sample preparation is necessary for the development of highly sensitive, accurate and specific steroid LC-MS/MS analysis (Shibata et al. 2014). Sample preparation involves extraction of the steroids typically with an organic solvent followed by purification step to remove unwanted matrix component from biological samples. Protein precipitation (PP), liquid-liquid extraction (LLE) and solid phase extraction (SPE) are common methods to separate analytes from sample matrix. However, it is important to evaluate whether the sample preparation technique selected: (1) provides a cleaner extract instead of magnifying (pre-concentrate) matrix effect and (2) is appropriate for the biofluids analyzed (Dams et al. 2003).

PP is achieved by adding solvent (e.g. acetonitrile, methanol and acetone) with low solubility and the precipitate of insoluble compounds is then separated from the soluble phase (e.g. centrifugation). The supernatant can be directly injected for analyte analysis or reconstituted in LC mobile phase before LC/MS analysis (Bakhtiar et al. 2002). PP is generally preferred for MS analysis for its simplicity but generally does not provide clean extract as many endogenous compounds such as fatty acids, lipids, phospholipids and endogenous peptides remains in the extract (Chambers et al. 2007). This is particularly a problem for ESI where the interfering compounds competes and co-elute with the target analyte by interfering with the droplet desolvation process (Bakhtiar and Majumdar 2007, Chambers et al. 2007). This co-eluting compound may also form adducts or react with the analyte of interest and interfere with the signal intensity (Gosetti et al. 2010). Studies have combined PP with other sample preparation to achieve cleaner samples (refer Table 1.3 for examples) (Carvalho et al. 2008). Some laboratories utilize a LC divert valve to elute early eluting compounds such as unwanted endogenous substances and salts to waste before the

extract is directed to the MS that may reduce matrix effect and MS contamination (Harwood and Handelsman 2009).

SPE is also widely used sample extraction method and provide cleaner extracts in comparison to PP (Chambers et al. 2007, Dams et al. 2003). This method involves separation of compounds between mobile and stationary phases which can be carried out either off-line (manual extraction) or on-line (automated extraction that is directly connected to the chromatographic system). On-line separation is less labour-intensive and time consuming compared to off-line SPE. The separation mechanism for SPE is similar to analytical chromatography where the analytes are retained in the stationary phase through the reverse-phase or ion exchanged SPE than removal of sample matrix followed by eluting the analyte with a strong organic solvent at the appropriate pH (Berrueta et al. 1995). Although SPE provides a cleaner extract compared to PP, studies have shown occurrence of matrix effect with this sample preparation method (Souverain et al. 2004). This is due to the pre-concentration step that increases unwanted interfering substance together with the target analyte(s). Possible alternative to remove the pre-concentration step (i.e. direct injection or dilution) but this will reduce the sensitivity (Dams et al. 2003).

LLE is widely used for extraction of small molecules such as drugs and hormones which gives clean extracts with high reproducibility (Janzen et al. 2008, Souverain et al. 2004, Xu et al. 2005). Besides being cost effective and highly selective, LLE sample extraction method is less susceptible to matrix effects compared to PP and SPE for common API ionization sources (Souverain et al. 2004). However, recovery of polar compounds has been reported to be low using LLE extraction depending on solvent pairs (Chambers et al. 2007). This extraction method involves separation of analytes from biological sample based on two different solubility properties. Non-polar analytes in aqueous sample (biological fluid) are extracted using an immiscible solvent (e.g. ethyl acetate, methyl tert-butyl ether and

hexane), with phase separation leaving the salts and proteins in the aqueous phase. Samples are normally vortex-mixed with the organic solvents followed by centrifugation to separate the solvent from aqueous phase. The organic solvent is recovered by freezing the aqueous phase or pipette. The organic layer is then dried and the residue that consist the analyte is reconstituted in the LC mobile phase. However, in some cases, the hydrophobic extract is directly injected upon method optimization (Medvedovici et al. 2011). The drawbacks of using LLE include low recovery for polar analyte and ionic compounds, multiple extraction steps may be required, difficulty to automate the extraction method and formation of emulsion in samples containing high levels of phospholipids that may affect the accuracy and extraction recovery of the target analyte (Leung and Fong 2014, Van Eeckhaut et al. 2009). Neutralizing compound with ionizable functional groups by adjusting the pH prior to organic solvent extraction helps to achieve high extraction recovery (Hendriks et al. 2007). Examples of studies utilizing different sample purification methods for MS steroid analysis are listed in Table 1.3.

1.9 Aims of study

The overall aim of this study is to develop and validate sensitive LC-MS/MS assays for quantitative endogenous and exogenous steroids analysis from various biological matrices for specific clinical applications. Androgens (testosterone, DHT, nandrolone), pro-androgens (DHEA) and estrogen (17 β -estradiol) were measured in various biological matrices including urine, serum and dried blood spots (DBS). LH was measured using validated ICL and IF assays for urine and serum. Urine is a preferred sample collection method as it provides convenience and is less intrusive especially for longitudinal field studies in children and adolescents. Urine sampling also avoids impracticality of multiple blood sampling for healthy volunteers and provides an integrated measurement especially for hormones secreted in pulsatile (LH) or diurnal (sex steroids in early puberty) manner. DBS is also a less invasive sampling method that requires only small volume of blood, simplified sample processing and is cost effective (i.e. shipping and sample storage without needing refrigeration). DBS sampling method is suitable for long-term pharmacological studies because the samples can be collected by the patients themselves with minimum training without the need of frequent visits to the clinic.

The specific aims of this thesis were:

1. To determine whether an androgen ester (nandrolone decanoate) marketed for intramuscular injection can be delivered effectively and safely as subcutaneous injection. To achieve this aim, DBS sampling method was optimized and LC-MS/MS method was developed and validated to measure testosterone and nandrolone from DBS.

- II. To determine whether commercially available IF and ICL LH immunoassays optimized for blood samples can be used for urine samples kept after prolonged frozen storage.
- III. To determine whether first morning void hormonal assessments in growing adolescents at various stages of pubertal progression requires adjustment to correct for hydration status and, if so, to determine whether creatinine or specific gravity are better adjustments.
- IV. To validate the feasibility of frequent urine sampling regimen and urine assay methodology for LH and sex steroids measurements using ICL and LC-MS/MS, respectively. Samples were collected from growing adolescents for a longitudinal study to assess changes in urine LH, estradiol and testosterone over 12 months by reference to contemporaneous changes in anthropometry and self-reported Tanner stages.

Chapter 2 Materials and Methods

The chemicals, sample preparation and instrument settings used in this study are described in this section.

2.1 LC-MS/MS assay

2.1.1 Chemicals

The chemicals and reagents used are listed in Table 2.1 and Table 2.2. All reagents used were analytical and chromatographic grade.

2.1.2 Instrumentation

LC analysis was carried out on a Shimadzu Nexera UHPLC system (Shimadzu Scientific Instruments, Columbia, MD). MS/MS analysis was performed on an API-5000 triple-quadrupole mass spectrometer (Applied Biosystem/MDS SCIEX, Ontario, Canada) equipped with an APPI source. The MS/MS nitrogen gas was supplied by a nitrogen gas generator (Peak Scientific Instruments Ltd, Scotland).

2.1.3 LC-MS/MS method for DBS steroids analysis

2.1.3.1 Preparation of calibration standards and quality control

Calibration standards and quality controls (QCs) were made from artificial blood according to a modified method described previously (Higashi et al. 2008). Briefly, venous whole blood was collected from a volunteer in a lithium heparin tube (Vacuette[®], Greiner Bio-one). The plasma separated from red blood cells by centrifugation at 1500 x g (at 4°C, 15 min) was discarded and the red blood cells were washed with 30 mL of saline (0.9% NaCl in distilled water) (to remove remaining plasma), centrifuged at 1500 x g for 15 min at 4 °C followed by discarding the supernatant; this step was repeated four times to remove any remaining plasma. Charcoal treated plasma was prepared by adding 50 mg of activated charcoal (BDH

Table 2.1 List of chemicals for steroid LC-MS/MS assay.

Chemical	Chemical name	Type	MW (g/mol)	Manufacturer
Testosterone	17 β -hydroxyandrost-4-en-3-one	Standard	288.4	NMI, Sydney, Australia
Nandrolone	17 β -hydroxy-19nor-4-andro-sten-3-one	Standard	274.4	Steraloids, Newport, RI, USA
17 β -Estradiol	17 β -estra-1,3,5(10)-estratriene	Standard	272.4	Steraloids, Newport, RI, USA
Dihydrotestosterone	17 β -hydroxy-5 α -androstan-3-one	Standard	290.4	NMI, Sydney, Australia
Dehydroepiandrosterone	5-androsten-3 β -ol-17-one	Standard	288.4	NMI, Sydney, Australia
Testosterone glucuronide	17 β -3-oxoandrost-4-en-17-yl b-D-glucopyranosiduronic acid	Standard	464.6	NMI, Sydney, Australia
17 β -Estradiol glucuronide	1,3,5(10)-estratrien-3, 17 β -diol 17-glucosiduronate	Standard	448.5	Steraloids, Newport, RI, USA
Dihydrotestosterone glucuronide	3-oxo-5 α -androstan-17 β -yl glucosiduronic acid	Standard	466.6	NMI, Sydney, Australia
Dehydroepiandrosterone glucuronide	5-androsten-3 β -ol-17-one glucosiduronate	Standard	464.5	Steraloids, Newport, RI, USA
d ₃ -Testosterone	16,16,17-d ₃ -17 β -hydroxyandrost-4-ene-3-one	Internal standard	291.4	NMI, Sydney, Australia
d ₄ -Estradiol	2,4,16,16-d ₄ -17 β -estra-1,3,5(10)-estratriene	Internal standard	276.4	Cambridge Isotope Laboratory, USA
d ₃ -Dihydrotestosterone	5 α -(16,16,17 α - ² H ₃)-5 α -Androstan-17 β -ol-3-one	Internal standard	293.5	NMI, Sydney, Australia
d ₂ -Dehydroepiandrosterone	16,16- d ₂ -5-androsten-3 β -ol-17-one	Internal standard	290.4	Steraloids, Newport, RI, USA

Abbreviations: NMI: National Measurement Institute; MW: molecular weight; d: deuterated; AR: analytical reagent; HPLC: high performance liquid chromatography.

Table 2.2 List of reagents for steroid LC-MS/MS assay.

Reagent	Type	MW (g/mol)	Manufacturer
Methanol	Solvent (HPLC grade)	32.04	RCI LabScan, Bangkok, Thailand
Toluene	Solvent (HPLC grade)	92.14	RCI LabScan, Bangkok, Thailand
Methyl tert-butyl ether	Solvent (AR grade)	88.15	RCI LabScan, Bangkok, Thailand
Potassium carbonate (K ₂ CO ₃)	Buffer	138.21	Sigma-Aldrich, St Louis, MO, USA
Disodium hydrogen phosphate (NaHPO ₄ anhydrous)	Buffer	141.98	Sigma-Aldrich, St Louis, MO, USA
Sodium dihydrogen phosphate (NaH ₂ PO ₄ ·2H ₂ O)	Buffer	156.01	UNIVAR Analytical Reagent, NSW, Australia
Sodium chloride (NaCl)	Salt	58.44	UNIVAR Analytical Reagent, NSW, Australia
Sodium azide (NaN ₃)	Preservative	65.01	Ajax Chemical, Sydney, Australia

Chemicals, Victoria, Australia) to every milliliter of plasma. The mixture was stirred gently for an hour at room temperature followed by centrifugation at 1200 x g for 30 min. The supernatant was then filtered (filter paper #1, Advantec Co, Tokyo, Japan) to remove the remaining charcoal. The steroid-free plasma (tested with LC-MS/MS assay to ensure the plasma is free from endogenous testosterone) was added to the washed red blood cells to obtain a hematocrit of 0.45. The artificial blood prepared was then spiked with stock solution of testosterone (T) and nandrolone (N) to attain final concentrations of 0.05-32 ng/mL for T and 0.156-10 ng/mL for N. QCs were made up from a separate lot of artificial blood at low, medium and high concentrations (0.1, 1, and 16 ng/mL for T; 0.3, 1.25 and 5 for N). Fifty microliters of standards and QCs was spotted onto filter card (Whatman 903 protein saver cards, WHAT10534612; GE Healthcare, Westborough, MA), allowed to dry overnight at room temperature and stored in a sealed plastic bag at room temperature until analysis.

2.1.3.2 DBS sample preparation

Steroids were extracted from the whole DBS which were cut and transferred into 15 mL disposable borosilicate glass tubes (16×150 mm). One milliliter of methanol:water (1:1) was added followed by 10 µL of internal standard (25 ng/mL d₃-T). The mixture was shaken mechanically for 30 min and then again for another 20 min after addition of methyl tert-butyl ether (MTBE) (1.5 mL). The tubes were centrifuged at 300 x g for 5 min and followed by the transfer of the organic layer into 5 mL disposable borosilicate glass tubes tube (12 × 75 mm). The solvent was evaporated to dryness in heating block at 50 °C overnight in a fume hood. The dried residue was reconstituted in 70 µL of 50% methanol in water, transferred into 96-well polypropylene V-bottom microtiter plate (PerkinElmer, MA, USA) and 45 µL was injected into the LC-MS/MS system.

2.1.3.3 *Blood volume determination*

We aimed to use the whole capillary blood volume on the filter card rather than taking a subsample (e.g. by a punch) as that risked non-homogenous distribution of blood impregnation on the filter paper. To determine the capillary blood volume on the filter card, a linear equation was derived from a plot of weight of blood on filter card (weight of blood-impregnated filter paper minus weight of unused filter paper) versus volume of blood spotted on filter card ($R^2 = 0.997$) (Figure 2.1). To generate this calibration, venous blood was collected from a volunteer (hematocrit, 0.45) and immediately a set of increasing volume of blood (10-250 μL) was spotted using a calibrated pipette onto filter cards with five replicates. The spots were dried overnight, cut out and weighed. To determine the accuracy of this equation, known volumes (40, 50, 60, 70 μL) of whole venous samples collected from 10 male volunteers (hematocrits 0.40-0.50) were spotted onto filter cards in triplicate and dried overnight. The estimated weight of the blood spot on the filter card (using a Mettler balance AE240) was then compared with the nominal volume of blood and accuracy (nominal volume \times 100/actual volume) was 95-106% with coefficient of variation (CV) of 0.2-7.1% for all volumes tested.

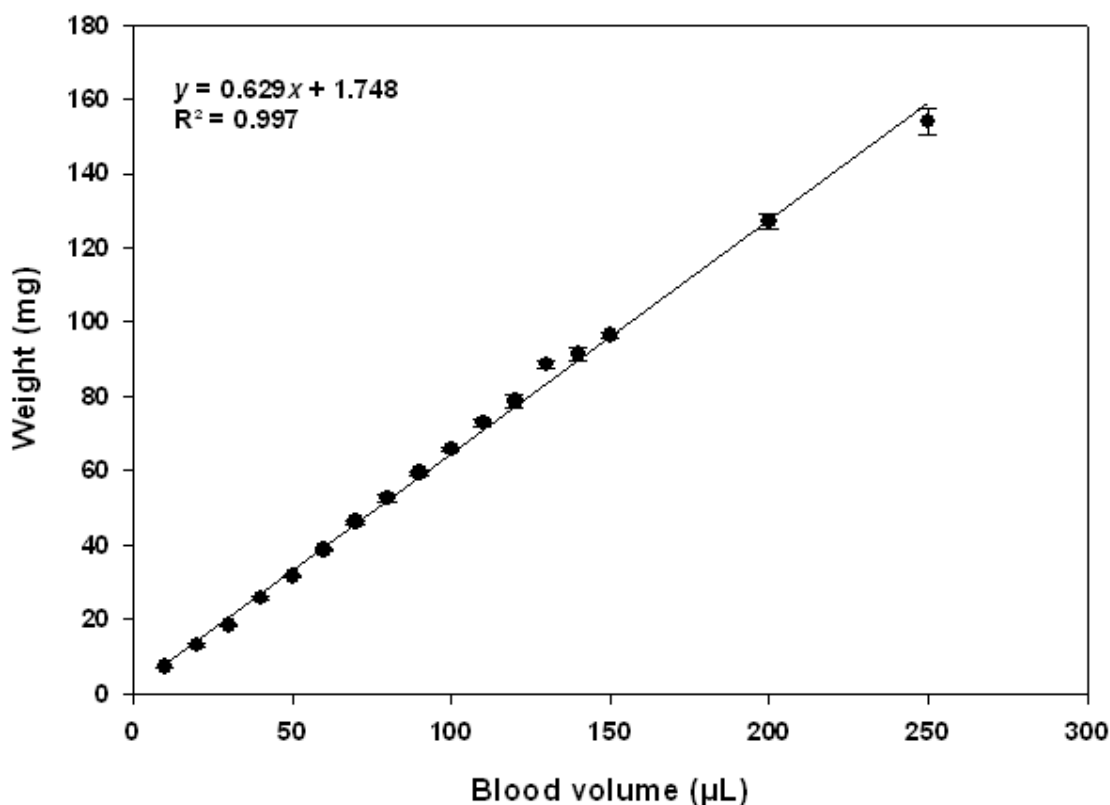


Figure 2.1 Relationship between amount of blood and weight of filter card (n=5).

To determine the capillary blood volume on the card, a linear equation derived from a plot; weight of blood on filter card versus volume of blood spotted on filter card ($y = 0.629x + 1.748$; $R^2 = 0.997$) was used.

2.1.3.4 Comparison between whole DBS and fixed-sized disc

To determine the variation using whole DBS and fixed-sized paper disc, correlation between T venous DBS concentration obtained from two different sampling methods (1) whole blood spot and (2) 6 mm punch disc, were compared against plasma T concentration. For this purpose, venous blood was collected in lithium heparin tube from twenty male volunteers (hematocrit, 0.40-0.51). Fifty microliters of blood was spotted directly on the filter card using a calibrated pipette and the remaining blood was centrifuged at $1500 \times g$ for 15 min at 4°C to separate plasma. Plasma was extracted according to method described in Section 2.1.5.1. After overnight drying at room temperature, the DBS was either cut out entirely using a pair scissors or discs were punched out using a 6 mm puncher (n=3) from the same blood sample

followed by extraction and measured using LC-MS/MS assay. The plasma and DBS T concentration were correlated according to the formula $[\text{plasma}_T = \text{DBS}_T / (1 - \text{hematocrit})]$. Venous whole DBS T was unbiased in relation to plasma T (standard deviation 6.3 ± 7.2 (SD) % in Bland-Altman analysis; Pearson correlation $r=0.98$) whereas the punch disc produced an upward bias (deviation 28 ± 9.2 %; $r=0.97$) (Figure 2.2). The finding indicates that the venous whole DBS T measurements correlate well with the corresponding plasma T levels. However, the punch disc overestimates the T concentration in comparison to plasma T levels. All further DBS measurements used whole blood spotted on the filter card and the volume of blood was determined by first cutting the whole DBS and weighing the blood spot followed by calculation using the equation from Figure 2.1 and adjusted for hematocrit.

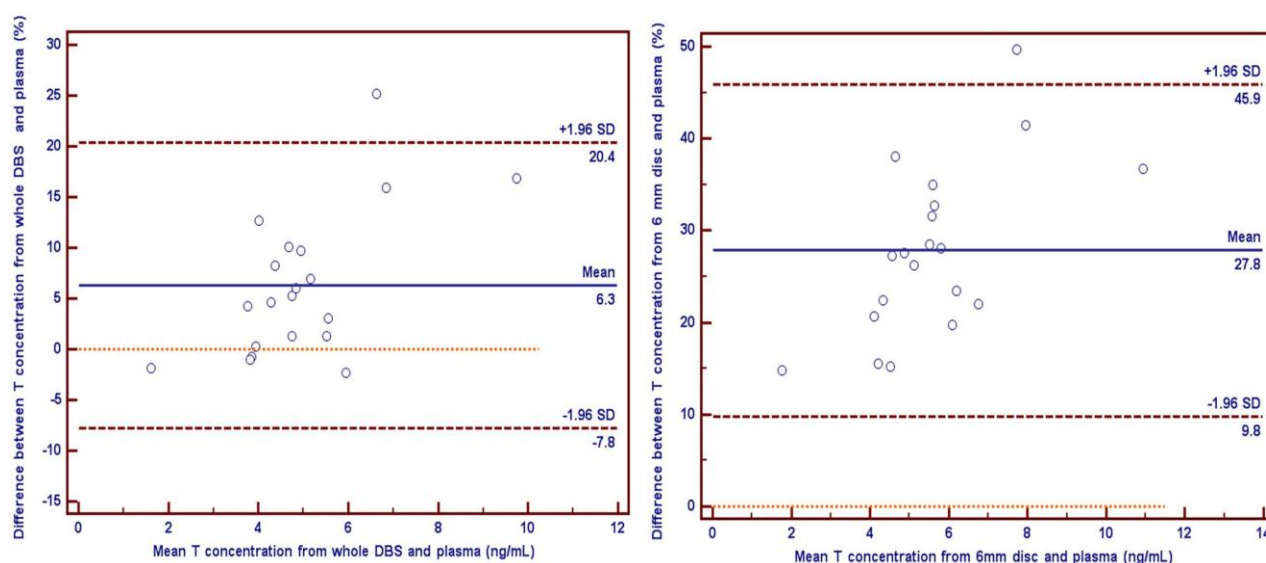


Figure 2.2 Bland-Altman plots for comparison of testosterone (T) concentration obtained from whole DBS versus plasma (left panel) and 6 mm punch disc versus plasma (right panel).

The Bland-Altman plots represent the difference between two sampling methods: 1) whole blood spot and 2) 6 mm punch disc against plasma T concentration. The solid and the dashed lines represent the observed average and 95% limit of confidence (± 1.96 SD), respectively.

2.1.3.5 LC-MS/MS parameters

The LC column was an Ascentis[®] Express Phenyl-Hexyl column (10 cm x 2.1 mm, 2.7 μ m; Supelco, Sigma-Aldrich, PA; Cat. no. 53336-U) equipped with an Ascentis[®] Express Phenyl-Hexyl guard cartridge (0.5 cm x 2.1 mm, 2.7 μ m; Supelco, Sigma-Aldrich, PA; Cat. no. 53524-U). The column temperature and autosampler were set at 35 and 4 $^{\circ}$ C, respectively. The elution solvents were water (A) (18M Ω quality; Millipore Milli-Q system, Bedford, MA, USA) and methanol (B). The gradient elution was performed at the flow rate of 0.75 mL/min with the organic solvent started with 10% B (0-0.10 min), 55-65% B (0.11-4.99 min), 100% B (5.00-5.70 min), 10% B (5.71-6.50 min). Toluene was used as the APPI dopant, delivered at the flow rate of 0.07 mL/min. T and N MS/MS analysis was carried out in positive ion mode. The MS conditions of N, T and d₃T are listed in Table 2.3. N, T and d₃T eluted at 3.62, 4.15 min and 4.19 min, respectively (Figure 2.3). The following MS parameters were used: ion source gas 1: 55 psi; ion source gas 2: 50 psi; curtain: 12 psi; collision gases: 6 psi; ion source temperature: 500 $^{\circ}$ C; ion spray voltage: 750V. Data were quantified using Analyst software (version 1.6, AB Sciex).

Table 2.3 Mass spectrometry parameters for nandrolone, testosterone and d₃-testosterone measurements.

Steroid Ion Fragmented		MRM transition Q1 \rightarrow Q3	Dwell time (msec)	DP	EP	CE	CXP
N	[M+H] ⁺	275.2 \rightarrow 109.1	500	190	10	40	12
T	[M+H] ⁺	289.3 \rightarrow 109.1	500	190	10	35	12
d ₃ T	[M+H] ⁺	292.3 \rightarrow 109.1	250	190	10	35	12

Abbreviations: N: nandrolone; T: testosterone; d₃T: deuterated testosterone; MRM: multiple-reaction-monitoring; DP: declustering potential; EP: entrance potential; CE: collision energy; CXP: collision cell exit potential.

2.1.3.6 Method validation

Linearity, lower limit of quantification (LLOQ), recovery, process efficiency, within and between day precision and accuracy were evaluated during the validation of the analytical method according to FDA guidance (FDA 2001). The linearity was evaluated on the basis of three calibration curves. Response of peak area ratio of T and N to internal standard (d_3T) was plotted against known steroid concentrations. The assay acceptance criterion for each back-calculated standard concentration was 15% CV from the nominal value. The LLOQ was evaluated by five replicates of the lowest concentrations of the calibration curve with the accepted deviation values of 20%. The calibration curve was quadratic for both T and N with $1/x$ weighing with correlation coefficient (r) greater than 0.999. The LLOQ was 50 pg/mL for T and 156 pg/mL for N using a 50 μ L blood sample.

