Cardenolide Biosynthesis in Foxglove

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Received: January 28, 1998; Accepted: March 28, 1998

Abstract: The article reviews the state of knowledge on the biosynthesis of cardenolides in the genus Digitalis. It summarizes studies with labelled and unlabelled precursors leading to the formulation of the putative cardenolide pathway. Alternative pathways of cardenolide biosynthesis are discussed as well. Special emphasis is laid on enzymes involved in either pregnane metabolism or the modification of cardenolides. About 20 enzymes which are probably involved in cardenolide formation have been described "downstream" of cholesterol, including various reductases, oxido-reductases, glycosyl transferases and glycosidases as well as acyl transferases, acyl esterases and P450 enzymes. Evidence is accumulating that cardenolides are not assembled on one straight conveyor belt but instead are formed via a complex multidimensional metabolic grid. For example "fucose-type" cardenolides and "digitoxose-type" cardenolides seem to form via different biosynthetic branches and the "norchloranic acid pathway" identified recently seems to be operative only in the formation of fucose-type cardenolides.

Key words: Biosynthesis, cardenolides, cardiac glycosides, glycosidase, glycosyl transferase, enzymes, feeding experiments, Digitalis, oxido-reductases, secondary metabolism, Scrophulariaceae, tracer studies.

Abbreviations: GPC: gel permeation chromatography SDS-PAGE: sodium dodecyl sulphate polyacrylamide gel electrophoresis

Introduction

About 80 different glycosides of the cardenolide-type occur in the genus Digitalis (1). The Digitalis cardenolides are characterized by a steroid nucleus with rings connected cis-trans-cis; it has a 14β-hydroxy group, and an unsaturated five-membered lactone ring is substituted at C-17β. A sugar side chain with up to five carbohydrate units containing glucose and various rare 6-deoxy, 2,6-dideoxy and 6-deoxy-3-methoxy sugars, such as δ-fucose, δ-digitoxose or δ-digalactose, is attached at position 3β. According to their genin part they are divided into 6 series, termed A through F (Fig. 1). Most of the genuine cardiac glycosides present in Digitalis species have a terminal glucose; these cardenolides have been termed primary glycosides. After harvest or during the controlled fermentation of dried Digitalis leaves most of the primary glycosides are hydrolyzed to yield the so-called secondary glycosides. Digitalis cardenolides are valuable drugs in the medication of patients suffering from cardiac insufficiency. In therapy genuine glycosides, such as the lanatosides, are used as well as compounds obtained after enzymatic hydrolysis and chemical saponification, for example digitoxin (31) and digoxin, or chemical modification of digoxin, such as metildigoxin. Digitalis lanata Ehrh. and D. purpurea L are the major sources of the cardiac glycosides most frequently employed in medicine.

The putative biosynthetic pathway leading to the cardenolides (Fig. 2) is basically deduced from studies using radiolabelled precursors. For more details, the reader is referred to previous reviews by Grunwald (2) and Schütte (3). The more recent identification and characterization of various enzymes involved in pregnane and cardenolide metabolism have further clarified the pathway and this knowledge may now open up a possible route for manipulating cardenolide biosynthesis in plants. In this review emphasis is laid on cardenolide formation, whereas cardenolide degradation, bio-transformation and storage are not discussed in great depth.

Fig. 1 The Digitalis cardenolides are composed of six different genins and various sugars including 6-deoxy and 2,6-dideoxy sugars.
Studies with Precursors in vivo

