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Selenoproteins and tRNA-Sec: regulators of cancer redox homeostasis

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Abstract

In the past two decades, significant progress has been made in uncovering the biological function of selenium. Selenium, an essential trace element is required for the biogenesis of selenocysteine, which is then incorporated into selenoproteins. These selenoproteins have emerged as central regulators of cellular antioxidant capacity and maintenance of redox homeostasis. This review provides a comprehensive examination of the multifaceted functions of selenoproteins, with a particular emphasis on their contributions to cellular antioxidant capacity. Additionally, we highlight the promising potential of targeting selenoproteins and the biogenesis of selenocysteine as avenues for therapeutic intervention in cancer. By understanding the intricate relationship between selenium, selenoproteins, and ROS, insights can be gained to develop therapies that exploit the inherent vulnerabilities of cancer cells.

Keywords

Selenium; selenoprotein; redox; oxidative stress; ROS; ferroptosis

Reactive Oxygen Species Emerge as Novel Therapeutic Targets in Cancer

Oncogenic transformation is accompanied by a host of changes to cellular genetics, epigenetics, metabolism, and to the cellular environment. An increase in reactive oxygen

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Declaration of interests

None are declared by the authors.

species (ROS) and dysregulation of redox homeostasis and signaling are hallmarks of cancer [1,2]. Mitochondria are major consumers of cellular oxygen, reducing divalent oxygen to produce carbon dioxide and water. However, reduced forms of oxygen including superoxide (O_2^-) and hydrogen peroxide (H_2O_2) can be generated as reactive byproducts of mitochondrial respiration, later producing highly reactive hydroxyl radicals ($HO\bullet$) via the iron (Fe) dependent Fenton reaction. Thus the mitochondrial dysfunction often observed in cancer cells generates an environment primed for formation of high levels of ROS.

Observations of elevated levels of ROS in cancer cells initially led to hypotheses that treatments to reduce ROS in cancer could provide therapeutic benefit [3,4]. While elevated levels of ROS can increase protein, lipid, and DNA oxidation [5], ROS can also activate a variety of signaling pathways such as the DNA damage response (DDR), iron homeostasis, and the anti-oxidant and anti-inflammatory responses [6], supporting key aspects of oncogenesis such as cell proliferation, survival, and metastasis [7,8]. Thus, initial clinical trials were conceived to neutralize ROS in cancer utilizing antioxidant therapy [9] and uses of adjuvant antioxidant supplements persists into treatment strategies today with many reported studies of diets high in vitamins and antioxidants reducing chemotherapy toxicity and correlating with increases in survival [10]. However, antioxidant therapy rapidly emerged as a double-edged sword. Several cancers with extremely high native levels of ROS, such as melanoma, are able to become more aggressive and invasive following adjuvant antioxidant therapy [11]. In these cancers ROS are both necessary for growth through addiction to the ROS mediated signaling cascade, and limiting for growth due to the effects of oxidative stress [12].

Over the past several years the field has shifted from attempting to reduce ROS levels to instead using them as a targetable vulnerability [13,14]. Cancer cells require a robust antioxidant defense system to protect them from the high levels of ROS generated by altered metabolism and extrinsic stresses. Selenoproteins, enzymes that selectively include the amino acid selenocysteine, make up major classes of antioxidant proteins critical for the protection of cancer cells to elevated ROS.

There are 25 selenoproteins encoded within the human genome, with the majority of selenoproteins involved in cellular antioxidant capacity [15]. Nearly all glutathione peroxidase (GPx) and thioredoxin reductase (TrxR) enzymes fall into this category as a catalytic selenocysteine is essential for their activities. Studies replacing the catalytic selenocysteine of GPx4 for the sulfur containing cysteine result in highly reduced protein activity and increased susceptibility toward peroxide-induced cell death [16]. Therefore, selenoproteins and their biogenesis may serve as novel targets to induce synthetic vulnerabilities in ROS dependent cancers. In this review we will discuss the role of selenium in human biology and cancer.

Selenium - The Essential Poison and The Selenium-Cancer Hypothesis

Selenium, a trace metal, was discovered in 1817 [17]. Its essential role as a micronutrient for *Escherichia coli* enzyme activity was confirmed in 1954 [18], followed by the discovery of its importance for animals in 1957 [19,20]. Deficiency in selenium can lead to Keshan

Disease (a cardiomyopathy) and Kashin-Beck Disease (a severe rheumatoid arthritis-like osteoarticular disorder) [21–24] (Box 1). However, intake of more than 400 µg/day of selenium can cause acute toxicity [25]. Currently, the US Department of Agriculture recommends a daily intake of 55 µg of selenium to prevent disease caused by selenium deficiency. In Finland, where selenium soil levels are naturally low, there is government mandated selenium supplementation in fertilizers to prevent dietary deficiency in the general population [26,27]. Interestingly, selenium supplementation has been recently implicated in viral defense, as Finland observed significantly lower death rates from the SARS-CoV-2 pandemic compared to neighboring countries with similar infection rates and similarly low native soil selenium levels [28].

Early research in the 1940s reported that high dietary selenium intake led to the development of liver tumors in rats [29], causing global concerns about selenium consumption. However, subsequent studies demonstrated protective effects against tumors in various cancer models, leading to further investigations [30]. The Nutritional Prevention of Cancer Trial (NPCT) in 1996 ultimately defined low plasma selenium levels (<121 µg/l)[31] as an increased risk factor for the development of prostate cancer (Box 1).