For within and between-day assay validation, QC samples were prepared in artificial blood as described in Section 2.1.3.1 with the T and N at three concentration levels of low, medium and high (0.1, 1, and 16 ng/mL for T; 0.3, 1.25 and 5 ng/mL for N) in five separate runs. The within-day precision (% CV) was 2.5-4.4% with accuracies of 95-108% and the between-day precision was 4.9-13.5% with accuracies of 100-106% at all QC levels (Table 2.4).

The recovery, matrix effect and process efficiency of the method was carried out according to the method described previously (Matuszewski et al. 2003) at low, medium and high concentrations of each compound. All extraction recoveries and process efficiencies were between 96-107% with no ion suppression or enhancement for either analyte (matrix effect recoveries between 96-102%). Refer Table 2.4 for the detailed validation data.

Specificity of T against isomers with same molecular weight, DHEA and epitestosterone (16 ng/mL) were evaluated. The retention time of these compounds did not co-elute with the retention time of T.

Stability of T and N on DBS was evaluated at 4°C, room temperature and 37°C for short term (42 days) and long term (742 days) at low, medium and high concentrations (0.1, 1, and 16 ng/mL for T; 0.3, 1.25 and 5 ng/mL for N) measured against fresh calibration spotted onto filter card and extracted immediately after overnight drying.

The stability of T on DBS was well maintained at 3 temperatures and all QCs tested with accuracies of 79.2-113.7% (CV 0.4 -11.8%) (Table 2.4). N was also stable on DBS at all 3 conditions and all QCs tested up to 42 days (accuracies 82.5-110.7%; CV 0.4-13%). Long term storage of DBS showed a decline in N stability at room temperature and 37°C in the medium and high QCs (accuracies 65.6-75.7%; CV 0.9-9.6%). The N stability was well maintained at 4°C for all QCs up to 742 days with accuracies of 99.9-116.6% (CV 4.2-7.7%) (Table 2.5).

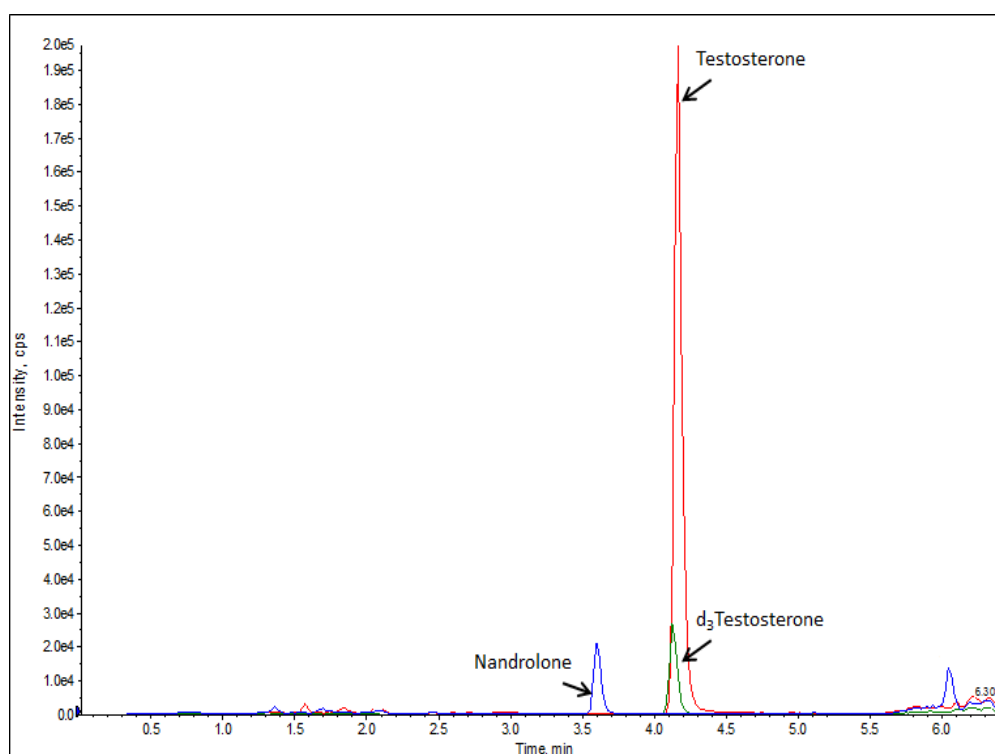


Figure 2.3 Dried blood spot method analytes chromatogram.

Table 2.4 LC-MS/MS DBS method validation data.

Analyte	LLOQ (pg/ml)	QC	Within-day (%)		Between-day (%)		ER (%)	ME (%)	PE (%)
			Accuracy	CV	Accuracy	CV			
T	50	Low	99.8	4.4	100.3	13.5	104.2	99.8	104.0
		Medium	98.4	3.0	103.1	5.2	106.4	95.6	101.7
		High	107.5	2.5	105.9	4.9	106.3	96.3	102.4
N	156	Low	95.0	3.0	101.5	10.6	106.5	95.8	102.0
		Medium	105.8	4.1	102.6	8.4	96.4	100.9	97.3
		High	105.2	3.8	103.8	5.7	99.5	101.7	101.2

Abbreviations: LLOQ: lower limit of quantitation; QC: quality control; ER: extraction recovery; ME: matrix effect; PE: process efficiency; CV: coefficient of variation

Table 2.5 Stability data of testosterone and nandrolone on DBS at three different storage conditions for short (42 days) and long term storage (742 days).

Time (days)	Storage condition	Testosterone						Nandrolone					
		Low		Medium		High		Low		Medium		High	
		Accuracy	CV	Accuracy	CV	Accuracy	CV	Accuracy	CV	Accuracy	CV	Accuracy	CV
3	RT	90.9	7.4	106.7	3.0	105.6	5.3	105.3	5.5	105.7	4.2	106.3	6.2
	4C	97.6	3.1	101.1	3.4	107.3	5.5	110.7	2.8	93.8	9.2	105.5	7.0
	37C	94.4	3.5	96.7	1.6	108.7	3.7	98.6	6.2	107.0	2.4	107.7	3.9
7	RT	91.8	9.0	98.7	4.0	103.9	4.0	99.4	6.8	94.6	5.2	96.3	2.2
	4C	101.3	5.5	104.7	3.9	105.3	0.6	108.3	0.9	103.3	4.3	100.7	1.2
	37C	94.0	11.6	99.5	3.5	108.3	0.9	90.4	4.5	103.2	3.6	101.7	1.4
14	RT	96.5	7.1	94.8	4.4	98.2	1.9	103.8	6.9	87.6	1.1	88.7	0.9
	4C	104.6	5.7	99.9	4.5	98.7	3.5	91.4	5.2	98.1	6.0	98.1	1.0
	37C	93.2	6.0	97.5	5.8	93.7	5.0	88.3	2.9	85.7	5.2	85.5	3.2
28	RT	99.0	8.0	97.0	1.5	101.5	4.7	85.7	2.1	86.6	12.2	91.5	3.8
	4C	88.1	8.1	103.0	8.3	106.0	2.4	94.2	9.5	94.8	2.6	97.0	4.6
	37C	87.0	11.8	95.0	4.4	95.6	4.4	86.4	13.0	82.5	8.1	88.4	6.4
42	RT	105.0	11.0	89.9	3.1	91.1	4.2	87.0	3.0	85.7	2.3	91.2	6.4
	4C	101.4	6.8	99.5	10.1	98.3	0.4	99.9	7.5	92.8	11.0	98.1	0.4
	37C	93.8	2.3	86.3	2.1	87.9	5.2	86.3	3.6	83.0	7.3	85.0	7.0
742	RT	107.0	8.1	92.9	1.4	94.4	0.7	101.4	4.3	75.7	9.6	74.0	4.0
	4C	109.3	6.7	104.3	2.4	107.7	2.9	111.6	7.7	109.63	7.4	99.9	4.2
	37C	113.7	5.2	89.2	4.3	79.2	3.9	106.7	3.0	74.1	6.6	65.6	0.9

Abbreviations: RT: room temperature; CV: coefficient of variation

2.1.4 LC-MS/MS method for urinary steroids analysis

2.1.4.1 Urine sample preparation

Urine samples were extracted by LLE. Urine (500 μL) was transferred into 15 mL disposable borosilicate glass tubes (16 \times 150 mm), spiked with 10 μL of internal standards (25 ng/mL d_3T , 75 ng/mL d_4E_2 , 200 ng/mL d_2DHEA and 250 ng/mL d_3DHT) and had 500 μL of 0.1M phosphate buffer (pH 6.2) and 10 μL β -glucuronidase from *Escherichia coli* K12 (Roche Diagnostic, Mannheim, Germany; Cat. no.: 03707598001) added. After overnight incubation at room temperature, 100 μL of potassium carbonate (20%: w/v) was added followed by 1.5 mL of MTBE. The mixture was shaken mechanically for 15 min, centrifuged at 2700 x g for 15 min followed by transfer of the organic layer into clean 5 mL disposable borosilicate glass tubes tube (12 \times 75 mm) and evaporated to dryness in a heating block at 50 C overnight in a fume hood. The dried residue was reconstituted in 75 μL of 20% methanol in water, transferred into 96-well polypropylene V-bottom microtiter plate and 50 μL was injected into the LC-MS/MS system.

2.1.4.2 LC-MS/MS parameters

The LC elution solvents were water (A) and methanol (B). For urine extracts, separation was achieved on a Ascentis[®] Express Phenyl-Hexyl column (10 cm x 2.1 mm, 2.7 μm) equipped with a Ascentis[®] Express Phenyl-Hexyl guard cartridge (0.5 cm x 2.1 mm, 2.7 μm). The gradient elution was performed at the flow rate of 0.6 mL/min with the organic solvent starting with 10% B (0-0.10 min), 55% B (0.11-4.99 min), 65% B (5.00-6.50 min), 65-100% B (6.50-7.00 min), 100% B (7.01-8.00 min), 10% B (8.01- 9.50 min). The column temperature and autosampler were set at 40 and 4 C, respectively. Toluene was used as the APPI dopant, delivered at the flow rate of 0.06 mL/min.

Following LC separation, samples were subjected to MS/MS analysis. E₂ was detected in negative ion mode whereas the androgens (T, DHT and DHEA) were detected in positive ion mode. The optimization of MRM settings and LC-MS/MS system conditions for each analyte have been listed in Table 2.6. The following MS parameters were used: ion source gas 1: 55 psi; ion source gas 2: 50 psi; curtain: 12 psi; collision gases: 6 psi; ion source temperature: 500 °C; ion spray voltage: 750V (for positive mode) and -750V (for negative mode).

Table 2.6 Mass spectrometry parameters for estradiol, testosterone, dihydrotestosterone, dehydroepiandrosterone and its corresponding isotopically labeled internal standards.

Steroid Ion Fragmented		MRM transition Q1→Q3	Dwell time (msec)	DP	EP	CE	CXP
E ₂	[M-H] ⁻	271.1→145.0	100	-100	-10	-57	-15
d ₄ E ₂	[M-H] ⁻	275.1→147.0	75	-100	-10	-57	-15
T	[M+H] ⁺	289.3→109.1	100	80	10	35	15
d ₃ T	[M+H] ⁺	292.3→109.1	75	80	10	35	15
DHT	[M-H ₂ O+H] ⁺	273.3→123.3	100	80	10	31	15
d ₃ DHT	[M-H ₂ O+H] ⁺	276.3→123.3	75	80	10	31	15
DHEA	[M-2H ₂ O+H] ⁺	253.1→197.1	100	80	10	30	15
d ₂ DHEA	[M-2H ₂ O+H] ⁺	255.3→197.2	75	80	10	30	15

Abbreviations: E₂: estradiol; d₄E₂: deuterated estradiol; T: testosterone; d₃T: deuterated testosterone; DHT: dihydrotestosterone; d₃DHT: deuterated dihydrotestosterone; DHEA: dehydroepiandrosterone; d₂DHEA: deuterated dehydroepiandrosterone; MRM: multiple-reaction-monitoring; DP: declustering potential; EP: entrance potential; CE: collision energy; CXP: collision cell exit potential; Q1: first quadrupole; Q3: third quadrupole.

2.1.4.3 Method validation

The LC-MS/MS method for urinary steroid quantitation was validated for linearity, LLOQ, recovery, matrix effects, process efficiency, within and between day precision and accuracy according to FDA guidance for bioanalytical method validation (FDA 2001). For the validation and calibration, blank urine comprised a pool of urine from two children aged 3-4 years of age was used. The linearity was evaluated on the basis of three calibration curves. Response of peak area ratio of the steroids to internal standard was plotted against known steroid concentrations using quadratic regression with $1/x$ weighing. The assay acceptance criterion for each back-calculated standard concentration was 15% CV from the nominal value. The LLOQ was evaluated by five replicates of the lowest concentrations of the calibration curve with the accepted deviation values of 20% using 500 μ L of urine.

The calibration curves fitted quadratic functions ranging from; 0.05-32 ng/mL E_2 , 0.025-32 ng/mL T, 0.1-32 ng/mL DHT and 0.2-128 ng/mL DHEA, with correlation coefficient (r) greater than 0.999. The precision was 2.6-7.2% (within-day) and 4.8-9.7% (between-day) with accuracies of 97-110% (within-day) and 95-108% (between-day) for all QC levels (steroids spiked as glucuronides at 0.2, 4 and 32 ng/mL for T; 0.8, 4 and 32 ng/mL for E_2 , DHT and DHEA) (Table 2.8).

The recovery, matrix effects and process efficiency were quantified as described previously (Matuszewski et al. 2003) at low (0.4 ng/mL), medium (1.6 ng/mL) and high (16 ng/mL) concentrations of each compound. The extraction recovery and process efficiency were between 91-118%, whereas the matrix effect recoveries were between 92-119% for all the analytes spiked at low, medium and high concentrations (Table 2.8).

The β -glucuronidase enzyme was evaluated for hydrolysis efficiency at room temperature (overnight). Five replicates were spiked with testosterone glucuronide (TG), estradiol

glucuronide (E₂G), dihydrotestosterone glucuronide (DHTG) and dehydroepiandrosterone glucuronide (DHEAG) at 40 ng/mL and another five replicates were spiked with the unconjugated steroid at the equivalent amount (25 ng/mL of T, DHT and DHEA; 24 ng/mL of E₂). The samples were then extracted according to the method described in section 2.1.4.1. The area ratios of the analyte to internal standards were compared and the enzyme deconjugation efficiency was between 88-102% after overnight incubation at room temperature for all the analytes.

For specificity, structurally related compounds that potentially may interfere with the method were also evaluated (Table 2.7). All the steroids listed did not interfere with the retention time of E₂, T, DHT and DHEA.

Table 2.7 List of possible interfering compounds for LC-MS/MS urinary and serum methods.

Analyte	Possible interfering compound(s)	Manufacturer
E ₂	Estrone (1,3,5[10]-estratrien-3-ol-17-one)	Steraloids, Newport, RI, USA
T	Epitestosterone (17 α -hydroxyandrost-4-ene-3-one) Dehydroepiandrosterone (5-androsten-3 β -ol-17-one)	National Measurement Institute, Sydney Australia
DHT	Androsterone (17 β -hydroxy-5 α -androstan-3-one), 3 α -diol (5 α -androstane-3 α ,17 β -diol) 3 β -diol (5 α -androstane-3 β ,17 β -diol)	National Measurement Institute, Sydney Australia
	Etiocholanolone (5 β -Androstan-3 α -ol-17-one), Epitiocholanolone (5 β -Androstan-3 β -ol-17-one), 5-androstenediol (5-androsten-3 β ,17 β -diol), Epiandrosterone (5 α -androstan-3 β -ol-17-one),	Steraloids, Newport, RI, USA

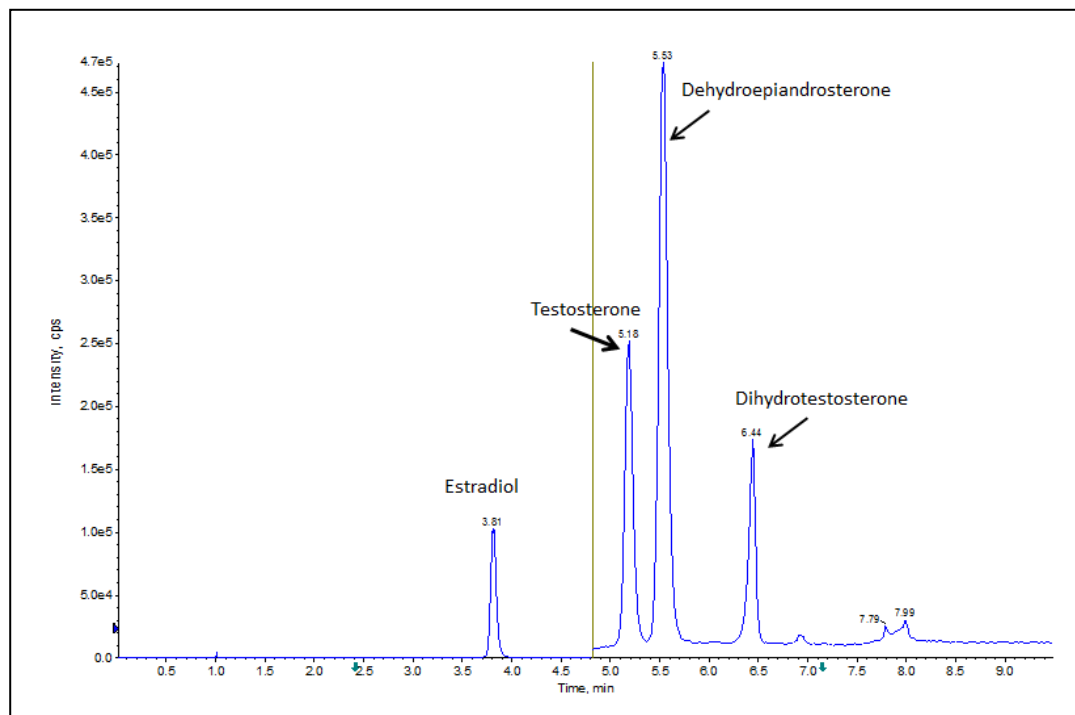


Figure 2.4 Urinary steroids method chromatogram.

Table 2.8 LC-MS/MS urinary steroids method validation data.

Analyte	LLOQ (pg/ml)	QC	Within-day (%)		Between-day (%)		ER (%)	ME (%)	PE (%)
			Accuracy	CV	Accuracy	CV			
E ₂	50	Low	99.9	4.5	95.4	6.3	97.0	106.4	103.2
		Medium	104.4	3.4	100.1	5.6	96.0	101.6	97.5
		High	105.0	2.6	104.2	9.7	95.1	106.3	101.1
T	25	Low	97.2	3.6	103.2	7.2	97.3	103.9	101.1
		Medium	100.7	4.4	104.3	7.8	94.4	106.0	100.0
		High	102.4	2.8	95.6	6.7	92.7	107.9	100.0
DHT	100	Low	103.4	7.2	99.1	6.6	100.5	105.0	105.6
		Medium	102.6	3.7	99.7	5.8	103.3	91.7	94.7
		High	102.6	4.4	95.6	7.7	90.6	107.7	97.6
DHEA	200	Low	110.2	5.2	97.3	4.8	97.5	118.6	115.6
		Medium	101.1	5.5	101.4	7.8	101.7	117.3	118.1
		High	99.3	5.6	107.9	6.4	98.5	111.5	109.8

Abbreviations: LLOQ: lower limit of quantitation; QC: quality control; ER: extraction recovery; ME: matrix effect; PE: process efficiency; CV: coefficient of variation.

2.1.5 LC-MS/MS method for serum steroids analysis

2.1.5.1 Serum sample preparation

Serum samples were extracted by LLE. Serum aliquots (200 μ L) were transferred into 5mL disposable borosilicate glass tubes (12 \times 75 mm), spiked with 50 μ L of internal standard (5 ng/mL d₃T and d₄E₂; 6.25 ng/mL d₃DHT; 7.5 ng/mL d₂DHEA) and had 1 mL of MTBE added. The tubes were vortex mixed for 1 min, allowed to phase separate at 4 °C for 1 h before being placed in a -80 °C freezer for 30 min to freeze the lower aqueous layer. The upper organic layer was decanted into clean glass tubes and the solvent evaporated overnight at 50 °C in a fume hood. The residue was then reconstituted in 75 μ L of 20% methanol in water, transferred into 96-well polypropylene V-bottom microtiter plate and 50 μ L was injected into the LC-MS/MS system.

2.1.5.2 LC-MS/MS parameters

LC separation was achieved on a Phenomenex Kinetex XB-C18 column (5 cm x 2.1 mm, 1.7 μ m; Cat. no. OOB-4498-AW) protected by Phenomenex C18 guard cartridge (Cat. no. AJO-8782). The LC column temperature and autosampler were set at 40 and 4 °C, respectively. The elution solvents were water (A) and methanol (B). A gradient elution was performed at a flow rate of 0.5 mL/min with 25% B (0-0.10 min), 52-62% B (0.11-4.30 min), 100% B (4.31-5.45 min), 25% B (5.46-7.00 min). Toluene was used as the APPI dopant, delivered at the flow rate of 0.05 mL/min. The optimization of LC-MS/MS MRM settings and system conditions for serum assay was identical with the urine assay. Please refer section 2.1.4.2 for the MS/MS parameters.

2.1.5.3 Method validation

The LC-MS/MS method for urinary steroid quantitation was validated for linearity, LLOQ, recovery, matrix effects, process efficiency, within and between day precision and accuracy according to FDA guidance for bioanalytical method validation (FDA 2001). For the validation and calibration, 4% bovine serum albumin in phosphate buffer was used. The linearity was evaluated on the basis of three calibration curves. Response of peak area ratio of

the steroids to internal standard was plotted against known steroid concentrations using quadratic/linear regression (according to analyte) with 1/x weighing. The assay acceptance criterion for each back-calculated standard concentration was 15% CV from the nominal value. The LLOQ was evaluated by five replicates of the lower concentrations of the calibration curve with the accepted deviation values of 20% using 200 μ L of serum.

The calibration curves were quadratic for T and DHEA (ranging between 0.01-16 ng/mL and 0.02-32 ng/mL, respectively) and linear for E₂ and DHT (ranging between 5-800 pg/mL and 0.01-16 ng/mL, respectively) with the r greater than 0.999. The precision was 5.3-13.5% (within-day) and 8.1-15.0% (between-day) with accuracies of 90-113% (within-day) and 95-111% (between-day) for all QC levels (0.01, 0.04 and 0.4 ng/mL for E₂; 0.025, 0.8, and 8 ng/mL for T; 0.2, 0.8 and 8 ng/mL for DHT; 0.05, 1.6, and 16 ng/mL for DHEA) (Table 2.9).

The recovery, matrix effects and process efficiency were quantified as described previously (Matuszewski et al. 2003) at low, medium and high concentrations of each compound (0.005, 0.08 and 0.4 ng/mL for E₂; 0.05, 0.4, and 8 ng/mL for T and DHT; 0.02, 0.8, and 16 ng/mL for DHEA). All the extraction recovery and process efficiency were within the range of 79-113%, whereas, the matrix effect were between the range of 81-107% for all the analytes spiked at low, medium and high concentrations (Table 2.9).

For specificity, structurally related compounds that potentially may interfere with the method were also evaluated (Refer Table 2.7 for compound list). All the steroids listed did not interfere with the retention time of E₂, T, DHT and DHEA.

Table 2.9 LC-MS/MS serum steroids method validation data.

Analyte	LLOQ (pg/ml)	QC	Within-day (%)		Between-day (%)		ER (%)	ME (%)	PE (%)
			Accuracy	CV	Accuracy	CV			
E ₂	5	Low	96	13.0	101	14.5	79	101	80
		Medium	90	11.2	104	11.0	103	93	96
		High	103	7.7	104	9.9	111	81	89
T	25	Low	104	13.4	103	15.0	92	87	91
		Medium	97	5.3	103	9.0	92	83	83
		High	113	8.4	105	11.0	100	103	105
DHT	100	Low	101	13.5	111	12.9	89	88	91
		Medium	102	8.9	95	10.4	112	107	113
		High	107	8.9	100	11.3	87	102	89
DHEA	50	Low	99	12.5	106	14.6	98	97	100
		Medium	110	7.1	106	8.1	99	104	95
		High	107	5.6	107	9.7	91	91	100

Abbreviations: LLOQ: lower limit of quantitation; QC: quality control; ER: extraction recovery; ME: matrix effect; PE: process efficiency; CV: coefficient of variation.