The putative pathway of cardenolide formation as found in standard text books was basically deduced from studies with radio-labelled precursors carried out mainly in the 1960s and 1970s. While summarizing the results from these studies it has to be considered that exogenous substances have to pass various barriers, such as biological membranes, before reaching the site of synthesis. In this respect, sterols seem to be particularly critical compounds, due to their affinity to membranes which may lead to false negative results, since these precursors may simply not enter the cardenolide pathway. In addition, compartmentalization and metabolite channelling have to be taken into consideration. Depending on the tissue investigated and the method and site of precursor application, the compound in question may be modified in various ways prior to reaching the site of cardenolide synthesis. Hence, results obtained in different experimental systems may differ and may sometimes lead to contradictory conclusions.
Cardenolides are steroids and thus supposed to be derived from mevalonic acid via the triterpenoid pathway. As early as 1960, it was found that 2-14C-mevalonic acid is incorporated into the steroid part of 31 (4). Later on, degradation experiments revealed that the label of 2-14C-mevalonic acid appeared in C-1, C-7 and C-15 of the cardenolide genin (5). In similar experiments with 3-14C-mevalonic acid the label appeared in C-18, C-19 and C-21 (6). Evidence against a route via a C20-steroid and in favour of a route via C21-pregnanes was obtained by feeding 3-14C-mevalonic acid (7) and [1,7,15,22,26-14C5]-cholesterol (1) (8). These results are consistent with a biosynthetic route via the mevalonic acid pathway. On the other hand, it was found that the carbon atoms C-22 and C-23 of the butenolide ring of the cardenolides are not derived from mevalonic acid (9). These findings led to the hypothesis that a pregnane has to be condensed with a C23 donor, such as acetyl CoA or malonyl CoA, to yield the cardenolide genin. In fact, labelled pregnenolone (2) accumulated to significant levels when [2-14C]-mevalonic acid was fed to D. purpurea plants (10). Since 1 is a major sterol in Digitalis plants and cell cultures (11, 12), it was hypothesized that pregnanes used for the formation of cardenolides are derived from 1. Actually, 2 was identified as the main bio-transformation product of 1 in D. purpurea plants (13). However, other phytosterols, such as β-sitosterol were also metabolized to yield pregnanes (14). Other steroids, such as smilagenin and sodium glycocholate, may also serve as cardenolide precursors (15). Indirect evidence of a favoured route not involving 1 was provided by studies with a specific inhibitor of 24-alkyl sterol biosynthesis. The feeding of 25-azacyclonanol led to an increase in endogenous 1 in D. lanata shoot cultures. Under these conditions the number of 24-alkyl sterols was dramatically reduced, as were the cardenolides (16).

Pregnenolone may be considered as the starting point for cardenolide formation regardless of the assumed sterol precursor. [21-14C]-Pregnenolone glucoside was incorporated into cardenolides (17) and it is interesting to note that small amounts of xysmalogenin, a A5,6-unsaturated cardenolide not found in Digitalis but in the related genus Isoplexis, were also detected. The incorporation of 2 into Digitalis cardenolides has been demonstrated in several studies (e.g., 18, 19). Compound 2 was incorporated into digoxigenin (13) more efficiently than into digoxigenin (23) or gitoxigenin. Since the 3α-H of [3α-1H, 4-14C]-pregnenolone was lost in cardenolide formation, it was inferred that 3-oxosteroids, such as progesterone (3), are intermediates of the cardenolide pathway. The conversion of 2 to 3 was actually seen in intact leaves (18) and in cell cultures (20) of the Digitalis species. After administration of radio-labelled 3 to D. lanata leaves the label was found not only in cardenolides (21) but in 2 as well, indicating that the pregnenolone oxidation/double bond migration is a reversible process (22). Since all Digitalis cardenolides are 5βH-configured, the administration of 3 should result in the formation of 5β-pregnanes. However, only small amounts of 5β-pregnan-3β,20-dione (4) and 5β-pregn-3β-ol-20-one (6) have been detected (22, 23), which may be best explained by the assumption that the steroespecific 5β-reduction of 3 is a rate-limiting step in cardenolide formation; once accomplished the products are rapidly processed and channelled into the cardenolides. In most of the feeding experiments carried out, 5α-pregnanes were the main pregnane products accumulating after the administration of 3 (20, 24, 25). 5α-Pregnanes were the only products formed from exogenous 3 in cardenolide-free suspension cultures and white dark-grown shoot cultures (25, 26). In this context it has to be added that 3 was also transformed to 20-hydroxy-pregnanes (27) and that the isomerisation of 5α-pregnanes to 5β-pregnanes has never been reported. Compound 4 was converted to 6 and vice versa (28) and both were incorporated into 13 by D. lanata leaves (28, 29) and shown to stimulate cardenolide production in D. lanata shoot cultures (25, 30).

The 14β-hydroxy group is an important structural feature of all cardiac glycosides. Neither 14α-hydroxysteroids (31) nor 5β-pregnan-8(14)-en-3,20-dione (29, 32) were incorporated into cardenolides. On the other hand, [8-3H]-cholesterol was incorporated into cardenolides without loss of radioactivity (31) and it was thus concluded that a route via Δ14(14) or Δ8(5) pregnenes or an 8,14-epoxide as once postulated (19) does not seem to be operative. This assumption was further substantiated by the findings that neither 14βH-steroids (33) nor Δ14(14)-cardenolides (34) were incorporated into cardenolides. Direct hydroxylation with a change in configuration at C-14 seems to be the most probable mechanism of 14β-hydroxylation, although according to another hypothesis, which has never been tested in detail, the 14α-hydrogen is replaced by a hydroxy group which is then converted into the 14β-hydroxy via a 14-oxo radical (17).

