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***In vitro* studies on the
biosynthesis and reduction
of ubiquinone**

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*To Veronica
& Tobias
with love*

ABSTRACT

This thesis concerns the role of ubiquinone, the only endogenously synthesised lipid soluble antioxidant, in the cellular defence against peroxidation of proteins and lipids.

The aims of the present investigations were to study the biosynthesis of ubiquinone in two different organelle fractions, i.e. microsomes and peroxisomes and to characterise the enzyme reactions of the three flavoenzymes, lipoamide dehydrogenase, glutathione reductase and thioredoxin reductase in the reduction of ubiquinone.

A semipreparative HPLC method was established to rapidly isolate different polyprenols with high purity. The isolated compounds could be used for studies of different enzyme reactions in the mevalonate pathway, and as standards for quantitative HPLC-analysis. Compared to conventional chromatographic methods this new technique was much more rapid and polyprenols with higher purity was isolated.

It was demonstrated that both peroxisomes and microsomes were involved in the biosynthesis of ubiquinone. Two enzymes involved in the synthesis of ubiquinone, *trans*-prenyltransferase and nonaprenyl-4-hydroxybenzoate (NPHB)-transferase, were investigated. The results clearly showed differences in the regulation of the synthesis of ubiquinone in those organelles. The specific activity of *trans*-prenyltransferase in peroxisomes was 30% of the total activity found in both organelles.

The characteristics of the regeneration of ubiquinol by the flavoenzymes, lipoamide dehydrogenase, glutathione reductase and thioredoxin reductase were investigated. These enzymes belong to the same family of enzymes and are defined as homo-dimeric pyridine nucleotide-disulfide oxidoreductases. The reduction of ubiquinone by lipoamide dehydrogenase and glutathione reductase was shown to be highly elevated by addition of zinc to the reaction mixture, whereas this reaction by thioredoxin reductase was inhibited by zinc. For lipoamide dehydrogenase and glutathione reductase the pH optimum for the reaction was found at acidic pH, but at physiological pH for thioredoxin reductase.

The reduction of ubiquinone by thioredoxin reductase was confirmed to be selenium dependent by use of full-length bovine and rat, *E. coli* (lacking selenocysteine), recombinant human (selenocysteine replaced by alanine), and truncated rat thioredoxin reductases, as well as with stable cell lines overexpressing thioredoxin reductase.

Altogether, the novel biological findings in this thesis are that; ubiquinone is not only synthesised in microsomes but also to a high extent in peroxisomes; ubiquinone is efficiently reduced by glutathione reductase and thioredoxin reductase; the reduction of ubiquinone by thioredoxin reductase is entirely selenium dependent.

LIST OF PUBLICATIONS

This thesis is based on the following publications, which will be referred to by their Roman numerals:

- I. **Tomas Carlson**, Karolina Skorupinska-Tudek, Jozefina Hertel, Tadeuz Chojnacki, Jerker M Olsson and Ewa Swiezewska. Single polyprenol and dolichol isolation by semipreparative high-performance liquid chromatography technique. *Journal of Lipid Research* 2000, 41: 1177-1180
- II. Michael Tekle, Magnus Bentinger, **Tomas Nordman**, Eeva-Liisa Appelkvist, Tadeusz Chojnacki And Jerker M. Olsson. Ubiquinone biosynthesis in rat liver peroxisomes. *Biochem Biophys Res Commun.* 2002, 291 (5): 1128-1133
- III. Ling Xia, Mikael Björnstedt, **Tomas Nordman**, Lennart C. Eriksson and Jerker M. Olsson. Reduction of ubiquinone by lipoamide dehydrogenase: an antioxidant regenerating pathway. *European Journal of Biochemistry* 2001, 268: 1486-1490
- IV. Ling Xia*, **Tomas Nordman***, Jerker M. Olsson, Anastassios Damdimopoulos, Linda Björkhem-Bergman, Ivan Nalvarte, Lennart C. Eriksson, Elias S.J. Arnér, Giannis Spyrou and Mikael Björnstedt. The mammalian cytosolic selenoenzyme thioredoxin reductase reduces ubiquinone. A novel mechanism for defense against oxidative stress. *Journal of Biological Chemistry* 2003, 278: 2141-2146
- V. **Tomas Nordman**, Mikael Björnstedt and Jerker M. Olsson. Reduction of ubiquinone by glutathione reductase. Submitted for publication, 2003.

* The authors contributed equally to this article.

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CONTENTS

Abstract.....	i
List of publications.....	ii
Contents.....	iii
List of abbreviations.....	iv
1 Introduction	1
1.1 General introduction.....	1
1.2 The mevalonate pathway.....	5
1.3 Ubiquinone	9
1.3.1 Biosynthesis of ubiquinones.....	11
1.3.2 Uptake and distribution of ubiquinone.....	13
1.3.3 Catabolism of ubiquinone.....	14
1.3.4 The functions of ubiquinone.....	15
1.3.5 Clinical relevance of ubiquinone.....	17
1.4 Regenerating enzymes systems.....	19
1.4.1 Lipoamide dehydrogenase.....	19
1.4.2 Glutathione reductase.....	20
1.4.3 Thioredoxin reductase.....	21
2 Present investigation	25
2.1 Aims.....	25
2.2 Results.....	25
2.2.1 Development of a rapid HPLC method for separation of polyprenols (Paper I).....	25
2.2.2 The biosynthesis of ubiquinone in peroxisomes (paper II)	27
2.2.3 Regeneration of ubiquinol by flavoenzymes (Paper III, IV and V).....	29
2.2.4 The role of selenium in the reduction of ubiquinone by thioredoxin reductase (paper IV).....	31
3 General discussion and future perspectives	32
4 Acknowledgements.....	35
5 References	37

LIST OF ABBREVIATIONS

DMAPP	Dimethylallyl pyrophosphate
FPP	Farnesyl pyrophosphate
GPP	Geranyl pyrophosphate
GPx	Glutathione peroxidase
GR	Glutathione reductase
GSH	Reduced glutathione
GSSG	Oxidized glutathione
HMG-CoA	3-Hydroxy-3-methylglutaryl coenzyme A
IPP	Isopentenyl pyrophosphate
LDL	Low density lipoproteins
LipDH	Lipoamide dehydrogenase
Prx	Peroxiredoxin
ROS	Reactive oxygen species
Sec	Selenocysteine
Ser	Serine
SREBP	Sterol regulatory element binding protein
Trx	Thioredoxin
Trx-(SH) ₂	Reduced thioredoxin
TrxR	Thioredoxin reductase
TrxR2	Mitochondrial TrxR
Trx-S ₂	Oxidized thioredoxin
VLDL	Very low density lipoproteins

1 INTRODUCTION

1.1 General introduction

The biomembranes of mammalian cells consists of a hydrophobic lipid bilayer that is able to keep apart the interior of the organelle from the exterior and uphold transmembrane gradients for different kinds of ions, like protons, calcium, sodium and potassium but also of other organic molecules like carbohydrates and proteins. The membrane is not only separating the different environments but actually contains components that build up the gradients. The cellular metabolism, that constitutes cell function, consists of a constant interaction between reactive, polarized molecules that are able to form new combinations and build up new constitutive components of the cell or form and store energy necessary for the metabolism.