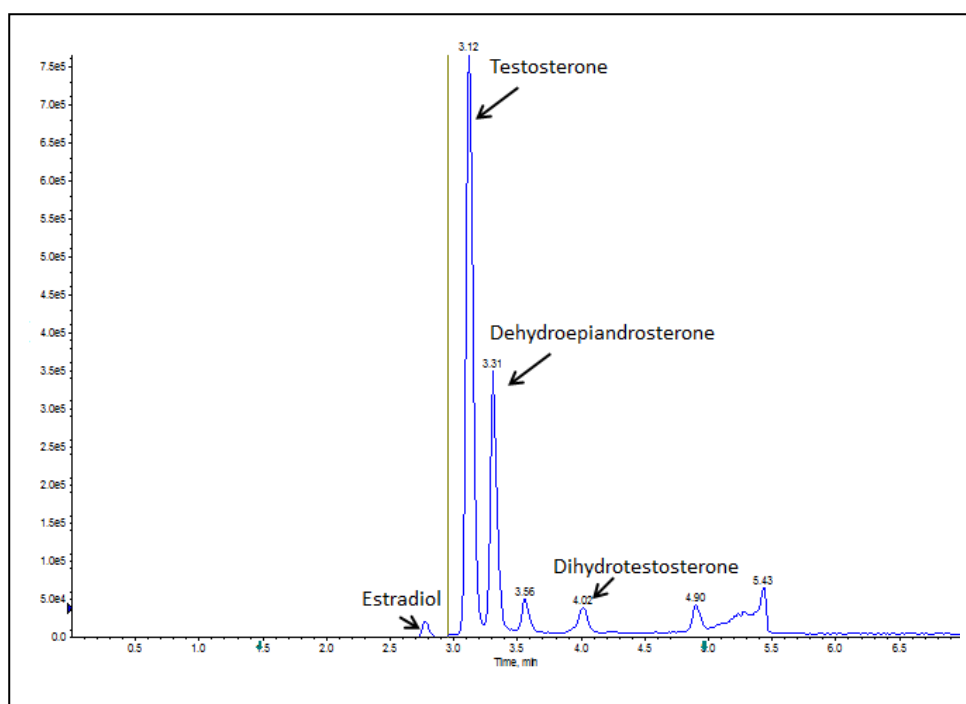


Figure 2.5 Serum steroids method chromatogram.

2.2 LH immunoassay

Urine and serum LH were measured by commercially available immunoassays an ICL immunoassay system: IMMULITE[®] 1000 LH, Siemens and IF assay: Delfia hLH assay, Perkin Elmer, Rowville, Melbourne, Victoria. The within-assay CV were <10%. Urine FSH assays (Immulite, DELFIA) did not pass validity tests (dilutional linearity, quantitative spike recovery) and were not used in this study.

2.2.1 *Immulite*

The ICL is a solid-phase two-site chemiluminescent immunometric assay that detects intact LH and LH β subunit. The solid phase of the system consists of a polystyrene bead sealed in the test unit and coated with a capture monoclonal antibody against LH. The standards or samples (approximately 100 μ L) were first aliquot in the disposable sample cups. Each sample cup was loaded on the loading rack followed by a test unit containing the bead. The sample (50 μ L) and alkaline phosphatase (conjugated to polyclonal goat anti-LH) were automatically pipetted into the test unit by the programmed Immulite system. Following incubation (with intermittent agitation), the reaction fluid was removed by high speed mixing followed by series of washing to remove the unbound material. Chemiluminescent substrate added to the complex undergoes hydrolysis through the action of the alkaline phosphatase enzyme creating unstable anion that emits sustained light emission measured by the photon counter.

2.2.2 *DELFLA*

The IF assay utilizes the immobilized monoclonal human LH β subunit as capture antibody and europium-labeled human LH β subunit as detector antibody. The assay was carried out according to the manufacturer instructions. Briefly, 25 μ L of standards and samples were aliquot in microtitration strip coated with mouse monoclonal anti-hLH followed by 200 μ L of

assay buffer. The strips were incubated for an hour on a plate shaker (Wallac 1296-001 Plateshaker) at room temperature. The strips were then aspirated and each strip was washed with a plate washer (Wallac 1296-026 Platewasher). Two hundred microliter of tracer solution (europium labeled anti- β human LH IgG) was added followed by 15 min incubation on a shaker at room temperature. The strips were aspirated and washed before adding 200 μ L of enhancement solution. The fluorescence was read using a time-resolved fluorometer (Perkin Elmer Multimode Plate Reader Enspire).

2.3 Urine creatinine measurement

Creatinine concentrations were determined by the colorimetric alkaline-picrate (Jaffé) method (CREJ2, Roche Diagnostics, Cat. No. 04810716 190) on a Cobas C501 analyzer (Roche Diagnostics GmbH, Indianapolis, IN). Calibrators (Roche Diagnostics, Cat. No. 10759350 190) were used for this automated system to generate a linear curve ranging between 375 and 55000 μ mol/L and the limit of detection of 375 μ mol/L. The assay requires 13 μ L of potassium hydroxide (900 mmol/L, phosphate 135 mmol/L, pH > 13.5) and 17 μ L of picric acid (38 mmol/L, pH 6.5) diluted in 77 μ L and 30 μ L of distilled water, respectively for sample volume of 10 μ L. All reagents were from ready to use cassettes and were handled automatically by the analyzer.

2.4 Urine specific gravity measurement

Urine specific gravity (SG) was measured by immersing a reagent strip (ChoiceLine 10, Roche Diagnostics) in freshly voided urine sample. Dipstick color changes were compared visually with the color chart to estimate the SG (range between 1.000 and 1.030; 0.005 unit difference between consecutive colour).

Chapter 3

Pharmacokinetic-Pharmacodynamic Study of Subcutaneous Injection of Depot Nandrolone Decanoate Using Dried Blood Spots Sampling Coupled With LC-MS/MS Assays

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Chapter 3 Pharmacokinetic-Pharmacodynamic Study of Subcutaneous Injection of Depot Nandrolone Decanoate Using Dried Blood Spots Sampling Coupled With LC-MS/MS Assays

3.1 Introduction

Since the first clinical use of T in 1937 (Hamilton 1937), two years after its Nobel Prize-winning discovery as the primary mammalian androgen (Butenandt and Hanisch 1935, David et al. 1935, Ruzicka and Wettstein 1935), its sole unequivocal therapeutic indication remains as replacement therapy for T deficiency states due to usually life-long hypothalamic, pituitary or testicular disorders (Handelsman 2010). Although exogenous T can be administered by implantable, transdermal or oral products, depot injectable formulations have long been the most widely used and affordable products for delivering T treatment aiming to maintain long-term adherence and sustained effective T replacement therapy for many years.

Depot injectable T products consist of T esterified to fatty acid side-chains with the length increasing hydrophobicity for partitioning into the vegetable oil vehicle as a depot for deep intramuscular (im) injection. These injections require skilled medical personal for slow administration, usually into the upper outer quadrant of gluteal muscle. While self-injection is feasible for the dexterous, most patients consider it too difficult so self-administration is rare. Im injections cause local pain or discomfort (Mackey et al. 1995, Sartorius et al. 2010), risk local injection site infection or bruising and, rarely, pulmonary oil micro-embolisation (Gu et al. 2009, Mackey et al. 1995, Svendsen and Aaes-Jorgensen 1979, Svendsen et al. 1980). Among patients with bleeding disorders or those taking anti-coagulants or antiplatelet therapy, deep im injections may be less suitable due to risk of im hematoma. In those situations daily-use oral or transdermal T products can be substituted; however, they have

high rates of discontinuation (Schoenfeld et al. 2013) as they lack the convenience of low-demand reliability of long-acting depot T products. Hence, a more convenient, self-administered method to inject T esters would be advantageous and cost-saving.

Clinical pharmacological studies to define drug pharmacokinetics and pharmacodynamics requires frequent blood sampling to generate sufficient data to define the time of peak and peak concentrations as well as circulating half-times and other derived pharmacological variables (Gibaldi and Perrier 1982, Minto et al. 1997). For long-acting depot products, this makes necessary many clinic visits for venesection followed by sample processing to separate serum for frozen storage until assay. These features add greatly to cost and complexity of conducting such pharmacological studies. We previously validated DBS technology for field studies of steroid pharmacology (Howe and Handelsman 1997) and now apply this remote sampling technology for repeated blood sampling at convenient times in the participants own home. This eliminate the need for medical professional to take blood samples, process and freeze samples while reducing the total blood sampled. As the time course of subcutaneous (sc) injections of steroids in an oil vehicle is not reported and may differ from the im route of administration (Handelsman et al. 1995, Minto et al. 1997), we investigated the pharmacokinetics of a single sc injection of nandrolone decanoate (ND) and the pharmacodynamics of its effects on endogenous serum T. As a generic androgen ester in an oil vehicle, this may demonstrate the feasibility of sc injection of T esters in an oil vehicle with potential to simplify injectable T replacement therapy. Nandrolone (N), also known as 19-nortestosterone has structural similarities with T but lacking a methyl group at the 19th position (Hemmersbach and Grobe 2009) (Figure 3.1). ND consists of a long aliphatic side chain (10 carbons) (Figure 3.1) that provides sustained release of this steroid into the circulation. ND is further hydrolyzed into its active steroid, N which inhibits the pituitary

gonadotropin release through the negative feedback loop resulting in decrease of endogenous T production (Minto et al. 1997).

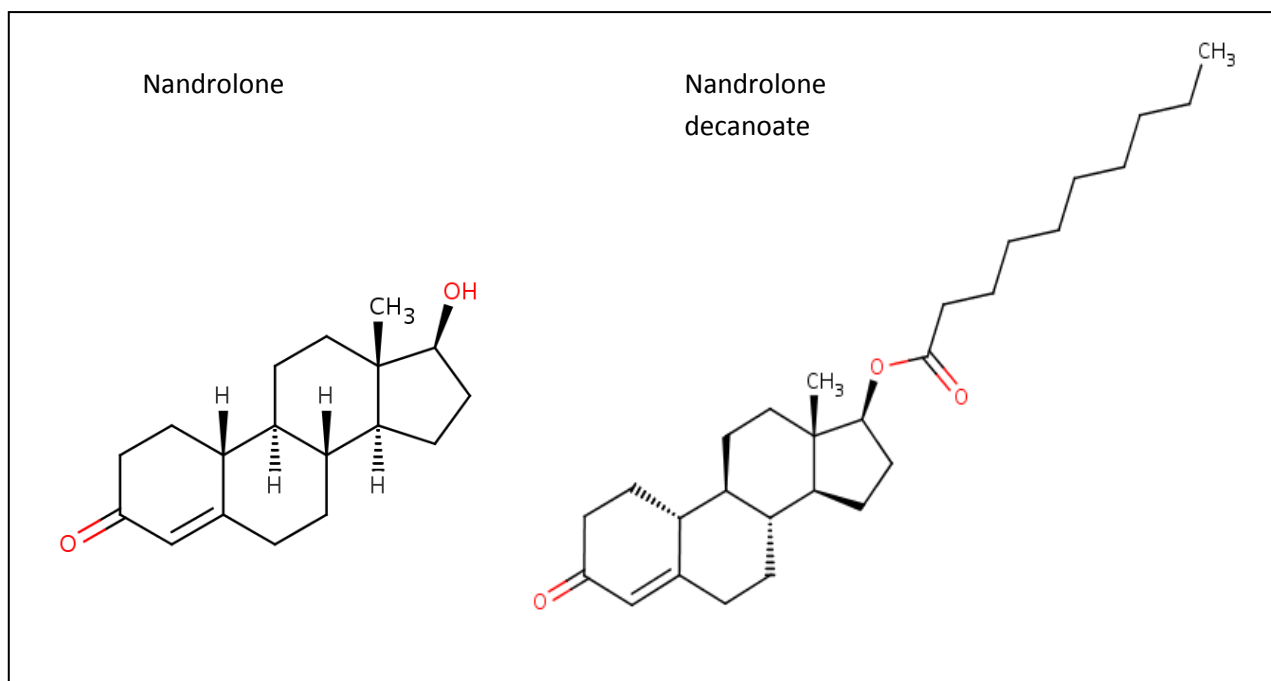


Figure 3.1 Structures of nandrolone and nandrolone decanoate.

Nandrolone decanoate, a synthetic anabolic steroid has a long duration of action due to its 10-carbon aliphatic side chain. Nandrolone decanoate is released into the extracellular fluid gradually with oil/water partitioning of the steroid ester from the oil vehicle with rapid hydrolysis of the ester to form active steroid (nandrolone) in the bloodstream (Minto et al. 1997).

3.2 Study Design

Healthy eugonadal volunteer men ($n=8$, age 31 ± 10 (SD) year, height 175 ± 7 cm, weight 80.7 ± 0.8 kg, BMI 26.3 ± 3.0 kg/m²) were administered 100 mg ND in 2 mL arachis oil vehicle (MSD, Australia) by sc injection (21 gauge needle (0.8x25mm) Becton Dickinson Medical) into a single subdermal abdominal site. Participants were instructed in collecting capillary blood by finger prick using a single-use lancet (BD Microtainer, Contact-Activated Lancet 2.0x1.5mm; Becton Dickinson, Franklin Lakes NJ 07417) and applying blood onto filter cards (McDade 2014). Blood spots were applied to the 1st, 3rd and 5th of the five pre-

marked rings allowing for a gap to avoid overlap of blood samples. Capillary blood was obtained before and daily for 21 days recording the exact time of sampling. Venous blood was also sampled before and at weekly intervals to store serum and to spot venous blood directly onto filter cards. Serum samples were stored at -20°C until assayed. The dried blood spots were allowed to dry overnight at room temperature and were then stored in a sealed paper bag at room temperature until extracted. The participants provided written informed consent and the study was approved by the Sydney Local Health District Human Ethics Committee within National Health and Medical Research Council Guidelines for Human Experimentation (NHMRC) guideline for human experimentation. Volunteers received \$200 for their time and effort on completing the full study (5 visits, 22 finger-prick blood samples).

3.3 Data analysis

Comparison of T and N concentrations in different fluids (serum, capillary blood, venous blood) was performed by non-parametric (Passing-Bablok) regression, deviance analysis of differences (modified Bland-Altman) and Spearman rank correlation using NCSS and MedCalc software. Peak or nadir concentrations and time of peak or nadir were determined directly from the serial daily hormone concentrations as well as from population pharmacokinetic/pharmacodynamic modelling using the exact time of finger-prick sampling (rather than nominal day) by non-linear curve fitting (Gibaldi and Perrier 1982, Minto et al. 1997). Data were expressed as mean and standard error of mean (SEM) for data with a Gaussian distribution and median (range) otherwise.

3.4 Results

All scheduled samples (finger-prick, venous) were collected without complaints about finger-prick blood collection. There were no complaints of discomfort following the injections. Hematocrit was unchanged by participation in the study (pre 0.45 ± 0.01 , post 0.45 ± 0.01 , difference 0.0 ± 0.01 or -0.5 ± 2.4 % of baseline, paired t-test $p > 0.8$).

Capillary T and N concentration displayed a high correlation ($r=0.95$, 0.96 , respectively) and was unbiased (mean deviation -2.5 ± 60 (SD) %, -27 ± 39 %) compared with measurements in serum for T (Figure 3.2) and for N (Figure 3.3). Similar findings were obtained with high correlation ($r=0.97$ for all) and lack of bias between venous whole blood spot and serum or capillary T and N.

Serum N rose to a peak concentration of 2.50 ± 0.25 (SEM) ng/mL at a median (range) of 6 (4-13) days (Figure 3.4). Serum T declined from 3.50 ± 0.57 ng/mL at baseline to a nadir of 0.38 ± 0.13 (SEM) ng/mL representing 89 ± 3 % maximal suppression at a median (range) of 8 (5-16 days) (Figure 3.5). Using non-linear curve fitting, N peaked at 1.72 ng/ml at 6.4 days while serum T reached a nadir of 0.53 ng/ml (suppressed by 2.9 ng/ml) at 10.3 days (Figure 3.5). Capillary T and N displayed virtually identical patterns following sc ND injection (Figure 3.6). Serum LH and FSH were both suppressed maximally at day 7 (median 7 days, range 7-14 days) to reach a nadir of 1.2 IU/L (LH) and 1.1 IU/L (FSH) after injection, representing a median 60% and 49% suppression from baseline, respectively, and recovered towards, but not full reaching, baseline by day 21 (Figure 3.6).

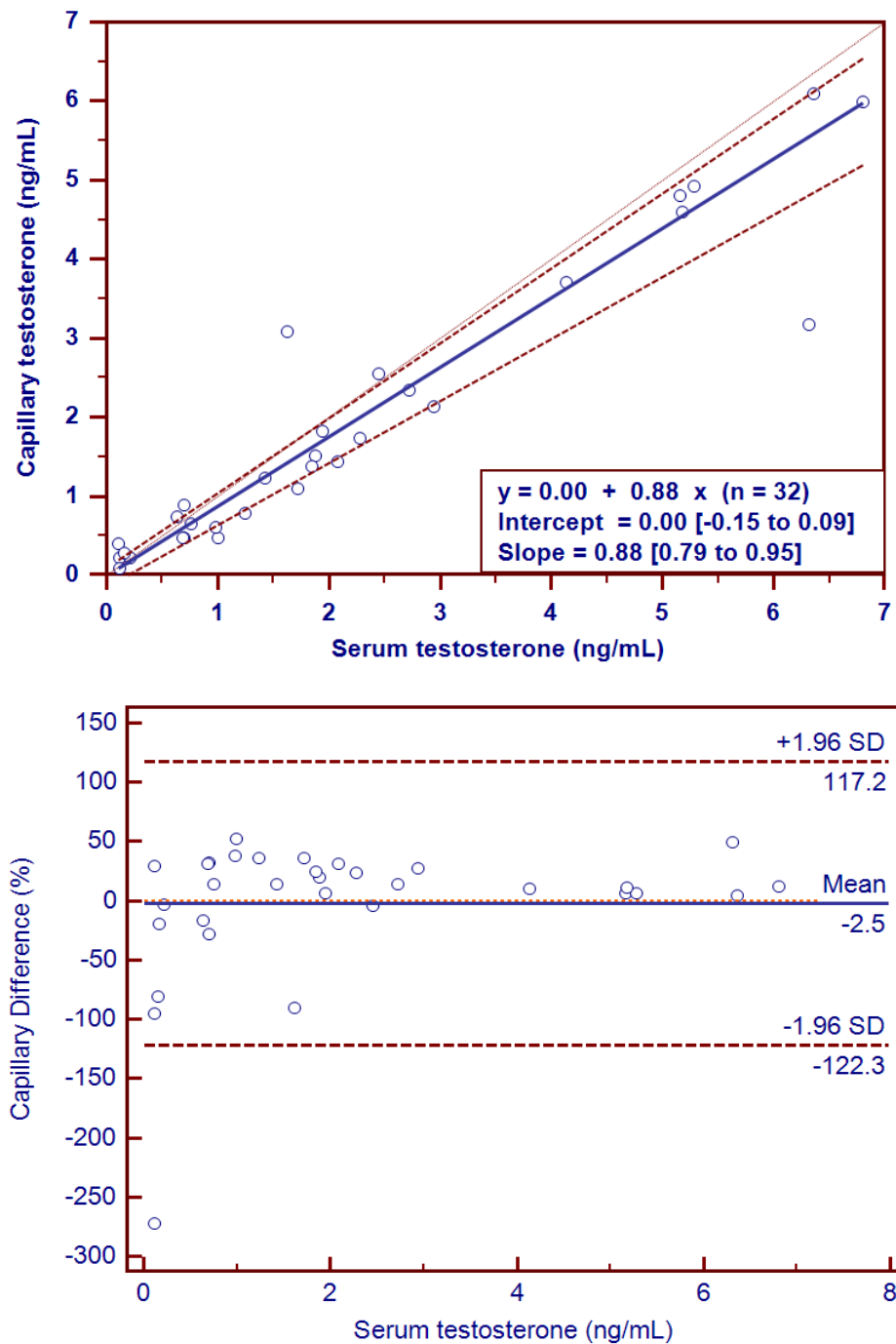


Figure 3.2 Plot of correlation (Passing-Bablok-upper panel) and deviance (modified Bland-Altman-lower panel) of individual capillary and serum testosterone in 32 samples obtained from 8 participants before and weekly for 3 weeks after sc injections of ND

Line of best fit is shown as a solid line with upper and lower 95% confidence intervals in dashed lines and the line of identity shown as a dotted line. Inset are the (Passing-Bablok) regression formula and 95% confidence limits on intercept and slope. The deviance (modified Bland-Altman) plot shows the deviation of capillary from serum testosterone expressed as a percentage. For further details see text.

