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Current knowledge of the multifunctional 17β**-hydroxysteroid dehydrogenase type 1 (HSD17B1)**

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1. The origin and evolution of the 17β**-HSD1 gene (HSD17B1)**

As early as the late 1940s and early 1950s, an enzyme regulating the balance between estrone (E1) and estradiol (E2) was discovered in human placenta (Langer & Engel, 1958). Enzyme activity in both prokaryotic and eukaryotic species was described about this first discovered member of the 17β-hydroxysteroid dehydrogenase family, i.e. 17β-HSD1. During the course of evolution, genes encoding the 17β-HSD enzymes developed individually approximately 540 million years ago parallel to those for steroid receptors (Baker, 2004; Jansson, 2009). This implies an important evolutionary role for the 17β-HSD enzyme family.

Human 17β-HSD1 was the first 17β-HSD to be cloned and sequence identified (Luu-The et al., 1989; Peltoketo et al., 1988). Its three-dimensional structure is also the first example of any human steroid-converting enzyme (Ghosh et al. 1995; Azzi et al. 1996; Lin et al., 1996). The 17β-HSD1 gene was determined to be located in the q.12.1 band of chromosome 17 through gene mapping by in situ hybridization. This enzyme contains 327 amino acids and exists as a homodimer with two identical subunits of 34.5 kDa (Lin et al., 1992; Peltoketo et al., 1988). 17β-HSD1 uses NADPH as a co-factor to catalyze the conversion of E1 to E2, and to a minor extent that of androgens such as 4-androstenedione (4-Adione) to testosterone (T) (Lukacik et al., 2006). 17β-HSD1 can bind to both triphosphate cofactors (NADPH) and NAD (H) at the molecular level but with much higher specificity to the former, which is rich in cells that largely governs the enzyme's catalytic direction towards estrone reduction (Karavolas et al., 1970; Lin et al. 1992; Sherbet et al., 2007). Enzyme kinetics and X-ray crystallographic studies have shown that 17β-HSD1 has the potential to bind C-19 steroids in both normal and reverse orientations resulting in the 3β-reduction of DHT into 5-androstane-3,17-diol (3β-diol) and 17β-oxidation of DHT into A-dione, both

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leading to the inactivation of the most potent androgen DHT (Gangloff et al., 2003). 17β-HSD1 expression positively correlates to estrone activation, E2 levels, and proliferation of breast cancer cells (Aka et al., 2010). The multi-specificity of 17β-HSD1 is structurally based on the pseudo-symmetric structures of androgens that can accommodate the narrow enzyme substrate tunnel by both normal and alternative binding (Lin et al., 2013). Thus, 17β-HSD1 up-regulates breast cancer cell growth by a combined action on estradiol synthesis and DHT inactivation.

In primates, 17β-HSD1 is primarily expressed in the placenta and ovarian granulosa cells and to a lesser extent in the endometrium, adipose tissue and prostate. It is not expressed in the testes or adrenals (Schwabe et al., 2001; Takeyama et al., 2000). This tissue-specific expression makes 17β-HSD1 an attractive pharmaceutical target in women's diseases (Lukacik et al., 2006), particularly the breast cancer. Today, fifteen 17β-HSD enzymes have been discovered in mammals and the nomenclature of these enzymes follow their discovery order. All of these belong to the short-chain dehydrogenase/reductase family (SDR) with the exception of 17β-HSD5, which is an aldo-keto-reductase (AKR). Short-chain dehydrogenase/reductase enzymes are multimeric in nature, expressed in a variety of organisms with NADPH as co-factor. Aldo-keto-reductase enzymes act as monomers and also use NADPH as co-factor. A high degree of substrate variability is shown by SDR enzymes including: steroids, retinoids, fatty acids and prostaglandins. 17β-HSD enzymes are localized in different parts of the cell across diverse tissues and show preference for a variety of substrates and co-factors. A feature common to all 17β-HSD enzymes is the ability to catalyze oxidation or reduction of the carbon at position 17 in the steroids. These enzymes have different substrate preferences such as E1, E2, T, 3beta-diol and DHT. They possess distinct physiological functions (Jansson, 2009).