Well aware of the necessity for molecular interaction and metabolism of formation and handling of reactive molecules I will, in this theses, deal with the potential hazard for the cell with the reactive intermediates. Any molecule with a reactive center or a free radical may form a covalent binding to a structural part of the cell or to its DNA or RNA and disturb cellular function. In the worst scenario the cell may be injured and collapse. It is obvious that the cell needs systems to protect it self from these oxidative attacks and systems that repair or regenerate damaged components of the cell. The role of ubiquinol for this cellular defence is the topic of this thesis.

Reactive molecules that may cause an oxidative hazard to the cell is constantly formed. Five percent of the oxygen used in cell respiration form oxygen radicals and other metabolic processes like cytochrome P450 catalyse hydroxylations that produces an excess of these reactive oxygen

species (ROS). Oxidative stress is a common term used to describe a state caused by reactive oxygen species. ROS formation, e.g. superoxide radicals (O_2^-), hydrogen peroxide (H_2O_2) and hydroxyl radicals (OH) (Cadenas 1989; Cadenas & Davies 2000; DiGuseppi & Fridovich 1984), are seen in many different locations i.e. the mitochondrial respiratory chain, reduction by superoxide dismutase (SOD), the Fenton reaction, and reduction by the cytochrome P450 systems (Dröge 2002). ROS are not only harmful for the cell but also crucial for normal metabolism playing an essential role in the biosynthesis of complex organic molecules, detoxification of xenobiotic chemicals, and defence against pathogens such as virus, bacteria or other microorganism (Dröge 2002; Finkel 1998; Kamata & Hirata 1999; Moran et al 2001; Rhee 1999).

Macromolecules such as DNA, proteins, and lipids that are damaged by high oxidative stress may eventually lead to apoptosis or cell death. ROS can affect proteins and lipids by peroxidation (Ernster 1993). Lipid peroxidation is a threat to the integrity of the biomembrane and to the structure and function of the membranous organelle itself. Rupture of lysosomal compartments is a direct threat to the existence of the cell. The lipid peroxidation in cellular membranes is a chain reaction that is self-propagating once initiated by different ROS (Fig. 1).

The target of ROS in the initial step is the unsaturated fatty acids of the phospholipids in the biomembrane. In this first step a carbon centered lipid radical (L \cdot) is formed that immediately can react with oxygen and form a lipid peroxy radical (LOO \cdot). In the phase called propagation this lipid peroxy radical can react with unsaturated fatty acids of other, closely located phospholipids in the membrane.

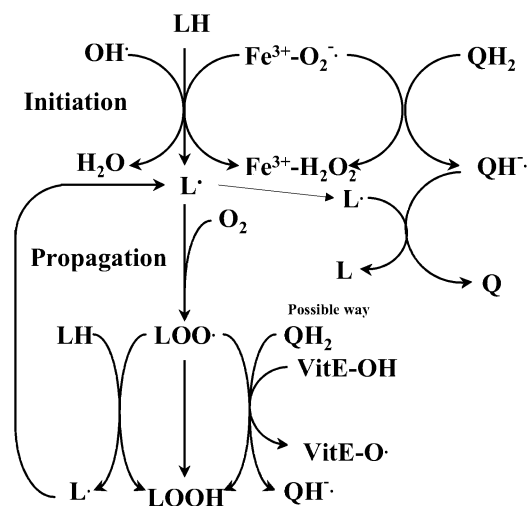


Figure 1. A simplified scheme of the lipid peroxidation. $\text{Fe}^{3+}\text{-O}_2\cdot$, perferryl radical; $\text{OH}\cdot$, hydroxyl radical; $\text{L}\cdot$, carbon centred lipid radical; LH, unsaturated fatty acid; $\text{LOO}\cdot$, lipid peroxy radical; LOOH , lipid hydroperoxide; QH_2 , ubiquinol; $\text{QH}\cdot$, semiquinones; Q, ubiquinone; VitE-OH , vitamin E or α -tocopherol; $\text{VitE-O}\cdot$, α -tocopheryl radical.

The final product of each chain reaction of lipid peroxidation is lipid hydroperoxides (LOOH). The breakdown of the lipid membrane may lead to increased fluidity as well as inactivation of membrane proteins and receptors. The permeability of the membrane is also hampered making the maintenance of cellular compartments impossible. Unless the cell can protect itself against these reactions and maintain, an appropriate cellular life would be impossible. It has to balance the formation of radical from different sources by regulation of the defence systems.

Cellular defence aims to trap and neutralise (reduce) the free radicals formed. This can be done by either scavenging of the radicals by molecules that can participate in a redox reaction or by enzymatic conjugation and excretion of the reduced and conjugated molecules. To

protect the cell against the cellular damages caused by lipid peroxidation defence mechanisms scavenging free radicals and lipid hydroperoxides are of great importance. As an example the initiation of the lipid peroxidation was inhibited by the reduced form of ubiquinone (Q), ubiquinol (QH₂) (Fig. 1) (Ernster 1993; Forsmark-Andree et al 1997). Furthermore, the lipid peroxy radical formed, was in these investigations, trapped by another lipid soluble antioxidant, vitamin E (α -tocopherol) that terminated the propagation phase. It was also proposed that ubiquinol is a scavenger of this radical (Ernster & Dallner 1995). The lipid soluble antioxidant, Vitamin E, is easily taken up via the intestinal system and transported to the liver and from this organ transported in VLDL via the blood to different organs in the body (Herrera & Barbas 2001; Traber 1999). There are today no enzymatic systems known, that can regenerate vitamin E to its reduced form from α -tocopheryl radical, but both vitamin C (ascorbate) and ubiquinol have been shown to efficiently do this (Beyer 1994; Ernster & Dallner 1995). Several factors affect the function and the levels of these lipid soluble antioxidants. One important factor is selenium which has been suggested to have functional connections to vitamin E and ubiquinol since selenium deficiency is associated with lower concentrations of vitamin E and ubiquinol (Chen & Tappel 1995; Scholz et al 1997; Vadhanavikit & Ganther 1993; Vadhanavikit & Ganther 1994).

To maintain a high capacity of this very important antioxidative function of ubiquinol it is required that this molecule is either synthesised in sufficient amounts or that it is regenerated by other enzyme systems.

1.2 The mevalonate pathway

The mevalonate pathway is a sequence of enzyme catalysed events that besides cholesterol, that is the main known lipid product generated in this pathway, also contributes to the production of several other neutral lipids i.e. ubiquinone, dolichol and dolichyl phosphate (Fig. 2). Furthermore, this pathway is also involved in the regulation of features such as signal transduction by isoprenylation of proteins, isopentenylation of tRNA for efficient selenoprotein synthesis, and N-linked glycosylation of proteins (Diamond et al 1996; Faust & Dice 1991; Goldstein & Brown 1990; Schroepfer 1981).