These findings prompted the National Institutes of Health (NIH) to conduct the Selenium and Vitamin E Cancer Prevention Trial (SELECT) [34]. This trial investigated selenium (in the form of L-selenomethionine, as this was determined to be the major selenium species in the NPCT) and vitamin E supplementation (as a general antioxidant) as a preventive measure for prostate cancer in a large-scale, placebo-controlled study. Despite being one of the largest human cancer prevention trials ever performed, the group receiving both vitamin E and selenium demonstrated a significantly increased risk of prostate cancer [35,36] (Box 1).

Selenium, as an essential poison, has a narrow window of benefit for human health (Figure 1). When measuring selenium blood plasma levels, too little selenium (<70µg/l) is associated with deficiency diseases, low plasma selenium (<120µg/l) is linked to an increased risk of cancer, selenium and vitamin E supplementation with levels >140µg/l can significantly increase cancer risk, elevated plasma selenium levels (>400µg/l) are associated with increased risks of selenosis, and highly elevated plasma levels (>1000µg/l) are seen in cases of acute toxicity [38]. Optimal baseline selenium levels have been established at 110–135µg/l correlating with a plateau in production of plasma selenoproteins at 130µg/l [39]. Interestingly, other further large scale studies have observed decreases in cancer mortality risk with increases in plasma selenium up to a level of 130µg/l, with increases in mortality risk observed at levels >150µg/l [40]. Overall, these studies suggest that the association between cancer risk and selenium follows the trends observed with ROS in cancer. In the early stages of tumorigenesis, elevated levels of ROS may increase the risk of cancer progression due to their ability to cause DNA damage and promote genomic instability. Thus antioxidant and/or selenium supplementation may provide significant benefits in the prevention of cancer. However, in established tumors, ROS are often elevated and the tumor must limit ROS to survive. Consequently, supplementation of an established tumor with antioxidants may lead to worsened outcomes. Given that many selenoproteins with antioxidant roles exhibit increased translation following selenium supplementation [41–44]

it is a distinct possibility that observed effects of selenium supplementation are due to increased production of selenoproteins.

Cysteine versus Selenocysteine

A fundamental question that arises concerning selenoproteins is “why?”. Cysteine is an abundant and readily incorporated amino acid, yet this small class of enzymes specifically requires incorporation of a highly toxic trace mineral. From a chemical perspective, selenocysteine offers several unique advantages over cysteine. Selenium, positioned as the 34th element on the periodic table, resides one row below sulfur, the 16th element. Although sulfur and selenium share the same valence shell electron configuration, selenium’s larger atomic radius grants it superior nucleophilic properties compared to sulfur, resulting in heightened reactivity. This distinction becomes apparent when examining the pKa values of the amino acids: selenocysteine possesses a pKa of 5.24, whereas cysteine exhibits a pKa of 8.25. In a cellular environment with a pH of approximately 7.4, selenocysteine predominantly exists in a deprotonated state, while cysteine is primarily protonated [45,46]. Consequently, these different protonation states lead to significantly disparate rates of reactivity.

Furthermore, the divergent reactivity between selenocysteine and cysteine contributes to considerably reduced rates of terminal oxidation for selenocysteine enzymes [45]. In the ACS article “Why Nature Chose Selenium”, Reich and Hondal state that “almost all chemical reactions involving selenium are faster in comparison to the same reaction with sulfur” [45]. While it is tempting to conclude that nature selected selenium to replace sulfur due to its heightened chemical reactivity, thereby expediting enzymatic reactions, their viewpoint diverges from this notion, suggesting that nature specifically chose selenium for its unique capacity to engage with oxygen and ROS in a *readily reversible* manner. In a biological system, terminal oxidation of an enzymatic active site would require a complete resynthesis of the affected enzyme, leading us into discussion of nature’s redox machinery: selenoproteins.

Mammalian Selenoproteins

Glutathione Peroxidases (GPx1–4,6)—The functions of GPx in cancer have been extensively reviewed [47,48]. GPx enzymes play a crucial role in detoxifying RO by utilizing glutathione (GSH) as a reducing agent (Figure 2). GPx1–4 and 6 are selenoproteins while GPx5, 7 and 8 are cysteine variants. All GPx enzymes operate through a conserved catalytic mechanism, relying on a tetrad of conserved amino acids: Sec/Cys, Gln, Trp, and Asn [49]. While structurally and functionally similar, GPx enzymes diversify their functions through differences in active site structure, substrate accommodation, tissue expression and subcellular localization [50]. GPx1 was the first characterized selenoprotein and is expressed ubiquitously across most cell types with cytoplasmic localization, making it one of the most active and critical cellular antioxidant defense enzymes [51]. GPx2 is found in the intestinal epithelium and is often referred to as the intestinal GPx. In colorectal adenocarcinoma loss of GPx2 has been linked to the development of microsatellite instability and immune infiltration [52]. GPx3 is secreted in plasma and has been implicated as a tumor suppressor

gene in breast and lung cancers [53,54]. While the exact function of GPx3 is under debate as glutathione is rapidly catabolized in the plasma, it has been hypothesized that GPx3 may be active at hubs of ROS generation and may localize to basement membranes, providing antioxidant capability to the cellular microenvironment [55]. GPx4, originally called Phospholipid Hydroperoxide Glutathione Peroxidase (PHGPX) is essential for lipid peroxide detoxification and has emerged as a central regulator of ferroptosis [56], a non-apoptotic form of regulated cell death that has been extensively reviewed elsewhere. While the primary function of GPx4 is cytoplasmic lipid peroxide detoxification, GPx4 also has a nuclear isoform that can act as protein thiol peroxidase [57] and a mitochondrial isoform that protects against mitochondrial dependent ferroptosis [58]. Recently a R152H missense mutation in GPx4 was found in a patient with sedaghaton-type spondylometaphyseal dysplasia (SSM) [59]. This mutation provided additional structural basis for GPx4 activity and further demonstrated the central role of GPx4 in human health. Little is known about GPx6 besides that it is expressed during embryonic development and in the olfactory epithelium [60].