2. Comparison of particular gene expression in different organisms, animals and human

The sequence identities between human 17β-HSD1 and other species range from 51% (zebra fish) to 99% (chimpanzee) and homologies range from 70% to 100%, respectively. The biggest differences are located in the F/G segment (residues191–230), which lines the hydrophobic substrate binding site (SUB) and in the C-terminal region (Miyoshi et al., 2001).

Human 17β-HSD1 catalyzes the reduction of the weak estrogen E1 to the most potent, E2. This occurs in target cells where the estrogenic effect is exerted *via* the estrogen receptor (ER). Estrogens, especially E2, are known to stimulate the proliferation of hormonedependent diseases (Chetrite GS., 2005) such as breast cancer. The risk of breast cancer is positively correlated with a high level of E2 (Pasqualini et al., 1996), because this potent estrogen plays an important role in the proliferation of cancer cells (Castoria et al., 2010). It has been confirmed by microarray analysis that E2 regulates estrogen response elements (EREs), progesterone receptor (PR), pS2 and cathepsin D that affects the cell growth and differentiation (Laganière et al., 2005; Cicatiello et al., 2004).

The majority of breast cancer tumors (60–80%) express high levels of ERs, which accounts for the proliferative effect of estrogens. They tend to have a higher intratumoral estrogen concentration in comparison to normal breast tissue and plasma (Labrie et al., 2000). There is a direct relation between high [E2]/[E1] ratio and breast cancer cell proliferation. Strategies targeting the reduction of $[E2]/[E1]$ ratio, are proposed to be an effective means of facilitating breast cancer therapy (Zhang et al., 2012). In situ synthesis and metabolism of estrogens is believed to be of great importance for the development and progression of breast cancer. In fact, 17β-HSD1 is overexpressed in many breast tumors and as such it is an attractive target for the treatment of these diseases (Frotscher et al., 2008).

In accord with its role in sex-hormone signaling, 17β-HSD1 is expressed in placenta, endometrium and ectopic pregnancy. Immunohistochemical assays revealed that 17β-HSD1 is present in syncytiotrophoblast (ST) cells (Li et al., 2005), a large portion of extravillous cytotrophoblast (EVCT) cells and 20% of column cytotrophoblast (CCT) cells. On the other hand, no expression of 17β-HSD1 was detected in villous cytotrophoblast (VCT) cells. Localization of 17β-HSD1 was found on the surface of glandular epithelial cells when progesterone was present at typical ovulatory cycle concentrations (Mäentausta et al., 1991). It was also associated with endometrial carcinoma. In addition, 17β-HSD1 is found in epithelial cells of the fallopian tube. Interestingly, the expression level of 17β-HSD1 in the fallopian tube epithelium during tubal pregnancy is significantly higher than that found during a normal cycle. There is evidence that normal and tubal pregnancies possess identical expression of P450 aromatase and 17β-HSD1 in ST cells implicating similar E2 production in the placenta (Li et al., 2003). Furthermore, the association of 17β-HSD1 with EVCT cells indicates that 17β-HSD1 perhaps plays a role in trophoblast invasion. Increased expression of 17β-HSD1 in the epithelial cells of the fallopian tube may lead to a local E2 supply sufficient for the maintenance of tubal pregnancy (Li et al., 2003). The synthesis of estrogens was recently demonstrated in non-small cell lung carcinomas (NSCLCs) via aromatase activity. Moreover, an aromatase inhibitor (AI) did suppress estrogen receptorpositive NSCLC growth (Hershberger et al., 2005; Verma et al., 2011). Recent studies highlights the importance of 17β-HSD1 as an important prognostic factor in NSCLC patients making it an attractive target that can improve the clinical response in estrogenresponsive NSCLC patients (Verma et al., 2013).