Since 14β-hydroxyprogesterone was incorporated into cardenolides, it was concluded that 14β-hydroxylation must occur prior to the formation of the butenolide ring. This assumption was recently substantiated by the finding that 5β-pregnan-3β,14β,21-triol-20-one (8) increased cardenolide production in D. lanata shoot cultures by more than 4-fold (30).

Steroid 12β-hydroxylation and 16β-hydroxylation can occur at the pregnane level, the cardenolide genin and the glycoside level (35, 36, 37). 16β-Hydroxylation is achieved by direct replacement of the 16β-hydrogen (38). There is circumstantial evidence that 16β-hydroxylation is preferably performed at the C14-stage, whereas 12β-hydroxylation occurs mainly at later stages of cardenolide biosynthesis.

According to the putative pathway, 8 is the last C21-intermediate in the cardenolide pathway. Actually, this compound has been shown to be a much better precursor of cardenolides than, for example, 5β-pregnan-3β,21-diol-20-one (12) or 9 (30). However, 5β-pregnan-3β,14β-diol-20-one (15) has not yet been tested as a substrate and hence it still remains unclear whether pregnane 14β-hydroxylation precedes 21-hydroxylation or vice versa.

At this point it can be assumed that 2, derived from a sterol precursor, is modified in a sequence of stereo- and site-specific modifications, the crucial reactions being progesterone 5β-reduction and 14β-hydroxylation. There is strong evidence, however, that another route of cardenolide genin formation is operative in Digitalis. Feeding experiments with labelled C23 steroids revealed that 23-norcholesteric acids can serve as cardenolide precursors. It has been shown that the radioactivity of side-chain labelled 23-norcholesteric acids appears in the butenolide ring, thus indicating the incorporation of the C23 steroid without degradation (39). 23-Nor-5-cholesteric acids were better precursors than the respective 5β-steroids and the highest incorporation was seen with 23-nor-5,20(22)E-
The formation of cardenolide tridigitoxosides either.

observed in these studies. Administration of cardenolide.

epidigitoxigenin 3-O-3-glucoside, glucodigifucoside (26)
3-epidigitoxigenin, digitoxigenin 3-O-β-D-glucoside (24), 3-

ase. The formation of the sugar side chain of the cardenolides, especially the
implies that the various sugars are attached at the cardenolide genin formation. Hence, the “norcholanic acid” pathway should not be regarded as an alternative pathway, but rather as the discovery of a new set of tubes of a branched, anastomosing canal system funneling precursors to the desired end products, the cardenolides.

It has already been mentioned that the carbon atoms C-22 and C-23 of the butenolide ring of the cardenolides are not derived from mevalonic acid. Nucleophilic attack at the C-20 carbonyl of a properly activated acetate or malonate is proposed as one possible mechanism of attaching C-22 and C-23 to the pregnane skeleton. The formation of the butenolide ring system can then be accomplished by formal elimination of water and lactonization. Experimental evidence for these steps is still lacking and a different mechanism of butenolide ring formation has recently been suggested, involving the formation of a pregnane 21-O-malonyl hemiester with subsequent intramolecular condensation under decarboxylation and dehydratiation (41).

So far, only a few investigations have focussed on the forma-
tion of the sugar side chain of the cardenolides, especially the stage at which the characteristic 2,6-dideoxy sugars are attached to the cardenolide genin. The hypothetical pathway implies that the various sugars are attached at the cardenolide aglycone stage, although it cannot be ruled out that pregnane glycosides are obligate intermediates in cardenolide formation. Some results indicate that digitoxose is formed from glucose without rearrangement of the carbon skeleton (42) and that nucleotide-bound deoxysugars are present in cardenolide-producing plants (43). Recent investigations into cardenolide biosynthesis showed high incorporation of 14C-labeled malonate into cardenolides, but one third of the radioactivity was recovered in the butenolide ring. The radioactivity of the C6 fragment formed from the cleavage of [26-14C]-cholesterol (49) or quantification of the product 2 by a sophisticated HPLC-MS method (50). Lindemann and Luckner (50) found the enzyme associated with mitochondria and microsomal fractions of proembryogenic masses, somatic embryos and leaves of D. lanata. Formation of 2 was highest with sitosterol as the substrate, however, other sterols were also accepted.

