

Review

Selenium Biotransformation by Food-Relevant Microorganisms: Bacterial and Fungal Differences in Diversified Uptake, Metabolic Partitioning, and Terminal Fate

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Abstract

Selenium (Se) biotransformation by microorganisms determines how inorganic selenium is redistributed into organic selenium, selenium nanoparticles (SeNPs), methylated species, and other intracellular or extracellular pools. Although microbial selenium metabolism has been extensively studied, evidence supporting individual mechanisms remains uneven, and bacterial and fungal observations are often compared without sufficient consideration of energetic context, cellular architecture, or evidence strength. This review reorganizes the field around an evidence-graded mechanistic framework. We distinguish direct functional validation from convergent pathway evidence and association-level observations, compare bacterial and fungal selenium handling across uptake, redox metabolism, sulfur assimilation, methylation, compartmentalization, and terminal localization, and introduce cellular selenium loading as a conceptual bridge between uptake and downstream metabolic partitioning. We further emphasize that methylation is not equivalent to volatilization and that terminal selenium fate is best resolved by combining chemical speciation with spatial localization. These mechanisms are integrated into strain-specific selenium-transformation profiles and linked to representative applications and evidence-guided microbial engineering. This synthesis aims to shift microbial selenium research from empirical total-selenium accumulation toward mechanism-resolved, testable, and engineerable selenium biotransformation.

Keywords: selenium biotransformation; bacterial–fungal differences; cellular selenium loading; metabolic partitioning; selenium nanoparticles



Academic Editors: Yiannis Kourkoutas and Young Hoon Jung

Received: 10 August 2026

Revised: 7 September 2026

Accepted: 18 September 2026

Published: 20 September 2026

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1. Introduction

Selenium (Se) is an essential trace element required for the synthesis of a defined group of selenoproteins involved in redox regulation, thyroid hormone metabolism, immune function, and other physiological processes [1,2]. Both selenium deficiency and excessive intake can produce adverse effects, reflecting the relatively narrow physiological window of this element [1,3]. Importantly, the biological behavior, retention, nutritional relevance, and safety of selenium depend strongly on chemical speciation rather than on total selenium concentration alone [3,4]. Organic selenium compounds, particulate selenium such as selenium nanoparticles (SeNPs), and residual inorganic Se(IV) or Se(VI) differ substantially in stability, reactivity, bioaccessibility, and metabolic fate. Controlled conversion of inorganic selenium into defined selenium species has therefore become an important objective in selenium enrichment.

Microbial biotransformation provides a versatile route for this conversion because selenium exposure, nutrient supply, growth conditions, and cellular physiology can be manipulated simultaneously [5]. Selenium-enriched yeasts, lactic acid bacteria, and other food-associated microorganisms have consequently been investigated in food fortification, fermentation, probiotic, supplement, and feed-related systems [6–9]. Mechanistic research has progressed from measurements of selenium accumulation and tolerance to characterization of selenium transport, respiratory and non-respiratory reduction, glutathione- and thioredoxin-associated redox processes, sulfur metabolism, selenium-containing amino acid formation, methylation, SeNP biogenesis, intracellular sequestration, and extracellular redistribution [4,5,10]. Studies based on genetics, selenium-speciation analysis, targeted perturbation, adaptive evolution, and multi-omics have further increased mechanistic resolution. Recent work has extended this knowledge to selenium uptake and metabolic reprogramming in *Saccharomyces cerevisiae* [11], food-grade bacterial SeNP formation [12–14], integrated redox and sulfur metabolism [15–17], and membrane-associated nanoparticle export [18]. The field has therefore advanced beyond establishing whether individual selenium-transforming reactions occur. The more important question is how these processes interact to determine the final chemical form and cellular location of selenium. However, pathway-centered descriptions provide limited explanations for why microorganisms exposed to similar selenium conditions generate different selenium species, localization patterns, and retention outcomes.

Comparing selenium biotransformation among different microbial groups is essential for answering this question. Similar selenium exposure does not necessarily produce similar selenium outcomes because microorganisms differ in cellular architecture, energetic organization, redox buffering, sulfur assimilation, compartmentalization, and selenium-containing amino acid utilization [10,19,20]. Selected selenium-respiring bacteria can couple oxyanion reduction to electron transfer and energy conservation, whereas many food-associated bacteria appear to integrate selenium transformation mainly with redox adaptation, tolerance, and stress-associated reduction. Fungal systems more frequently involve glutathione-dependent redox buffering, intracellular compartmentalization, and, in selenium-enriched yeasts, substantial retention of selenomethionine (SeMet)-containing proteins [11,20,21]. These differences are informative but remain strain- and condition-dependent rather than defining absolute bacterial–fungal boundaries. Cross-taxon comparison can therefore distinguish broadly shared transformation principles from taxon- or strain-associated tendencies and identify the physiological features that most strongly influence selenium partitioning. This distinction has practical consequences. For selenium-enrichment processes, microorganisms can be selected according to the desired selenium form and retention pattern rather than total selenium accumulation alone, and cultivation conditions can then be adjusted according to the dominant physiological constraints of the selected strain. For mechanistic research, comparison across taxa also helps determine which mechanisms may be transferable among microorganisms, which require taxon-specific validation, and which apparent differences may partly reflect unequal experimental resolution rather than true biological divergence. Cross-taxon comparison is therefore essential for distinguishing conserved selenium-transformation principles from physiological strategies that determine taxon-associated selenium partitioning.