3. Structure–biological functions: dual estrogen and androgen activities and disease implications

The homogeneity and high activity of the enzyme preparation developed in early 1990s, significantly improved from former purifications, laid down the enzyme's crystallization and structural determination as the first human steroid-converting enzyme (Lin et al. 1992; Zhu et al. 1993; Ghosh et al. 1995a, 1995b). It has been elucidated by structural and mutagenesis studies that in the Rossmann fold (Breton et al., 1996; Buehner et al., 1973) of 17β-HSD1, a positively charged amino acid is able to form a salt bridge with the 2′-phosphate group of the cofactor NADP(H), *i.e.* Arg37 in 17β-HSD1 (Huang et al., 2001). Structural analysis, mutagenesis studies and sequence alignment have resulted in the identification of features essential for the catalytic process namely three conserved amino acid residues, Ser142,

Tyr155 and Lys159 constituting a "catalytic triad" with a water molecule (Puranen et al., 1994, Ghosh et al. 1995). Further investigations showed that an additional conserved water molecule stabilized by an H-bond interaction with an Asn114 residue (together with the "catalytic triad" to form a "catalytic tetrad") plays a critical role in the enzymatic process for HSDs (Filling et al., 2002; Hwang et al., 2005). Three catalytic mechanisms are proposed for 17β-HSD1 (Ghosh et al. 1995; Ghosh & Vihko, 2001; Penning, 1997): one concerted (simultaneous transfer of hydride and proton, not shown) and two stepwise. The latter differs in the intermediate presence of either an oxyanion or a carbocation. (A) Firstly, the pro-S hydride of NADPH is transferred to the α-face of E1 at the planar C17 carbon resulting in an energetically favorable aromatic system; the resultant oxyanion is subsequently protonated by the acidic -OH group of Tyr155 (A2). (B) In the second proposed mechanism, initially the keto oxygen of E1 is protonated by the acidic -OH of Tyr155; the resultant carbocation then accepts the pro-S hydride of NADPH at the α-face. The proton relay is facilitated by a H-bond network involving Lys159, two water molecules and Asn114, an electrostatic interaction between the protonated side chain of Lys159 and the phenyl ring of Tyr155 (Ghosh et al. 1995; Ghosh & Vihko, 2001) as well as T-stacking between Phe192 and Tyr155 (Negri et al., 2010). Hydrogen bonds are represented by dashed lines in Figure 1 and π –π-interactions are not depicted for the sake of clarity. Despite the availability of enormous structural information, the most likely mechanism is highly debated (Marchais-Oberwinkler et al., 2011).

To date, 20 crystal structure forms of 17β-HSD1 are available in the protein data bank (PDB) as: apo-enzyme (1bhs), holo-enzyme (1fdv, 1qyv), binary complex with E2, androgens or inhibitors (1fds, 1fdw, 1dht,3dhe, 1jtv, 1iol, 3dey, 1i5r, 3hb4, 3klm) and ternary complex with cofactor and E2 or inhibitors (1fdt, 1equ, 1fdu, 1a27, 1qyw, 1qyx,3hb5). Remarkably, no crystal structure has been determined with the E1 substrate (Marchais-Oberwinkler et al., 2011).

All crystals reveal an overall identical tertiary structure: a rigid cofactor binding site (COF) and a narrow, hydrophobic SUB, which constitutes a "substrate recognition domain" delimited by the C-terminal region (Alho-Richmond et al., 2006; Azzi et al., 1996). Estradiol is stabilized by hydrogen bonds between the O3 and His221/ Glu282, as well as between the O17 and Tyr155/ Ser142 (Azzi et al., 1996). Flexible βFαG′ loop accounts for the major differences in the structures. This loop is not resolved in twelve crystal structures and can occupy three possible orientations depending on the presence of cofactor and ligands: an opened, a semi-opened and a closed enzyme conformation (Negri et al., 2010). The binding mode is known for some steroidal inhibitors as they have been co-crystallized in complex with 17β-HSD1 (1equ, 3hb5, 1i5r). The data revealed the importance of a defined βFαG′ loop conformation for compound binding. Since no protein structure complex with non-steroidal inhibitors exists, computational studies have been performed to investigate their binding. These studies showed that the choice of the crystal structure was the determinant for the identification of a binding mode and that the latter was strongly dependent on the loop conformation (Bey et al., 2009). The multi-specificity of the enzyme has been studied and reviewed (Lin et al. 1999). The cofactor hydrogen bonding onto the enzyme main chain was found to be conserved in 17β-HSD1 as well as in other short-chain

dehydrogenase/reductase family and contributes to nicotinamide orientation (Shi & Lin, 2004).