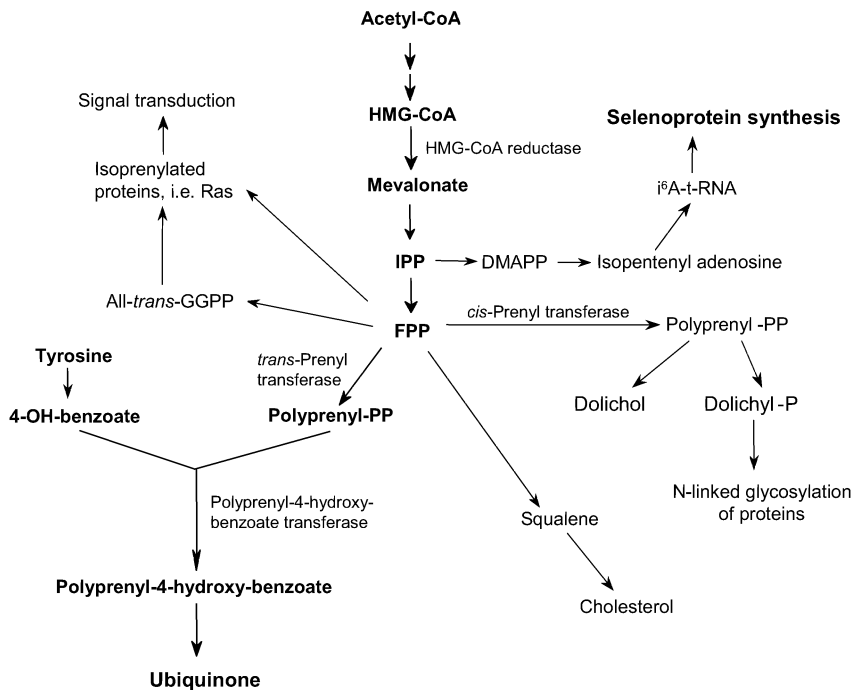


Figure 2. Schematic scheme of the mevalonate pathway.

In the initial part of the mevalonate pathway the formation of the branch-point product, farnesyl pyrophosphate (FPP), is mainly regulated by the enzyme HMG-CoA reductase (Goldstein & Brown 1990). Although, this pathway has been one of the most intensely studied there are still many unsolved questions that further need to be clarified.

The first reaction in this pathway, that was demonstrated in cytosol, was a condensation of two acetyl-CoA catalysed by the enzyme acetoacetyl-CoA thiolase, also accepted as the committed step in the isoprenoid biosynthesis (Schroepfer 1981). Thompson and Krisans demonstrated also that this reaction was catalysed by a peroxisomal thiolase and suggested that this organelle may be involved in the isoprenoid production (Thompson & Krisans 1990).

The next reaction in this pathway is the formation of HMG-CoA catalysed by HMG-CoA synthase, present mainly in cytosol but also in mitochondria (Ayte et al 1990; Clarke et al 1987; Clinkenbeard et al 1975; Goldstein & Brown 1990). HMG-CoA is the substrate for the most studied enzyme in the mevalonate pathway, 3-hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA reductase). This enzyme catalyses a two step reduction of HMG-CoA to the formation of mevalonate. The enzyme was primarily found to be located in the endoplasmic reticulum, integrated in the membrane with its catalytic site facing the cytosol but later on also discovered in peroxisomes (Keller et al 1985; Keller et al 1986; Kovacs et al 2001). HMG-CoA reductase is well investigated and is regarded to be the major rate-limiting enzyme in the biosynthesis of cholesterol, highly feedback regulated by its metabolites i.e. oxysterols (Goldstein & Brown 1990; Ness & Chambers 2000; Åkerlund & Björkhem 1990). The amounts and the activation of this enzyme are regulated by different

mechanisms e.g. phosphorylation/dephosphorylation causing inactivation/activation (Beg et al 1987; Clarke & Hardie 1990), transcriptionally by regulation of the Sterol Regulatory Element Binding Protein (SREBP) (Ericsson & Edwards 1998; Hua et al 1996; Kawabe et al 1994), and by proteolytic degradation (McGee et al 1996; Miller et al 1989; Parker et al 1986). Pharmaceutical drugs called statins are used to efficiently inhibit the enzyme HMG-CoA reductase in order to regulate the high levels of cholesterol in persons with hypercholesterolemia causing atherosclerosis, one of the most common diseases in the western world (Alberts 1988; Vaughan et al 2000). Although, these drugs are lowering the cholesterol levels in blood it may also have other unexpected effects that today is not completely evaluated. Thus, some investigations have shown that the incidence of cardiac incompensation is increased among people on statins. Furthermore, other investigators have reported a lower incidence of colon cancer in patients supplemented with statins (Agarwal et al 2002; Viner et al 2002).

The mevalonate is further phosphorylated in two steps forming the mevalonate-5-pyrophosphate catalysed by mevalonate kinase and phosphomevalonate kinase a reaction that requires both ATP and Mg^{2+} for optimal activity. These enzymes were purified from liver cytosol, but high levels of the mevalonate kinase activity were also demonstrated in peroxisomes (Biardi et al 1994; Stamellos et al 1992; Tanaka et al 1990).

The mevalonate pyrophosphate decarboxylase catalyse the formation of the product isopentenyl pyrophosphate (IPP) that is, the five-carbon compound, known to be the main substrate for FPP synthesis (Alvear et al 1982; Chiew et al 1987)

The enzyme, isopentenyl pyrophosphate isomerase (IPP isomerase) is mainly associated with the cytosol, but later studies have also indicated enzyme activities in mitochondria and peroxisomes (Ericsson et al 1992; Runquist et al 1994). The isomerisation reaction of IPP to dimethylallyl pyrophosphate (DMAPP) requires the presence of either Mg^{2+} or Mn^{2+} . The condensation of DMAPP and one IPP lead to the formation of geranyl pyrophosphate (GPP). A further condensation of one IPP to GPP forms FPP. These reactions are catalysed by farnesyl pyrophosphate synthase (FPP synthase) (Poulter & Rilling 1981). Both GPP and FPP were shown to feedback down regulate the IPP isomerase activity *in vitro* (Rilling & Chayet 1985). Another possibly important function of the synthesis of the DMAPP is the isopentenylation of tRNA^{Ser/Sec} necessary for effective synthesis of selenoproteins i.e. glutathione peroxidase (GPx) and thioredoxin reductase (TrxR) (Diamond et al 1996; Faust et al 1980; Moustafa et al 2001; Warner et al 2000).

1.3 Ubiquinone

Ubiquinone was discovered 1955 by Morton and co-workers (Festenstein et al 1955). By investigation of the physiological and chemical properties, Crane *et al.* proved that this compound contain a quinoid part and they were also able to isolate this lipid from mitochondria of bovine hearts (Crane et al 1957). At the same time Morton *et al.* introduced the name ubiquinone, based on that this compound is ubiquitously present in all biological systems (Morton et al 1957). In 1958, Folkers and his colleagues synthesised the complete structure; 2,3-dimethoxy-5-methyl-6-all-trans-polyprenyl-1,4-benzoquinone, and produced it by fermentation (Wolf et al 1958). Later it was shown that ubiquinone was an essential component in the mitochondrial respiratory chain (Ernster et al 1969; Mitchell 1975). However, it has been established that ubiquinone is present also in all extramitochondrial membranes including the plasma membrane with other vital functions for the cell (Kalén et al 1987; Zhang et al 1996). The distribution of ubiquinone in different subcellular fractions of rat liver cells is shown in table 1.

Table 1. Subcellular distribution of ubiquinone-9 in rat liver cells.

Fraction	Q9
Nuclear fraction	0.2
Mitochondria	1.4
Microsomes	0.15
Lysosomes	1.9
Golgi vesicles	2.6
Peroxisomes	0.3
Plasma membranes	0.7

(Kalén et al 1987; Zhang et al 1996) The values are given in µg/mg protein.

Ubiquinone consists of a redox active quinone ring that in different species has a condensed all-*trans*-isoprenoid side chain with various lengths (Fig. 3).