Thioredoxin Reductases (TXNRD1–3)—Thioredoxins are small ~12kDa redox regulatory enzymes with two active site internal cysteine residues, capable of forming cis and trans disulfide bridges to assist in protein folding as well as a multitude of cellular processes. Thioredoxins are a key component of cellular redox homeostasis and are essential for the maintenance of a reductive environment through reduction of oxidized cysteine residues. While we will not discuss the function of the thioredoxin system in depth here, we recommend these excellent reviews to the reader [61–63]. Instead, we will focus on the FAD and NADP(H) dependent thioredoxin recycling systems, Thioredoxin Reductases (TrxRs) (Figure 3). There are three TrxRs in the human genome (TXNRD1–3), all of which are selenoproteins. Similarly to GPxs, TrxRs also display specific function due to subcellular localization. TrxR1 is cytosolic, TrxR2 is mitochondrial localized, and TrxR3 is testes-specific [60].

MSRB1, SELENOH, SELENOO—Other key redox involved selenoproteins are the methionine sulfoxide reductase MSRB1 and the enzymes SELENOH and SELENOO. MSRB1 mediates reduction of oxidized methionine to protect the proteome from effects of ROS. MSRB1 activity has been implicated in overall redox homeostasis [64] as well as pro-inflammatory cytokine production in macrophages, implicating this enzyme in the inflammatory response [65]. SELENOH is a nuclear oxidoreductase with DNA binding activity capable of regulating p53 in response to oxidative stress [66]. SELENOO is the largest human selenoprotein and is selectively localized to the mitochondria. While the exact function of SELENOO is still unknown it has been implicated in redox homeostasis and is suspected to have an active kinase domain [67].

Other Mammalian Selenoproteins—While in this review we focus primarily on the 11 redox active selenoproteins, we will also briefly touch upon the other 14 selenoproteins encoded within the human genome. Selenoproteins F, K, M, N, S, and T have been implicated in ER homeostasis and utilize their oxidative capabilities in protein folding [68,69]. The enzymes DIO1–3 are essential for thyroid hormone metabolism and are

likely responsible for some of the pathological presentation of selenium deficiency[70]. Selenoprotein P is a selenium chaperone as it contains 11 selenocysteine residues, is synthesized in the liver, and secreted to selectively carry selenium throughout the body[71,72]. SEPHS2 is a selenium donor utilized for the biosynthesis of selenoproteins and has been implicated in the cellular detoxification of selenide, a byproduct of selenocysteine biosynthesis [73,74]. Still the function of several selenoproteins, namely V and W, remain unknown. Broad classification, substrate specificity, and kinetic details of many selenoproteins remain difficult to study due to extreme difficulty in the production of these enzymes in recombinant or overexpression systems[75].

Inhibition of Selenoproteins for Cancer Therapy

To further explore the potential of selenoproteins as novel targets for cancer treatment, publicly available survival data was analyzed. Survival graphs and hazard ratios for all 25 selenoproteins across 27 different types of cancer were assessed. Using a strict significance cutoff of $p < 0.05$, the hazard ratios were generated as a heatmap and plotted using unguided hierarchical clustering (Figure 5, Key figure). While many significant survival correlations are found, minimal significant clustering of selenoprotein hazard ratios across different cancers was observed. This finding supports previous research suggesting that the selenoproteome is highly complex, and its involvement in cancer is highly context dependent. For example, cervical squamous cell carcinoma has multiple selenoprotein hazard ratios < 1 , indicating that higher expression correlates with increased survival. These data would suggest that cervical squamous cell carcinoma patients may benefit from selenium supplementation, in support of already underway clinical trials testing this hypothesis and already demonstrating reduced chemotherapy toxicity [76]. Furthermore, liver hepatocellular carcinoma has multiple selenoprotein hazard ratios > 1 , indicating negative correlations between selenoprotein expression and survival. Liver hepatocellular carcinoma is a known ROS-driven cancer with recent data pointing to a complex regulatory role of TrxR1 in development [77]. These observations may help explain the conflicting results found in the existing literature on selenoproteins, as significant and contrasting survival correlations of the same gene across various cancer types are observed in this dataset.

In 2014, the compound (1S, 3R)-RSL3 was characterized as a GPx4 inactivator capable of driving ferroptosis [56,78]. While the poor pharmacokinetics of RSL3 have prevented its transition to clinical settings, a new RSL3 derivative with greatly improved bioavailability and plasma half-life has recently been developed [79]. However, in addition to GPx4 there is evidence that RSL3 can bind to other targets including TrxR1 and its effects may not be strictly GPx related [80]. As RSL3 utilizes a chloroacetamide functional group to covalently bind to an active site selenocysteine, it is possible there are still undiscovered RSL3 targets to be found. Furthermore, it was demonstrated that the mechanism of action of ferroptosis inducing compounds RSL3, ML162, and FIN56 is chemical induction of GPx4 proteasomal degradation [81]. While the exact biochemical mechanisms of small molecule induced GPx4 degradation is unclear, recent advances in the understanding of targeted protein degradation may eventually lead to the development of the next generation of ferroptosis inducing compounds in a specific targeted degrader of GPx4.

TrxRs have been implicated in redox homeostasis across many cell types due to their inherent role in thioredoxin function and have emerged as promising cancer targets [62,63,82–84] with several developed inhibitors [85–88]. The most prominent TrxR inhibitor is the FDA approved gold containing compound Auranofin (Ridaura). While Ridaura is FDA certified for rheumatoid arthritis it has demonstrated potent anti-cancer activity and trials are underway to assess its effectiveness[89].