Two principal pathways are implicated in the final steps of E2 activation in breast cancer tissue. The aromatase pathway transforms androgens into estrogens (Batzl et al., 1996), the sulfatase pathway converts DHEA sulfate into DHEA and estrone sulfate (E1S) into E1 (MacIndoe, 1988; Pasqualini et al., 1989), followed by E1 conversion into the potent E2 by the action of reductive 17β-HSDs (Aka et al., 2009; Nguyen et al., 1995; Pasqualini, 2004, Lin et al. 2010). Quantitative evaluation indicates that in human breast tumors, DHEAS and E1S via sulfatase is a much more likely precursor for E2 than androgens via aromatase (Santner et al., 1984). 17β-HSD1 remains an important enzyme for E2 production because it can use E1 as substrate for both aromatase and sulfatase pathways with NADPH as cofactor (Nguyen et al., 1995; Poutanen et al., 1995). Moreover, the expression and activity of 17β-HSD1 are significantly higher in breast cancer than in normal breast tissue (Pasqualini, 2004) and it has been suggested that this higher expression could explain the elevated E2 concentration in breast tumors. 17β-HSD1 is a major player for E1–E2 conversion and cell viability in estrogen-dependent breast cancer cells, particularly in the T47D cell line (Zhang et al., 2014). Epidemiological evidence indicates that most breast cancer risk factors are associated with prolonged exposure of the mammary gland to high levels of estradiol (E2). This potent estrogen plays a crucial role in the development and evolution of hormonedependent breast cancer. Approximately 60% of premenopausal and 75% of postmenopausal breast cancer patients is hormone dependent (Aka et al., 2012).

17β-HSD1/ DHT complex crystals were obtained by soaking the apo-enzyme crystals and the complex formation was confirmed after structure determination. The complex structure was solved at 1.7 Å resolution (Aka et al., 2010). Stereo representation showed the H-bond of DHT with the residues His221 in the reverse binding mode, whereas the normal binding mode lacks this H-bond interaction. Distances between DHT, Tyr155 and the cofactor NADP are different. In the reverse mode, the distance between the O3 of DHT and NC4 of NADP is 4.35 Å and between Tyr155 to NC4 of NADP is 5.4 Å whereas in the normal mode, the distance between the O17 of DHT and NC4 of NADP is 3.75 Å and between Tyr155 to NC4 of NADP is 5.4 Å (Fig.2). The reduction of DHT into both 3β-diol and 3αdiol by 17β-HSD1 points towards the potential of DHT binding to the enzyme in two orientations. These results strongly support the rationale for inhibiting 17β-HSD1 in breast cancer therapy to eliminate estrogen activation via the sulfatase pathway while avoiding the deprivation of DHT (Aka et al., 2010). It was recently found that 17β-HSD1 increases breast cancer cell migration in spite of its positive regulation of the anti-metastatic gene nm23. This also correlates with its capacity to stimulate breast cancer cell growth, further confirming the necessity of targeting this enzyme in ER-positive breast cancer. These novel findings suggest several directions for future research with regard to the contribution of 17βHSD1 to breast cancer progression and related treatment (Aka et al., 2012)

4. Inhibitor design

The search for inhibitors of 17β-HSDs began in the 1970s and gradually gained momentum thereafter before culminating during the first decade of the 2000s. Significantly more