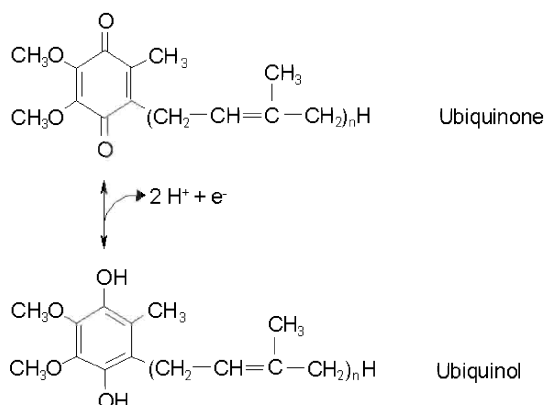


Figure 3. The chemical structures of the oxidized and reduced form of ubiquinone.

The predominant form of ubiquinone in humans has the longest known isoprene side chain with ten isoprene units (Q10) (Olson & Rudney 1983). Thus, other species show different homologues with various chain lengths indicating not only species variations but also functional varieties of ubiquinone depending on the length of the hydrophobic side chain (Table 2).

Table 2. Different ubiquinone homologues in various species.

Homologue	Occurrence
Q0	African Millipede
Q5	E. Coli
Q6	E. Coli, S. cerevisiae
Q7	E. Coli, Torula
Q8	E. Coli, Algae
Q9	Mouse, Rat
Q10	Human, Pig, Tobacco leaf

1.3.1 Biosynthesis of ubiquinones

The intracellular biosynthesis of ubiquinone, illustrated in figure 4, involves several events i.e. synthesis of the quinoid ring from aromatic amino acids and the synthesis of the isoprenoid side-chain.

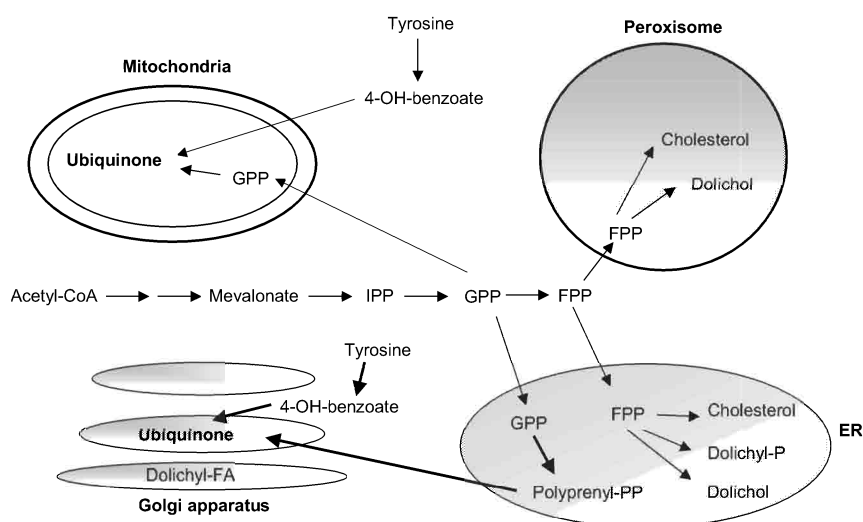


Figure 4. Schematic illustration of where mevalonate pathway enzyme reactions are located in the cell.

The condensation of the isoprenoid moiety with the ring, 4-hydroxybenzoate, is known predominantly to occur in the endoplasmic reticulum/Golgi system (Kalén et al 1990), but total biosynthesis was also demonstrated in mitochondria (Trumpower et al 1974). After prenylation of the ring, several modifications such as decarboxylation, hydroxylations, O-methylations, and a C-metylation have to take place in order to yield a functional ubiquinone (Fig. 5).

In mammals the aromatic amino acids tyrosine and phenylalanine are proposed to be the precursors required for the synthesis of 4-

hydroxybenzoate, necessary for ubiquinone biosynthesis (Booth et al 1960; Olson & Rudney 1983).

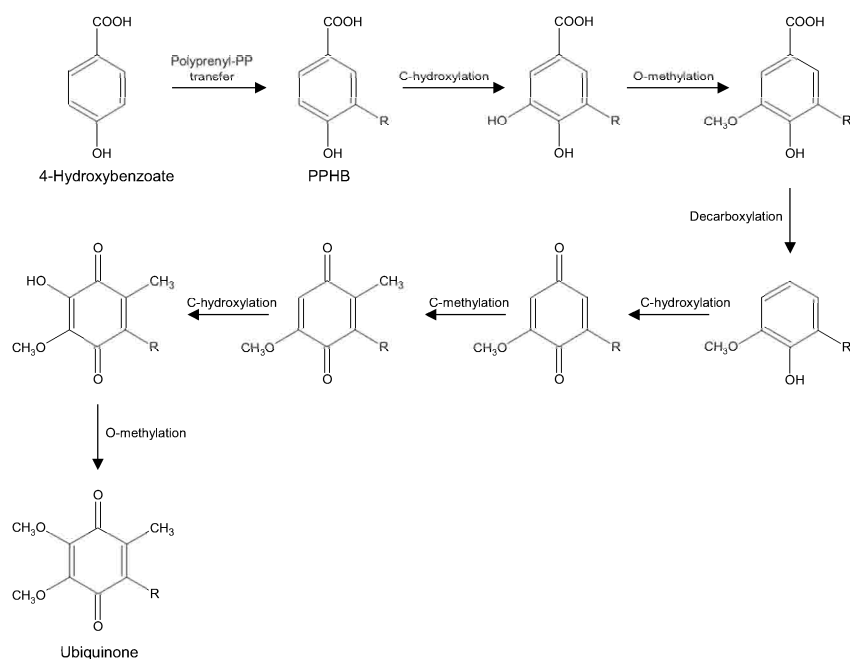


Figure 5. The eight last terminal steps in the biosynthesis of ubiquinone. R=polyisoprenoid chain; PPHB=polyprenyl-4-hydroxybenzoate.

The synthesis of the isoprenoid side-chain in mammals is catalysed by *trans*-polyprenyltransferase, an enzyme that has different intracellular locations (Grünler et al 1994). *In vitro* studies showed that the substrate for this reaction was unexpectedly GPP and not FPP (Teclebrhan et al 1993). This enzyme condenses isoprene units in *trans*-configuration to its final chain length. The polyprenyl-4-OH-benzoate transferase catalyses the condensation of the polyprenyl side chain to the ring structure, 4-hydroxybenzoate (Gupta & Rudney 1985; Kalén et al 1990).

1.3.2 Uptake and distribution of ubiquinone

Different studies when radioactively labelled ubiquinone was used showed that the dietary uptake of ubiquinone is limited and only a small amount of exogenous ubiquinone was detected in various tissues (Ramasarma 1985; Zhang et al 1995). Although, ubiquinone is administrated in its oxidised form the major part (80-90%) is found in reduced antioxidant form, ubiquinol (Zhang et al 1995; Åberg et al 1992). The mechanism for the reduction of ubiquinone is so far not completely evaluated.

The predominant form of ubiquinone is in rat Q9 and in human Q10 (Dallner & Sindelar 2000). The distribution of those ubiquinones in different organs is shown in table 3.

Table 3 Amounts of Q9 and Q10 in tissues of rats and humans.