To study cardenolide genin glycosylation in more detail 13 was fed to light-grown and dark-grown D. lanata shoot cultures, as well as to suspension-cultured cells (45). In either system the substrate was converted to 23, digitoxigenin-3-one, 3-epidigitoxigenin, digitoxigenin 3-O-β-D-glucoside (24), 3-epidigitoxigenin 3-O-β-D-glucoside, glucodigifucoside (26) and additional cardenolide products. Digitoxosylation was not observed in these studies. Administration of cardenolide mono- and bisdigitoxosides or cardenolide fucosides did not lead to the formation of cardenolide tridigitoxosides either. These results support the hypothesis that cardenolide fucosides and digitoxosides may be formed via different biosynthetic routes and that glycosylation may be an earlier event in cardenolide biosynthesis than previously assumed. Only recently was a set of pregnane and cardenolide fucosides synthesized (46) and it was shown that feeding of the 3-O-β-D-

fucoside of 9 to D. lanata shoot cultures leads to a 25-fold increase in the formation of 26 when compared to a control where the respective aglycone was fed (47).

Enzymes Involved in the Formation of the Cardenolide Genins

I. Cholesterol side-chain cleaving enzyme (SCCE)

Compound 1 is supposed to be a precursor of cardenolides (see above) during the formation of which the side chain of 1 has to be cleaved between C-20 and C-22 to yield 2 (Fig. 2). Analogous to the formation of steroids in animals this reaction is thought to be catalyzed by P450scs (“cholesterol side chain-cleaving enzyme”), however, this enzyme has never been characterized in detail in plants. The enzyme activity was determined by measuring either the decrease in 1 (48), the radioactivity of the C6 fragment formed from the cleavage of [26-14C]-cholesterol (49) or quantification of the product 2 by a sophisticated HPLC-MS method (50). Lindemann and Luckner (50) found the enzyme associated with mitochondria and microsomal fractions of proembryogenic masses, somatic embryos and leaves of D. lanata. Formation of 2 was highest with sitosterol as the substrate, however, other sterols were also accepted.

II. NAD: Δ⁵-3β-hydroxysteroid dehydrogenase/Δ⁵,Δ⁴-ketoster-

oid isomerase (3β-HSD)

The conversion of 2 into 3 involves two steps: The first reaction is the NAD-dependent oxidation of the 3-hydroxy group yielding Δ⁵-pregnen-3-one catalyzed by the Δ⁵-3β-hydroxysteroid dehydrogenase. The double-bond is shifted from position 5 to position 4 by the action of Δ⁵,Δ⁴-ketoster-oid isomerase (51). The enzyme system is referred to in toto as 3β-HSD (Fig. 2). The enzyme exhibited maximal activity at pH 8.0 and around 50°C.

3β-HSD was isolated from phytohormone-habituated D. lanata cell suspension cultures as well as from shoot cultures and leaves of D. lanata plants. NAD is the preferred proton acceptor. The addition of Triton X-100 (0.1 %) to the extraction buffer resulted in an almost 70 % loss of 3β-HSD activity. In addition to the NAD-dependent dehydrogenase, an oxidase requiring only molecular oxygen acts on the substrate. The enzyme was partially purified only recently. The molecular weight as determined by GPC was 80–90 kDa (52).

III. NADPH: progesterone 5β-reductase (5β-POR)

The 5β-POR catalyzes the transformation of 3 into 4, i.e., the rings A and B of the steroid are then connected cis (Fig. 2). Hence, one of the important structural characteristics of the Digitalis cardenolides seems to be accomplished at this stage. Optimal enzyme activity was seen at 30 °C and pH 8.0. The 5β-POR requires NADPH as the co-substrate and 3 was the preferred substrate. The relative conversion rates for other steroids such as testosterone, cortisone and cortisol were much lower. The enzyme was purified 770-fold to homogeneity from the cytosolic fraction of shoot cultures of D. purpurea. The molecular weight as determined by GPC was 280 kDa (53).

With the exception of the 5β-POR, all known enzymes of the putative biosynthetic pathway were detected in plants, organ
cultures and suspension cultures of *D. lanata* (54) supporting the view that 5β-POR is a key enzyme in cardenolide biosynthesis as proposed by Gätter and Seitz (55). This concept, however, was not accepted by Lindemann and Luckner (50), who found 5β-POR expressed in a cardenolide-free embryogenic cell line of *D. lanata* and they speculated that cardenolide formation is mainly regulated by the availability of 1 and its transport into mitochondria, where the SCEE is assumed to be located.