Additional mechanisms to target ferroptosis in cancer have discovered that the lipoprotein receptor LPR8 is an essential ferroptosis resistance gene [90,91]. Interestingly, LPR8 is a key member of the complex responsible for endocytosis of Selenoprotein P [92,93]. Once Selenoprotein P undergoes endocytosis it is rapidly degraded and selenocysteine lyase (SCLY) breaks down free selenocysteine to alanine[94], releasing selenium for use in synthesis of new selenoproteins, a topic that will be covered in more detail in the next section of this review.

Selenoprotein Biogenesis

While inhibitors are being developed to target specific selenoproteins, it is important not to overlook the biosynthetic cascade required for selenoprotein biogenesis, which could represent a novel and exciting area of research with the potential to broadly regulate the selenoproteome. Mammalian incorporation of selenocysteine is characterized by several unique features. First, selenocysteine does not have its own codon; instead, it reprograms a UGA-STOP codon through a complex translational process [95,96]. In all mammalian mRNA encoding selenoproteins, there is a conserved hairpin structure in the 3' UTR known as the selenocysteine incorporation sequence (SECIS). This structure is recognized and bound by a multiprotein complex consisting of SECIS binding protein 2 (SECISBP2), Eukaryotic Elongation Factor Selenocysteine (EEFSEC), and tRNA selenocysteine 1 associated protein 1 (TRNAU1AP) [97–99]. The complex facilitates the positioning of tRNA^{Sec} into the elongating ribosome [100]. Ribosomal protein L30 (RPL30), eukaryotic translation initiation factor 4A3 (eIF4A3), and nucleolin (NCL) also play roles in regulating selenocysteine insertion. Mutations in SECISBP2 have been associated with thyroid disorder and multisystem selenoprotein deficiency disorder[101–103].

Second, tRNA^{Sec} stands out from other tRNA species as it lacks its own aminoacyl-tRNA synthetase (aaRS) [104]. Instead, tRNA^{Sec} is initially aminoacylated as serine by the enzyme Seryl-tRNA synthetase 1 (SerRS) [105]. The resulting seryl-tRNA^{Sec} is then phosphorylated by Phosphoseryl tRNA Kinase (PSTK) to create a phosphate leaving group for subsequent reactions [106]. The enzyme SEPSECS, in complex with the selenium donor SEPHS2, catalyzes the substitution of the oxygen moiety for selenium via a PLP intermediate [107]. However, even after synthesis, tRNA^{Sec} must undergo additional post-transcriptional modifications before it can be used for translation.

While human tRNAs carry on average 13 post-transcriptional modifications per molecule [108], tRNA^{Sec} is unique in its hypomodification status as it contains only four: mcm5U(m)34, i6A37, PseudoU55, and m1A58 [104]. PseudoUridine 55 and m1A58, which are critical for proper tRNA folding, are placed by PUS4 and TRM6/61, respectively.

The remaining modifications occur in the anticodon region and are essential for proper codon recognition [109]. Isopentylation of A37 (i6A) by TRIT1 is commonly observed in conjunction with modification at position 34 and has moderate effects on selenoprotein translation [110], while modification of U34 is vital for selenoprotein translation [111,112]. The post-transcriptional modification of U34 involves a multifaceted enzymatic process. The Elongator Complex, through the radical SAM and acetyl-CoA dependent enzyme Elp3, introduces the chemical modification 5-carboxymethyl-Uridine (cm5U) [113]. Subsequently, cm5U is methylated by the tRNA methyltransferase AlkBH8, resulting in 5-methoxycarbonylmethyl-Uridine (mcm5U) [114]. Further modification at U34 can occur via 2'-O-methylation by the enzyme FTSJ1, although the function and regulation of this modification in mammalian systems are still unknown [115] (Figure 4).

The biosynthesis of tRNA^{Sec} represents a complex and coordinated system for incorporating selenocysteine into a limited number of enzymes. This system presents a unique opportunity: by disrupting the mechanisms of tRNA^{Sec} biogenesis, post-transcriptional modification, or translational incorporation, it may be possible to dysregulate selenoproteins on a global scale as seen in genetic mutations of tRNA^{Sec} [116]. While caution must be exercised when modulating the selenoproteome, our data and historical perspectives strongly suggest that this enzymatic cascade offers multiple novel therapeutic targets capable of modulating cellular redox homeostasis.

Concluding Remarks

Understanding the role of ROS and redox signaling in cancer has evolved significantly. Initially, the focus was on reducing ROS levels in cancer cells through antioxidant therapy. However, it became evident that ROS also play important roles in cancer progression and survival, activating signaling pathways essential for oncogenesis. This realization led to a shift in perspective, with ROS being recognized as targetable vulnerabilities in cancer cells. Selenoproteins, which incorporate the amino acid selenocysteine, have emerged as crucial players in cellular antioxidant defense mechanisms. GPx and TrxR are two major classes of selenoproteins involved in ROS detoxification. GPx enzymes protect cells from oxidative damage by utilizing glutathione as a reducing agent, while TrxRs maintain redox homeostasis by recycling oxidized thioredoxin. Recent advances have shed light on the role of selenoproteins in cancer biology. GPx4 has emerged as a central regulator of ferroptosis, a form of regulated cell death that shows promise as a therapeutic target in various cancers. Inhibitors targeting GPx4 and TrxRs have demonstrated anticancer activity in preclinical studies, with some compounds showing potential for clinical development. While links between inhibition of selenoprotein function and inducing cancer cell death have been uncovered, there are still gaps in our knowledge of how to design therapies that target selenoprotein function or selenocysteine biogenesis (see Outstanding questions). Moreover, the field of selenium and selenoprotein research in cancer is complex and evolving. The dual nature of selenium's effects, as both a beneficial micronutrient and a potential toxin, highlights the importance of understanding its role within a narrow range. The specific functions of selenoproteins in cancer cells and their potential as therapeutic targets provide exciting avenues for future research and the development of novel anticancer strategies. Further investigations into the redox biology of selenium and selenoproteins

will undoubtedly contribute to our understanding of cancer biology and may lead to the development of innovative approaches to cancer treatment.

