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Phytochemistry 67 (2006) 225-231

PHYTOCHEMISTRY

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# Molecular cloning and heterologous expression of progesterone 5 $\beta$ -reductase from *Digitalis lanata* Ehrh. $\stackrel{\text{tr}}{\approx}$

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Received 5 September 2005; received in revised form 11 November 2005 Available online 28 December 2005

Dedicated to the memory of Prof. Dr. Ernst Reinhard.

#### Abstract

A full-length cDNA clone that encodes progesterone 5 $\beta$ -reductase (5 $\beta$ -POR) was isolated from *Digitalis lanata* leaves. The reading frame of the 5 $\beta$ -POR gene is 1170 nucleotides corresponding to 389 amino acids. For expression, a *Sph1/Sal*1 5 $\beta$ -POR fragment was cloned into the pQE vector and was transformed into *Escherichia coli* strain M15[pREP4]. The recombinant gene was functionally expressed and the recombinant enzyme was characterized. The  $K_m$  and  $v_{max}$  values for the putative natural substrate progesterone were calculated to be 0.120 mM and 45 nkat mg<sup>-1</sup> protein, respectively. Only 5 $\beta$ -pregnane-3,20-dione but not its  $\alpha$ -isomer was formed when progesterone was used as the substrate. Kinetic constants for cortisol, cortexone, 4-androstene-3,17-dione and NADPH were also determined. The molecular organization of the 5 $\beta$ -POR gene in *D. lanata* was determined by Southern blot analysis. The 5 $\beta$ -POR is highly conserved within the genus *Digitalis* and the respective genes and proteins share considerable homology to putative progesterone reductases from other plant species.

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Keywords: Digitalis lanata; Plantaginaceae; Veronicaceae; Progesterone 5β-reductase (5β-POR); Cardenolide biosynthesis; Over-expression

#### 1. Introduction

Leaves of *Digitalis* plants are still the major source for the isolation of cardenolides that are used to treat cardiac insufficiency in humans. Cardenolides are characterized by a steroid nucleus with its four rings connected *cis*– *trans–cis*, having a 14β-hydroxy group and an unsaturated five-membered lactone ring at C-17β. Typically, sugar side chains of variable length are attached at position C-3 of the cardenolide genins. Through studies using radiolabelled precursors, the putative biosynthetic pathway was basically deduced, but it is not yet fully understood on a biochemical level (Kreis et al., 1998).

Taking cholesterol as the starting point, about 20 enzymes which probably affect the formation of cardenolides have been identified and characterized in *Digitalis* (Lindemann and Luckner, 1997; Kreis et al., 1998). But only some of them have been purified, including the progesterone 5 $\beta$ -reductase (5 $\beta$ -POR), a key enzyme of cardenolide biosynthesis catalysing the conversion of progesterone to 5 $\beta$ -pregnane-3,20dione. The enzyme has been partially sequenced (Gärtner et al., 1994). To find a possible route for manipulating cardenolide biosynthesis in plants, a more detailed knowledge of the enzymes and genes involved in cardenolide formation is necessary for studying the regulation and engineering of

Abbreviations: 3β-HSD,  $\Delta^5$ -3β-hydroxysteroid dehydrogenase/ $\Delta^5$ - $\Delta^4$ ketosteroid isomerase; 5β-POR, progesterone 5β-reductase; RT-PCR, reverse transcriptase polymerase chain reaction;  $t_R$ , relative retention time.

<sup>&</sup>lt;sup>★</sup> The nucleotide sequences reported in this paper have been submitted to GenBank<sup>™</sup> Data Base with the corresponding Accession Numbers AY574950/AY585867.

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<sup>0031-9422/\$ -</sup> see front matter © 2005 Elsevier Ltd. All rights reserved. doi:10.1016/j.phytochem.2005.11.013

the cardenolide pathway (Kreis et al., 1998; Eisenbeiß et al., 1999; Luckner and Wichtl, 2000).