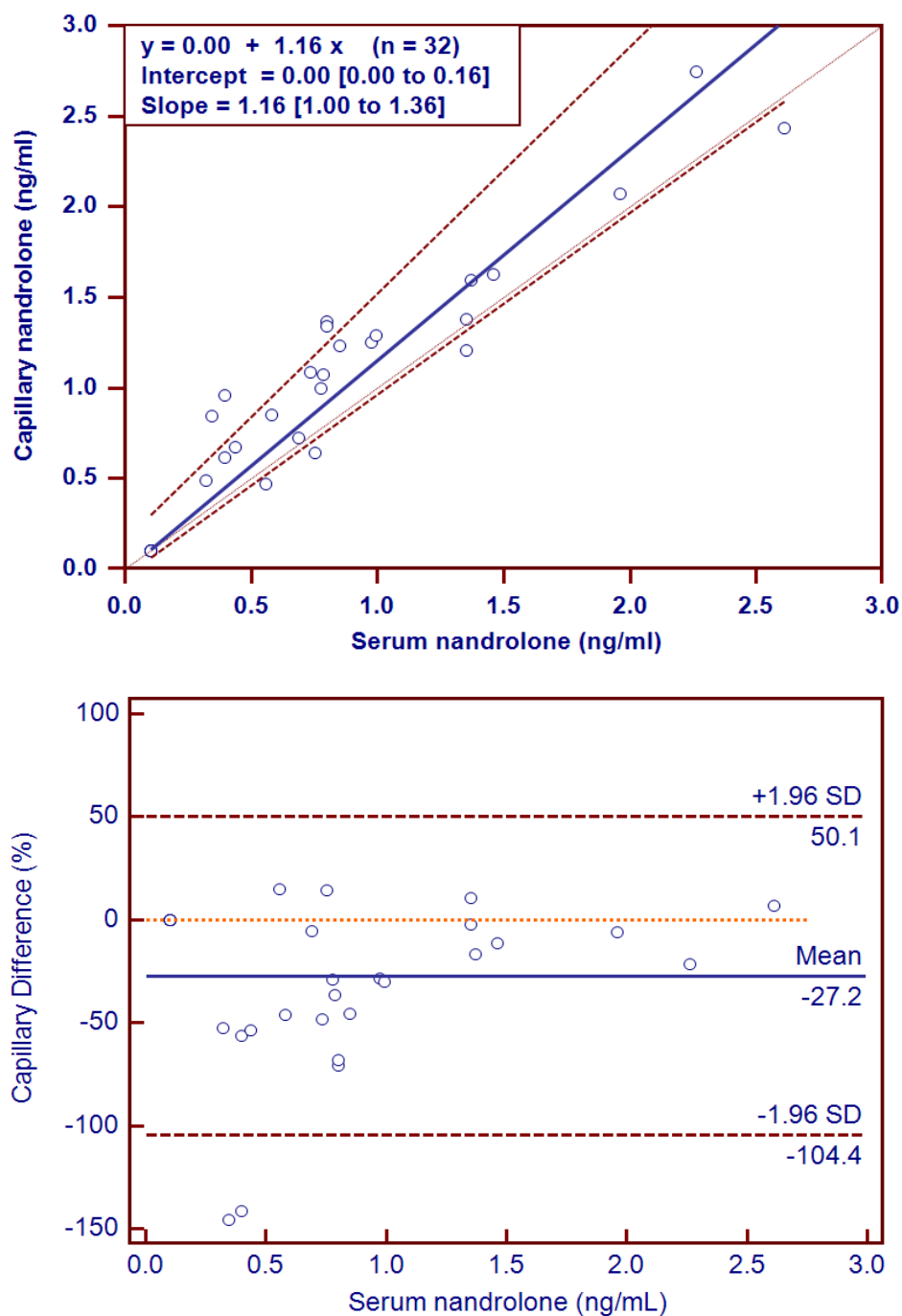
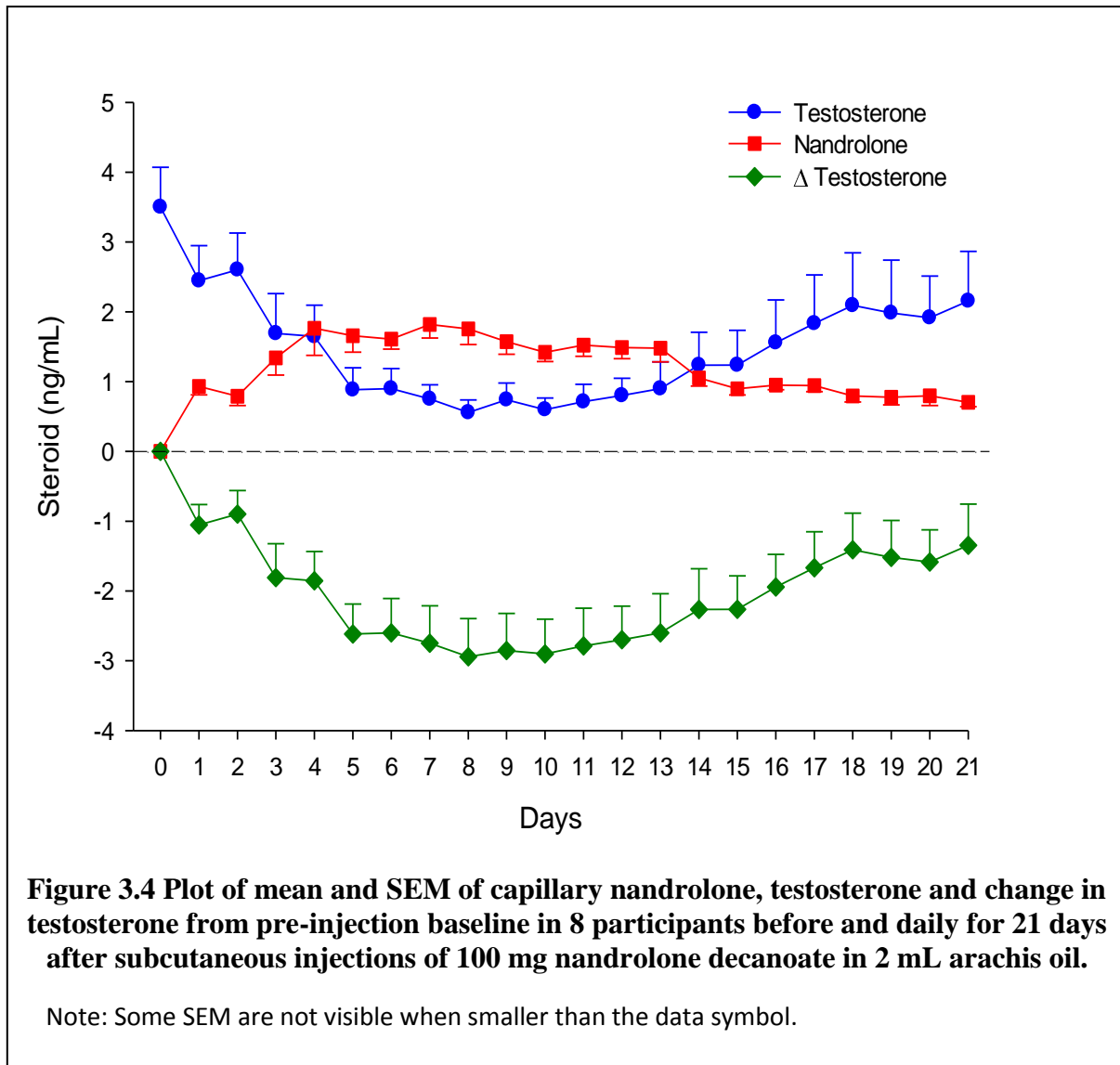


Figure 3.3 Plot of correlation (Passing-Bablok-upper panel) and deviance (modified Bland-Altman-lower panel) of individual capillary and serum nandrolone in 32 samples obtained from 8 participants before and weekly for 3 weeks after sc injections of ND.

Line of best fit is shown as a solid line with upper and lower 95% confidence intervals in dashed lines and the line of identity shown as a dotted line. Inset are the (Passing-Bablok) regression formula and 95% confidence limits on intercept and slope. The deviance (modified Bland-Altman) plot showing the deviation of capillary from serum nandrolone expressed as a percentage. For further details see text.



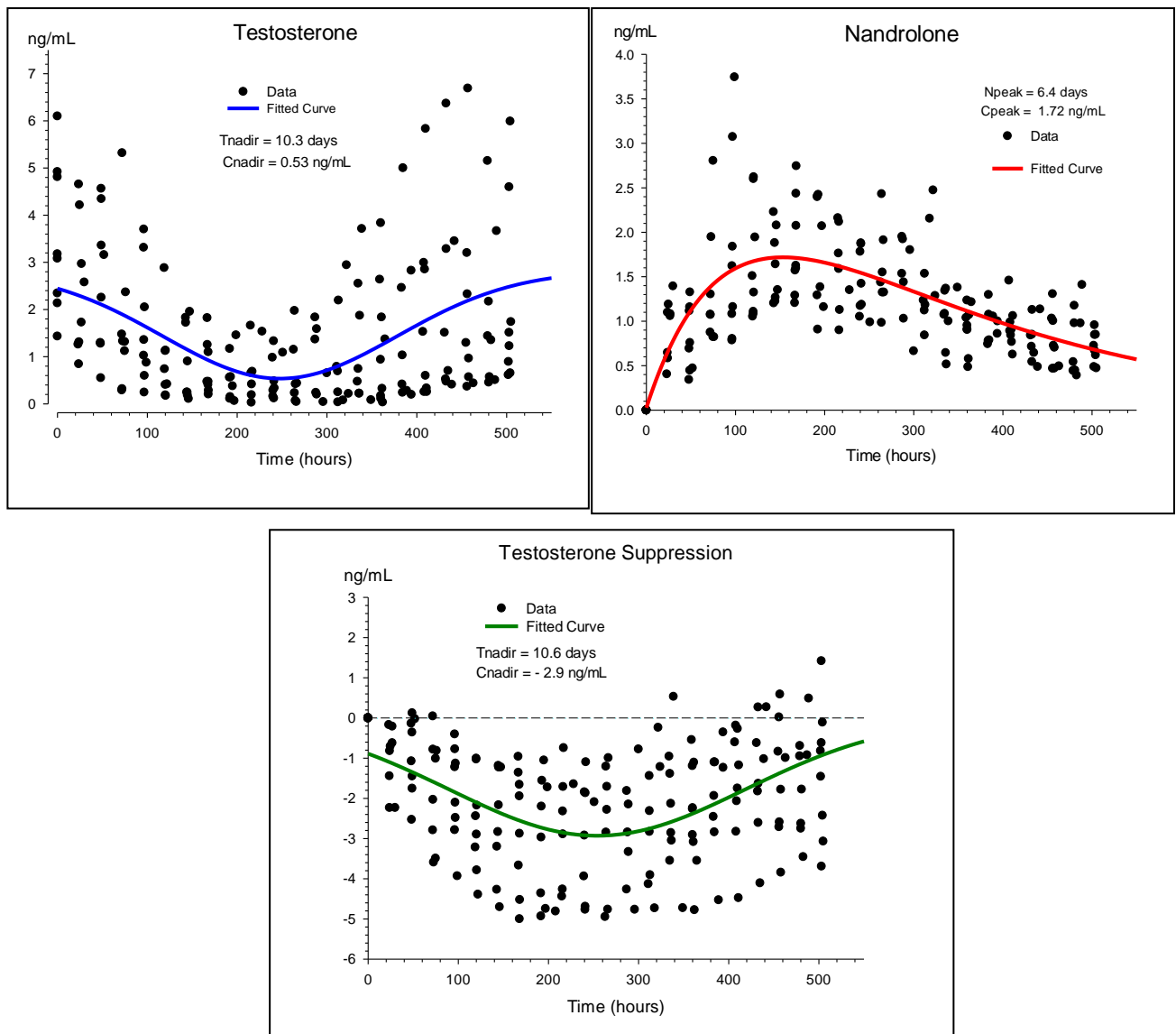


Figure 3.5 Plots of non-linear curve fitting of T (left panel), N (right panel) and T suppression (lower panel) of capillary blood collection from 8 participants before and daily according to exact individual collection time points after SC injection of ND

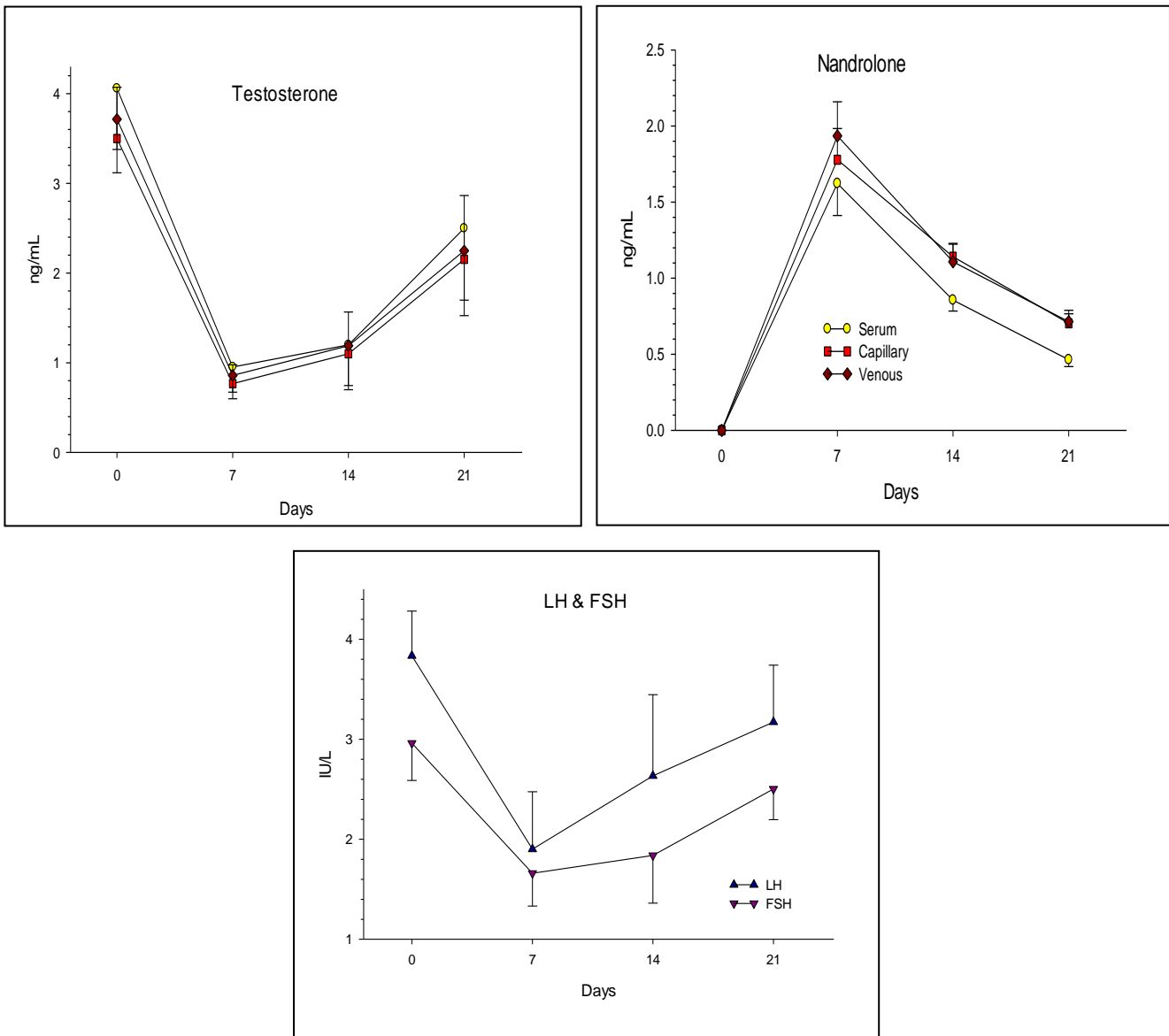


Figure 3.6 Plot of mean and SEM of capillary, serum and venous nandrolone (left panel), testosterone (right panel) and serum LH and FSH (lower panel) in 8 participants before and weekly for 3 weeks after subcutaneous injections of 100 mg ND

3.5 Discussion

DBS technology has been used for over 50 years mostly to measure individual analytes at a single time-point in screening assays or cross-sectional studies (McDade 2014, McDade et al. 2007) for its simplified sample collection, processing and storage. It has been extended to measuring multiple analytes from a single filter spot (Edelman et al. 2007, Magnisali et al. 2011, Worthman and Stallings 1997) but few studies have reported serial DBS sampling of ambulatory, community-dwelling individuals (Howe and Handelsman 1997) and its feasibility has been doubted (Kissinger 2011). This study shows that this advantageous feature is feasible for pharmacological studies of depot steroids, where remote sampling at home is more convenient than requiring repeated clinic visits for venipuncture as well as centrifugation for separating serum or plasma and bulky, frozen sample storage until assay and decreases in hemoglobin from frequent venesection. Furthermore, the use of population PK/PD modelling employing the exact time of finger-prick sampling also relaxed the stringency of time of day requirements for remote sampling. By reducing cost and complexity, thereby features facilitate community-based studies involving steroid measurements such as for the pharmacology of long-acting depot steroids and drugs.

For over 6 decades, injectable T esters have been administered in a vegetable oil vehicle marketed solely for im injection (Junkman 1957). The pharmacokinetics and pharmacodynamics are primarily determined by ester chain side-length, volume of oil vehicle and injection site, all determining the hydrophobic physicochemical partitioning between the oil vehicle and aqueous extracellular fluid wherein ubiquitous esterases liberate the free steroids from their esters (Minto et al. 1997). However, there are no reports of the pharmacology of sc injections of androgen esters in an oil vehicle, other than a pilot study of 22 hypogonadal men where blood T was measured by immunoassay a day before and a day after sc injection of low dose of T enanthate (mean 55 mg weekly, <0.3 ml oil) (Al-Futaisi et

al. 2006). No adverse effects or discontinuations were reported but the data provides minimal insight into the pharmacology of sc injection of androgen esters. In the present study using DBS technology to facilitate intensive and yet simplified blood collection from participants at home, we provide the first detailed pharmacological analysis of sc injection of ND in arachis oil vehicle. The present finding of sustained depot-like effects is expected given the known pharmacology of im N esters (Bagchus et al. 2005, Howe and Handelsman 1997, Minto et al. 1997) together with the observations that most im injections are actually sc (see below). Using prior pharmacological data of im ND injections with steroids measured by immunoassays, sc injection of 100 mg in 2 mL oil most closely resembles gluteal injection of 100 mg in 4mL (rather than gluteal or deltoid in 1 mL) in pharmacokinetics (time of peak 6.0 vs 5.0 days; peak concentration 2.5 vs 3.7 ng/mL) and pharmacodynamics (time of nadir 8.0 vs 9.2 days; nadir concentration 0.38 vs 0.69 ng/mL) (Minto et al. 1997). Another study of gluteal im injection of 100 mg ND in 1 mL oil reported higher peak N concentrations (4.9 ng/mL) and earlier (1.25 days) peak time (Bagchus et al. 2005) consistent with the reported effects of injection volume (Minto et al. 1997).

Nevertheless, inadvertent and unrecognized sc injection of T and N esters in oil vehicle is common. It has been known for decades that sc fat is so thick that gluteal im injections frequently deposit the injectate into sc fatty tissue rather than muscle tissue (Cockshott et al. 1982). Using computed tomography or ultrasound scanning to measure sc fat thickness and placement of injectate or comparison with length of injection needles, it is estimated that 12-85% of im injections in men and 55-95% in women are actually sc (Boyd et al. 2013, Burbridge 2007, Chan et al. 2006, Cockshott et al. 1982, Haramati et al. 1994, Joo and Sohng 2010, Nisbet 2006), the higher estimate in women corresponding to their greater sc fat thickness. This may also explain our observation that im T injections were less painful in overweight or obese men (Sartorius et al. 2010). Experimental studies in pigs show that sc

and im injections of drugs in an oil vehicle have similar pharmacokinetics (Perry et al. 1997, Svendsen et al. 1985). Although injection site granulomata have been reported more frequently in sc fat compared with muscle (Baumann 2012, Cockshott et al. 1982), this observation is derived from hospital-based im injections, usually non-steroids in aqueous solutions, rather than the smaller minority of less toxic, oil vehicle based im injections typically administered in ambulatory care settings (Svendsen 1983, Svendsen et al. 1985).

Although the tolerability of sc injections of androgen esters in an oil vehicle requires more extensive validation through further pharmacological studies of T esters as well as experience in its use, it is likely to be safe and tolerable. Extensive experience with T pellets indicates that sc implantation of pure crystalline T is safe and acceptable for months to years, marred only by a low rate of extrusions (Handelsman et al. 1997) due to a sterile reaction to implantation which is unrelated to mechanical factors (Kelleher et al. 2001, Kelleher et al. 1999) or prevented by antibiotic cover (Kelleher et al. 2002). Similarly, the vegetable oils used as injection vehicles (e.g. sesame, arachis, castor, cottonseed and mellaleuca oils) for androgen esters are well tolerated clinically when administered intramuscularly (Mackey et al. 1995). They are better tolerated than mineral oils which are much more irritating when injected subdermally (Darsow et al. 2000, McWilliams 1927, Rollins et al. 1997, Symmers 1955) whereas vegetable oils also reduce local muscular damage compared with aqueous injections (Svendsen 1983, Svendsen et al. 1985). Previous studies have already shown that the pharmacology of androgen esters depends on site and volume of injection (Minto et al. 1997) and further studies using T esters in men with differing body weight and after repeated injections are required to evaluate duration of action and usefulness in clinical practice of sc relative to im injections.

The present study suggests that sc injections of T esters may prove safe and tolerable. If so, this would make self-injection of T esters feasible with the potential benefits of reducing

medical care costs, demand on medical personnel time and injection site pain or bruising as well as allowing freer use among those with bleeding disorders or on anticoagulants to use this more convenient long-acting depot form of T delivery.

Chapter 4

Immunoreactive LH in long-term frozen human urine samples

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Chapter 4 *Immunoreactive LH in long-term frozen human urine samples.*

4.1 Introduction

LH together with FSH are principal pituitary hormones exerting dynamic neuroendocrine control of the initiation and maintenance of mature reproductive functions. In addition to initiating puberty, in women LH drives follicle maturation and ovulation while in men it governs Leydig cell production and secretion of T. Consequently measuring LH is fundamental to understanding of reproductive neuroendocrinology. Urine has always been the preferred sampling format for anti-doping testing as well as for long-term and field studies such as neonatal (Kuijper et al. 2006), adolescent (Hayes and Johanson 1972, McNeilly et al. 2012), occupational (Kesner et al. 1999, Whelan et al. 2002) or toxicological (Kesner et al. 1999, Kuijper et al. 2006, Whelan et al. 2002) cohort studies where urine collections avoid the need for repeated venipuncture. Urinary LH measurement has a role in confirming androgen doping because exogenous androgens suppress urinary LH (Cowan et al. 1991, Goebel et al. 2009, Handelsman et al. 2009, Kicman et al. 1990). Furthermore, abuse of anti-estrogens, GnRH analogs and recombinant LH (Handelsman 2006) may also be detected by increased urinary LH levels.

One limitation is that modern commercial human LH immunoassays have been established and validated solely for blood samples and not urine sample, unlike hCG immunoassays which were always developed for qualitative urine pregnancy testing as well as for blood samples although quantitative urinary hCG assays are described (Cole and Khanlian 2009). Urine LH immunoreactivity may depend on urine sample storage conditions as well as immunoassay epitope specificity. For example, pre-storage extraction by acetone precipitation (Reiter et al. 1973, Saketos et al. 1994) or by addition of glycerol or albumin

(Kesner et al. 1995, Livesey et al. 1983, Saketos et al. 1994) stabilize immunoreactivity. Furthermore, whereas two-site assays with epitopes on different subunit of the heterodimer optimizes detection of intact LH (Alonso-Whipple et al. 1988, Nilsson et al. 2001, Pettersson et al. 1991), dissociation of LH into its subunits, influenced by exposure to high urinary concentrations of urea (Lempiainen et al. 2012), may be reflected in loss of immunoreactivity whether or not the subunit remain intact especially at -20 °C storage (Lempiainen et al. 2012). This is consistent with the stability of a urinary LH assay based on a different strategy of pre-assay dissociation into subunits with detection aimed at the LH β subunit (Brindle et al. 2006), an assay displaying prolonged stability during frozen storage (Brindle et al. 2006, O'Connor et al. 2006). However, it is simpler for field studies to implement urine LH immunoassays that do not require pre-storage manipulation. In addition, as glycerol is on the World Anti-Doping Prohibited List as a banned chemical for athletes, it cannot be used with urine samples collected for anti-doping testing. Therefore, this study aimed to evaluate the stability of urinary LH immunoreactivity using two commercially available immunoassays, an immunofluorometric (IF, Delfia, Perkin-Elmer) and an immunochemiluminometric (ICL, Immulite, Siemens) assay, before and after 4 years of storage at -20 °C without addition of any preservatives.

4.2 Study Design

Urine samples were obtained from a previous study that evaluated the potential of recombinant hCG (rhCG, Ovidrel, MerckSerono Pty Ltd) as an indirect androgen doping agent (Handelsman et al. 2009). The effects of two doses of rhCG, with or without concomitant administration of ND (Deca-Durabolin, Organon Australia Pty Ltd, Lane Cove, Sydney) to suppress endogenous LH and T (Minto et al. 1997), on urine and serum LH and testosterone were examined in 24 healthy young men aged 18-45 years who received a single sc injection of rhCG (250 or 750 μ g). Spot urine samples were collected before and daily for

8 days after dosing and stored frozen at -20 °C until analysis in a single batch at the end of study (2008) and then again (2012) after 4 years of unthawed storage at -20 °C. At both times, the full batch was analysed in duplicate by ICL (Immulite 1000 LH, Siemens) and IF (Delfia hLH assay, Perkin Elmer, Rowville, Melbourne, Victoria) assays (refer Chapter 2 for assay details). Urinary SG was measured by a refractometer and urine LH values were adjusted to a standard SG of 1.020. Prior to assay, urine samples were thawed and warmed at 37°C in a sealed container for 10-15 minutes with shaking to redissolve sediments.

4.3 Data analysis

Results are expressed as mean \pm SEM. The LH concentrations measured in either assay at each time were compared by Passing-Bablok non-parametric regression and deviance (Bland-Altman plot) analysis using MedCalc software.

4.4 Results

The comparison of urinary LH concentrations measured using IF and ICL immunoassays, adjusted to standard SG, when run in either 2008 or after 4 years frozen storage (2012) is shown in Figure 4.1. The comparison between the two LH assays when both were run in 2008 and then again when both were run in 2012 after 4 years frozen storage, is shown in Figure 4.2. The details of the Passing-Bablok regression equations to compare urinary LH using the IF and ICL at both times is given in Table 4.1.

The urine LH concentrations measured using the ICL assay when comparing measurements in 2008 and 2012 shows good correlations (Figure 4.1, Table 4.1). By contrast, the IF assay showed marked reduction (~70%) in LH concentration when measured in 2012 compared to 2008 (Figure 4.1, Table 4.1).

When comparing LH assays performed in 2008, and then again after 4 years frozen storage, the two LH assays were discrepant. In 2008 the IF assay provided LH measurements which

were ~50% of those in the concurrent ICL LH assay (Figure 4.2, Table 4.1). In 2012, the IF LH assay was reduced to ~30 % compared with the contemporaneous ICL assay (Figure 4.2, Table 4.1).