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Box 1.**Historical perspectives on the role of selenium in cancer prevention**

Shamberger and Frost's influential letter to the Canadian Medical Association Journal in 1969 established an inverse correlation between selenium concentration in forage crops and cancer death rates in the U.S., which aligned with a study in 1977 showing a similar inverse correlation of selenium soil concentration and cancer risk when measuring selenium blood levels across several U.S. cities and 27 countries [32]. The NPCT was published in 1996 by Clark and Combs as a large-scale, double-blind, randomized, placebo-controlled cancer prevention trial that was initially designed to measure recurrence of nonmelanoma skin cancer over a 10-year period through dietary intake of 200 µg/day of selenium in the form of selenized yeast tablets. However the trial ultimately demonstrated significant reductions (HR = 0.61) in colon, prostate, and lung cancer incidence through this dietary intervention [33]. Following the success of the blinded portion of the study, the trial was then unblinded and participants were followed for several more years. Subsequent analysis of the unblinded portion of the study refined the benefits of selenium supplementation to males with baseline levels of plasma selenium <121 µg/L, with the largest cancer prevention effects of selenium supplementation seen in prostate cancer [31].

Since the early 2000s, numerous studies have attempted to replicate the NPCT findings, yielding varying results. However, it is possible that these results stem from missteps in patient selection, specifically baseline plasma selenium levels [37]. The NPCT specifically recruited patients from regions with low selenium, resulting in a study cohort with a mean plasma selenium level of 114µg/l. In contrast, several follow-up studies, including SELECT, selected patients with median plasma selenium levels as high as 143µg/l, exceeding the beneficial range of selenium supplementation as defined by the NPCT (<121µg/l). While the negative results of SELECT and other selenium supplementation trials have temporarily halted most selenium-focused studies, these results underscore the dual nature of the benefits and risks associated with selenium supplementation.

Outstanding Questions

- Do the benefits of selenium supplementation result from increases in plasma levels of selenoprotein P?
- Given the narrow window between benefit and toxicity, can we create a comprehensive guideline for ideal plasma selenium levels?
- Why do different tumor cell types and normal cells display unique dependencies on selenoproteins and selenocysteine biogenesis enzymes?
- What are the redundant and distinct functions for redox active selenoproteins in cancer progression?
- Will specific selenoprotein inhibitors become clinically viable?
- Will targeting the selenocysteine biogenesis pathway to alter the selenoproteome show promise as a viable therapeutic strategy?

Highlights

- Reactive oxygen species (ROS) are tightly regulated to promote tumor growth.
- Disruption of key ROS detoxification enzymes or pathways induce ferroptosis, a non-apoptotic cell death pathway.
- Many key ROS detoxification enzymes are selenoproteins.
- The incorporation of selenocysteine into proteins involves a complex multistep mechanism.
- The selenocysteine biogenesis pathway is emerging as a novel target for cancer treatment as its disruption is capable of inducing ferroptosis