IV. NADPH:progesterone 5α-reductase (5α-POR)

5α-POR, which catalyzes the reduction of 3 to 5α-pregnane-3,20-dione (5), probably in a competitive situation with the 5β-POR, was isolated and characterized from cell cultures of *D. lanata* where it was found to be located in the endoplasmic reticulum (56). 5α-POR requires NADPH as a reducing cosubstrate, and optimum conditions for the 5α-POR were at pH 7 and 40°C. At temperatures below 45°C, the product of the enzyme reaction, 5, was enzymatically reduced to 5α-pregnan-3β-ol-20-one (22) (see below).

V. NADPH:3β-hydroxysteroid 5α-oxidoreductase (3β-HS-5α-OR)

The enzyme catalyses the conversion of 5 to 22. 3β-HS-5α-OR was first isolated and characterized in the microsomes of *D. lanata* cell cultures (57). The enzyme worked best at pH 8.0 and 25°C. Just slightly increasing the temperature to 27°C resulted in a marked reduction of 3β-HS-5α-OR activity. Both NADPH and NADH were able to provide the necessary reduction equivalents to drive the reaction.

Differential centrifugation as well as linear sucrose density gradient centrifugation revealed that most of the 3β-HS-5α-OR is soluble and it was thus inferred that it is not associated with a specific cell compartment.

VI. NADPH:3β-hydroxysteroid 5β-oxidoreductase (3β-HS-5β-OR)

The 3β-HS-5β-OR catalyzes the conversion of 4 to 6 (Fig. 2). It was found to be a soluble protein (55). Optimum enzyme activity was found at a pH-value of 6.5 and at around 40°C. The 3β-HS-5β-OR was catalytically active in the presence of either NADPH or NADH, but NADPH was the preferred co-substrate. The reverse reaction was observed, yielding 4 when using 6 and NADP as a substrate and co-substrate, respectively.

VII. NADPH:3α-hydroxysteroid 5β-oxidoreductase (3α-HS-5β-OR)

This enzyme catalyses the conversion of 4 to 5β-pregnan-3α-ol-20-one (7). In a situation similar to that described for the progesterone reductases, the hydroxysteroid 5β-oxidoreductases may compete for 5β-pregnane-3-ones and part of these putative intermediates in the cardenolide pathway will be withdrawn due to the action of the 3α-HS-5β-OR. Actually, 3α-cardenolides have never been described in *D. lanata* and the final products of the 5α-pregnane pathway are not yet known.

Cell-free buffered extracts from light-grown *D. lanata* shoots were shown to reduce 4 almost exclusively to 7 when 0.05 M MgCl₂ were present in the incubation mixture (25). These conditions were inhibitory for the formation of 6. The 3α-HS-5β-OR could be recovered from membrane-free protein extracts. Optimum enzyme activity was observed at pH 7.0 and 42°C. The enzyme reaction was found to be NAD(P)H-dependent and SH reagents were essential for enzyme activity. The enzyme seems to be specific for 5β-pregnane-3-ones; 5α-pregnane-3-ones or Δ⁴/Δ⁶-pregnanes were not accepted as substrates.

Pregnane 21-hydroxylation and 14β-hydroxylation: The enzymes involved in pregnane 21-hydroxylation and pregnane 14β-hydroxylation in the course of cardenolide formation have not been described as yet.

VIII. Malonyl-coenzyme A:21-hydroxyprogrenane 21-O-malonyltransferase (MHPPMT)

As far as the formation of the butenolide ring is concerned, it is supposed that the condensation of 8 with a dicarboxyl unit yields 13 (Fig. 2). When the 3β-O-acetate of 8 was incubated together with malonyl-coenzyme A in a cell-free extract of *D. lanata* leaves, a product was formed which was identified as the malonyl hemiesther of the substrate (41). The compound decomposes rapidly at temperatures higher than about 100°C and during prolonged storage and two products are formed, namely 5β-pregnan-1β-ol-20-one 3β,21-O-diacetate and the 3-O-acetate of 13. The enzyme catalysing the formation of the malonyl hemiesther was termed malonyl-coenzyme A:21-hydroxyprogrenane 21-O-malonyltransferase (MHPPMT).

The major part of the MHPMT was found to be soluble. Temperature and pH optima were at 50°C and pH 6.5, respectively. Thiol reagents stimulated MHPMT activity. Malonyl-coenzyme A and acetacetyl-coenzyme A were accepted as co-substrates. No ester formation was observed when acetyl-CoA or succinyl-CoA were added to the incubation mixture. CoA inhibited the malonylation reaction. Compound 8 and its 3β-O-acetate were the most suitable substrates for the transferase reaction. Pregnen-21-ol-20-one 9, corticosterone (10), 5β-pregnan-21-ol-3,20-dione (11) and 12 were only very poor substrates. The enzyme could so far be detected only in cardenolide-producing plants (41).