The mean urinary LH concentration (adjusted for urine SG) in the original study measured with IF and ICL in year 2008 and 2012 is depicted in Figure 4.3. The pattern of the urinary LH profile was very similar but not identical using either immunoassays at the end of study (2008) and again after 4 years of frozen (-20 °C) storage. Despite loss of immunoreactivity according to one (IF) but not the other (ICL) assays in all series the suppression of urine LH was clearly evident.

The details of the Passing-Bablok regression equations to compare urinary (ICL and IF) and serum LH (IF) is given in Table 4.2. The intercept of all the four comparisons was not significantly different from 0 although there were variations in the slope and correlations (Table 4.2).

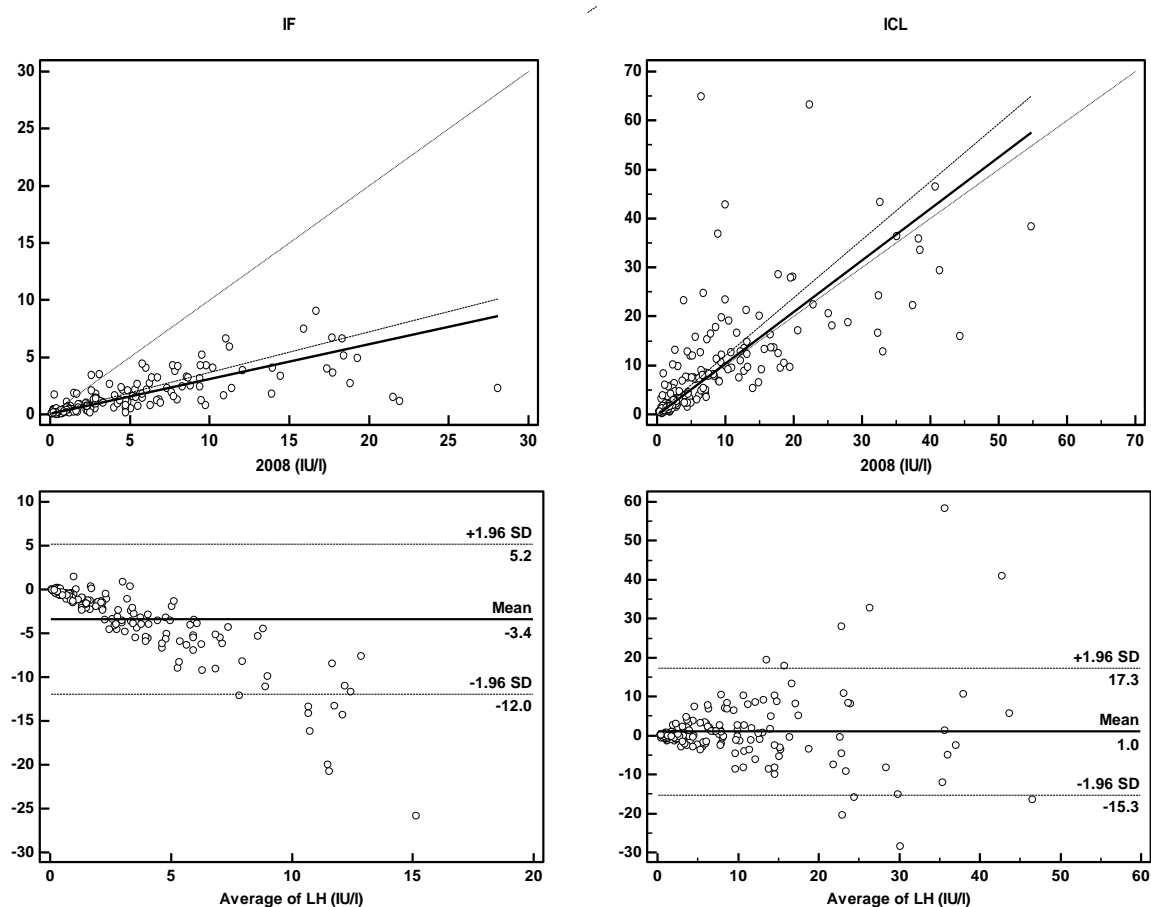


Figure 4.1 Comparison of urinary LH concentrations obtained using IF (left panels) and ICL (right panels) measured before and after four years of storage at -20°C .

Levels of urinary LH between the same assays were compared using Passing and Bablok regression analysis (upper panels). The slope (solid line) is calculated with 95% confidence bands (dotted lines) and line of identity (fine dotted line). The Bland-Altman plots (lower panels) represent urinary LH differences against averages of the two measurements. The solid line and the dotted line represent the observed average agreement and 95% limit of confidence respectively.

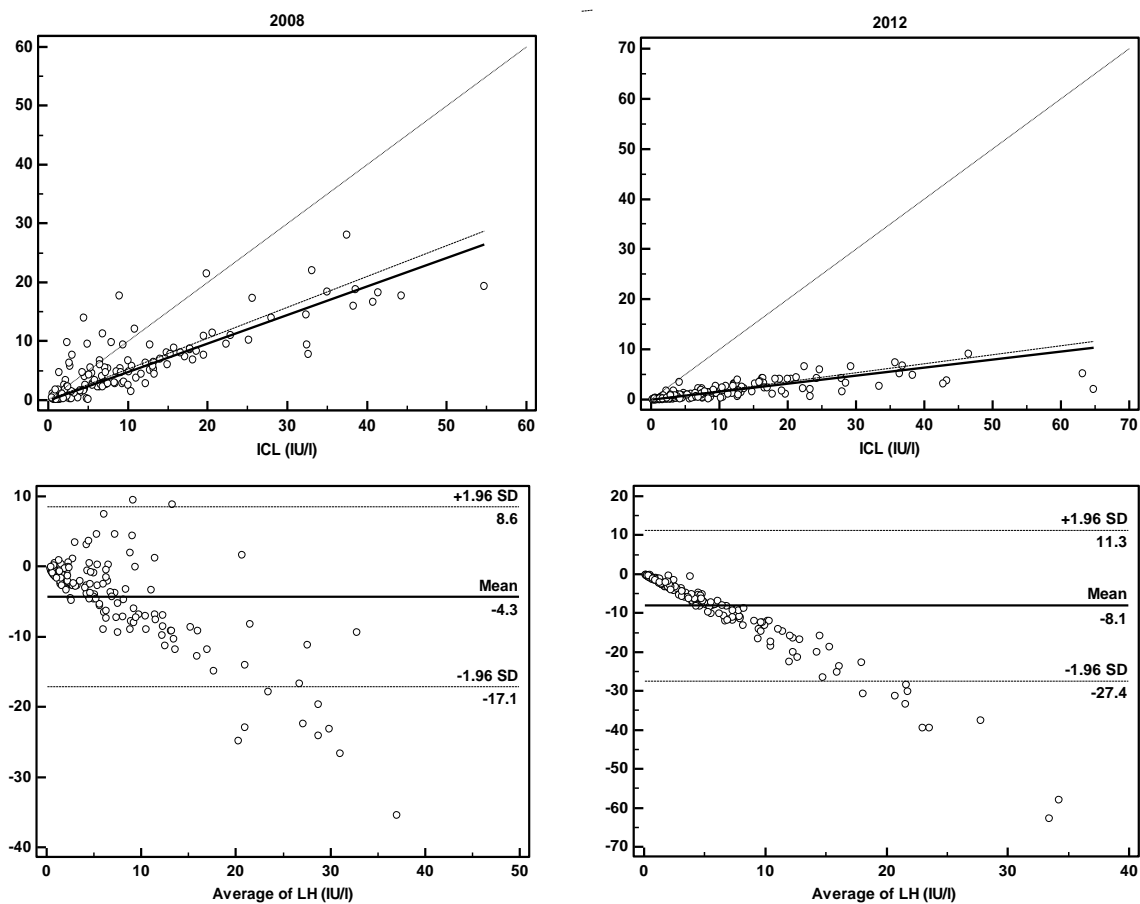


Figure 4.2 Comparison of urinary LH concentrations measured by IF and ICL in 2008 (left panels) and 2012 (right panels).

Levels of urinary LH between the two assays were compared using Passing and Bablok regression analysis (upper panels). The slope (solid line) is calculated with 95 % confidence bands (dotted lines) and line of identity (fine dotted line). The Bland-Altman plots (lower panels) represent urinary LH differences against averages of the two measurements. The solid line and the dotted line represent the observed average agreement and 95 % limit of confidence respectively.

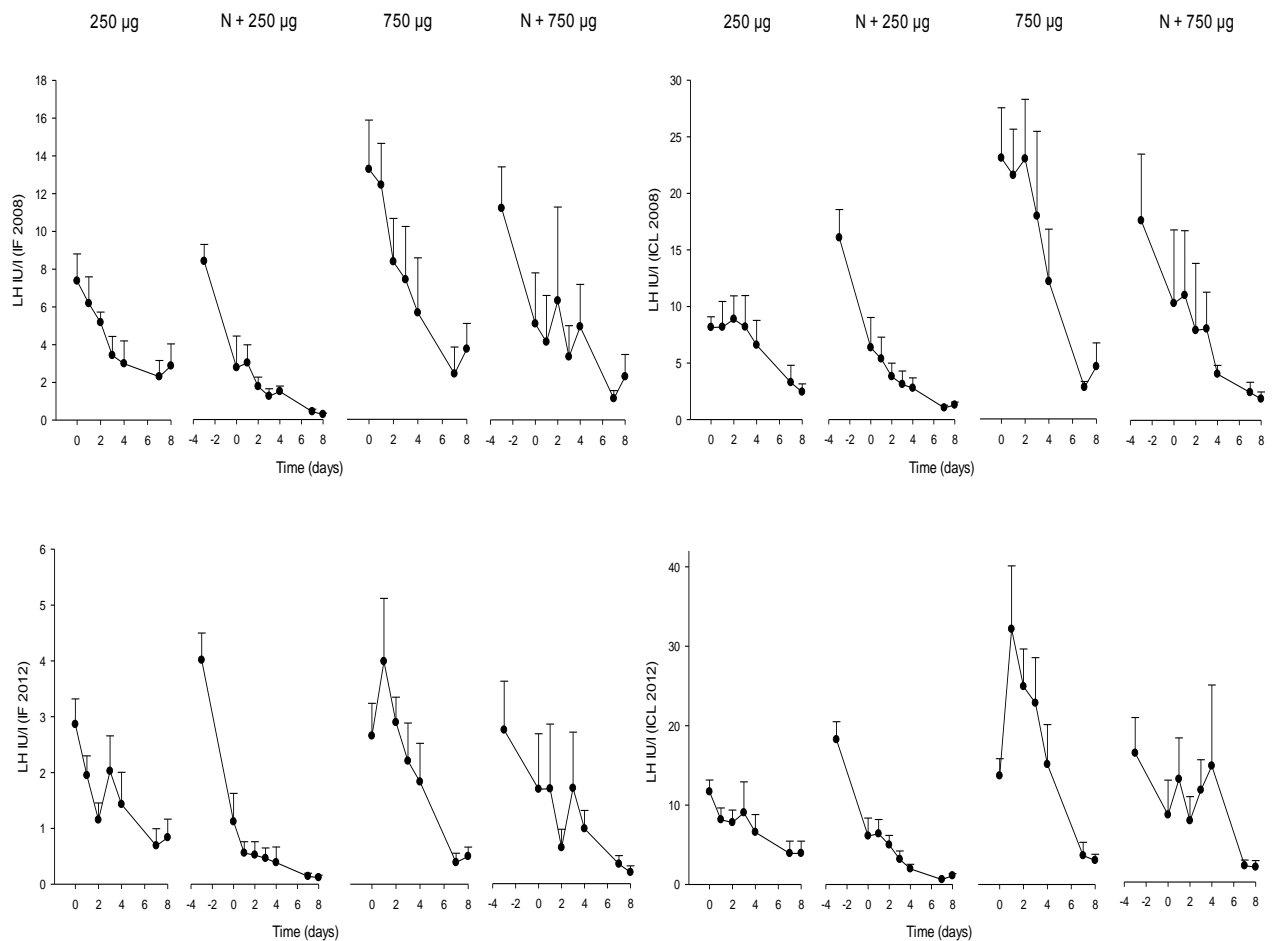


Figure 4.3 Plot of urine LH assayed with Delfia (left panels) and Immulite (right panels) for year 2008 (upper panels) and 2012 (lower panels).

Data represents the mean and SEM of spot urine collected before and after dosing of hCG (with or without nandrolone suppression). Note all LH concentrations are adjusted to standard urine SG of 1.020.

Table 4.1 Comparison of urine LH determined using two immunoassays.

The number of urine samples (n) with the slope, intercept and correlation coefficient (r) and their 95% confidence intervals in parentheses determined by Passing-Bablok regression.

Assays compared	n	Slope	Intercept	r
Delfia 2008 vs 2012	156	0.30 (0.27, 0.36)	0.04 (-0.01, 0.10)	0.72 (0.63, 0.78)
Immulite 2008 vs 2012	180	1.06 (0.94, 1.19)	-0.25 (-0.57, 0.15)	0.70 (0.61, 0.76)
Immulite vs Delfia 2008	156	0.49 (0.45, 0.53)	-0.11 (-0.41, -0.02)	0.84 (0.79, 0.88)
Immulite vs Delfia 2012	156	0.16 (0.14, 0.18)	-0.03 (-0.07, 0.00)	0.78 (0.71, 0.83)

Table 4.2 Comparison of urine LH determined using Immulite and Delfia (2008 and 2012) versus serum LH determined using Delfia (2008).

The number of samples (n) with the slope, intercept and correlation coefficient (r) and their 95% confidence intervals in parentheses determined by Passing-Bablok regression.

Urine LH vs Serum LH (Delfia 2008)	n	Slope	Intercept	r
* Delfia 2008	156	0.34 (0.28, 0.40)	0.02 (-0.05, 0.09)	0.70 (0.61, 0.77)
Delfia 2012	180	1.22 (1.04, 1.41)	-0.03 (-0.11, 0.04)	0.61 (0.51, 0.69)
*Immulite 2008	180	0.16 (0.13, 0.19)	-0.03 (-0.08, 0.02)	0.64 (0.54, 0.72)
Immulite 2012	180	0.15 (0.11, 0.19)	0.03 (-0.05, 0.07)	0.43 (0.30, 0.54)

* Note: Data obtained from (Handelsman et al. 2009)

4.5 Discussion

The present study demonstrated that two available commercial LH immunoassays optimized for blood samples can also be used for urinary LH measurement. However, the performance of both LH assay with urine samples differed markedly. The ICL immunoassay showed quantitatively reproducible LH measurement even after prolonged storage at -20 °C for 4 years without addition of preservatives. By contrast, the IF immunoassay demonstrated consistently but proportionately lower LH measurements relative to the ICL assay both initially and then exhibited a further decrease after 4 years of frozen storage. Yet, despite the reduced absolute LH measurements by the IF immunoassay, both LH immunoassays displayed sufficiently similar patterns of urine LH measurements to confirm the findings of the original study that hCG administration produces LH suppression (Handelsman et al. 2009). Hence either assay used before or after prolonged frozen storage may be sufficient for a research study whereas only one provides quantitative results after frozen storage as might be required for look-back of stored anti-doping samples, an application which requires reproducible quantification of absolute levels. Similar findings were reported for serum LH measurements where the performance of the ICL was reported to be more sensitive and accurate compared to the IF immunoassay for the determination of reference range during sexual development in normal children (Resende et al. 2007).

Commercially available immunoassays designed for serum or plasma LH measurements require careful validation for use with urine samples particularly when inference is to be drawn from suppressed urine LH values (Cowan et al. 1991, Goebel et al. 2009, Kicman et al. 1990, Mareck et al. 2010, Palonek et al. 1995, Perry et al. 1997). In addition to the two LH immunoassays in this study, thorough validation has been published for two LH immunoassays (Access and Elecsys) (Robinson et al. 2007) and indirectly for a third (AxSYM) (Llouquet et al. 2013, Perry et al. 1997). Other studies reported good correlation of

urine and serum LH in children and cycling women as determined by IF immunoassay (Demir et al. 1994, Saketos et al. 1994). Validation after prolonged frozen conditions has not been evaluated by available commercial immunoassays.

These discrepancies between LH immunoassays most probably reflect the diversity of immunoreactive LH species in human urine compared with the bloodstream (Birken et al. 2001, Birken et al. 2007, Stenman et al. 2008). This diversity reflects the metabolism of the gonadotropins which produces nicked dimers and free subunits including the core fragment. Like hCG where the metabolism is more fully characterized (Bristow et al. 2005), the homologous LH heterodimer is metabolized and excreted in the urine in various fragments which are largely in the forms of free subunits and fragmented forms of LH β (Birken et al. 1996, Kovalevskaya et al. 1995). The differences between the two LH assays presumably reflect on the capability of the two-site immunoassays to detect various LH epitopes (O'Connor et al. 1998). Both the assays detect intact LH and some fragmented forms probably including the core beta fragment. It is possible that the ICL immunoassay detects other unknown fragment(s) which are not detected by the IF immunoassay. This could explain the consistently lower LH levels measured by the IF assay than the ICL assay. Earlier studies have also reported IF immunoassays meant to detect intact LH failed to detect variant forms either in urine or serum samples that lead in discrepancies in measurements of LH using different immunoassays (Nilsson et al. 2001, Pettersson et al. 1991). LH immunoassays with both β -directed monoclonal antibodies are reported to give higher urinary LH concentrations compared to assays that only detect intact LH (Nilsson et al. 2001). Assays that have highly specific antibodies may also be problematic in that they may not measure all forms of LH (Pettersson et al. 1991, Pettersson et al. 1992, Pettersson and Soderholm 1991).

Loss in urinary LH and hCG immunoreactivity after 7 to 70 days of storage at -20 °C (unpreserved) measured with the IF immunoassay (Lempiainen et al. 2012, Saketos et al. 1994), RIA (Livesey et al. 1983) and immunoenzymatic assay (Robinson et al. 2007) was also reported previously which was attributed to the dissociation of the heterodimeric glycoprotein into its subunits in the presence of urinary urea in specimens (Lempiainen et al. 2012, Livesey et al. 1983). Loss of immunoreactivity of urinary LH (measured with IF immunoassay) was also reported after 24 weeks of -80 °C storage (Kesner et al. 1995). Acetone extraction and addition of preservatives such as bovine serum albumin and glycerol was reported to stabilize LH immunoreactivity in frozen storage (Kesner et al. 1995, Livesey et al. 1983, Saketos et al. 1994). However, using sample preservatives for research sample collection is inconvenient and adds to time and expense (Brindle et al. 2006) and similarly some preservatives such as glycerol are unsuitable for anti-doping purpose. Previous studies have reported that plasma LH is stable after storage for 8 and 14 days after refrigeration (4 °C) (Kubasik et al. 1982, Livesey et al. 1980), for 14 days stored frozen (-6 °C) (Kubasik et al. 1982) and for up to 9 months after -20 or -70 °C storage (Tsatsoulis et al. 1988).

The quantitative reproducibility of the ICL immunoassay indicates it is more robust for measurements of urinary LH for anti-doping purposes compared with the IF assay. Nevertheless despite the quantitative reduction in urine LH by the IF assay, the reduction was proportionate over the four years frozen storage. Consequently the IF assay remains applicable in research studies where, rather than absolute quantification, relative measurements confined to within-study inference, may still be useful.

Chapter 5

Requirement for Specific Gravity and Creatinine Adjustments for Urinary Steroids and Luteinizing Hormone Concentrations in Adolescents

The content in this chapter has been accepted for publication in *Annals of Clinical Biochemistry* 2015

Chapter 5 Requirement for Specific Gravity and Creatinine Adjustments for Urinary Steroids and Luteinizing Hormone Concentrations in Adolescents

5.1 Introduction

Measurements of urinary gonadotropins and steroids in children and adolescents emerged as methods to estimate pubertal development and gonadal function early in the immunoassay era (Kulin and Santner 1977, Raiti et al. 1969, Vestergaard et al. 1966). Subsequently, urine sampling was replaced by serum or plasma immunoassays due to preferences for blood collection over cumbersome and time-consuming urine collections (e.g. 24 hr sampling) and extraction procedures required to assess urine solute concentrations. In recent years, however, measurements of urinary gonadotropins and steroids have reappeared with the development of highly sensitive assays that can measure urinary gonadotropins without extraction (Brindle et al. 2006).

Urine may be collected either as untimed spot collection at random times, first morning void or timed (e.g. 24 hours urine collection) collections. Urine sampling provides an integrated measurement especially for hormones secreted in pulsatile manner such as LH (Kulin et al. 1975) or diurnally like sex steroids in early puberty, and is more acceptable to children and adolescents than venipuncture. Further, for longitudinal studies, spot urine hormone measurements are more convenient and/or less intrusive than blood or saliva collections, a simplification which enhances the feasibility and participant compliance with repeated sampling over time. The relatively high hormone concentrations in urine compared with blood or saliva, together with the ability to concentrate urine, is advantageous for assays with low sensitivity or analytes at low concentrations. However, an inherent problem of using urine is the wide and unregulated variation reflecting the individual's fluid status.

Urine dilution or concentration creates corresponding changes in urine solute concentrations so that adjustment of urine concentration may be required to avoid misinterpreting hormone excretion due to variation in hydration (Cone et al. 2009). Osmolality, SG and creatinine measurements are used to adjust for hydration (Barr et al. 2005). Although measurement of osmolality by freezing point depression is considered the reference method (Chadha et al. 2001), it is laborious, time consuming and expensive so is usually replaced by SG and creatinine measurements particularly for large scale, field studies. Urinary SG is measured using a refractometer to compare light refraction of a urine sample against pure water standard or by reagent strips which measure the ionic strength of urine by color changes. Urine SG of sample is normalized to a population reference value. While SG measurement has been largely superseded by urine creatinine adjustment in clinical laboratories, SG adjustment for urine dilution remains standard in anti-doping laboratories and is used in some toxicology studies (Aylward et al. 2014). Creatinine adjustment is based on the assumption that (a) this end-product formed endogenously from muscle creatine is released into the bloodstream and excreted in urine at a constant rate depending only on total muscle mass (Boeniger et al. 1993) and (b) endogenous hormones and creatinine undergo renal excretion at the same rate (Barr et al. 2005). Yet, creatinine excretion rate may be influenced by the growing muscle mass during puberty leading to potential systemic errors in using creatinine adjustments (Heavner et al. 2006).

Some (Denari et al. 1981, Haddow et al. 1994) but not other (Alessio et al. 1985, Berlin et al. 1985, Jatlow et al. 2003, Thompson et al. 1990, Zacur et al. 1997) studies suggest creatinine or SG adjustment for measurement of urinary substances although such adjustments may be either unnecessary or even introduce additional measurement errors. Furthermore, none have focused on situations where creatinine is changing systematically due to somatic growth. Thus the present study aimed to determine whether the first morning void hormonal

assessments carried out in growing young adolescents at various stages of pubertal progression require adjustments and, if so, to determine whether creatinine or SG adjustment was better.

5.2 Study Design

Urine samples were from the Adolescent Rural Cohort, Hormones, Health, Education and Relationships (ARCHER) study, a three year longitudinal study aiming to determine how temporal changes in pubertal hormones influence the physical status, behavior and mental health of adolescents. The details of the study design have been published previously (Steinbeck et al. 2012). Briefly, the study involves a total of 342 adolescents from the regional towns Dubbo, Orange and their surrounding rural region in western NSW, Australia. The samples reported in the present study were from those collected in the first year of the study (n=644; age distribution ranging between 10.1 and 14.3 years at initial sampling). Ethical approval was obtained from the Human Research Ethics Committee, University of Sydney (HREC 13094). Fasting morning blood samples were collected at 0 and 12 months (n=343) and first morning urine collected three monthly after 12 hr fasting at home by the adolescents between 7.00 am and 8.30 am (n=644). Post-menarcheal girls provided samples in the mid-follicular phase (day 7-10) with the assumption of 28-32 day cycle. Serum and urine samples were stored at -80 C until analysis. The adolescents also provided a self-rating of puberty using line drawings based on the Tanner stages at 0 and 12 months.

The LH and steroid concentrations were adjusted to standard SG of 1.020 according to the formula $[\text{hormone concentration}_{\text{sample}} \times (1.020-1)/(\text{SG}_{\text{sample}}-1)]$ (Wallis et al. 1985) and to standard CR measurement of the present study adolescent population (12.40 mmol/L [n=644; F 331]) using the formula $[\text{hormone concentration}_{\text{sample}} \times (\text{Creatinine}_{\text{population}}/\text{Creatinine}_{\text{sample}})]$ where $\text{Creatinine}_{\text{population}}$ was defined as the mean of the urinary creatinine of the whole sample.