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inhibitors are known for the 17β-HSD1 than the other isoforms in the family. Several review articles reported structure–activity relationship studies, which are crucial for drug design and illustrate the huge diversity of 17β-HSD1 inhibitors (Brozic et al., 2008; Day et al., 2008, 2010;Marchais-Oberwinkler et al., 2011;Penning, 1996; Poirier, 2003, 2009, 2010, 2011). Despite many years of research, there are no inhibitors in clinical use to date. This very likely results from the fact that 17β-HSD1 has estrogens as substrates and products such as E2 that also exhibits high affinity towards the estrogen receptor alpha (Huang et al., 2001; Jin & Lin, 1999; Lin et al. 2013). Therefore, the design of inhibitors that are analogues of estrogens makes it difficult to eliminate residual estrogenic activity (Lin et al. 2013, Mazumdar et al. 2009).With the emergence of personalized medicine and diagnostic tests, the arrival of a potent 17β-HSD1 inhibitor in a clinical setting is highly anticipated to provide a new option for the treatment of women found to have a high expression of 17β-HSD1 and a low expression of aromatase in breast cancer tumor biopsies (Ayan et al., 2012; Maltais et al., 2011). Finally, the use of 17β-HSD1 inhibitors is also a promising approach for the treatment of other estrogen-dependent diseases, such as endometrial cancer (de Cremoux, 2011) and endometriosis (Saloniemi T, 2010), where the enzyme has been shown to be overexpressed (Maltais et al., 2014).

Studies have shown that steroidal inhibitors preferably bind in the SUB, exhibiting interactions stabilized by hydrophobic contacts and hydrogen bonds with Tyr155/Ser142 and His221/Glu282 residues lining the pocket, whereas non-steroidal inhibitors bind partially to the SUB, but primarily to COF (Negri et al. 2010). However, competitive NMR-experiments suggested that phytoestrogens interact neither with the SUB nor with the COF.. The dimer interface of 17β-HSD1 was proposed to be a possible binding site by docking studies (Michiels et al., 2009). Hybrid inhibitors interacting with both steroid and cofactor binding sites resulted in nanomolar binding affinity at the molecular level, based on the available 3D structure of 17β-HSD1 (Qiu et al, 2002; Poirier et al. 2003). Further improvement of the cell penetration is necessary.

4.1.1. Non-steroidal compounds

Inhibitor I (Fig. 3) is a non-steroidal derivative with a pyrimidinone core, which was tested by Solvay Pharmaceuticals. In their animal model, human MCF-7 cells expressing 17β-HSD1 were inoculated in nude ovariectomized (OVX) mice and tumors generated in the presence of E1 (0.1 mol/kg/d) were treated for 28 days by subcutaneous (sc) injection with inhibitor I at a dose of 5 mol/kg/d (2.8 mg/kg/d) . Since the estrogen-dependent MCF-7 breast cancer cells express different 17β-HSD isoforms (Laplante et al., 2009), the authors stably transfected the HEK293 cells with a plasmid expressing human 17β-HSD1. Compared to the non-treated controls (in the presence or absence of estrone), inhibitor I reduced tumor weight by 54% and tumor area by 75%. The same group also tested five steroidal inhibitors (estrone derivatives B10721325, B10720511, B10720512, B10720440 and B10715817) in the tumor xenograft model (understanding the effect of inhibitors on estrone-stimulated human cancer cell growth in nude mice) at a dose of 5 mol/kg/d (Husen et al.,2006). Compound B10720511 was more potent than the other analogues and reduced tumor weight by 86%. This compound also showed a dose-dependent effect in this xenograft study with an estimated IC_{50} of 1.58 mol/kg/d (0.7 mg/kg/d). As an example, the

representative compound II (B10721325) reduced tumor weight by 60%. By measuring the uterine weight, the authors also observed that such compounds produced an antiestrogenic effect.

4.1.2. Steroidal compounds

Sterix Ltd. used extensive structure-based drug design with available crystal structures of 17β-HSD1 and developed a family of steroidal inhibitors of 17β-HSD1 and selected compound III (STX1040) as a non-estrogenic candidate to be tested in a xenograft model (Day et al., 2008; Lawrence et al., 2005). The authors inoculated estrogen-dependent human T47D breast cancer cells into nude OVX mice to generate tumors that could be stimulated by E1. Although T47D cells express additional 17β-HSDs, such as types 7 and 12, it was demonstrated in vitro that 17β-HSD1 is responsible for transforming all E1 to E2 (Poirier et al., 2009, Laplante et al., 2009). Breast tumor growth in T47D cells was stimulated by E1 injection (0.05 or 0.1 μg E1/mouse/d) for 35 days. Subsequently after 35 days, animals that showed response to E1 dosing were provided with an additional dose of 20 mg/kg/day STX1040 daily for 28 days. STX1040 significantly inhibited E1 stimulated T47D cell proliferation and decreased tumor volumes. STX1040 also decreased the plasma concentration of E2 in the xenograft experiments and the authors determined that it did not work via ER antagonism (antiestrogen).