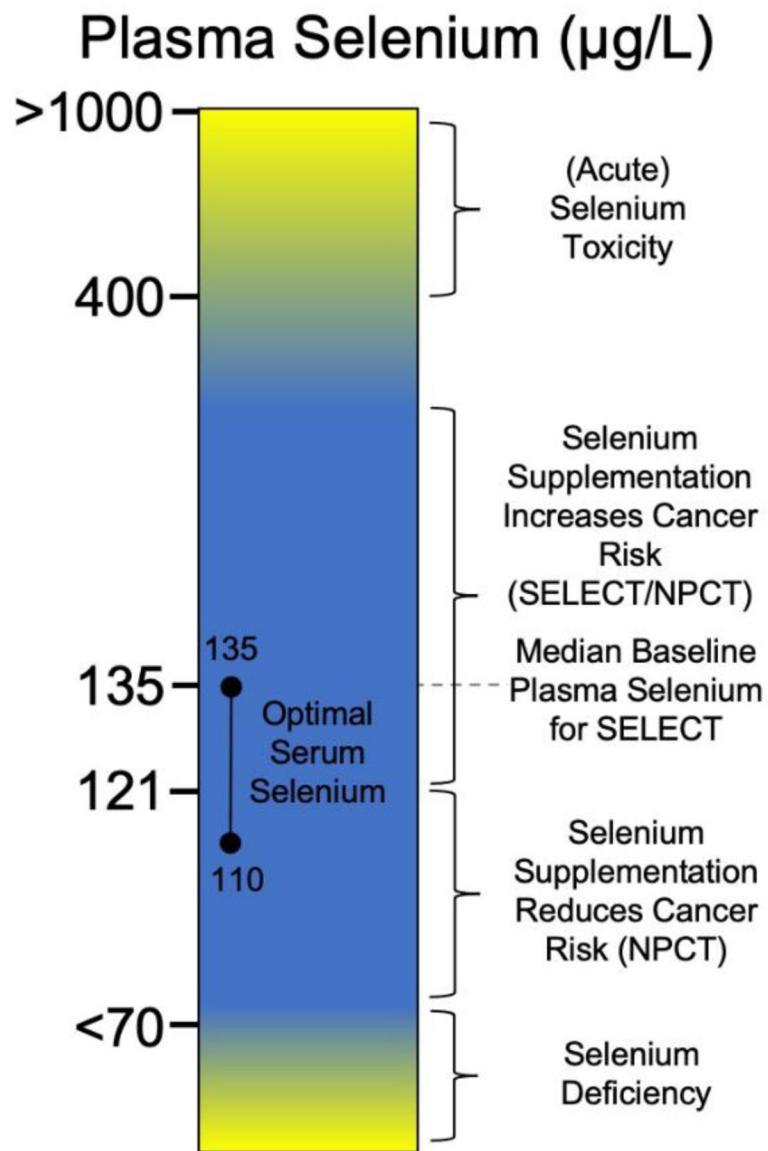


Figure 1. Relevance of human plasma selenium levels to human health.

A particular focus on key findings from selenium supplementation trials for cancer prevention. See [23,25,31,33,35,36,38,39].

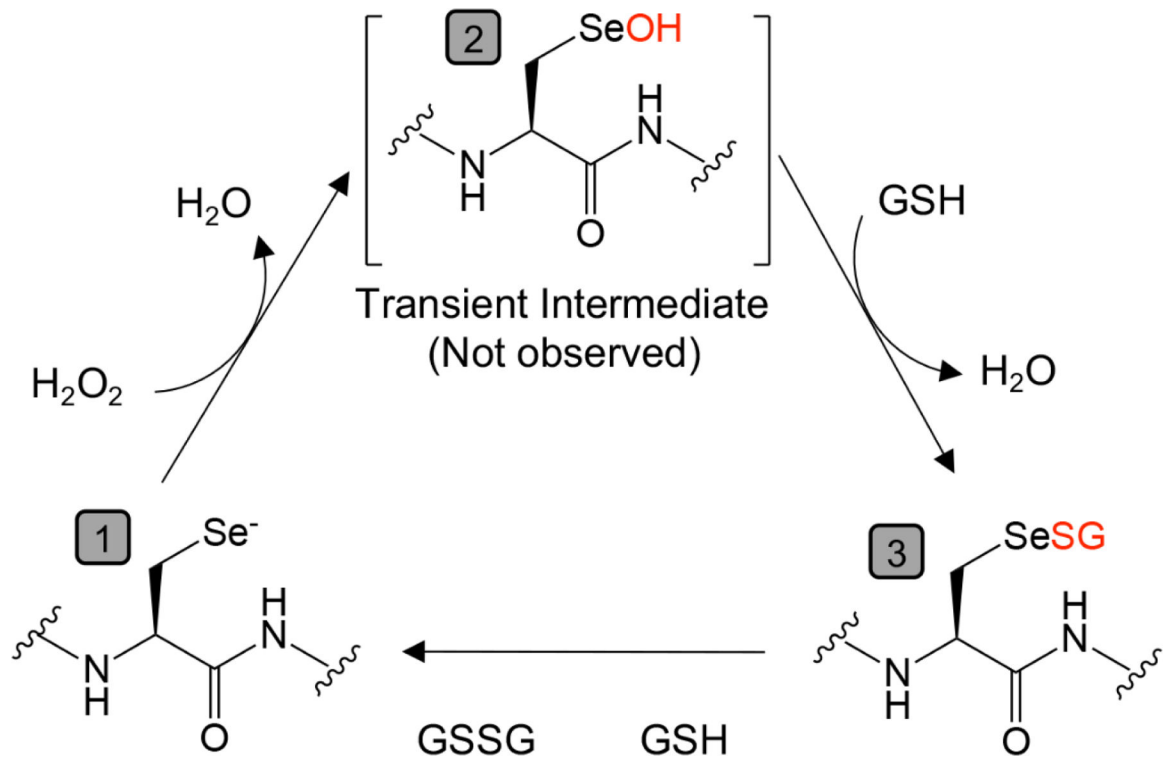


Figure 2. Conserved catalytic cycle of glutathione peroxidases.

Starting from (1), the catalytic selenocysteine exists in a base state as a selenol (Se^-) which quickly reacts with hydrogen peroxide to generate (2) selenenic acid (SeOH), a temporary intermediate that is rapidly replaced by reduced glutathione (GSH) to form (3) a selenenyl sulfide adduct (SeSG). The enzyme is subsequently regenerated to (1) through its reaction with a second GSH , resulting in the production of oxidized glutathione (GSSG).