5.3 Data Analysis

The steroid and LH concentrations unadjusted and adjusted for SG or creatinine were compared by Deming (orthogonal) regression and deviance (Bland-Altman) analysis using MedCalc software. Based on using the same analyte with different adjustments, the variance ratio in the Deming regression was assumed to be unity. Non-independence according to variations in the number of samples provided by each individual was ignored in this analysis. Descriptive statistics including mean, SD and SEM were performed by SPSS version 21. The F- ratios of age and Tanner stage group comparison for each hormone were calculated by one-way ANOVA separately for each gender.

5.4 Results

In first morning urine void samples (n=644), the mean (SD, range) creatinine concentration was 12.4 (4.5, 1.4 - 31.5) mmol/L with an overall gender difference being higher in males ($P < 0.05$). The SG was 1.020 (0.0054, 1.005 - 1.030) without significant gender difference ($P = 0.054$). Urine creatinine concentrations were progressively increased according to chronological age and to Tanner stage (Figure 5.1) for both genders. Pooling genders, there were significant differences in urine creatinine concentrations by age and Tanner stage ($P < 0.05$, two-way ANOVA) but not for urine SG according to age ($P = 0.29$) or Tanner stages ($P = 0.22$).

Urinary LH, E_2 , T, DHT and DHEA concentrations, adjusted for either SG or creatinine, are compared according to Deming regression line and the deviance plots are shown in Figure 5.2. For each urinary hormone concentration, there was a good correlation between the SG and creatinine adjusted concentrations (correlation of determination- R^2 : 0.69 - 0.85) free from proportional bias between adjustment methods.

Similarly, Deming regression and Bland-Altman comparison between the unadjusted and adjusted hormone concentrations with either SG or creatinine (Table 5.1) also demonstrate lack of bias whether adjusted or not by either creatinine or SG.

The mean, SD and F-ratios of the unadjusted, SG adjusted and creatinine adjusted hormones according to Tanner stages and age groups in females and males are shown in Tables 5.2-5.3 and Table 5.4-5.5, respectively. The results show consistent estimates and progression according to age and Tanner stage of unadjusted, SG adjusted and creatinine adjusted urine LH and steroid concentrations. The mean, SD and F-ratios of serum hormones according to Tanner stage and age groups are shown in Table 5.6 and 5.7.

The r of paired urinary and serum hormone concentrations is given in Table 5.8. The unadjusted and adjusted (creatinine and SG) urinary LH, E_2 , T, DHT and DHEA concentration showed similar correlation against serum. The samples were also grouped into three creatinine and SG percentile ranges (up to 25th percentile, between 25th to 75th percentile and above 75th percentile) and regression analysis was performed between unadjusted/adjusted urine hormone concentrations against serum hormone concentrations. There were no improvements in the r values within the groups. Dividing the same percentiles according to gender also did not improve the correlations between the urine unadjusted/adjusted hormones against serum hormones concentrations.

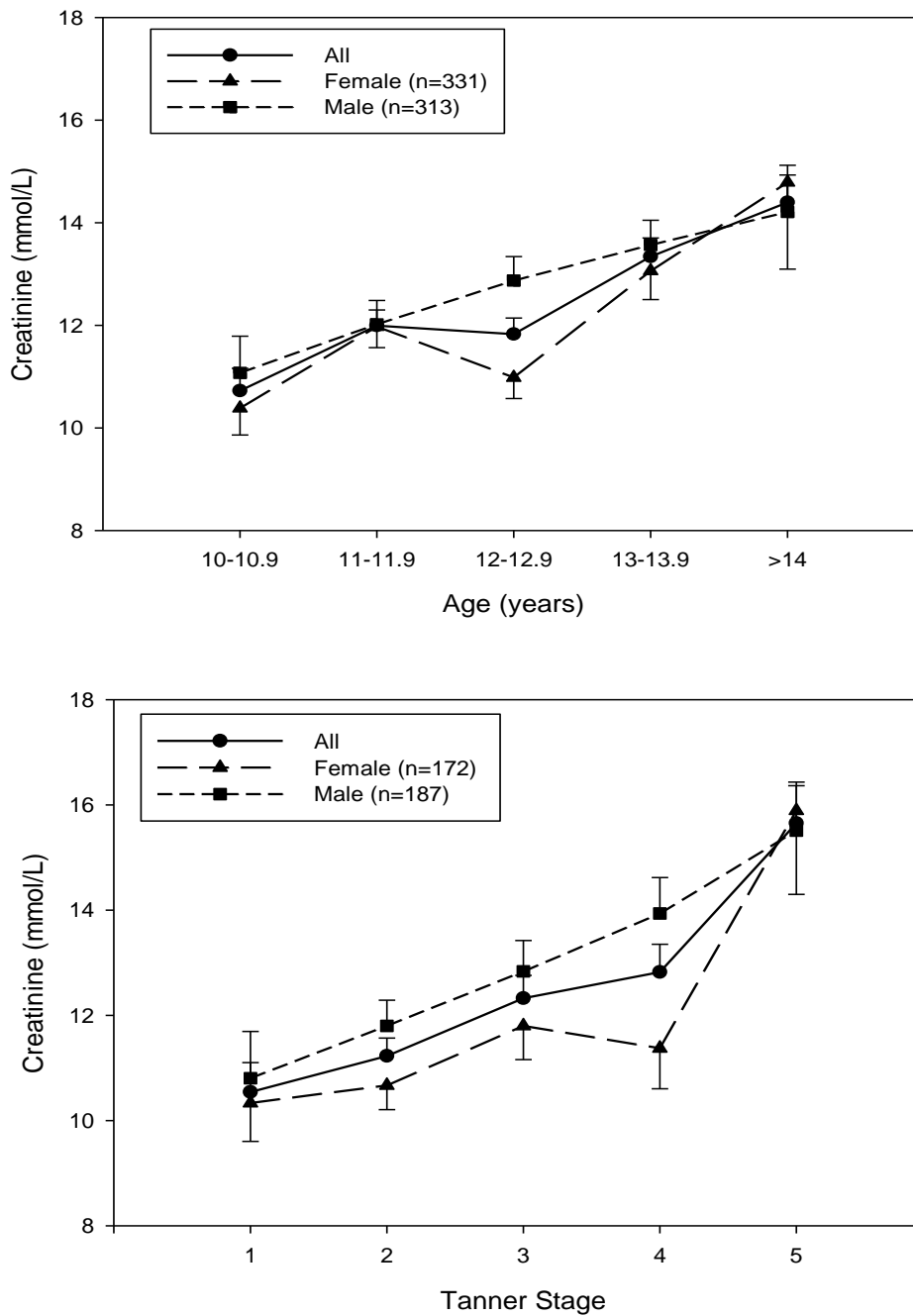


Figure 5.1 Plot of urinary creatinine measurements of adolescents groups according to age (upper panel) and Tanner stage (lower panel).

Data represents the creatinine mean and SEM. For the age plot, samples were from 3-monthly intervals ($n=644$) whereas for the Tanner stage plot, samples were from 0 and 12 months ($n=359$).

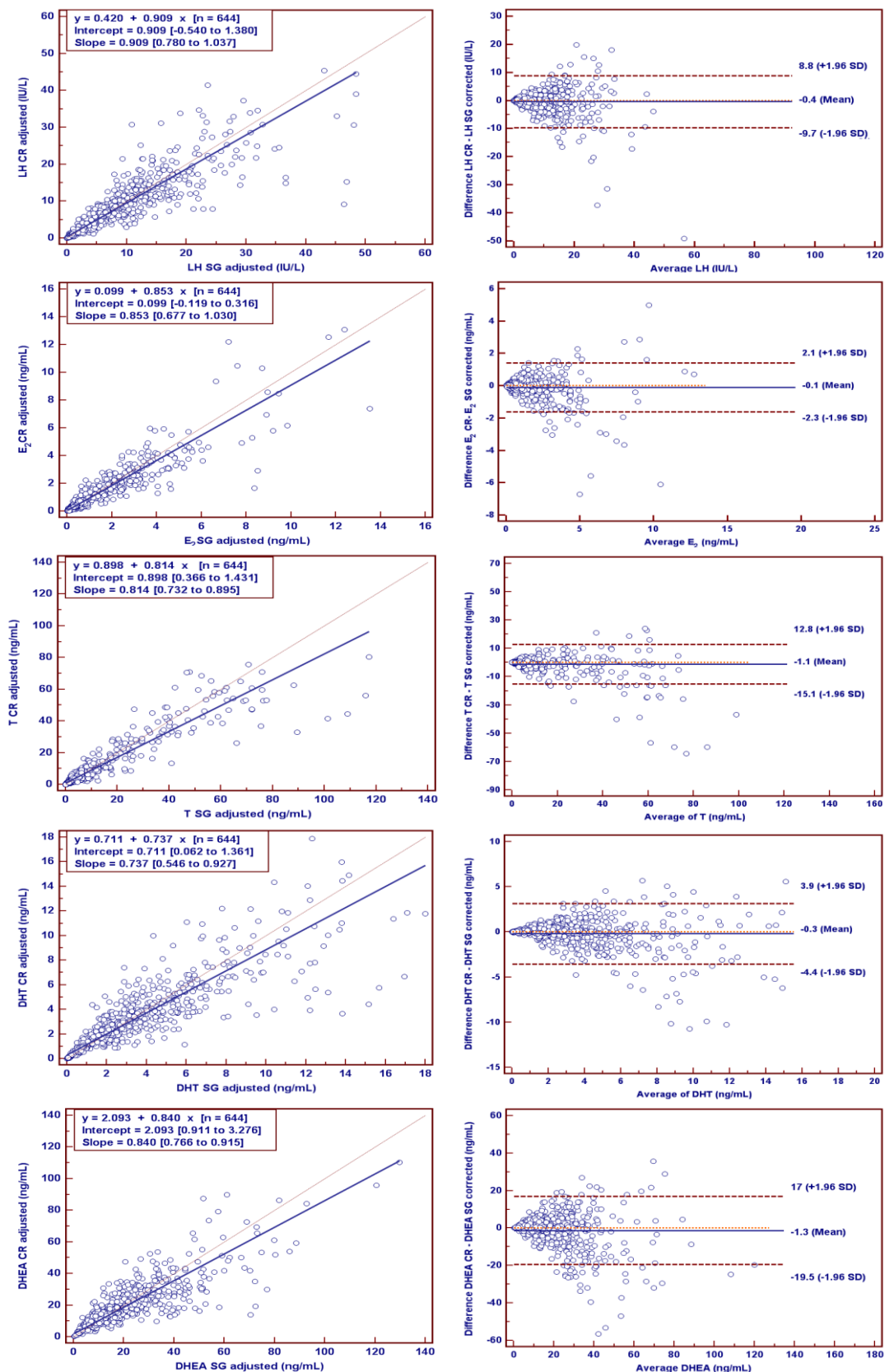


Figure 5.2 Comparison of urinary LH, E₂, T, DHT and DHEA concentrations adjusted by SG and creatinine.

Comparisons were made according to Deming regression analysis (left panels) and Bland-Altman plots (right panels). For the Deming plots, the slope is shown as a solid line and line of identity in fine dotted line. Insets are the regression formula and 95% confidence limits on the intercept and slope. The Bland-Altman plots represent the differences between creatinine and SG adjusted hormone concentrations against the averages of the hormone concentrations adjusted with the two-correction method. The solid line and the dashed lines represent the observed average and the 95% limit of confidence (± 1.96 SD), respectively. Note: A small number (n=6) of outliers were removed for graphical purposes. For the Deming regression, the variance ratio was assumed to be unity. To convert steroids from ng/mL to nmol/L multiply 3.47 for T and DHEA, 3.67 for E₂ and 3.44 for DHT

Table 5.1 Comparison of unadjusted against SG and CR adjusted urinary hormone measurements.

The slope, intercept and 95% confidence interval (CI) were determined by Deming regression. The mean and 95% CI (± 1.96 SD) were derived from the Bland-Altman plots.

	UA vs SG					UA vs CR				
	Deming Regression			Bland-Altman		Deming Regression			Bland-Altman	
	Slope (95% CI)	Intercept (95% CI)	R ²	Mean	95% CI	Slope (95% CI)	Intercept (95% CI)	R ²	Mean	95% CI
LH (IU/L)	0.94 (0.84 to 1.03)	0.03 (-0.67 to 0.73)	0.83	0.6	8.3, -7.2	1.03 (0.94 to 1.11)	-0.39 (-0.98 to 0.19)	0.80	0.1	8.1, -7.8
E2 (ng/mL)	0.92 (0.75 to 1.09)	0.02 (-0.19 to 0.22)	0.86	0.1	2.0, -1.8	1.08 (0.93 to 1.22)	-0.09 (-0.24 to 0.07)	0.85	0.0	1.8, -1.8
T (ng/mL)	0.98 (0.89 to 1.06)	-0.17 (-0.75 to 0.42)	0.90	0.4	11.5, -10.7	1.20 (1.08 to 1.31)	-1.23 (-1.99 to -0.47)	0.88	-0.7	11.7, -13.2
DHT (ng/mL)	1.12 (0.74 to 1.50)	-0.63 (-1.94 to 0.68)	0.89	0.2	3.5, -3.2	1.53 (0.71 to 2.35)	-1.75 (-4.44 to 0.94)	0.82	-0.1	4.8, -5.0
DHEA (ng/mL)	0.90 (0.81 to 0.99)	0.65 (-0.92 to 2.22)	0.75	1.5	17.9, -14.9	1.07 (0.94 to 1.20)	-1.58 (-3.67 to 0.50)	0.67	0.2	17.6, -17.2

Note: UA- unadjusted; SG- specific gravity adjusted; CR- creatinine adjusted; R²-correlation of determination. For the Deming regression, the variance ratio was assumed to be unity.

Table 5.2 Comparison of mean urinary hormone measurements (unadjusted, SG adjusted and CR adjusted) and F- ratios according to Tanner stage in female.

Mean (SD) (n) [#]	Tanner Stage					F Ratio*
	1 (24) [#]	2 (54) [#]	3 (50) [#]	4 (30) [#]	5 (14) [#]	
Unadjusted						
LH (IU/L)	3.59 (6.20)	6.90 (9.69)	9.84 (8.67)	11.59 (6.71)	10.52 (9.28)	4.01
E2 (ng/mL)	0.67 (1.12)	1.21 (1.30)	2.06 (1.59)	2.96 (2.33)	5.72 (4.24)	19.59
T (ng/mL)	1.95 (2.49)	2.99 (2.85)	4.70 (3.54)	5.70 (4.45)	6.57 (3.60)	7.75
DHT (ng/mL)	2.05 (1.98)	2.62 (1.88)	2.20 (1.39)	2.84 (2.73)	2.85 (2.52)	0.95 (P=0.44)
DHEA (ng/mL)	11.51 (8.67)	16.62 (14.97)	18.98 (11.95)	24.56 (17.79)	29.34 (11.69)	5.39
SG adjusted						
LH (IU/L)	3.64 (5.09)	7.67 (10.01)	11.08 (9.59)	12.63 (7.54)	12.54 (12.62)	4.57
E2 (ng/mL)	0.67 (0.90)	1.36 (1.28)	2.34 (1.90)	3.12 (2.28)	6.65 (5.53)	19.92
T (ng/mL)	2.11 (2.24)	3.49 (3.36)	5.36 (5.00)	5.94 (4.58)	7.22 (4.07)	5.95
DHT (ng/mL)	2.22 (1.74)	3.09 (2.42)	2.38 (1.61)	3.03 (3.06)	2.88 (2.19)	1.11 (P=0.35)
DHEA (ng/mL)	14.30 (14.06)	20.00 (19.67)	20.94 (15.52)	26.59 (20.23)	32.58 (16.97)	3.08
Creatinine adjusted						
LH (IU/L)	3.70 (5.33)	7.64 (9.65)	10.83 (8.87)	13.52 (6.94)	9.73 (9.21)	5.43
E2 (ng/mL)	0.67 (0.84)	1.34 (1.17)	2.23 (1.62)	3.27 (2.25)	4.68 (3.06)	18.50
T (ng/mL)	2.13 (1.82)	3.46 (2.92)	4.86 (3.27)	6.28 (4.61)	5.91 (4.23)	7.02
DHT (ng/mL)	2.42 (2.04)	3.09 (2.01)	2.42 (1.41)	3.16 (3.45)	2.63 (2.89)	0.95 (P=0.44)
DHEA (ng/mL)	13.73 (8.78)	19.55 (15.07)	20.45 (12.44)	28.75 (23.33)	26.18 (18.53)	3.58

*All the P values were <0.05 unless indicated in parentheses
(n)[#] Indicates number of samples

Table 5.3 Comparison of mean urinary hormone measurements (unadjusted, SG adjusted and CR adjusted) and F- ratios according to Tanner stage in male.

Mean (SD) (n) [#]	Tanner Stage					F Ratio*
	1 (19) [#]	2 (53) [#]	3 (52) [#]	4 (39) [#]	5 (24) [#]	
Unadjusted						
LH (IU/L)	2.33 (2.77)	4.26 (4.69)	4.79 (4.32)	11.24 (8.14)	11.24 (8.36)	15.46
E2 (ng/mL)	0.15 (0.17)	0.20 (0.26)	0.29 (0.39)	0.96 (0.90)	1.26 (0.85)	24.30
T (ng/mL)	2.00 (2.26)	3.86 (7.33)	6.33 (9.23)	25.55 (21.59)	42.14 (34.07)	31.25
DHT (ng/mL)	2.30 (1.58)	2.35 (2.18)	2.24 (2.01)	5.26 (3.46)	6.19 (3.78)	16.73
DHEA (ng/mL)	10.13 (8.68)	10.25 (7.47)	13.68 (10.86)	21.00 (12.99)	25.15 (13.60)	12.15
SG adjusted						
LH (IU/L)	2.39 (2.68)	4.48 (4.68)	5.21 (5.03)	11.21 (8.09)	11.52 (8.76)	13.90
E2 (ng/mL)	0.16 (0.16)	0.20 (0.23)	0.32 (0.40)	0.95 (0.83)	1.25 (0.83)	25.31
T (ng/mL)	2.04 (2.00)	3.87 (6.75)	7.59 (13.26)	27.21 (25.31)	43.06 (33.50)	27.57
DHT (ng/mL)	2.44 (1.45)	2.84 (3.36)	2.51 (2.31)	5.29 (3.77)	6.31 (4.18)	10.01
DHEA (ng/mL)	11.98 (11.63)	11.86 (11.07)	15.18 (12.42)	20.42 (11.70)	24.44 (12.97)	6.56
Creatinine adjusted						
LH (IU/L)	2.59 (2.75)	4.50 (4.88)	4.64 (4.56)	10.29 (6.57)	9.17 (6.24)	12.77
E2 (ng/mL)	0.16 (0.15)	0.20 (0.21)	0.28 (0.32)	0.79 (0.55)	1.04 (0.72)	27.99
T (ng/mL)	1.99 (1.74)	4.00 (6.95)	6.52 (9.90)	22.97 (19.26)	34.45 (24.35)	30.45
DHT (ng/mL)	2.67 (1.59)	2.48 (2.71)	2.32 (2.23)	4.61 (2.83)	5.02 (2.95)	8.85
DHEA (ng/mL)	11.78 (8.24)	10.87 (6.86)	13.60 (10.56)	18.27 (8.10)	20.78 (12.06)	7.13

*All the P values were <0.05 unless indicated in parentheses
(n)[#] Indicates number of samples

Table 5.4 Comparison of mean urinary hormone measurements (unadjusted, SG adjusted and creatinine adjusted) and F- ratios according to age groups in female.

Mean (SD) (n) [#]	Age (years)					F Ratio*
	10-10.9 (21) [#]	11-11.9 (57) [#]	12-12.9 (50) [#]	13-13.9 (36) [#]	>14 (10) [#]	
Unadjusted						
LH (IU/L)	4.61 (6.25)	6.76 (8.57)	9.23 (9.37)	11.66 (9.14)	8.80 (4.68)	3.00
E2 (ng/mL)	0.94 (1.22)	1.26 (1.32)	1.80 (1.84)	2.99 (1.85)	6.74 (4.74)	21.71
T (ng/mL)	2.23 (1.84)	3.48 (3.26)	4.35 (3.51)	5.39 (4.38)	5.57 (4.31)	3.61
DHT (ng/mL)	1.89 (1.43)	2.53 (1.87)	2.69 (1.98)	2.31 (2.18)	2.97 (2.99)	0.82 (P=0.52)
DHEA (ng/mL)	12.97 (7.98)	15.73 (11.41)	18.41 (15.63)	23.60 (14.95)	36.98 (14.35)	7.52
SG adjusted						
LH (IU/L)	5.42 (7.01)	6.70 (7.58)	10.55 (10.25)	13.88 (11.48)	9.87 (5.56)	4.57
E2 (ng/mL)	1.04 (1.16)	1.32 (1.40)	2.04 (1.77)	3.43 (2.40)	7.57 (6.05)	21.38
T (ng/mL)	2.66 (2.16)	3.61 (3.31)	5.14 (4.44)	6.12 (5.58)	5.77 (4.16)	3.57
DHT (ng/mL)	2.47 (2.43)	2.62 (2.00)	3.13 (2.39)	2.53 (2.26)	3.11 (2.95)	0.62 (P=0.65)
DHEA (ng/mL)	17.15 (14.01)	16.47 (12.75)	22.57 (21.65)	26.16 (17.16)	41.04 (20.44)	5.48
Creatinine adjusted						
LH (IU/L)	5.68 (8.00)	7.00 (7.90)	10.52 (9.68)	12.59 (8.93)	9.21 (6.64)	3.49
E2 (ng/mL)	1.09 (1.26)	1.36 (1.27)	1.96 (1.63)	3.02 (1.73)	5.86 (3.67)	19.98
T (ng/mL)	2.76 (2.36)	3.77 (2.86)	4.90 (3.95)	5.21 (3.74)	5.34 (5.52)	2.50
DHT (ng/mL)	2.30 (1.72)	2.83 (1.74)	3.09 (2.43)	2.38 (2.18)	3.31 (4.46)	0.89 (P=0.47)
DHEA (ng/mL)	15.76 (9.76)	18.07 (11.18)	21.56 (19.65)	23.92 (13.44)	37.84 (27.70)	4.34

*All the P values were <0.05 unless indicated in parentheses.

(n)[#] indicates number of samples

Table 5.5 Comparison of mean urinary hormone measurements (unadjusted, SG adjusted and creatinine adjusted) and F- ratios according to age groups in male.

Mean (SD) (n) [#]	Age (years)					F Ratio*
	10-10.9 (29) [#]	11-11.9 (54) [#]	12-12.9 (45) [#]	13-13.9 (42) [#]	>14 (17) [#]	
Unadjusted						
LH (IU/L)	2.52 (4.16)	4.07 (4.50)	7.61 (5.55)	10.38 (8.19)	9.21 (8.90)	10.44
E2 (ng/mL)	0.11 (0.09)	0.21 (0.28)	0.42 (0.42)	1.03 (1.00)	1.15 (0.73)	20.77
T (ng/mL)	1.33 (2.96)	4.60 (9.48)	11.19 (14.46)	27.63 (25.63)	36.99 (34.82)	19.96
DHT (ng/mL)	1.77 (1.29)	2.65 (2.27)	3.09 (2.72)	5.01 (3.71)	5.57 (3.90)	9.37
DHEA (ng/mL)	6.94 (6.33)	11.15 (8.69)	16.60 (11.04)	21.41 (13.33)	24.72 (12.85)	13.63
SG adjusted						
LH (IU/L)	2.66 (3.95)	4.24 (4.45)	7.51 (5.93)	11.36 (8.82)	8.63 (7.34)	11.59
E2 (ng/mL)	0.12 (0.08)	0.21 (0.23)	0.41 (0.39)	1.08 (0.95)	1.09 (0.68)	24.48
T (ng/mL)	1.29 (2.35)	4.82 (10.45)	11.03 (14.16)	32.25 (31.29)	34.36 (28.89)	20.40
DHT (ng/mL)	1.87 (1.20)	3.30 (3.83)	3.02 (2.67)	5.43 (3.82)	5.25 (3.73)	6.84
DHEA (ng/mL)	7.71 (6.00)	13.01 (12.50)	16.18 (10.69)	23.13 (13.00)	23.69 (12.75)	10.71
Creatinine adjusted						
LH (IU/L)	2.56 (3.41)	4.19 (5.00)	6.92 (5.08)	9.54 (6.89)	8.07 (5.52)	10.05
E2 (ng/mL)	0.12 (0.08)	0.21 (0.23)	0.38 (0.34)	0.86 (0.71)	1.00 (0.47)	26.39
T (ng/mL)	1.31 (2.19)	4.26 (7.09)	10.26 (14.12)	24.28 (20.14)	33.08 (25.23)	24.36
DHT (ng/mL)	2.00 (1.48)	2.78 (2.88)	2.78 (2.37)	4.46 (2.83)	4.85 (3.23)	6.29
DHEA (ng/mL)	7.68 (5.56)	11.80 (9.21)	14.91 (8.85)	19.37 (9.52)	22.00 (9.20)	12.13

*All the P values were <0.05 unless indicated in parentheses.
(n)[#] indicates number of samples

Table 5.6 Comparison of mean serum hormone measurements and F- ratios according to Tanner stage in female and male.