Tissue	Q9		Q10	
	Rat	Human	Rat	Human
Heart	202.0	2.5	16.9	114.0
Kidney	123.9	3.3	22.0	66.5
Liver	130.9	1.8	21.3	54.9
Muscle	42.6	1.0	3.1	39.7
Brain	37.4	1.0	18.9	13.4
Pancreas	37.2	1.6	2.8	32.7
Spleen	22.9	0.7	9.2	24.6
Lung	16.9	0.6	2.4	7.9
Thyroidea	43.5	1.2	6.6	24.7
Testis	32.4	0.4	4.7	10.5
Intestine	50.9	0.5	19.0	11.5
Colon	47.5	0.4	8.4	10.7
Ventricle	55.6	n.d	5.3	11.8

(Åberg et al 1992) The values are given in µg/g tissue, n.d = not determinated

1.3.3 Catabolism of ubiquinone

The endogenous catabolism of ubiquinone varies in different rat tissues with half-life times from 49 to 125 hours (Table 4) (Andersson et al 1990; Thelin et al 1992).

Table 4. Half-life time (hours) of ubiquinone in rat tissues.

Tissue	Ubiquinone
Kidney	125
Thymus	104
Pancreas	94
Brain	90
Liver	79
Stomach	72
Spleen	64
Heart	59
Colon	54
Intestine	54
Muscle	50
Testis	50
Thyroid	49

(Andersson et al 1990; Thelin et al 1992)

Interestingly, the half-life times for cholesterol and dolichol in the liver is almost the same as for ubiquinone but is 40- and 10-fold longer, respectively, in brain (Andersson et al 1990). These findings indicate that the biosynthesis and metabolism of these lipids are regulated in different ways.

The catabolism of ubiquinone has only to a limited extent been studied. The breakdown products of ubiquinone that so far have been identified have the same ring structure but the side-chain was shown to be much shorter and carboxylated (Imada et al 1970; Nakamura et al 1999). By

these changes of the side-chain the product will be more hydrophilic and, thereby, easier to excrete from the cell.

1.3.4 The functions of ubiquinone

Ubiquinone possesses many essential functions depending on its localisation (Nohl et al 2001). Besides its most known function as an electron carrier in the mitochondrial respiratory chain it is also an antioxidant, involved in extramitochondrial electron transport, regulate mitochondrial permeability pores, and destabilise membranes and participate in plasma membrane electron transport necessary for the control of intracellular pH among other things (Crane & Navas 1997; Fontaine & Bernardi 1999; Gille & Nohl 2000; Villalba et al 2001)

1.3.4.1 The respiratory chain

As a component of the respiratory chain ubiquinone plays a vital role in oxidative phosphorylation. Located in the inner mitochondrial membrane ubiquinone shuffles electrons from complex I and II to complex III (Crane 2001; Mitchell 1975; Nohl et al 2001). The unique function of ubiquinone in the mitochondria where it is the only non-protein component involved in cell respiration, enable it to freely participate and transfer electrons between cytochromes and flavoproteins. Therefore, ubiquinone plays an essential role in the adenosine triphosphate (ATP) production (Schultz & Chan 2001).

1.3.4.2 The function as an antioxidant

More than 30 years ago reduced ubiquinone-6 was proposed to possess antioxidant properties (Mellors & Tappel 1966a; Mellors & Tappel

1966b). An effective role of ubiquinol as antioxidant was later demonstrated to prevent lipid peroxidation in liposomes, lipid emulsions, phospholipids, and LDL (Fiorentini et al 1993; Frei et al 1990; Landi et al 1990; Pobezhimova & Voinikov 2000; Takahashi et al 1995; Thomas et al 1997; Yamamoto et al 1990). Furthermore, supplemented ubiquinone-10 was also shown to protect DNA and membrane proteins (Ernster & Dallner 1995; Tomasetti et al 2001; Tomasetti et al 1999).

The protective role of ubiquinol as an inhibitor of lipid peroxidation has been widely discussed. According to some investigator ubiquinone was shown to prevent lipid peroxidation at the same rate as vitamin E (Yamamoto et al 1990). Other studies have shown an even higher effectiveness of ubiquinol in prevention of LDL oxidation than vitamin E (Frei et al 1990; Stocker et al 1991). This inhibition of lipid peroxidation by ubiquinol was further confirmed by the use of submitochondrial particles in which lipid peroxidation was initiated by ascorbate and ADP-Fe³⁺ (Forsmark et al 1991). Furthermore, ubiquinol was shown to be required in order to maintain vitamin E in its reduced active form (Fig. 1) (Frei et al 1990; Kagan et al 1990; Mukai et al 1990; Nohl et al 1999).

For the antioxidant function of ubiquinol and because it is widely spread in all membranes it is of high importance that the reduced form can be regenerated at all these locations. Many investigators have so far studied the regeneration of ubiquinone and different quinone reductases have been proposed as reduction enzymes (Kishi et al 1999; Takahashi et al 1996; Takahashi et al 1995). The most studied enzyme is DT-diaphorase, a cytosolic homodimeric enzyme (Beyer et al 1996; Beyer et al 1997; Landi et al 1997). Recently, it was shown *in vitro* that the homodimeric enzyme

lipoamide dehydrogenase efficiently could reduce ubiquinone (Olsson et al 1999).

1.3.5 Clinical relevance of ubiquinone

Several studies have shown that the ubiquinone concentrations are decreased during ageing (Kalén et al 1989; Lönnrot et al 1995). In addition, it has been shown that deficiency of ubiquinone is associated with several disease conditions, i.e. cardiomyopathies, muscle degenerative and neurogenerative diseases (Littarru 1995; Rosenfeldt et al 1999; Shults et al 1998). The lowered concentration of ubiquinone found in these different diseases may suggest a very important function of this compound in different biological systems.

The uptake of supplemented ubiquinone, under normal conditions, is restricted and it is obvious that under normal conditions the endogenous synthesis of ubiquinone is enough to provide all the cells with this compound necessary for its membrane functions. However, under conditions where ubiquinone is not synthesised or regenerated in adequate levels a supplementation is probably required for the maintenance of its functional properties.

One very severe disease, mitochondrial encephalomyopathy, caused by a gene mutation leads to deficiency in synthesis of ubiquinone and thereby dysfunction of the electron transfers in the respiratory chain (Rötig et al 2000). In a clinical trial supplementation with ubiquinone-10 was shown to mostly restore the ubiquinol levels and to reduce the symptoms of the disease (Rötig et al 2000).

It was shown that oral supplementation to healthy subjects with 30 mg Q10/day for 3 to 9 months increased the blood concentration from 1mg Q10/l to 2mg Q10/l (Folkers et al 1994). This dietary uptake of ubiquinone was suggested to only have a primary role in the blood but lower importance in (other) different tissues. These elevated concentrations in the blood may serve several important functions, i.e. an enhanced protection of LDL from oxidation, a prevention of free radical damage caused by neutrophils in inflammatory diseases, and prevention of oxidative injury by endothelial cells resulting from ischemia-reperfusion (Ernster & Dallner 1995; Kontush et al 1995). These and possibly other protective functions against free-radical damage in the circulation may account for the majority of the beneficial effects of ubiquinone supplementation in experimental and clinical medicine. Furthermore, supplementation of ubiquinone has shown to have beneficial effects on diseases in the cardiovascular system (Langsjoen et al 1994; Langsjoen & Langsjoen 1999).

1.4 Regenerating enzymes systems

The redox status of the cell is of vital importance for cellular activities. Many enzymes and transcription factors have to be kept in reduced form to be functionally active and able to remain in the right configuration in the cell. Several redox systems, such as the thioredoxin system, the glutathione system and also many other systems participate in this mission of keeping vital biological molecules in an optimal redox state.