IX. Digitoxin 12β-hydroxylase (D12H)

This microsomal cytochrome P-450-dependent monooxygenase is capable of converting digitoxigenin-type cardenolides to their corresponding digoxin-type cardenolides (58). The enzyme was first isolated from cell suspension cultures of *D. lanata*, where the enzyme was found to be located in the endoplasmic reticulum.

The pH optimum of the D12H was at pH 7.5 and the temperature optimum at 20°C (Table 1). Compound 31, β-methyldigitoxin and α-acetyldigitoxin (33) as well as digitoxigenin-type cardenolides with shorter or no sugar side chain were hydroxylated (59). Gitoxigenin, k-strophanthin-β and cymarin, on the other hand, were not accepted as substrates. NADPH and O₂ are essential for the catalytic activity and the enzyme reaction is competitively inhibited by NADP⁺ and cytochrome c. The D12H was inhibited by CO, but illumina-ton with blue light (λₘₜₐₓ 450 nm) reversed this inhibition almost totally. KCN stimulated hydroxylation in
vitro, whereas Co²⁺, Zn²⁺ and Hg²⁺ were strongly inhibitory. After immobilization in alginate the enzyme retained 70 % of its original activity. The kinetic data of D12H immobilized in alginate were the same as for the enzyme in freely suspended microsomes (60).

It should be mentioned that digitoxin 16β-hydroxylase (D16H) has been detected in protein extracts prepared from D. purpurea cell suspension cultures but the enzyme has not yet been characterized in detail (61).

Enzymes Involved in the Formation of the Sugar Side Chain

X. UDP-glucose:sterol 3-O-glucosyltransferase (SGT)

This enzyme catalyzes the transfer of the sugar moiety of UDP-glucose to a steroid substrate (Fig. 3). [4-14C]-Epiandrosterone was used as the standard substrate. In the cultured cells the enzyme was not associated with a specific subcellular fraction. However, almost 60 % of the enzyme isolated from leaves was associated with the microsomal fraction from which it could be solubilized with 0.1 % sodium deoxycholate (62).

SGT was partially purified from cell cultures and leaves of D. purpurea. The purified enzyme had its pH optimum at pH 7.5. All Δ²-steroids tested were good substrates for the SGT. 5αH-Steroids, such as epiandrosterone and 5α-pregnan-3β-ol-20-one, were better substrates than their corresponding 5βH-analogues. Epiandrosterone (5αH-configured) containing a 3β-hydroxy group was a better substrate than its 3α-hydroxy analogue, whereas of the 5βH-steroids tested, those with a 3α-hydroxy group were better substrates than the respective 3β-hydroxy compounds. Compound 13 was only a poor substrate for the SGT. However, taking into consideration the small amounts of glucodigitoxigenin genuinely found in Digitalis it may well be that the sterol glucosyltransferase is involved in the formation of this compound. It should be mentioned that quite large amounts of glucodigitoxigenin were formed when 13 was fed to suspension-cultured cells of D. purpurea (36) or shoot cultures of D. lanata (63). To summarize, it still remains to be clarified whether sterol glycosyltransferases, like the enzyme isolated from D. purpurea, are actually involved in the formation of Digitalis glycosides.

XI. UDP-glucose:digitoxin 16-O-glucosyltransferase (DGT)

The enzymatic glucosylation of secondary glycosides to their respective primary glycosides (Fig. 3) was first shown by Franz and Meier (64) in particulate preparations from D. purpurea leaves and was investigated in more detail in cell cultures of D. lanata (65). The DGT requires two substrates: a secondary cardiac glycoside and a sugar nucleotide. Of 6 sugar nucleotides tested only UDP-α-D-glucose served as a glycosyl donor, whereas other glucose nucleotides (65) or UDP-α-D-fucose (66) were not accepted. As far as pH and temperature are concerned, the highest glucosylation rates were found at pH 7.4 and 40°C, respectively.