The last steroidal inhibitor of 17β-HSD1, compound IV (PBRM) has distinct mechanism of action, differing from the others. By replacing the phenolic -OH of E2 by a bromoethyl group and adding a characteristic carbamoyl benzyl side chain, the authors obtained a nonestrogenic compound that inhibited the enzyme (Maltais et al., 2011). This compound exhibited no binding to the ER, with no antiestrogenic function. The structure activity relationship study provided a new potent and steroidal nonestrogenic inhibitor of 17β-HSD1 named 3-{[(16β,17β)-3-(2-bromoethyl)-17-hydroxyestra-1(10),2,4-trien-16 yl]methyl}benzamide(23b). This compound specifically inhibited the transformation of E1 into E2 by 17β-HSD1 in T-47D cells (IC₅₀ = 83 nM) with no effect on 17β-HSD2, 17β-HSD7, 17β-HSD12, or CYP3A4 and did not stimulate the proliferation of estrogen-sensitive MCF-7 cells. Compound 23b is a competitive and irreversible inhibitor of 17β-HSD1 (Ayan et al.,2012; Maltais et al., 2014), compound IV (10 mg/kg/d, sc) completely blocked tumor growth stimulated by $E1(0.1 \text{ g/mouse/d}, \text{sc})$ comparable to that of the control group level (without E1) (Lin et al.,2013). A compound 6-(3-hydroxyphenyl) naphthalene-2-ol (Compound 5 in Frotscher et al., 2008) was identified as a highly active inhibitor of 17β-HSD1 showing good selectivity towards 17β-HSD2, ERα and ERβ. Furthermore it displays a medium Caco-2 permeability, reasonable metabolic stability and low inhibition of the most important hepatic CYP enzymes. This compound will be used as a primary lead in subsequent drug design process (Frotscher et al., 2008).

Recently, it is reported that 6-hydroxybenzothiazole ketones as a new class of 17β-HSD1 inhibitors with a notable activity/selectivity profile (Miralinaghi et al., 2014). They modified the benzothiazole core by a systematic bioisosteric replacement for the purpose of further optimizing parameters. Thus, they identified a new 6-hydroxybenzothiophene derivative that displayed stronger inhibition of 17β-HSD1 (IC_{50} =13nM) with higher selectivity than a

benzothiazole analog. Another study focused on rational structural modifications to this compound class with the aim of gaining more insight into its structure-activity relationship (SAR). (4-Hydroxyphenyl)-(5-(3-hydroxyphenylsulfanyl)-thiophen-2-yl) methanone was discovered as a member of a novel potent class of human 17β-HSD1 inhibitors. Computational methods were used to elucidate its interactions with the target protein. The compound also showed activity towards the murine 17β-HSD1 enzyme and is thus a starting point for the design of compounds suitable for evaluation in an animal disease model (Abdelsamie et al., 2014).

5. Some disease-related mutations

Certain mutations in the 17β-HSD family are related to disease. 17β-HSD1 polymorphisms were investigated for 16 different indications, most of which deal with breast cancer (8 studies) (Sasano et al., 2008; Subramanian et al., 2008; Suzuki et al., 2007). Three of these eight breast cancer studies have some direct associations with 17β-HSD1 SNPs (Singlenucleotide polymorphism). In multiethnic women from the US (Feigelson et al., 2001) and in Malaysian women (Wu et al., 2003) the A-allele of the SNP rs605059 (A/G: Gly312Ser) was claimed to be of high-risk. However, this observation was not repeated by the same author (Feigelson et al., 2006). In one study the AA allele in SNP rs605059 correlated with higher serum estradiol concentrations in lean women (Setiawan et al., 2004), and in another study a 12 bp deletion in the 5′ flanking area of 17β-HSD1 was only shown to influence the recurrence rate of breast cancer (Kristensen et al., 2001). AG- and AA-alleles of SNP rs605059 (A/G: S312G) in 17β-HSD1 in Chinese women seem to relate to endometrial cancer, but there is no comparable situation in US women (Setiawan et al., 2004). Conversely, the A-allele has a higher risk of endometrosis in Japanese women.