Although this field has by now been insufficiently investigated we know that several enzymes are involved in the redox processes. One important group is the FAD-containing enzymes lipoamide dehydrogenase, glutathione reductase and thioredoxin reductase, each enzyme catalysing electron transfer between pyridine nucleotide, FAD and a disulfide moiety. These enzymes are homodimeric enzymes with subunits that have a molecular weight of about 55 kDa and belong to a family of pyridine nucleotide disulfide oxidoreductases sharing both structural and functional similarities (Burleigh & Williams 1972; Jones & Williams 1975; Krohne-Ehrich et al 1977; Ronchi & Williams 1972; Williams 1992).

1.4.1 Lipoamide dehydrogenase

The first known function of lipoamide dehydrogenase was its participation in the three α -ketoacid complexes located in the inner mitochondrial membrane (Hayakawa et al 1969; Hirashima et al 1967). Figure 6 demonstrate the function of this enzyme (E_3) in the pyruvate dehydrogenase complex. By oxidation of the lipoic acid linked to a lysine at E_2 it transfers electrons to NAD^+ , generating NADH (Spencer et al 1984). Lipoic acid in its free form can be reduced to dihydrolipoic acid by lipoamide dehydrogenase with NADH as cofactor (Biewenga et al 1996;

Kamata & Akiyama 1990; Podda et al 1994). Two other enzymes of the same family, thioredoxin reductase and glutathione reductase, can also reduce this compound, but with NADPH as cofactor (Arnér et al 1996; Pick et al 1995). In turn dihydrolipoic acid was demonstrated to be able to reduce ubiquinone (Kozlov et al 1999). Lipoamide dehydrogenase was *in vitro* also shown to effectively reduce ubiquinone (Olsson et al 1999). It is obvious that these enzyme systems are connected and contribute to an elevated level of resistance against oxidative stress in the cell.

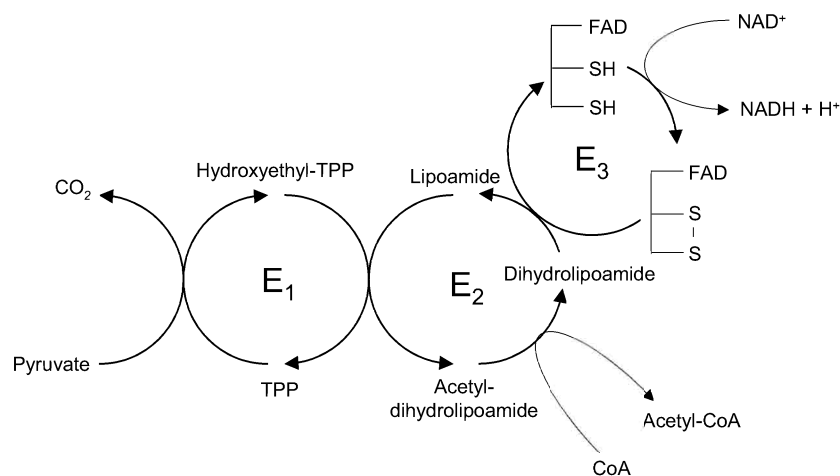


Figure 6. Schematic illustration of the pyruvate dehydrogenase complex. E1 = Pyruvate dehydrogenase; E2 = Dihydrolipoyl transacetylase; E3 = Lipoamide dehydrogenase.

1.4.2 Glutathione reductase

Glutathione reductase is known to effectively reduce oxidised glutathione (GSSG) with NADPH as cofactor and thereby maintain the essential pool of reduced glutathione (GSH) (Meister 1995; Williams 1992). This enzyme is located mainly in the cytosol. Comparisons between enzymes isolated from various species showed high degree of similarities both

structurally and functionally with lipoamide dehydrogenase (Greer & Perham 1986; Krauth-Siegel et al 1982; Stephens et al 1983; Williams et al 1982). The homology of these enzymes was demonstrated to be associated with their redox active disulfide sites (Jones & Williams 1975; Williams 1992).

GSH is a water-soluble compound consisting of the three amino acids, glutamate, cysteine and glycine, that is involved in both non-enzymatic and enzymatic reactions (Meister 1995). The main non-enzymatic functions are to effectively reduce disulfides, serve as a thiol buffer and conjugate hydrophobic compounds to facilitate an efficient excretion (Hathcock 1985; Lu 1999; Sharma et al 2000; Suzuki & Sugiyama 1998). Enzymatically GSH serves as an electron donor in several reactions catalysed by i.e. glutathione transferases (GST) and glutathione peroxidases (GPx) (Brigelius-Flohe 1999; Mannervik 1985; Mannervik & Danielson 1988; Rinaldi et al 2002; Ursini et al 1995).

1.4.3 Thioredoxin reductase

Although, thioredoxin reductase belongs to the same family as lipoamide dehydrogenase and glutathione reductase there are crucial structural differences affecting the functions of this enzyme (Ronchi & Williams 1972; Thelander 1970; Williams 1992). The C-terminal part of mammalian thioredoxin reductase is in comparison with the two other enzymes elongated with about twenty amino acids and containing cysteine and selenocysteine adjacent to each other (Williams 1992; Zhong et al 2000). The incorporation of selenium as selenocysteine in proteins has been suggested to be facilitated by isopentenylation of the tRNA^{ser/sec} via the mevalonate pathway (Ding et al 1998; Warner et al 2000). The

exceptionally broad substrate specificity is connected to this selenenylsulfide as it is located closely to the active disulfide site consisting of the conserved sequence Cys-Val-Asn-Val-Gly-Cys at the N-terminal of the other subunit (Fig. 7) (Williams 1992; Zhong et al 2000).

The thioredoxin system consists of thioredoxin (Trx), thioredoxin reductase (TrxR) and NADPH (Fig. 7). Trx are small ubiquitous dithiol proteins that exist in both mammalian cells and in prokaryotes (Holmgren 1985). Examples of three distinct thioredoxins are the classical Trx (cytosol), Trx2 (mitochondria) and SpTrx (testis) (Masutani et al 1996; Miranda-Vizuete et al 2001; Spyrou et al 1997). The most studied thioredoxin is the 12 kDa cytosolic form (Eklund et al 1991; Holmgren 1985). The functional role of Trx is depending on the essential and well-characterized redox-active disulfide/dithiol moiety, -Cys-Gly-Pro-Cys- (Gleason & Holmgren 1988; Holmgren 1989).

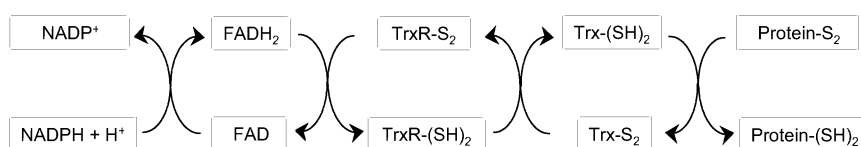


Figure 7. A simplified scheme of the thioredoxin system.

All thioredoxins are reactivated by TrxR with NADPH as cofactor. One specific function for Trx is as an electron donor to ribonucleotide reductases (Miranda-Vizuete et al 1996; Padovani et al 2001; Reichard 1993). However, Trx is also important in a variety of other cellular

activities, such as thiol redox control of enzymes, receptors and transcription factors, redox signalling, and cellular growth including tumor cell proliferation (Holmgren et al 1998). More interestingly, thioredoxins were also shown to be involved in apoptosis, by regulation of the apoptosis signal-regulating kinase-1 (ASK-1), in a redox-controlled manner (Saitoh et al 1998). Additionally, thioredoxins can reduce disulfides in proteins that have been formed by hydrogen peroxide as well as directly scavenge free radicals (Nordberg & Arnér 2001). Other more recently discovered functions of thioredoxins are the reactivation of peroxiredoxins (Prx) (Chae et al 1994). Peroxiredoxins are a relatively recently discovered family of antioxidant proteins. These proteins are peroxidases and by its location in the cytosol, they catalyse the degradation of hydroperoxides to either water or alcohol, depending on the substrate (Chae et al 1994; Chae et al 1999; Rhee et al 1994).