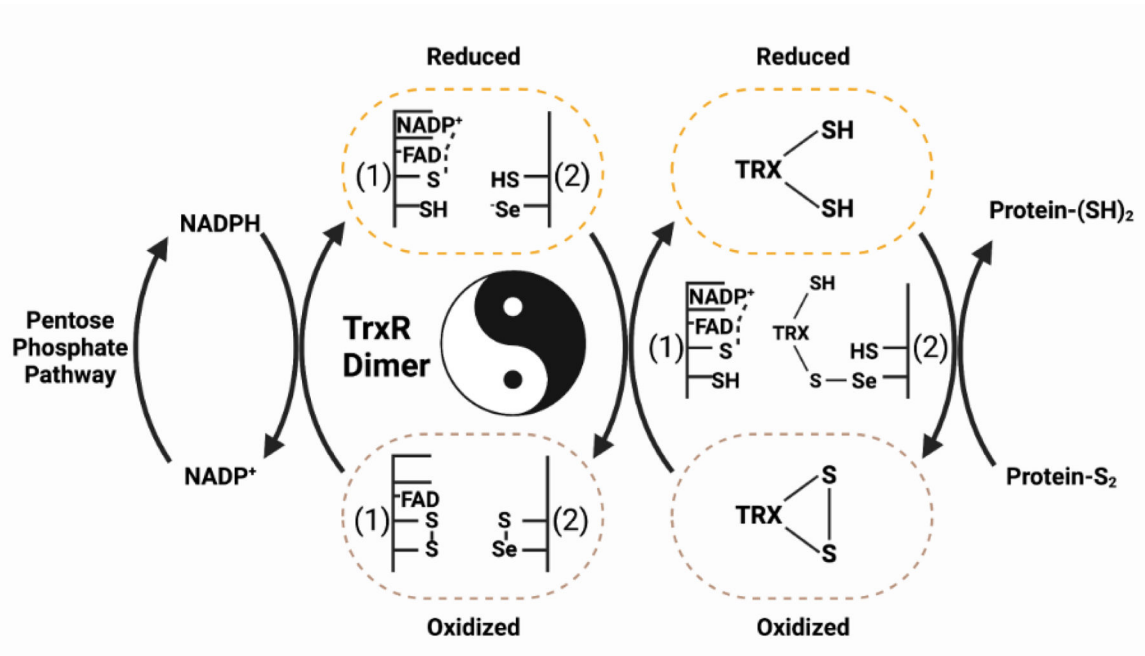


Figure 3. Conserved biological mechanism of thioredoxin.

The thioredoxin pathway allows electrons from metabolism to cycle through the redox machinery, thereby maintaining a reduced cellular environment. From left to right, NADPH generated from the pentose phosphate metabolic pathway binds to a dimer of oxidized thioredoxin reductase (TrxR). Next, the TrxR dimer forms a yin-yang orientation where the “head” of protein 1 (1) binds into the “tail” of protein 2 (2) to reduce a Se-S bond mediated through an FAD cofactor. This process is performed in duplicate with the “tail” of (1) binding into the “head” of (2) (not shown). Third, the reduced TrxR dimer can then recycle oxidized thioredoxin by binding to the selenocysteine of the reduced TrxR. The resulting electron shuttle restores thioredoxin to its reduced form, thus regaining its cellular redox capabilities.

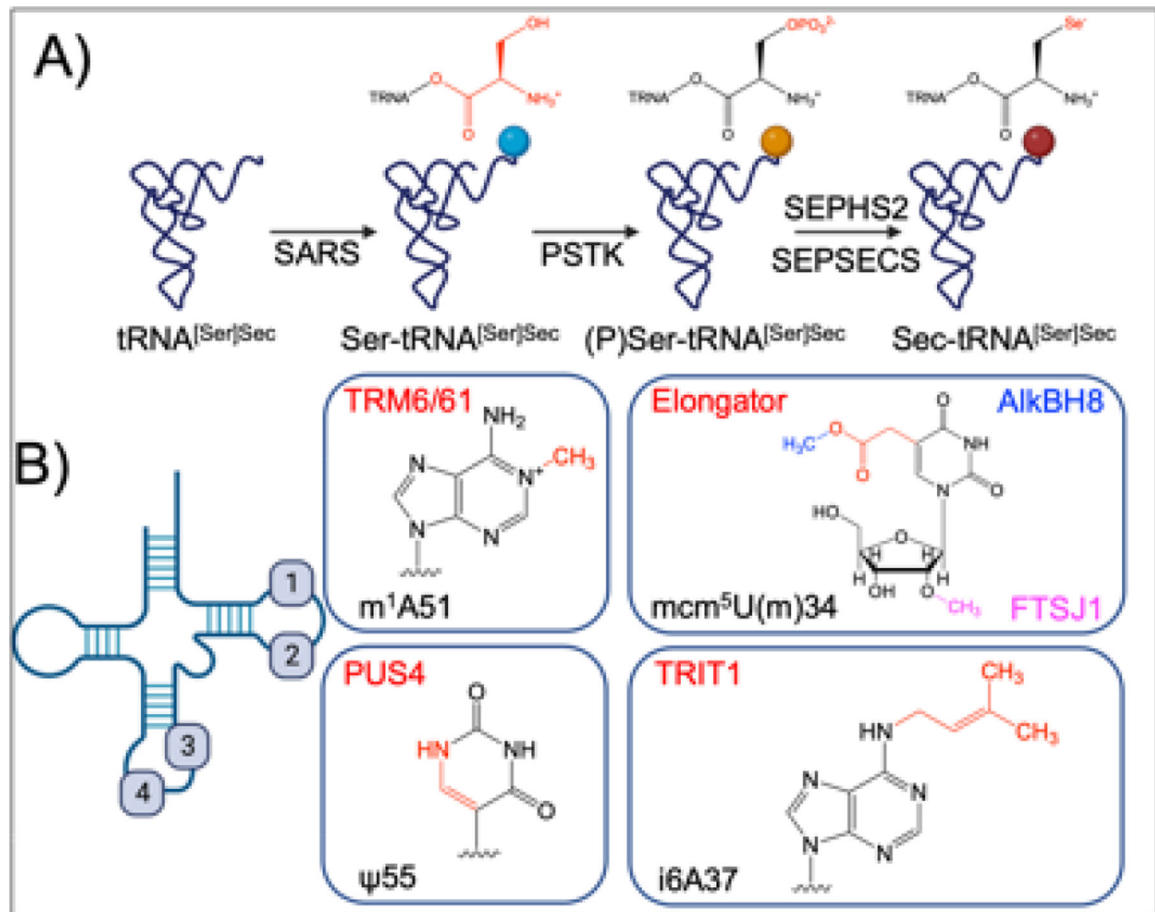


Figure 4. Selenocysteine biosynthesis and post transcriptional modifications of tRNA-selenocysteine (tRNA^{[Ser]Sec}).