![Fig. 3 Enzymes involved in the formation of the sugar side chain of Digitalis cardenolides. 13, digitoxigenin; 24, digitoxigenin 3-0-β-glucoside; 25, digiproside; 26, glucodiglucoside; 27, digitoxigenin 3-0-β-quinovoside; 28, glucodigitoxigenin 3-0-β-quinovoside; 29, evatromonoside; 30, glucosevatromonoside; 31, digitoxin; 32, purpureaglycoside A; 33, β-acetyldigitoxin. X, UDP-glucose: sterol 3-0-glucosyltransferase (SGT); XI, UDP-glucose: digitoxin 16-0-glucosyltransferase (DGT); XII, UDP-fucose: digitoxigenin 3-0-fucosyltransferase (DFT); XIII, UDP-quinovose: digitoxigenin 3-0-quinovosyltransferase (DQT); XIV, UDP-glucose: digiproside 4-0-glucosyltransferase (DPGT); XV, acetyl coenzyme A: digitoxin 15'-0-acetyltransferase (DRAT); XVI, lanatoside 15'-0-acetylersterase (LAE); XVII, cardenolide 16-O-glucohydrolase I (CGH I); XVIII, cardenolide glucohydrolase II (CGH II); XIX, cardenolide β-0-fucohydrolase (CFH).]
Strong DGT activity was found in buffered extracts from young leaves, roots and flowers of Digitalis lanata plants, whereas only weak activity could be detected in stems and mature leaves. DGT was demonstrated in leaves, callus and suspension-cultured cells of D. lanata, D. purpurea and D. heywoodii (67). The DGTs of the three Digitalis species examined differed considerably with regard to their substrate preferences. Compound 31 and digoxin were glucosylated much better by cell-free extracts from D. lanata than their 15′-O-acylated derivatives. Although 15′-O-acylated glycosides do not occur in D. purpurea, they were glucosylated to their corresponding primary glycosides by enzyme preparations from D. purpurea cell cultures (65). Cardenolide monoglycosides, such as evatromonoside (29) were accepted very well, whereas cardenolide genins or bisdigitoxosides were glucosylated at a much slower rate (68). Digitoxigenin quinovoside (27) was glucosylated by partially purified DGT to yield glucodigitoxigenin quinovoside (28). Under the same conditions glucosylation was not observed when digiprose (25) was tried as the glucosyl acceptor, indicating that DGT accepts only substrates with an equatorial OH group in the 4′ position (66).

XII. UDP-fucose:digitoxigenin 3-O-fucosyltransferase (DFT)

The DFT catalyzes the transfer of the sugar moiety of UDP-α-D-fucose to a cardenolide aglycone, such as 13 or 23 (66) (Fig. 3). Compound 25, the product formed in the presence of 13 is a minor glycoside in D. lanata (1). DFT is a soluble enzyme in D. lanata leaves. Fucosylation activity was highest at pH 5.7 and 37 °C. Gitoxigenin and 13 were much better substrates than 23. The apparent molecular weight of DFT is about 60 kDa, as determined by GPC (69).

XIII. UDP-quinovose:digitoxigenin 3-O-quinovosyltransferase (DOT)

Incubation of crude protein extracts together with 13 and UDP-fucose not only resulted in the formation of 25 but also of 27 (Fig. 3), the 4′-epimer of 25, which is a minor glycoside in D. lanata (1). DFT is a soluble enzyme in D. lanata leaves. Fucosylation activity was highest at pH 5.7 and 37 °C. Gitoxigenin and 13 were much better substrates than 23. The apparent molecular weight of DFT is about 60 kDa, as determined by GPC (69).

XIV. UDP-glucose:digiprose 4′-O-glucosyltransferase (DPGT)

Glucodigifucoside (26) was formed upon incubation at 37 °C and pH 5.7 of a soluble enzyme preparation from young leaves of D. lanata in the presence of UDP-α-D-glucose and 25 (66) (Fig. 3). The enzyme is not identical with the glucosyltransferases described above, but has not been characterized in detail as yet. Compound 26 is a major cardenolide in D. lanata leaves during all stages of development and may be regarded as the end-product of the “fucose pathway” (see above).

XV. Acetyl coenzyme A:digitoxin 15′-O-acetyltransferase (DAT)

This soluble, cytosolic enzyme catalyzes the 15′-O-acetylation of cardenolide tri- and tetrasaccharides (Fig. 3). Using acetyl coenzyme A as the acetyl donor, DAT activity was detected in partially purified protein extracts from D. lanata and D. grandiflora, both known to contain lanatosides (70). The enzyme from either source exhibited its pH optimum at pH 6.0 and about 40 °C.