So far, molecular data from *Digitalis* are available only for a few house keeping genes (tRNA-Leu, 18S ribosomal RNA) and several enzymes like aldo-keto reductase (Gavidia et al., 2002), acyl-CoA-binding protein (Metzner et al., 2000), cyclophilins (Scholze et al., 1999; Küllertz et al., 1999), for review see Luckner and Wichtl (2000). Cardenolide specific genes are described for: cardenolide-16'-Oglucohydrolase (Schöninger et al., 1998; Framm et al., 2000), lanatoside-15'-O-acetylesterase (Kandzia et al., 1998), and  $\Delta^5$ -3 $\beta$ -hydroxysteroid dehydrogenase (Finsterbusch et al., 1999; Lindemann et al., 2000). The gene for progesterone 5 $\beta$ -reductase of *D. obscura* (*Dop5\betar*; AJ555127) was reported by Roca-Perez et al. (2004). The  $p5\beta r$  gene from *D. purpurea* was cloned and a partial genomic clone from D. obscura has been used to analyse the cardenolide production in 10 natural populations under seasonal aspects. We here report for the first time the cloning and heterologous functional expression of 5 $\beta$ -POR from leaves of Digitalis lanata Ehrh. and the biochemical characterization of the recombinant enzyme.

### 2. Results and discussion

#### 2.1. PCR amplification and cloning

The early steps of cardenolide biosynthesis are usually described as outlined in Fig. 1 (for review, see Kreis et al., 1998). We here focussed on the crucial step leading to  $5\beta$ -configured pregnanes supposed to be the direct precursors of *Digitalis* cardenolides.

Initial experiments were carried out using degenerated oligo nucleotide primers derived from the peptide sequences of progesterone 5 $\beta$ -reductase from *D. purpurea* (Gärtner et al., 1990, 1994) taking Kazusa's codon usage system into

account (www.kazusa.or.jp). The resulting fragments showed high sequence homology to the genomic clone of  $Dop5\beta r$  gene of *D. obscura* and to the progesterone 5 $\beta$ reductase ( $p5\beta r$ ) from *D. purpurea*. After submission of the sequence for  $p5\beta r$  gene (AJ310673; Roca-Perez et al., 2004) the results were confirmed by PCR amplification with distinct primers. The 5 $\beta$ -POR was amplified by RT-PCR from cDNA prepared from *D. lanata*, *D. purpurea* and *D. obscura*. DNA fragments of nearly identical length were also obtained when genomic DNA of *D. purpurea* was used as template. After subcloning of the PCR fragments into the TOPO cloning vector system the nucleotide sequence was elucidated by MWG<sup>®</sup> Biotech AG (Ebersberg, Germany).

We here isolated a full-length cDNA clone that encodes a progesterone 5 $\beta$ -POR from leaves of *D. lanata*. An identical match was observed between the deduced and directly determined amino acid sequence of the progesterone 5 $\beta$ reductase peptides from *D. purpurea* (Gärtner et al., 1994). RT-PCR using RNA and/or mRNA from mature leaves resulted in one single DNA fragment of the appropriate size. The DNA fragments and the nucleotide sequences obtained from *D. lanata*, *D. purpurea* and *D. obscura* did not differ in size (Fig. 2A). PCR amplification with genomic DNA as a template resulted in a fragment of 1247 bp, slightly different in size from the cDNA fragments (Fig. 2A, Lane 4). Actually, the sequence of the genomic clone contained a small intron as obtained after sequencing data analysis.

## 2.2. Alignments

Several authors proposed that 5 $\beta$ -POR has a key function in cardenolide biosynthesis (Gärtner et al., 1990; Lindemann and Luckner, 1997) producing the required 5 $\beta$ -configured pregnane intermediates leading to the various cardenolide genins. Fig. 3 shows the alignment of deduced 5 $\beta$ -POR protein sequences for *D. lanata* 



Fig. 1. Early steps in cardenolide biosynthesis.

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