Mean (SD)	Tanner Stage					F Ratio*
	1	2	3	4	5	
	Female					
(n) [#]	(24) [#]	(50) [#]	(43) [#]	(32) [#]	(12) [#]	
LH (IU/L)	0.88 (1.54)	2.06 (2.12)	3.47 (2.33)	4.39 (2.57)	5.70 (3.14)	14.90
E2 (pg/mL)	26.26 (23.00)	36.86 (23.48)	54.76 (28.76)	56.58 (22.32)	74.43 (41.57)	10.80
T (ng/mL)	0.10 (0.06)	0.16 (0.10)	0.22 (0.16)	0.82 (1.84)	0.31 (0.13)	4.09
DHT (ng/mL)	0.08 (0.05)	0.10 (0.07)	0.11 (0.07)	0.15 (0.10)	0.16 (0.08)	4.69
DHEA (ng/mL)	2.26 (1.11)	2.94 (1.62)	3.45 (2.17)	4.01 (2.50)	5.10 (1.70)	5.92
	Male					
(n) [#]	(17) [#]	(52) [#]	(48) [#]	(34) [#]	(22) [#]	
LH (IU/L)	0.50 (0.58)	0.81 (0.81)	1.17 (1.02)	2.64 (1.51)	2.73 (1.53)	24.52
E2 (pg/mL)	11.88 (6.97)	10.54 (5.44)	13.73 (7.56)	22.28 (11.65)	25.52 (11.19)	18.80
T (ng/mL)	0.09 (0.08)	0.64 (0.92)	0.93 (1.26)	3.55 (2.09)	4.58 (2.08)	51.04
DHT (ng/mL)	0.12 (0.08)	0.17 (0.14)	0.26 (0.66)	0.33 (0.16)	0.35 (0.15)	1.85 (P=0.12)
DHEA (ng/mL)	1.74 (1.23)	2.11 (0.99)	2.42 (1.38)	3.37 (1.73)	3.43 (1.46)	8.41

*All the P values were <0.05 unless indicated in parentheses
(n)[#] indicates number of samples

Table 5.7 Comparison of mean serum hormone measurements and F- ratios according to age groups in female and male.

Mean (SD)	Age (years)					F Ratio*
	10-10.9	11-11.9	12-12.9	13-13.9	>14	
	Female					
(n) [#]	(20) [#]	(54) [#]	(48) [#]	(36) [#]	(9) [#]	
LH (IU/L)	0.90 (1.18)	2.14 (2.44)	3.00 (2.38)	4.38 (2.17)	6.09 (3.40)	13.20
E2 (pg/mL)	29.10 (22.51)	31.44 (20.44)	48.80 (21.79)	64.87 (27.98)	88.42 (42.14)	19.86
T (ng/mL)	0.12 (0.08)	0.15 (0.10)	0.24 (0.26)	0.56 (1.27)	1.15 (2.44)	4.17
DHT (ng/mL)	0.08 (0.05)	0.12 (0.69)	0.10 (0.06)	0.14 (0.08)	0.20 (0.14)	6.43
DHEA (ng/mL)	2.54 (1.07)	2.82 (1.51)	2.96 (1.84)	4.05 (1.84)	6.81 (3.69)	12.27
	Male					
(n) [#]	(26) [#]	(55) [#]	(40) [#]	(40) [#]	(15) [#]	
LH (IU/L)	0.65 (0.74)	0.79 (0.84)	1.34 (0.86)	2.27 (1.33)	3.57 (1.98)	28.43
E2 (pg/mL)	11.38 (5.59)	10.37 (6.68)	15.46 (9.35)	21.09 (9.22)	29.76 (10.90)	22.80
T (ng/mL)	0.14 (0.18)	0.52 (1.04)	1.77 (1.83)	3.26 (2.11)	4.67 (2.00)	37.66
DHT (ng/mL)	0.13 (0.08)	0.22 (0.62)	0.23 (0.18)	0.30 (0.15)	0.37 (0.15)	1.44 (P=0.22)
DHEA (ng/mL)	1.89 (1.20)	2.04 (1.29)	2.60 (1.31)	3.13 (1.32)	4.15 (1.69)	10.92

*All the P values were <0.05 unless indicated in parentheses

(n)[#] indicates number of samples

Table 5.8 Pearson's correlation coefficient and confidence intervals (in parentheses) of paired urinary and serum LH, E2, T, DHT and DHEA (n=343).

Urine versus serum	LH	E2	T	DHT	DHEA
UA	0.56 (0.48 to 0.63)	0.73 (0.67 to 0.77)	0.79 (0.74 to 0.82)	0.44 (0.35 to 0.52)	0.63 (0.56 to 0.69)
SG	0.57 (0.50 to 0.64)	0.72 (0.66 to 0.77)	0.79 (0.74 to 0.83)	0.42 (0.33 to 0.50)	0.60 (0.52 to 0.66)
CR	0.56 (0.48 to 0.63)	0.79 (0.74 to 0.82)	0.80 (0.76 to 0.84)	0.35 (0.25 to 0.44)	0.66 (0.59 to 0.71)

Note: UA- unadjusted; SG- specific gravity adjusted; CR- creatinine adjusted.

5.5 Discussion

Urinary measurement of reproductive hormones is a convenient means to evaluate pubertal status and gonadal function for field population studies. In clinical settings, adjustment based on the assumption of stable urine creatinine excretion is commonly used to adjust for variations in hydration although other techniques such as regression normalization or log transformation are proposed (Gaines et al. 2010, Heavner et al. 2006). As an end metabolite of muscle creatine, urine creatinine is determined by total muscle mass in addition to other factors such as age, gender, diet (meat consumption), physical activity, and BMI some of which exert their effects via changes in muscle mass (Alessio et al. 1985, Barr et al. 2005, Carrieri et al. 2000, Suwazono et al. 2005). Hence one aim of the present study was to determine for the first time whether creatinine adjustment was valid or required for longitudinal studies of growing adolescents.

Our findings confirm that the first morning urine creatinine concentration increases with age and Tanner stages and was higher among males. However, adjustment for urine creatinine was no better or worse than adjustment for SG or even no adjustment. This may reflect the fact that we studied first morning void urine samples which control hydration, whereas similar interpretation may not apply to urine sampled at random when hydration state may

vary more. Our findings are consistent with previous studies showing prominent intra- and inter-individual variability in creatinine excretion of second morning and 24h urine samples in adults due to variable fluid intake (Alessio et al. 1985). Significantly higher creatinine levels in morning versus afternoon (Colombi et al. 1983), in evening spot samples (Barr et al. 2005) and creatinine loss due to multiple freeze-thaw cycles have also been reported (Garde et al. 2003, Schneider et al. 2002) all of which introduce systematic errors in use of urine creatinine for dilution adjustments. Thus, although studies have suggested alternative adjustment based on SG in adult humans and primates (Miller et al. 2004, White et al. 2010), none have focused on the need for SG adjustments in first morning voids of growing adolescents.

SG is readily measured by reagent strip for field studies without needing a laboratory. Previous studies demonstrate good agreement between SG measurements by reagent strip versus refractometer (Frew et al. 1982, Moore Jr et al. 1997) or osmolality (Dorizzi et al. 1987, Frew et al. 1982, Gounden and Newall 1983). SG measurement by reagent strip is widely used in clinical applications (Burkhardt et al. 1982, Gounden and Newall 1983). Although refractometer urine SG may be influenced by disease states leading to high serum protein or glycosuria,(Chadha et al. 2001, Voinescu et al. 2002) reagent strip SG is not affected by glucose, only minimally by urea and albumin, but may be affected by the rare instances of alkaline urine (Dorizzi et al. 1987). Urine SG reading may also be influenced by diet, environment and the renal reabsorption capacity (Trevisan 1990). Among adolescents, we find that urine SG measured with reagent strips is systematically not influenced by age or gender consistent with previous reports (Nermell et al. 2008, Suwazono et al. 2005).

Limits of acceptable creatinine and SG measurements vary between studies. Generally, urine is considered too dilute when the SG and creatinine levels are lower than 1.010 and 0.5 g/l (4.4 mmol/L), respectively, and too concentrated where SG and creatinine levels higher than

1.030 (or 1.035) and 3 g/l (26.5 mmol/L), respectively (Alessio et al. 1985, Trevisan 1990). However, due to the standardized method of collection and hydration (first morning void), the present study did not discard any samples as too dilute or too concentrated.

The present study demonstrated that the fasting first morning void urine hormone concentrations adjusted by creatinine correlated well with those adjusted by SG in this adolescent population. This is consistent with previous reports that used randomly collected or timed urine collection from children and adults showing good correlations when creatinine and SG adjustments were compared directly (Carrieri et al. 2000, Cone et al. 2009, Gaines et al. 2010, Haddow et al. 1994, Parikh et al. 2002, Trevisan 1990) or with adjustment according to both (Cone et al. 2009, Miller et al. 2004, White et al. 2010) including a reduced variation using these adjustments in some studies (Haddow et al. 1994, Heavner et al. 2006). However, the present study shows that neither of the adjustment methods for first morning void urine sample of adolescents were significantly improved compared to unadjusted hormone concentrations. These observations are consistent with previous reports for creatinine adjustment of urine steroid measurements in adult women (Hakim et al. 1994, Miyakawa et al. 1981).

In studies where the urinary hormone concentrations were correlated with paired circulating serum concentrations, the urinary unadjusted concentration or concentration expressed by volume of urine correlates better than the adjustment based on analyte to creatinine ratios (Demir et al. 1994, Denari et al. 1981, Zacur et al. 1997), although some studies have shown improved correlation with creatinine adjustments (Munro et al. 1991, Seki et al. 1985). The present study demonstrated that the urinary hormone concentrations adjusted with creatinine and SG did not improve the correlation with paired serum concentrations. These samples were also grouped into three creatinine and SG percentile ranges (25th, 25-75th and 75th) to replicate non-fasting conditions with wider variation in hydration status. However, no

improvement was observed in terms of correlation between the unadjusted or adjusted urine hormone and paired serum concentrations. These findings further support that the adjustments may not be necessary for first morning void urine samples.

In conclusion, the present study shows that adjustment of urinary steroid and LH concentration for hydration state may not be required for first morning void specimens of even growing adolescents. If adjustments are required, then either creatinine or SG are equally suitable and provide comparable results. Reagent strip SG measurements are simple and sufficiently reliable, economical and time-saving for large numbers of urine sampling in long-term field studies.

Chapter 6

Urinary Sex Steroids, Luteinizing Hormone and Anthropometric Markers of Puberty

Chapter 6 Urinary Sex Steroids, Luteinizing Hormone and Anthropometric Markers of Puberty

6.1 Introduction

The circulating gonadotropin, T and E₂ changes that drive the external manifestations of puberty are well described from cross-sectional studies according to chronological age or Tanner staging interpreted quasi-longitudinally (Dorn et al. 2006, Lee and Houk 2006). Such cross-sectional analysis artificially smooths longitudinal data due to a low resolution in temporal sampling, markedly underestimating the underlying within-subject variability. Hence the large, normal variability in both time of onset and tempo of completing puberty has been insufficiently considered as important intermediate factors in the marked physical and psychological changes wrought by puberty. Furthermore previous studies have relied upon older methods of often direct (unextracted) sex steroid immunoassays, an inaccurate technology especially at low circulating steroid levels concentrations (Handelsman and Wartofsky 2013), which is now being supplanted by more sensitive and specific MS-based steroid assays (Handelsman and Wartofsky 2013, Sikaris et al. 2005). Similar more sensitive MS-based methods have been recently described for serum sex steroids in pre-pubertal children (Courant et al. 2010).

In clinical settings the usual methods to appraise pubertal development comprise hormone measurements and anthropometry, with emphasis on timing of the height growth spurt, clinical inspection and bone age (Biro et al. 1995, Bordini and Rosenfield 2011). In epidemiological studies the definition of puberty has to be simplified to be based on adolescent self-report or parental report against either Tanner stage line drawings (Marshall and Tanner 1969, Marshall and Tanner 1970) or Petersen's Pubertal Development Scale

(Dorn et al. 2006). Self-rated Tanner staging is less intrusive and more feasible than clinician assessment for epidemiological studies despite some loss of reliability, especially in early puberty, which can be overcome by larger sample size (Bonat et al. 2002, Desmangles et al. 2006, Hergenroeder et al. 1999, Morris and Udry 1980). Menarche (a late pubertal event), spermarche (Ji 2001, Nielsen et al. 1986) which is difficult to evaluate (Sivananthan et al. 2012), semenarche, and voice breakage have all been described in relation to age and/or Tanner stage (Laron 2010, Sun et al. 2012) but as solitary time points provide minimal information on either timing of onset or tempo of puberty. To date there have been no reports describing individual puberty hormone change with sufficient measurement frequency to adequately capture individual variation, which is necessary to adequately describe onset and tempo of puberty for a community-based study.

The first aim of this study is to validate the feasibility of the frequent urine sampling regimen and the urine assay methodology for LH, E₂ and T. The second aim is to validate the changes in urine LH, E₂ and T over 12 months by reference to contemporaneous changes in anthropometry and self-reported Tanner stage.

6.2 Study design

Adolescents between the ages of 10 and 12 years were recruited from local schools of two regional towns in the state of New South Wales (NSW), Australia. Fasting morning blood samples were collected at 0 and 12 months for the measurement of LH, E₂ and T, and first morning (fasting) urine collected three monthly for the same measures. No participants had an endocrine disorder or were on any type of gonadal steroid hormone therapy. Height was measured using a portable stadiometer (to 0.1 cm). Weight was measured in light clothing using a Tanita TBF-300 Pro Body Composition Analyzer (Kettaneh et al. 2005). Height, weight and BMI (kg/m²) were expressed as z-scores using the Centres for Disease Control

(CDC 2000) and World Health Organization (WHO 2006) standard age and gender reference charts. The adolescents provided a self-rating of puberty using line drawings based on the Tanner stages (Marshall and Tanner 1969, Marshall and Tanner 1970). Self-report of Tanner stage (Bonat et al. 2002, Desmangles et al. 2006, Hergenroeder et al. 1999, Morris and Udry 1980) was the only feasible and ethically acceptable measure of pubertal staging available to the investigators.

First morning urine following a 12 hour fast was collected at home before blood samples were collected between 7:00 am and 8:30 am to minimise the effects of diurnal hormone variation (Bremner et al. 1983, Dorn et al. 2006). Serum and urine were stored at -80 °C. Post-menarcheal girls provided urine and blood specimens in the mid-follicular phase (Day 7-10) of their menstrual cycle. Serum and urine steroids were measured by LC-MS/MS assay (Chapter 2). Blood and urine samples with hormone values less than the LLOQ for E₂ and T were taken as half the LLOQ.

Serum and urine LH were measured by Immulite 1000 LH (Chapter 2). The within-assay coefficients of variation were <10%. Serum and urine LH values below the detection limit (0.1 IU/L) were set at zero. Urine FSH assays (Immulite, Delfia) did not pass validity tests (dilutional linearity, quantitative spike recovery) and were not used in this study. All urine hormone concentrations were adjusted for urine SG measured by reagent strip (Chapter 2) to a standard SG of 1.020.

The study has ethical approval from the Human Research Ethics Committee, University of Sydney (HREC 13094) within the NHMRC, which are consistent with the Declaration of Helsinki. All participants assented, and a parent provided written informed consent prior to commencing the study.

6.3 Data analysis

Two-way ANOVA was used to determine effects of gender and scheduled sampling time and their interaction on anthropometric and hormone outcomes. ANCOVA was used to assess the relationship between serum hormones with changes in anthropometric variables. Mixed models linear regression was used to assess the relationship between longitudinal changes in urinary hormones and changes in anthropometric values. Baseline hormone values and baseline anthropometric measurements were covariates. All statistical analyses were conducted using Stata 12.1 (StataCorp, Texas, USA). Statistical significance was set at the 0.05 level.

6.4 Results

6.4.1 Cohort characteristics

One hundred and four participants were recruited. The mean ages (SD) for the study participants at baseline were 12.5 (0.93) years for males and 11.8 (0.98) years for females. At follow-up, the ages were 13.5 (0.94) years for males and 12.9 (0.97) years for females. For the females, 22 (39%) had menarche prior to the study and one additional girl experienced menarche during the follow-up year. Post-menarcheal girls were significantly older than their pre-menarcheal counterparts (12.9 years vs. 11.9 years, $p < 0.001$). A high proportion of scheduled samples were collected for urine (484, 92%) and serum (194, 93%). There was a low loss to follow-up (7, 6.7%).

Mean anthropometric measurements, other than BMI, increased significantly over 12 months (Table 6.1) whereas age- and gender-standardized z-scores did not change over the 12 months follow-up (Table 6.2). Pre-menarcheal girls significantly increased their age-standardized weight ($p < 0.001$) and height z-scores ($p = 0.002$), whereas these z-scores did not change for

post-menarcheal girls. Rate of change in anthropometric measurements were similar between genders (interaction $p > 0.05$).

Self-rated Tanner staging increased with fewer in stage 1 and more in stage 5 at 12-month follow-up. During the year, 14 participants (13.5%) progressed two Tanner stages, 43 (41.3%) progressed one stage and 41 (39.4%) did not change in their self-rated Tanner stage (Table 6.3). Six (5.8%) participants (three boys) provided a lower self-rated Tanner stage at follow-up than baseline. One participant (1%, 1 boy) did not provide baseline Tanner staging and seven (6.7%, 1 boy, 6 girls) did not provide follow-up Tanner staging.

Table 6.1 Baseline and 12-month follow-up anthropometry measurements.

Mean (SD)	Baseline		12 Months		ANOVA F-statistic (p-value)		
	M (n=47)	F (n=57)	M (n=47)	F (n=57)	Gender	Time	Gender x Time
Height (cm)	156.8 (9.9)	150.8 (8.5)	163.8 (10.1)	157.1 (7.9)	25.7 (<0.001)	27.6 (<0.001)	0.08 (0.78)
Weight (kg)	49.3 (12.0)	44.1 (10.9)	55.2 (13.2)	50.1 (11.4)	9.7 (0.002)	13.2 (<0.001)	0.00 (0.99)
BMI (kg/m ²)	19.7 (3.5)	20.4 (3.8)	19.3 (3.7)	20.3 (4.0)	0.29 (0.59)	2.84 (0.09)	0.08 (0.77)

Table 6.2 Baseline and 12 month follow-up WHO and CDC z-scores (for age).

Mean (SD)	Baseline		12 months		Two-Way ANOVA F-statistic (p-value)		
	M	F	M	F	Gender	Time	Gender x Time
Height z (CDC)	0.50 (1.05)	0.16 (0.87)	0.50 (1.08)	0.25 (0.91)	4.81 (0.03)	0.13 (0.72)	0.12 (0.73)
Weight z (CDC)	0.43 (1.12)	0.19 (0.96)	0.46 (1.11)	0.35 (0.91)	1.46 (0.23)	0.44 (0.51)	0.19 (0.67)
BMI z (CDC)	0.28 (1.03)	0.18 (1.00)	0.27 (1.04)	0.27 (0.98)	0.12 (0.73)	0.09 (0.76)	0.12 (0.72)
Height z (WHO)	0.56 (1.11)	0.14 (0.92)	0.58 (1.12)	0.30 (0.93)	6.18 (0.02)	0.40 (0.53)	0.25 (0.62)
BMI z (WHO)	0.51 (1.24)	0.29 (1.18)	0.42 (1.21)	0.32 (1.18)	0.91 (0.34)	0.03 (0.87)	0.14 (0.71)

Table 6.3 Self-Rated Tanner staging at baseline and 12 month follow-up.

N Tanner	Baseline		12 Months	
	M	F	M	F
1	6	14	0	3
2	8	17	7	13
3	9	16	6	15
4	18	7	18	12
5	5	3	14	8
Total	46	57	45	51

6.4.2 *Hormone measurements*

Serum: Of the 194 serum collections, nine (5%) LH assays and two (1%) T (all in separate individuals) were below the LLOQ. No E₂ samples were below LLOQ. Those with LH samples below the limits of detection were significantly younger than their peers (mean difference = 1.47 years 95% CI 0.81-2.14 p<0.001). No difference in age was observed for those with serum T or E₂ samples below LLOQ. Hormone values all significantly increased over the 12-month period and were significantly different between genders, but rate of change was not statistically significant between gender (interaction p>0.05) (Table 6.4).

Table 6.4 Baseline and 12-month follow-up serum LH, E₂ and T.

Mean (SD)	Baseline		12 months		ANOVA F-statistic (p-value)		
	M (n=47)	F (n=57)	M (n=47)	F (n=57)	Gender	Time	Gender x Time
LH (IU/L)	1.7 (1.3)	2.3 (2.4)	2.5 (1.8)	3.6 (2.7)	9.4 (0.002)	11.2 (0.001)	0.70 (0.402)
E ₂ (pg/mL)	19.1 (8.5)	43.4 (29)	24.9 (9)	54.7 (30)	73.5 (<0.001)	6.4 (0.012)	0.74 (0.390)
T (ng/mL)	2.4 (2.3)	0.16 (0.10)	3.4 (2.55)	0.2 (0.12)	130.1 (<0.001)	5.0 (0.027)	3.80 (0.052)

Figure 6.1 shows serum LH, E₂ and T at baseline and follow-up, stratified by Tanner stages. Data stratified by chronological age were similar. Hormone concentrations increased through each Tanner stage and each year of age, although ordinal groupings overlap.