TrxR was originally purified and characterised from *E. coli* (Thelander 1967; Williams et al 1967). Later on this enzyme has also been cloned and sequenced (Russel & Model 1988). The molecular weight of the dimer was shown to be 70 kDa and each of the subunits contain a NADPH and a FAD binding domain in the active site specific for its homologues Trx, but have also reactivity with other prokaryotic Trx, i.e. *Anabena* (Gleason & Holmgren 1988).

Thioredoxin reductases have also been purified from different mammalian species, i.e. calf, rat and man (Holmgren 1977; Oblong et al 1993). The mammalian TrxR has very broad substrate specificity and reduce not only its homologous Trx, but also Trx from other species and several low molecular weight compounds including selenium compounds (Björnstedt et al 1997; Holmgren et al 1998), hydroperoxides (Björnstedt et al 1995)

and NK-lysin (Andersson et al 1996). Furthermore, TrxR1 is also an electron donor to human plasma GPx in the detoxification of hydroperoxides (Björnstedt et al 1994). The most studied TrxR in mammalian is the cytosolic form, but a mitochondrial TrxR have also been found (Miranda-Vizuete et al 1999).

2 PRESENT INVESTIGATION

2.1 Aims

- To develop a new method for rapid semipreparative isolation of polyprenols with very high purity that could be used as substrates and standards in studies of the biosynthesis of specific compounds of the mevalonate pathway, i.e. ubiquinone.
- To study and characterise the reduction of ubiquinone by the flavoenzymes lipoamide dehydrogenase, glutathione reductase and thioredoxin reductase.
- To study the role of selenium in the regeneration of ubiquinol by thioredoxin reductase.

2.2 Results

2.2.1 Development of a rapid HPLC method for separation of polyprenols (Paper I)

In this paper, a semi preparative HPLC method was established in order to rapidly isolate different polyprenols with high purity. The conventional chromatographic methods are time consuming and the purity of the polyprenols isolated is quite poor. By this new HPLC method we could reduce the time for isolation and collect fractions of polyprenols with very high purity (Fig. 8).

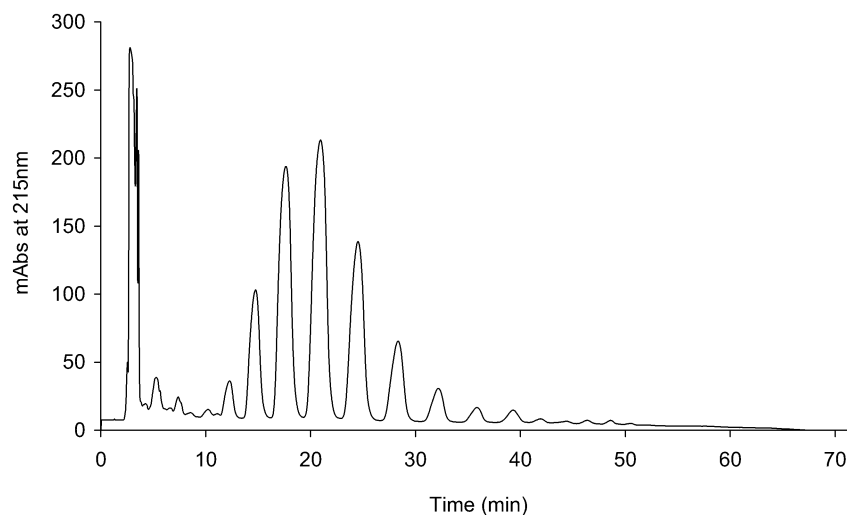


Figure 8. Chromatogram of semipreparative HPLC isolation of polyprenols.

Due to the high hydrophobicity of isoprenoid alcohols with significant chain lengths they are difficult to isolate in sufficient amounts and purity. In conventional chromatography time saving results in overlapping of the different polyprenols with decreased recovery and purity as a consequence. The results obtained by this new semipreparative HPLC method showed that 100 mg of material could easily be isolated within days in contrast to several weeks to months with old techniques.

In this paper we separated products synthesized via *cis*-prenyltransferase but, of course, products synthesized via *trans*-prenyltransferase can also be isolated.

The substances isolated have been used for development of radioactive substrates for the purpose to study different enzyme reactions in the

mevalonate pathway. They were also used as standards for quantitative HPLC-analysis.

2.2.2 The biosynthesis of ubiquinone in peroxisomes (paper II)

Since several enzymes from the mevalonate pathway, involved in both the initial and the terminal phases have been detected in peroxisomes (Grünler et al 1994; Thompson & Krisans 1990) the question was to presume whether peroxisomes also might contribute to the biosynthesis of the terminal part of ubiquinone (Fig 9).

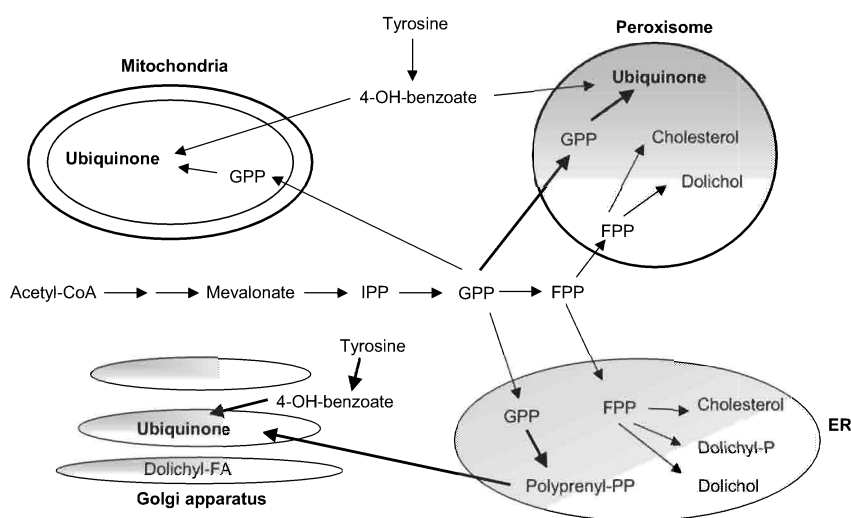


Figure 9. A schematic illustration of the locations of the mevalonate pathway reactions in the cell. The biosynthesis of ubiquinone in peroxisomes is bolded.

Many investigators have during decades shown that the biosynthesis of ubiquinone is mainly located in the endoplasmic reticulum/Golgi system.

In this investigation we analysed two enzymes, one that is involved in the synthesis of the isoprenoid side chain, *trans*-prenyltransferase, and the other enzyme that mediates the transfer of the isoprenoid side chain to the precursor ring, nonaprenyl-4-hydroxybenzoate (NPHB)-transferase.

These studies were performed in both peroxisomal and microsomal fractions isolated from normal rat liver.