XVI. Lanatoside 15′-O-acetyesterase (LAE)

An esterase converting acetyldigitoxose-containing cardenolides to their corresponding non-acetylated derivatives (Fig. 3) was demonstrated in D. lanata cell suspension cultures and leaves (71). The LAE was shown to be bound ionically to the cell wall, from which it could be solubilized with 0.1 M sodium citrate buffer, pH 6.0. Citrate is needed for enzyme extraction, but not for the enzyme activity itself. LAE was present in D. lanata leaves and cell cultures (71) but was not detectable in cell suspension cultures of D. grandiflora and D. purpurea (83), and in leaves of D. purpurea and D. heywoodii (71). The pH optimum of the purified enzyme was at 5.5, the temperature optimum was around 40 °C. The enzyme could not be inhibited by p-hydroxymercuribenzoate or eserine. The pl was at pH 8.7, as determined by chromatofocussing. The apparent molecular mass of the LAE, as determined by GPC, was 120 kDa. In SDS-PAGE one dominant protein band was seen at about 50 kDa. It was hence concluded that the LAE is composed of two identical subunits.

Lanatosides as well as their corresponding secondary glycosides were good substrates, α,β-diacyldigoxin was deacetylated to some extent, yielding small amounts of β-acetyldigoxin but not the respective α-derivative. Apigenin 7-O-acetylglicoside was not deacetylated. Hence, LAE seems to be a site-specific cardenolide acetylesterase capable of removing the 15′-acetyl group of lanatosides and their deglycosylated derivatives.

XVII. Cardenolide 16′-O-glucohydrolase I (CGH I)

In 1935, Stoll et al. (73) reported on enzyme activities in Digitalis leaves capable of hydrolyzing primary glycosides, such as the purpureaglycosides or the lanatosides (Fig. 3). These enzymes were called “desmoenzymes” because they could not be extracted from dried pulverized leaves. They are associated with plastids (74) and could be solubilized from leaves of various Digitalis species using buffers containing Triton X-100 or other detergents (67). The Digitalis species examined differed only slightly with regard to the assay conditions needed for optimum cardenolide glucosidase activity. The pH optimum was at around 4.5 and the highest conversion rates were found to occur at about 50–60 °C. However, considerable variations in substrate preferences were observed among the cardenolide 16′-O-glucosidases of the three species. The enzyme of D. lanata, termed CGH I, was purified from young leaves. The apparent molecular mass of the CGH I was 154 kDa, as determined by non-denaturating PAGE. Fragments of about 27, 37 and 76 kDa were obtained in SDS-PAGE (75). The pl of CGH I was 5.8, as determined by chromatofocussing.

XVIII. Cardenolide glucohydrolase II (CGH II)

Meanwhile, another cardenolide glucohydrolase, termed CGH II, was isolated from D. lanata and D. heywoodii leaves and cell cultures. This soluble enzyme hydrolyzes cardenolide disaccharides with a terminal glucose and seems to be quite specific for glucovatromonoside (30) (Fig. 3), which is suppos-
ed to be an intermediate in the formation of the cardenolide tetrasaccharides. The tetrasaccharides deacetyllanatoside C and purpureaglycoside A (32), which are rapidly hydrolyzed by CGH I (see above) were very poor substrates for CGH II. The enzyme was purified about 500-fold from leaves of D. heywoodii; it exhibited optimum activity at pH 6.0 and 50°C. The molecular mass of CGH II was determined as 69 kDa by GPC and 65 kDa by SDS-PAGE, the enzyme’s pI is at pH 6.2 (76, 77).

**Concluding Remarks**

Taking cholesterol as the starting point, about 20 enzymes which probably affect the formation of cardenolides have been identified in recent years. Among these are enzymes responsible for cardenolide formation and storage, as well as enzymes responsible for removing precursors from the cardenolide pathway. Only a few of them have been purified and just one, namely progesterone 1β-reductase, has been partially sequenced. The discovery of enzymes which have not yet been described but which might catalyze progesterone 1β- and 21β-hydroxylation may help to clarify the cardenolide pathway(s) further. In summary, a more detailed knowledge of the enzymes and genes involved in cardenolide formation is necessary for studying the regulation and engineering of the cardenolide pathway in future.

**Acknowledgements**

We thank E. Reinhard, M. Wichtl, M. Luckner and B. Dietrich for encouragement and fruitful discussions throughout the joint project on cardenolide formation, storage and degradation in the genus Digitalis (1990 – 1997). Our own work was in part financed by the Deutsche Forschungsgemeinschaft, the Fonds der Chemischen Industrie and the Bundesministerium für Bildung, Wissenschaft, Forschung und Technologie; their support is gratefully acknowledged.

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