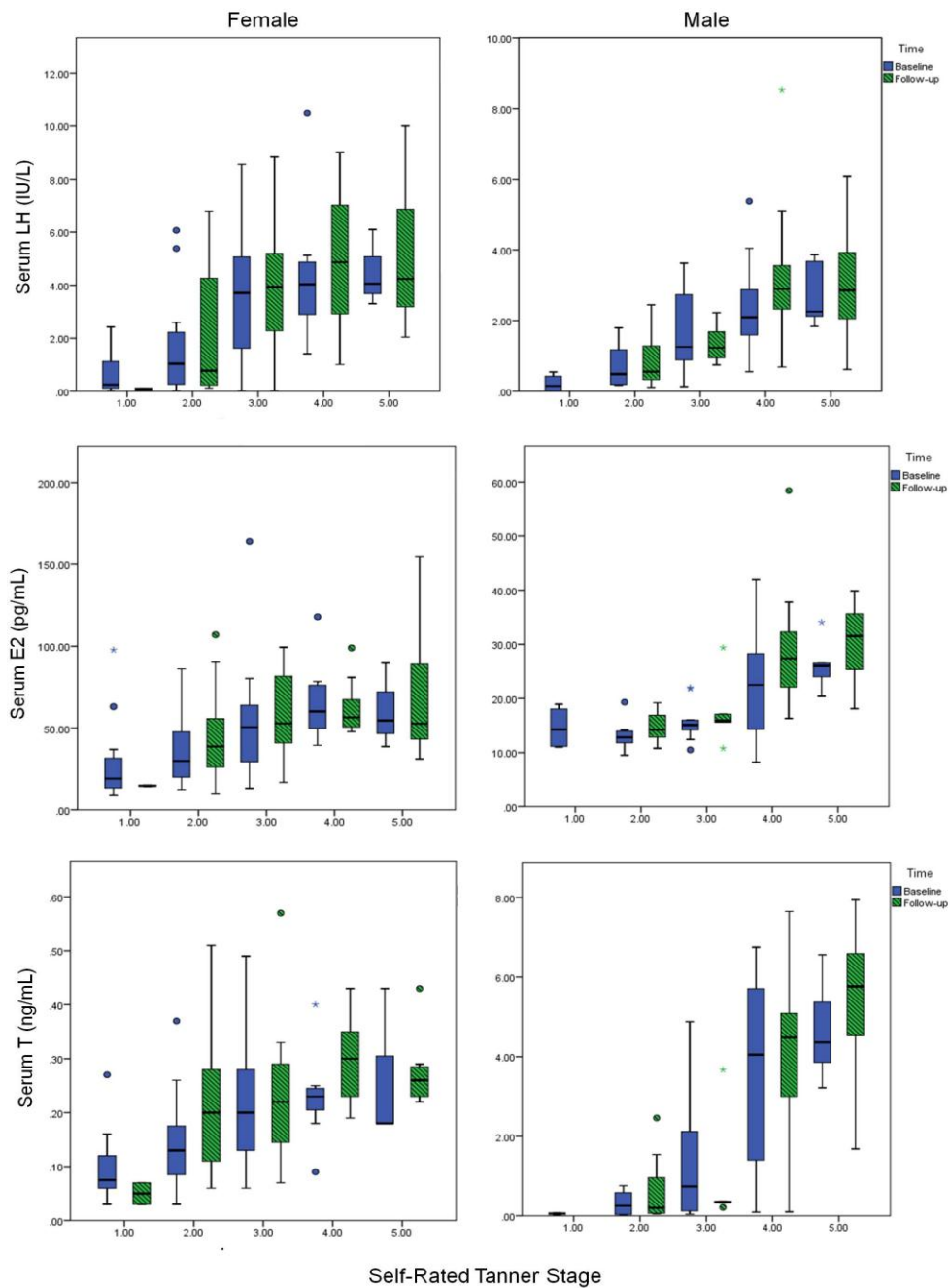


Figure 6.1 Cross-sectional plots of serum LH (top), E₂ (centre) and T (bottom) at baseline and 12-month follow-up, by self-rated Tanner stage.

Urine: For the 484 urine collections, five (1%) LH assays, 14 (3%) E₂ and nine (2%) T assays were below the LLOQ. For LH, these participants were younger than the rest of the cohort (mean difference 1.35 years; 95% CI 0.41-2.30; p=0.005), but there was no age difference between those with urine E₂ or T samples below or above the LLOQ. In five such cases (one urine and serum LH, one urine E₂, one urine E₂ and T, one urine T, one serum LH) the participant provided a Tanner stage 1 at baseline.

Figure 6.2 shows within-person changes from baseline over the 12-month collection period and Table 6.5 shows the mean three monthly values for urinary LH, E₂ and T over 12 months. There is a significant increase from baseline to follow-up in E₂, T and LH. The same pattern is seen in females when stratified by menarcheal status (Table 6.6). Urine hormone levels were not strictly progressive and in some instances decreased over time, though there was an overall increase in mean levels for all three hormones for males and females overall. For serum hormones, a decline from baseline to follow-up was observed in 26 adolescents (18 female) for LH, 22 adolescents (11 female) for E₂ and 19 (13 female) for T. Overall declines in urinary LH were observed in 48 adolescents (30 female), 23 (9 female) for urinary E₂, and 24 (14 female) for urinary T.

Urinary LH, E₂ and T all positively correlated with Tanner staging at baseline and 12-month follow-up (p<0.001 for all). Urinary LH, E and T all increased across Tanner stages.

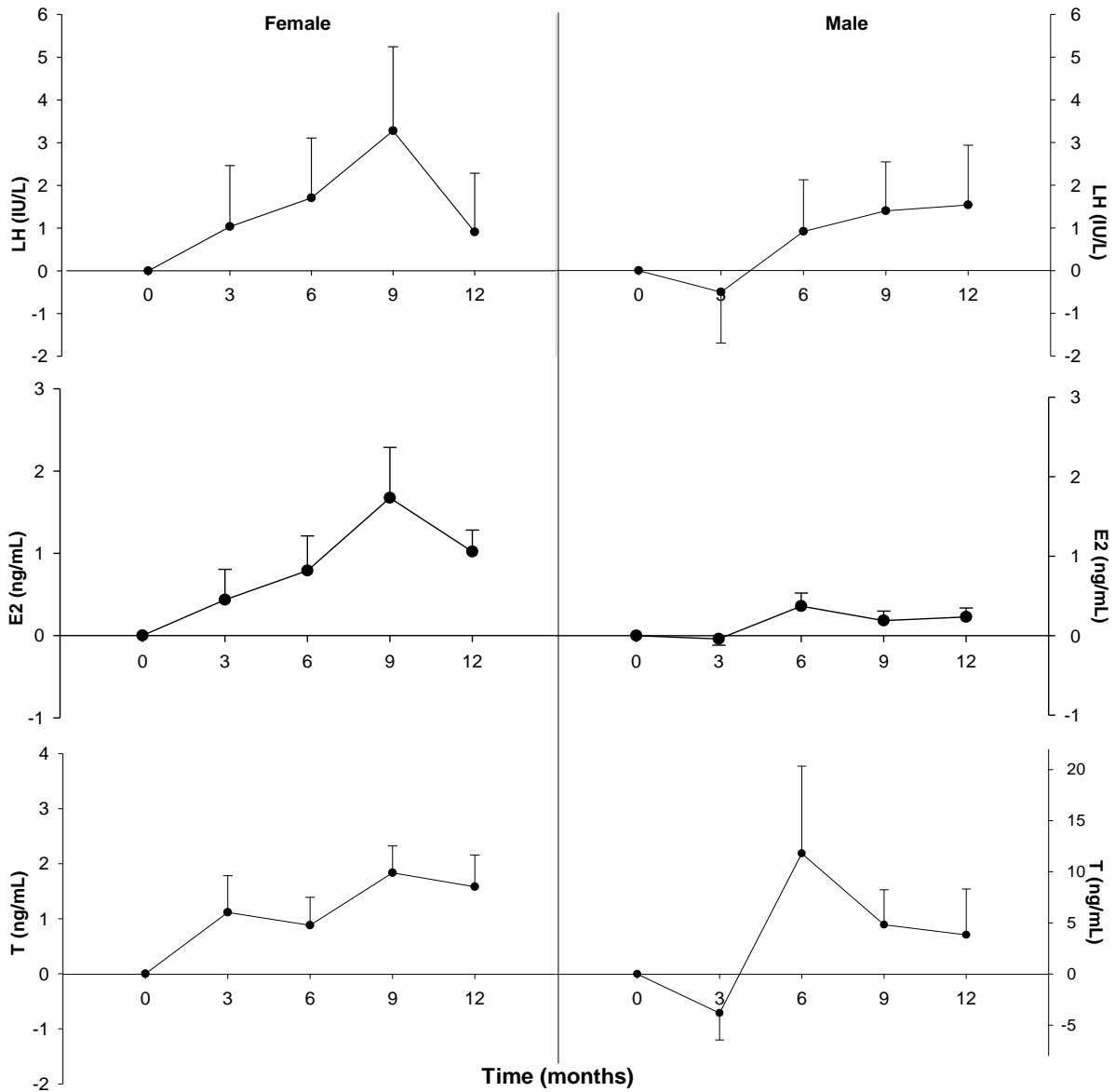


Figure 6.2 Plots of mean and SEM of individual changes from baseline (0) in urine LH, E2 and T concentrations in female (left panels) and male (right panels) at 3, 6, 9 and 12 months.

Note the y-axis scales of the T plots differ between genders.

Table 6.5 Mean urine LH, E2 and T.

Mean (SD)	Baseline		3 Months		6 Months		9 Months		12 Months (Follow-Up)		Two Way ANOVA F-statistic (p-value)		
	M	F	M	F	M	F	M	F	M	F	Gender	Time	Gender x Time
LH (IU/L)	8.7 (7.4)	9.6 (10.0)	8.4 (5.9)	10.2 (10.1)	9.6 (7.4)	11.5 (11.4)	9.8 (6.1)	13.3 (16.6)	10.1 (7.9)	10.1 (9.9)	3.2 (0.074)	0.9 (0.438)	0.4 (0.802)
E ₂ (ng/mL)	0.7 (0.9)	1.8 (2.0)	0.7 (0.9)	2.1 (2.8)	1.1 (1.6)	2.5 (3.1)	0.9 (1.1)	3.5 (4.8)	1.0 (1.0)	2.7 (2.8)	52.4 (<0.001)	2.3 (0.059)	1.3 (0.255)
T (ng/mL)	23.3 (35)	3.9 (3.8)	19.9 (26.1)	5.0 (6.2)	35.1 (80)	5.0 (4.1)	26.4 (34)	6.0 (4.1)	26.2 (28)	5.4 (5.1)	57.9 (<0.001)	0.9 (0.4870)	0.8 (0.548)

Table 6.6 Mean urine hormone measurements for girls by menarcheal status.

Mean (SD)	Baseline		3 Months		6 Months		9 Months		12 Months (Follow-Up)		Two-way ANOVA F-statistic (p-value)		
	Pre	Post	Pre	Post	Pre	Post	Pre	Post	Pre	Post	Menarcheal Status	Time	Menarcheal Status x Time
LH (IU/L)	6.5 (7.48)	14.6 (11.53)	6.8 (7.55)	16.1 (11.25)	7.6 (7.21)	17.4 (14.10)	9.0 (8.48)	19.2 (22.69)	9.5 (8.90)	11.0 (11.34)	30.34 (<0.001)	1.05 (0.384)	1.34 (0.255)
E ₂ (pg/mL)	0.7 (0.67)	3.4 (2.19)	0.9 (0.84)	4.1 (3.70)	1.1 (0.80)	4.7 (4.03)	1.5 (1.39)	6.4 (6.32)	1.7 (1.90)	4.3 (3.16)	95.54 (<0.001)	3.20 (0.014)	1.50 (0.201)
T (ng/mL)	2.4 (2.00)	6.3 (4.70)	2.7 (2.03)	8.9 (8.70)	3.2 (2.72)	7.7 (4.48)	4.5 (2.99)	8.0 (4.53)	4.3 (3.16)	6.9 (4.38)	57.21 (<0.001)	1.41 (0.232)	1.33 (0.258)

6.4.3 Association between Serum and Urine Hormone Measurements and Anthropometry

Change in serum LH was significantly positively associated with change in height and weight for females, but with neither in males (Table 6.7). Serum T was significantly positively associated with height changes in both sexes. Change in height was positively associated with urinary E₂ and T in females and urinary E₂ in males. No other significant associations were observed between urinary hormones and anthropometry over 12 months (Table 6.7).

Table 6.7 Regression results for serum (left) and urine (right) hormones and anthropometric markers of puberty.

Serum	β	95% CI	F-statistic	p-value	Urine	β	95% CI	p-value
<i>Change in Height</i>								
Female								
LH	0.53	0.21, 0.84	11.50	0.001	LH	0.01	-0.47, 0.48	0.979
E ₂	-0.001	-0.04, 0.03	0.01	0.943	E ₂	-0.25	-0.38, -0.12	<0.001
T	10.19	0.77, 19.61	4.73	0.035	T	-0.25	-0.44, -0.06	0.011
Male								
LH	-0.16	-0.92, 0.61	0.17	0.681	LH	0.31	-0.11, 0.72	0.149
E ₂	0.09	-0.02, 0.21	2.61	0.115	E ₂	-0.10	-0.16, -0.03	0.004
T	0.89	0.48, 1.31	19.26	<0.001	T	-1.05	-3.74, 1.64	0.446
<i>Change in Weight</i>								
Female								
LH	0.45	0.10, 0.81	6.67	0.013	LH	-0.13	-0.55, 0.28	0.535
E ₂	-0.01	-0.05, 0.03	0.20	0.656	E ₂	-0.02	-0.14, 0.09	0.695
T	11.81	1.15, 22.48	4.96	0.031	T	-0.14	-0.30, 0.03	0.110
Male								
LH	-0.10	-1.74, 1.54	0.02	0.900	LH	0.07	-0.13, 0.27	0.492
E ₂	0.07	-0.18, 0.31	0.31	0.583	E ₂	0.01	-0.02, 0.04	0.505
T	0.21	-0.86, 1.28	0.16	0.688	T	0.81	-0.48, 2.10	0.218
<i>Change in BMI</i>								
Female								
LH	0.03	-0.10, 0.16	0.24	0.625	LH	-0.79	-2.03, 0.45	0.214
E ₂	0.001	-0.01, 0.01	0.01	0.921	E ₂	0.03	-0.31, 0.37	0.858
T	2.18	-1.73, 6.09	1.25	0.269	T	-0.47	-0.97, 0.02	0.062
Male								
LH	-0.10	-0.46, 0.26	0.31	0.580	LH	-0.03	-0.89, 0.82	0.940
E ₂	-0.02	-0.07, 0.03	0.69	0.412	E ₂	-0.02	-0.16, 0.11	0.737
T	-0.01	-0.24, 0.23	0.00	0.963	T	1.33	-4.19, 6.86	0.636
<i>Change in Self-Rated Tanner Stage</i>								
Female								
LH	0.07	-0.04, 0.17	1.51	0.225	LH	0.46	-1.19, 2.11	0.583
E ₂	0.002	-0.01, 0.01	0.12	0.730	E ₂	-0.24	-0.70, 0.22	0.310
T	1.59	-1.25, 4.44	1.28	0.265	T	0.11	-0.56, 0.78	0.757
Male								
LH	-0.08	-0.33, 0.17	0.44	0.510	LH	-0.10	-1.23, 1.03	0.863
E ₂	0.03	-0.003, 0.07	3.38	0.075	E ₂	-0.15	-0.33, 0.03	0.100
T	0.16	0.02, 0.29	5.40	0.026	T	-0.27	-7.64, 7.09	0.942

6.5 Discussion

The two major findings of this study are the validation of a MS assay for pubertal urine steroids in a young adolescent population and the demonstration that it is feasible to collect urine samples from a community-based adolescent cohort at three-monthly intervals, with high compliance (93% serum and 92% urine collections completed) and low follow-up attrition rate.

In order to demonstrate the specific effects of puberty hormones on any biological aspect of adolescent development and health, a methodology that allows more frequent biological sampling than has been previously reported for epidemiological studies is essential. Urine samples have the advantage over blood samples that these are more acceptable both ethically and practically by adolescents, and each overnight sample provides a more time-integrated hormone measure. This is particularly true in early puberty when pubertal hormones commence pulsatile secretion nocturnally (Dorn et al. 2006), so that a morning overnight urine sample may be more informative than a serum sample at any single time point. Urine collections also allow for more frequent collection than repeated venepuncture would be tolerated (Aksglaede et al. 2009). Salivary samples are potentially easier to collect, but blood contamination and influence of flow-rate on measurements seriously limits validity and accuracy.

Anthropometric and serum hormone changes in our study revealed the anticipated increases over the course of one year in a cohort of young adolescents. The urine data also revealed anticipated hormone increases over the 12-months of observation. However, mean and individual urinary hormone changes were not strictly progressive; suggesting within-subject variability in early and mid-pubertal hormone levels may contain hitherto unexploited information on determinants of biological aspects of pubertal progression. This finding also

suggests that three monthly urine collections over an extended period have the capacity to provide new insights into the biology of puberty.

The cross-sectional associations between chronological age and self-reported Tanner stage and both serum and urinary hormones reveal considerable overlap between hormone levels at each age or stage, and emphasise the need to have better descriptors of puberty hormone change. Both Tanner stage and anthropometric change lag behind hormonal change. Using the former as surrogates for puberty hormone change will less accurately describe the relationship between hormone changes and the resultant physical changes, as well as any other adolescent health or developmental change of interest, such as mood or behaviour. Previous work has questioned the validity of self-rated Tanner staging (Bonat et al. 2002, Desmangles et al. 2006, Dorn et al. 2006, Hergenroeder et al. 1999, Morris and Udry 1980); however, our data support the validity of self-rated Tanner staging as a high proportion of adolescents completed the scales with findings of consistent or advanced Tanner stage at 12 months follow-up in all but 6% of adolescents and with the self-rated Tanner staging corresponding well with conventional anthropometric measures of puberty.

In conclusion, our work has used a robust methodology of urine sex steroid hormone measurement, using LC tandem mass spectrometry measurements for urine sex steroids (Handelsman and Wartofsky 2013), which display the high sensitivity and specificity to detect the lower levels of sex hormones, a particular challenge to the study of pubertal progression (Courant et al. 2010, Rosner et al. 2013). Based on previously recorded longitudinal growth data (Marceau et al. 2011, Steinbeck et al. 2012), it is anticipated that frequently measured urine samples over the two to three year window of puberty will not only provide a firmer biological basis for clinically observed patterns of puberty, such as early or late onset and rapid or slow tempo, but also allow determination of the true biological effects of puberty hormones on adolescent health and development.

Chapter 7 *Conclusions*

In this thesis, we successfully developed suitable sample preparation techniques and LC-MS/MS assays to measure steroids in various biological samples. The methods were further applied for clinical research studies including remote sampling and field studies. We also demonstrated that previously validated LH immunoassays for human blood samples are also suitable with qualifications for urine samples. This thesis consists of four research chapters as summarized in the sections below.

7.1 Blood spot sampling after sc steroid injection

This study was to assess the feasibility and pharmacology of sc injection of androgen ester in healthy men using DBS for frequent sampling. A sensitive and specific LC-MS/MS assay was developed and validated to measure steroids from DBS samples. To avoid common problems of using DBS samples such as non-homogenous distribution of blood on the filter card and hematocrit effect, we developed a novel sampling method which used the whole blood spotted onto the filter card instead of using a subsample (e.g. by a punch). The DBS technology provided intensive and simplified blood collection by the study participants at home without the need of clinic visit. This study provided a detailed pharmacological analysis of sc injection of ND in oil vehicle. We found a sustained release of this androgen ester which suggests that sc injections of T esters may prove to be safe and tolerable. This would make self-injection of long-acting depot form of T delivery more feasible with the potential benefits of reducing medical care costs demand on medical personnel time. Additionally this delivery method may also reduce injection site pain or bruising as well as allowing freer use among those with bleeding disorders or on anticoagulants. Further studies using T esters in men with differing body weight and after repeated injections are required to evaluate duration of action and usefulness in clinical practice of sc relative to im injections.

7.2 Urinary LH immunoassays in stored samples

This study was to assess whether commercially available LH immunoassays (ICL and IF) previously validated for human blood samples is suitable for urine samples kept at prolonged frozen storage (4 years) without addition of any preservative. Urinary LH may be dissociated into its subunits due to high urinary concentrations of urea that may cause loss in immunoreactivity after prolonged frozen storage. Using samples from a clinical study completed in 2008 and aliquots of the same samples stored frozen at -20 °C without added preservatives, this study describes the deviations in performance of ICL and IF immunoassays and their ultimate applicability for reliability clinical research and for anti-doping purposes. The study demonstrated that the two LH immunoassays optimized for blood samples can also be used for urinary LH measurement but the performance of both the assay differed markedly. The ICL immunoassay showed quantitatively reproducible LH measurement even after prolonged storage at -20 °C for 4 years without addition of preservatives. By contrast, the IF immunoassay demonstrated consistently but proportionately lower LH measurements relative to the ICL assay both initially (2008) and then exhibited a further decrease after 4 years of frozen storage (2012). Yet, both the assays displayed similar patterns of the time-course of urine LH measurement both before and after 4 years of frozen storage. In conclusion, we found that both immunoassays are suitable for urinary LH measurements with ICL assay being more robust for quantitative urinary LH measurement such as for anti-doping purpose whereas the IF could be applicable for research studies where urine LH levels are compared within-study but not in absolute terms.

7.3 SG and creatinine adjustments for urinary hormones

The study aimed to determine whether first morning void hormonal assessments carried out in growing young adolescents require adjustments to correct for variation due to hydration, and if so, to determine the best adjustment method based either on urinary creatinine or SG. While previous studies have examined broadly the issue of how to adjust urinary hormonal measurements none have focused on the specific situation where creatinine is changing systematically due to growth, hence this study contains novel information on whether urinary hormonal concentration adjustments are required in the setting of repeated serial sampling of a large adolescent population at various stages of pubertal progression. The present study demonstrated that unadjusted urinary steroids and LH concentration corresponded well with the concentration adjusted either with creatinine or SG when using first morning void urine samples, reflecting an overnight fast, even in growing adolescents. Based on these findings we suggest the possibility that the first morning void urine samples are not heavily influenced by the hydration status of study participants and may not require adjustments compared with randomly collected spot or timed urine collection methods. However, if the dilution adjustment is desired for the urine specimen, both the creatinine and SG appear equally suitable using first morning void urine samples. We also show that reagent strip SG measurements are simpler alternative to a refractometer and sufficiently reliable, economical and time-saving for large numbers of urine sampling in long-term field studies.

7.4 Urinary puberty hormones

The aim of this study was to develop and validate LC-MS/MS assay to measure urinary T and E₂ in adolescents and subsequently to relate the changes in the urinary sex hormones over 12 months to the standard anthropometric markers of puberty (height, weight, BMI, self-rated Tanner stage). Longitudinal relationships of within-individual hormone and anthropometric changes during puberty have not been fully described previously. Urine provides a more time-

integrated hormone measure compared to blood samples and is particularly important as pulsatile secretion during early progression of puberty occurs nocturnally. The study demonstrated feasibility of urine samples collection from a community based-adolescent cohort at three-monthly intervals with high compliance and low follow-up attrition rate. Both urine and serum hormone data showed anticipated increase over 12 months. This study successfully developed a robust LC-MS/MS method to measure urinary steroids that display high sensitivity and specificity. The study preliminary findings demonstrate the feasibility of intensive collection of urine samples together with validated urine assays for sex steroids and LH. These will allow a more accurate and sensitive, individual assessment of puberty timing and tempo. Currently, three monthly urine and a yearly blood collection for the ARCHER longitudinal study over three years is being carried out to better understand the role of puberty hormones on adolescent events. This longitudinal study aims to determine how temporal changes in T and E₂ independently affect physical status, social and emotional well-being, education, sleep, risk behaviours, and mental health in adolescents.

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Appendix

Chapter 3:

Gurmeet KS Singh was responsible to optimize the DBS sampling method, LC-MS/MS assay development and conducting the assays, as well as statistical analyses and involved in writing and editing the manuscript. Leo Turner is a nurse at the Andrology clinic, Concord Hospital that was responsible for recruiting of the volunteers, administrating the drug, monitoring, sample collection and editing the manuscript. Reena Desai was involved in the assay development and editing of the manuscript. Mark Jimenez conducted the gonadotropin assays and was involve in the editing of the manuscript. David J Handelsman was responsible for study design, assay development, statistical analyses, writing and editing the manuscript.

Chapter 4:

Gurmeet KS Singh was responsible for the statistical analyses and involved in writing the first draft and editing the manuscript. Mark Jimenez conducted the LH assays and was involved in the editing of the manuscript. Ron Newman was involved in the editing of the manuscript. David J Handelsman was responsible for study design, statistical analyses, writing and editing the manuscript.

Chapter 5:

Gurmeet KS Singh was responsible for assay development and conducting the assays, as well as statistical analyses, writing the first draft and editing the manuscript. Ben WR Belzer, Reena Desai and Mark Jimenez were involved in the writing and editing of the manuscript. Reena Desai was also involved in the assay development. Katharine S Steinbeck was involved in study design, study oversight, writing, and editing this manuscript. David J

Handelsman was responsible for study design, assay development, statistical analyses, writing and editing the manuscript.

Chapter 6:

Gurmeet KS Singh and Ben WR Balzer share equal authorship of this paper. Gurmeet KS Singh was responsible for assay development and conducting the assays, as well as authorship and editing the manuscript. Ben WR Balzer performed statistical analyses, wrote the first draft and contributed to the editing of the manuscript. Patrick J Kelly performed statistical analyses and contributed to editing the manuscript. Karen Paxton was involved in study design, sample collection, performed anthropometry assessments and edited the manuscript. Catherine I Hawke was involved in study design and oversight, as well as contributing to the writing and editing of the manuscript. David J Handelsman was involved in assay development and conduct, as well as statistical analyses and writing and editing the manuscript. Katharine S Steinbeck is the chief investigator of the ARCHER Study and was involved in study design, study oversight, writing, and editing this manuscript.