The *trans*-prenyltransferases in both of these organelles required *trans*-geranyl-PP as substrate and not *trans*-farnesyl-PP. However, the microsomal *trans*-prenyltransferase activity was highly activated in the presence of Mg^{2+} , whereas the peroxisomal *trans*-prenyltransferase activity reached the highest activity with Mn^{2+} . Moreover, in the presence of detergents, like digitonin, the microsomal *trans*-prenyltransferase activity was activated, while the peroxisomal enzyme was inactivated. These observations together with observations made after mechanical treatment such as sonication or freezing/thawing indicated that the location and the regulation of these isoenzymes differ. On a protein basis, the specific activity of the total *trans*-prenyltransferase, 30 % was found in the peroxisomal and 70% in the microsomal fraction. The effect of treatment with the HMG-CoA reductase inhibitor, mevinnolin was also investigated and the enzyme activity in both of these locations was enhanced by this compound. Treatment with clofibrate, a peroxisomal inducer, enhanced the microsomal activity, whereas the peroxisomal activity was decreased.

NPHB-transferase activity was also found in the peroxisomes, with an equal catalytic rate as in the microsomal fraction. Different regulatory patterns of the two enzymes were shown after treatment of the rats with

chemical compounds such as clofibrate and DEHP. By these treatments only the peroxisomal activity was affected, by decrease of the activity.

Altogether, the results presented suggest that at least two enzymes involved in the terminal part of the biosynthesis of ubiquinone are located in the peroxisomes.

2.2.3 Regeneration of ubiquinol by flavoenzymes (Paper III, IV and V)

The antioxidant function of ubiquinol is predominately to protect against lipid and protein peroxidation. Ubiquinone is synthesised in all cells and is integrated in all membranes. Its reduced form, ubiquinol, can inhibit the initiation of the peroxidation reaction by reducing the perferryl radical. It can also terminate the propagation phase by regeneration of vitamin E or, maybe act by itself to scavenge the lipidperoxyl radical formed in the process. Although the antioxidant function requires that ubiquinol is continuously regenerated the non-mitochondrial enzymatic systems involved are only characterised to a limited extent. The aim of these investigations was to characterise the reduction of ubiquinol by the three flavoenzymes, lipoamide dehydrogenase, glutathione reductase and thioredoxin reductase.

The reduction of ubiquinone by all three enzymes characterised was shown to have similar rates of reduction of ubiquinone with both NADH and NADPH as cofactors. However, the addition of zinc in the reaction mixture containing NADPH as cofactor, enhanced both LipDH and GR activity. Among other divalent ions tested only cadmium had the same effect on the reduction rate of ubiquinone by LipDH and GR. In contrast,

the reduction of ubiquinone by thioredoxin reductase was inhibited by zinc.

The pH optimum of the rate of reduction of ubiquinone was for lipoamide dehydrogenase and glutathione reductase acidic, pH 6 and 4.5, respectively. Under these acidic conditions the activities were almost the same for both enzymes as in the presence of zinc. This remarkable behaviour may be physiologically relevant during ROS generating conditions like ischemia/reperfusion. On the other hand, the pH optimum for thioredoxin reductase was found to be at physiological pH. All together, these observations indicate that ubiquinol-regeneration can operate during various intracellular conditions, maybe at different intracellular locations. Furthermore, the highest rate of reduction under physiological conditions was achieved by TrxR1.

By changing the ratio between NAD(P)H/NAD(P)^+ , regulatory mechanisms were studied using lipoamide dehydrogenase as enzyme. An inhibitory effect on the reduction of ubiquinone by this enzyme was only achieved when the NADPH/NADP^+ ratio was low. When GR was used in the reaction mixture it was shown that the reduction of ubiquinone was competitively inhibited by the traditionally known substrate, oxidised glutathione, but only at very high concentrations. The reduction of ubiquinone was also studied using FAD alone. It was found that a very low activity could be achieved. Thus, these results indicate that FAD plays an important role as a part of the enzymes studied.

2.2.4 The role of selenium in the reduction of ubiquinone by thioredoxin reductase (paper IV)

We also demonstrated the importance of selenium for the reduction of ubiquinone by TrxR1. In the study HEK293 cell lines overexpressing TrxR1, normal bovine and rat TrxR1, non-selenium containing *E. coli* enzyme, mutant human TrxR (selenocysteine replaced by alanine) and recombinant truncated rat TrxR lacking the two amino acids Sec and Gly at the C-terminal part were used. The results showed that there was almost no reduction of ubiquinone when the enzymes lacking selenocysteine was used in the reaction mixture. By incubation of the overexpressing HEK293 cell lines with selenite we also showed that the increase in TrxR1 activity in homogenates was accompanied by an increase in reduction of ubiquinone. In conclusion, those results strongly suggest selenium to be essential for reduction of ubiquinone by TrxR1.

3 GENERAL DISCUSSION AND FUTURE PERSPECTIVES

In this work the biosynthesis and reduction of ubiquinone with focus on the extra mitochondrial fraction of the compound was studied. It is obvious that the mevalonate pathway is complex in several aspects. First of all it is divided into several pathways that ends up in different products. The regulation of the different pathways is not fully discovered, but the fact that parts of the synthetic pathways are located in different subcellular compartments indicate a necessity of compartmentalization to guaranty the supply of ubiquinone in the different locations where it is needed. In this thesis we have shown that ubiquinone biosynthesis also occur in the peroxisomes suggesting a specific protecting role of this compound at this location. As many other enzymes of the mevalonate pathway have been discovered in this organelle it is reasonable to ask the question if not all of the enzymes of this pathway are located here.

Although the amounts of ubiquinol in the membranes are considerable it will not be enough for effective antioxidant function unless it can't be regenerated. The turnover of ubiquinol is much faster than can be explained by replacement via *de novo* synthesis. It has been shown that oxidative stress increases the amount of the oxidised ubiquinone in the cell and, thereby, also possibly enhances the degradation of this compound. To compensate for this depletion increased synthesis of ubiquinone, regeneration of ubiquinol and uptake from the blood or all three functions may occur.

In this thesis we investigated, as mentioned, other locations of ubiquinone biosynthesis but more intensively the characteristics of the reactions of

regeneration of ubiquinol by the flavoenzymes, lipoamide dehydrogenase, glutathione reductase and thioredoxin reductase.

The results obtained when the characteristics of the reduction of ubiquinone by glutathione reductase were investigated may suggest other functions of this enzyme. This proposal is based on that the highest rate of reduction of ubiquinone was shown at acidic pH and that zinc at physiological pH increased the reduction rate almost 3-fold.

In the studies with thioredoxin reductase we also used transfected stable cell lines overexpressing this enzyme. By this system together with enzymes lacking selenocysteine, we showed that the reduction of ubiquinone by this enzyme was selenium dependent. These results support the findings that deficiency of selenium decrease the concentrations of ubiquinone and vitamin E. The conclusion may be that if thioredoxin reductase is not sufficiently saturated with selenocysteine the reduction of ubiquinone is harmed and, thereby, the regeneration of vitamin E.

In the future it would be of great interest to also study cell lines overexpressing lipoamide dehydrogenase or glutathione reductase. As those latter enzymes are not selenium dependent these studies may add more physiological and molecular aspects onto the regulatory mechanisms of the reduction of ubiquinone. Other *in vitro* cell studies that could be interesting are the effect of oxidative stress on the biosynthesis and reduction of ubiquinone.

Supplementation of ubiquinone to different populations and species is today widely studied. In the future one target is to find a model to study

the effects of supplementation on both biosynthesis of ubiquinone and regeneration of ubiquinol.

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