Surprisingly, 17β-HSD1 polymorphisms might play a role in prostate cancer risk prediction. In a study with a large number of multiethnic men no overall association of haplotypes of four common SNPs in 17β-HSD1 (rs676387 (C/A), rs605059 (A/G), rs598126 (G/A), rs2010750 (C/T)) with prostate cancer were observed; however, two subgroups, Latinos and Japanese Americans, with the CAGC haplotype had a lower prostate cancer risk (Kraft et al., 2005). In non-Hispanic Caucasian men the minor allele of 17β-HSD1 SNP rs605059 (A/G) was more frequent among sporadic prostate cancer cases than among controls, but no statistically significant association could be detected (Cunningham et al., 2007). An Australian ovarian cancer study with patients and controls of Caucasian origin showed no association between ovarian cancer and 17β-HSD1 or 17β-HSD4 polymorphisms (Beesley et al., 2007). In addition to cancer, 17β-HSD1 polymorphisms were found to be related to other phenotypes including vasomotor symptoms (VMS) (Crandall et al., 2006), depression and some cognitive function in Chinese women (Kravitz et al., 2006). One study analyzed the association of three 17β-HSD1 SNPs, rs2830 (A/G), rs592389 (T/G), and rs615942 (G/T), with metabolic syndrome and diabetes in a group of multiethnic women (Lo et al., 2006). The likelihood of having diabetes among Caucasian women who are homozygous for the 17β-HSD1 polymorphisms is 4- to 7-fold greater compared with women who are heterozygous for these SNPs. On the other hand, the three 17β-HSD1 gene polymorphisms were not associated with metabolic syndrome in any racial/ethnic group (Lo et al., 2006).

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Fig 1.

Two possible stepwise catalytic mechanisms for 17β-HSD1. (A) In the first step the pro-S hydride of NADPH is transferred to the α-face of E1 at the planar C17 carbon (A1), resulting in an energetically favorable aromatic system; the resultant oxyanion is subsequently protonated by the acidic -OH group of Tyr155 (A2). (B) In the first step the keto oxygen of E1 is protonated by the acidic -OH of Tyr155 (B1); the resultant carbocation then accepts the pro-S hydride of NADPH at the α-face (B2). The proton relay is facilitated by a H-bond network involving Lys159, two water molecules and Asn114, an electrostatic interaction between the protonated side chain of Lys159 and the phenyl ring of Tyr155 (Ghosh & Vihko, 2001) as well as T-stacking between Phe192 and Tyr155 (Negri et al., 2010). Hydrogen bonds are represented by dashed lines. For the sake of clarity $\pi-\pi$ interactions are not depicted.

FIG. 2.

Crystal complex structure of 17β-HSD1/DHT. A and B, Electronic density of DHT for 2Fo-Fc map seen at 0.8σ cutoff in reverse binding mode (A) and normal binding mode (B). C, Stereo representation showing the H-bond of DHT with the residue His221 in the reverse binding mode (DHT represented in blue), whereas in the normal binding mode, there is no H-bond interaction present (DHT in green). D, Distances between DHT, Tyr155, and the cofactor NADP in 1) reverse mode (the distance between the O3 of DHT with NC4 of NADP is 4.35 Å and between Tyr155 to NC4 of NADP is 5.4 Å) and in 2) normal mode (the distance between the O17 of DHT with NC4 of NADP is 3.75 Å and between Tyr155 to NC4 of NADP is 5.4 Å). Note that the final model of the complex has been submitted to the protein data bank with PDB code 3KLM (Aka et al., 2010).

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Representative inhibitors of 17β-HSD1, which demonstrated efficacy in reducing estrogendependent breast tumors in vivo (animal models). Cited from Lin et al., 2013.