Interpretation across studies remains challenging because selenium transformation is strongly condition-dependent and because the underlying evidence is heterogeneous. Selenium species and dose, sulfur and phosphate availability, oxygen status, redox capacity, growth phase, and nutrient composition can redirect selenium among assimilation, particulate formation, methylation, sequestration, export, and residual inorganic pools [22–24]. At the same time, some transporter, reductase, efflux, and methylation mechanisms are

supported by targeted genetics, complementation, transport measurements, or biochemical validation [25,26], whereas many assignments in food-relevant microorganisms are supported mainly by physiological and multi-omics associations. Analytical endpoints add further variability because similar total selenium concentrations may represent different combinations of intracellular organic selenium, SeNPs, surface-associated selenium, soluble extracellular selenium, and volatile loss. Consequently, total selenium alone provides limited information on the physiological strategy by which a microorganism handles selenium.

This review therefore establishes a selenium partitioning framework in which microbial selenium biotransformation is interpreted as a continuum from selenium uptake and cellular loading to metabolic processing and terminal selenium allocation (Figure 1). Cellular selenium loading is used here as an integrative concept describing the metabolically accessible selenium presented to intracellular transformation systems rather than as a standardized analytical variable. Subsequent selenium partitioning is interpreted in relation to the balance between cellular selenium exposure and the redox, sulfur-metabolic, biosynthetic, and compartmental capacity available to process that exposure. Reduction is distinguished from assimilatory incorporation, methylation is treated as redistribution among selenium species rather than as synonymous with volatilization, and terminal selenium fate is resolved through the complementary dimensions of chemical speciation and spatial localization. Mechanistic claims are evaluated according to evidence strength, while bacterial and fungal systems are compared across common physiological dimensions. These elements are ultimately integrated into strain-specific selenium-transformation profiles, providing a basis for more rigorous microbial comparison, rational strain selection, targeted process control, functional validation, and evidence-guided engineering of microbial selenium biotransformation.

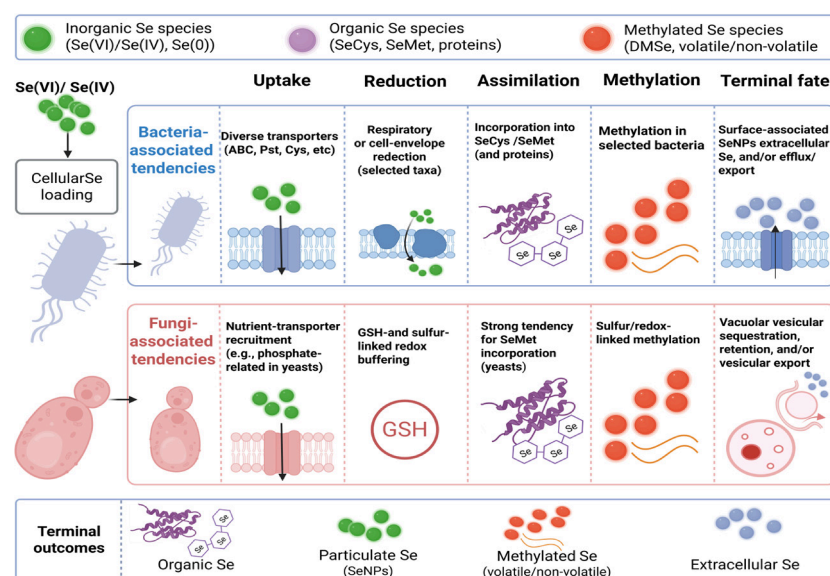


Figure 1. Conceptual overview of microbial selenium uptake, transformation, and terminal partitioning. Note. Colored bacterial- or fungal-associated routes summarize reported examples and should not be interpreted as universally taxon-specific pathways or conserved quantitative fluxes.

Scope and Evidence Grading

This review focuses primarily on selenium biotransformation in food-relevant bacteria and fungi. Model, environmental, selenium-respiring, and extracellular-electron-transfer microorganisms are included when they provide direct mechanistic evidence that is not yet available in food-associated strains. The review covers inorganic selenium uptake, reduction, assimilation, methylation, terminal selenium fate, and the engineering implications of

these processes. Broader clinical, nutritional, and environmental-remediation outcomes are considered only when they are required to define the biological significance or application boundary of a microbial selenium-transformation mechanism.