(A) Biogenesis of selenocysteine. tRNA-sec is initially aminoacylated with serine by seryl-tRNA synthetase (SARS). Phosphoserine tRNA Kinase (PSTK) phosphorylates Ser-tRNA^{[Ser]Sec}, allowing for substitution of the oxygen for a selenium by selenophosphate synthetase 2 (SEPHS2) and (Sep (O-Phosphoserine) TRNA:Sec (Selenocysteine) TRNA Synthase) SEPSECS, forming selenocysteine on the tRNA. (B) Post transcriptional modifications of tRNA-sec. tRNA-sec contains four post transcriptional modifications, 1-methyladenosine (m¹A) 51 placed by the tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit (TRM6) and TRNA (Adenine-N(1)-)-Methyltransferase Catalytic Subunit (TRM61), Pseudouridine (ψ) 55 placed by PseudoUridine Synthase 4 (PUS4), N6-isopentyladenosine (i⁶A) placed by tRNA isopentyltransferase 1 (TRIT1), and 5-methoxycarbonylmethyl-(2'-O-methyl)-uridine (mcm⁵U(m)) placed in conjunction by the Elongator Complex (cm⁵), AlkB Homolog 8, tRNA methyltransferase (AlkBH8) (mcm⁵), and FtsJ RNA 2'-O-Methyltransferase 1 (FTSJ1) (U_m). While mcm⁵ is essential for selenoprotein translation, the necessity for 2'-O-methylation is variable through poorly understood mechanisms.

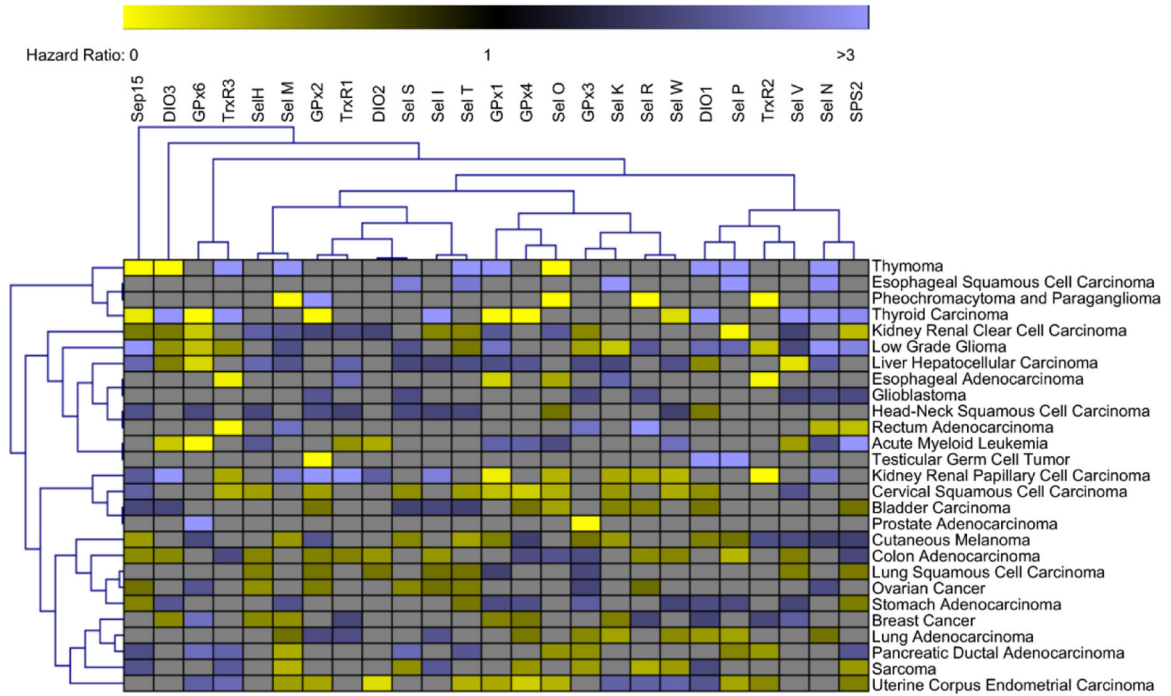


Figure 5. Key figure. Hazard ratios of selenoproteins across cancer types. Unbiased hierarchal clustering was used for visualization of statistically significant ($p < 0.05$) selenoprotein hazard ratios across various cancers with branches representing statistically similar groupings of genes or cancers. A hazard ratio of 1 indicates no difference between groups (high vs low expression of selected gene). Hazard ratios > 1 (Blue) indicates correlation between higher expression and lower survival of the indicated gene. Hazard ratios < 1 (Yellow) indicates correlation between lower expression and higher survival of the indicated gene. Hazard ratios with nonsignificant correlations ($p > 0.05$) were not included in the analysis and are represented as gray boxes. Several cancers such as liver hepatocellular carcinoma, glioblastoma, and head-neck squamous cell carcinoma have multiple selenoprotein hazard ratios > 1 indicating that efforts to reduce selenoprotein expression may provide therapeutic benefit. Other cancers such as cervical squamous cell carcinoma and uterine corpus endometrial carcinoma have multiple selenoprotein hazard ratios < 1 indicating that efforts to boost selenoprotein expression may provide therapeutic benefit. However, throughout the analysis of 25 selenoproteins across 27 cancers the only cancer with a net positive or negative survival correlation with selenoprotein expression is glioblastoma. Furthermore, many selenoproteins have significant and opposite correlations with patient survival across different cancer types. This data highlights the complexity and context dependent role of selenoproteins across different cancer types.

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