Evidence is evaluated at the level of individual mechanistic claims rather than entire studies. Level I denotes direct functional evidence, such as targeted genetic perturbation with complementation, substrate-specific transport measurements, or biochemical enzyme validation. Level II denotes convergent mechanism-oriented evidence, including selenium speciation combined with multi-omics, physiology, particle characterization, or protein-level assays without definitive causal perturbation. Level III denotes association-level evidence derived mainly from expression changes, pathway enrichment, or indirect phenotypic correlations. This evidence-gated approach is applied throughout the review to distinguish experimentally established mechanisms from pathway-supported interpretations while retaining the hypothesis-generating value of emerging multi-omics studies.

2. Selenium Uptake and Cellular Loading

The entry of inorganic selenium into microbial cells is the first determinant of its subsequent intracellular transformation. Microorganisms are exposed predominantly to selenate [Se(VI), SeO_4^{2-}] and selenite [Se(IV), SeO_3^{2-}], but neither oxyanion is generally handled through a universally conserved selenium-specific uptake system. Instead, current evidence indicates extensive recruitment of nutrient transporters whose physiological substrates are chemically related sulfur- [26,27], phosphorus- [25], or other anion-containing compounds [24,28]. The mechanistic significance of selenium uptake therefore lies not only in identifying individual membrane proteins but also in understanding how transporter promiscuity, nutrient competition, taxonomic background, and physiological state determine the amount of selenium ultimately presented to intracellular metabolism (Figure 2).

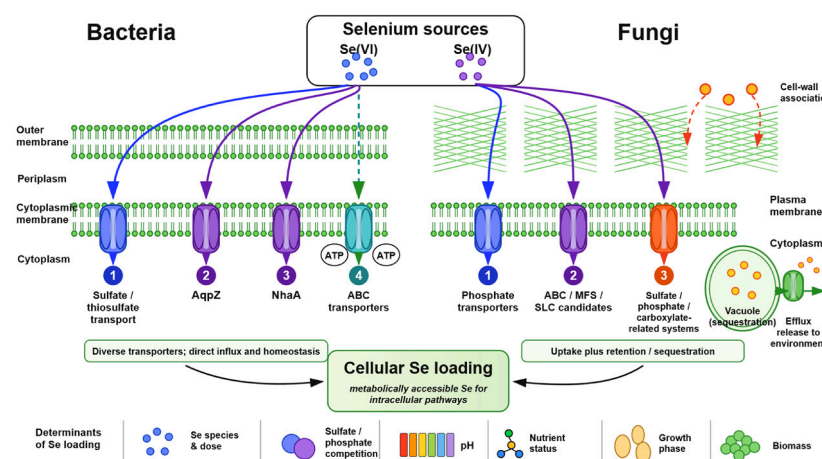


Figure 2. Comparative selenium uptake routes and cellular selenium loading in bacteria and fungi.

2.1. Uptake Routes

Selenate has a particularly close relationship with sulfate acquisition because selenium and sulfur share similar oxyanion chemistry. In *Escherichia coli* K-12, competition and genetic evidence support overlapping transport of sulfate and selenate through sulfur-oxyanion transport systems, while sulfate remains the principal physiological substrate [26,27]. Sulfur limitation can modify expression of the CysB-regulated sulfur-acquisition machinery and thereby alter the opportunity for Se(VI) to enter through these systems [29]. Se(VI) uptake can therefore be viewed as a well-supported example of substrate promiscuity within native nutrient transport (Figure 2).

Se(IV) uptake is more heterogeneous. In *Saccharomyces cerevisiae*, genetic analysis, substrate competition, and transport measurements support direct participation of phosphate transport systems [25]. Pho84p contributes substantially under phosphate-limited conditions, while lower-affinity phosphate transport becomes more relevant as phosphate availability increases. Competition between phosphate and selenite demonstrates that the effective uptake of Se(IV) depends on both transporter regulation and extracellular nutrient composition.

Other microorganisms use different membrane-associated routes. In *Rahnella aquatilis* HX2, gene deletion and complementation support roles for the aquaporin AqpZ and the Na⁺/H⁺ antiporter NhaA in Se(IV) uptake or cellular selenium homeostasis [28]. Sulfite-related, monocarboxylate-related, ATP-binding cassette (ABC), major facilitator superfamily (MFS), and solute carrier (SLC) systems have also been associated with selenium accumulation or selenium-stress responses in different bacterial and fungal systems [24,30–33]. These observations extend the range of candidate selenium-handling routes while indicating substantial organism dependence.

The available evidence therefore supports a useful distinction between the two major inorganic selenium substrates. Se(VI) has a relatively consistent relationship with sulfur acquisition, whereas Se(IV) can access a broader set of membrane processes whose contribution depends on the organism and culture environment. Selenium uptake is consequently better understood through chemical similarity, transporter promiscuity, and nutrient competition than through a single conserved selenium transporter.

2.2. Taxon Dependence

2.2.1. Selenium Uptake in Bacteria

Bacterial selenium uptake is dominated by recruitment of pre-existing ion and nutrient transport systems. Sulfate/thiosulfate transport in *E. coli* provides one of the best-characterized examples for Se(VI) [26,27]. Regulation of sulfur acquisition by nutritional status can further modify selenium entry, linking uptake directly to cellular sulfur demand [29].

For Se(IV), *R. aquatilis* HX2 demonstrates a different transport phenotype. Genetic perturbation and complementation support involvement of AqpZ and NhaA in selenium uptake or homeostasis [28]. These findings indicate that membrane proteins with primary physiological functions unrelated to selenium can make measurable contributions to cellular Se(IV) handling.

In many food-associated bacteria, current mechanistic resolution is lower. Transcriptomic and proteomic studies frequently identify ABC transporters and other membrane proteins that respond to selenium exposure [30,32,34]. Such responses support recruitment of membrane-associated networks and provide rational candidates for functional analysis. Their biological effects may involve selenium influx, efflux, ion homeostasis, membrane adaptation, or secondary stress responses, and their specific contributions are therefore best interpreted in the context of the evidence available for each system.

Environmental selenium-respiring or extracellular-electron-transfer bacteria remain useful mechanistic references where direct functional evidence is unavailable in food-relevant strains. However, transporter functions identified in such organisms should be transferred to food-associated microorganisms only when the relevant substrate, directionality, and cellular phenotype are experimentally supported.

2.2.2. Selenium Uptake in Fungi

Among fungi, *S. cerevisiae* provides the strongest direct evidence for inorganic selenium uptake. Phosphate-dependent Se(IV) transport has been resolved through targeted genetics,

competition experiments, and uptake measurements [25]. Because the contribution of high- and low-affinity phosphate transport changes with phosphate availability, nutrient status is intrinsically coupled to Se(IV) entry.

In *Aureobasidium melanogenum*, *Pichia kudriavzevii*, and *Aspergillus oryzae*, ABC-, MFS-, SLC-, sulfate-, phosphate-, and carboxylate-related transport systems have been associated with selenium accumulation or tolerance through transcriptomic, proteomic, and physiological evidence [24,31]. These studies support broad recruitment of nutrient and stress-associated transport networks and provide candidate components for more targeted mechanistic investigation.

Fungal cellular organization also affects the interpretation of apparent selenium accumulation. Cell-wall binding, vacuolar sequestration, endomembrane trafficking, and changes in efflux can increase selenium recovered with biomass without a proportional increase in plasma-membrane influx. Fungal biomass selenium therefore integrates both true cellular entry and subsequent retention or sequestration.

The comparison between bacteria and fungi also reveals an important evidence asymmetry. Direct transport kinetics and targeted genetic validation are concentrated in *S. cerevisiae* and a limited number of bacterial systems, whereas many food-associated microorganisms have primarily been examined by omics. Apparent taxonomic differences should therefore be interpreted through both biological divergence and differences in experimental resolution.

2.3. Cellular Loading

The amount of selenium presented to intracellular metabolism reflects the combined effects of selenium species and concentration, transporter availability, competing sulfate or phosphate, pH, nutrient status, membrane energetics, growth phase, and biomass [5,22,25,28]. Some variables influence selenium entry through direct substrate competition, whereas others act by modifying transporter expression, membrane physiology, nutrient demand, or cellular growth.

Process-level studies illustrate how these factors interact. Studies of *Saccharomyces* yeasts have associated ion homeostasis with selenium accumulation and organification [35], while a 2026 study of *S. cerevisiae* showed that siderophore-assisted cultivation increased selenium tolerance and cellular selenium accumulation while favoring SeMet within the measured selenoamino-acid pool [11]. Such findings demonstrate that cultivation conditions can simultaneously alter upstream selenium acquisition and downstream selenium retention.

Transmembrane influx, net cellular accumulation, and selenium organification should nevertheless be treated as distinct endpoints. Selenium recovered from biomass reflects influx together with surface association, intracellular retention, and sequestration. Efflux, extracellular conversion, volatilization, and biomass dilution can alter the same pool. High biomass selenium does not necessarily indicate rapid membrane influx, and increased cellular accumulation does not necessarily indicate preferential organic selenium formation.

Across currently characterized microorganisms, a recurring relationship is therefore apparent. Inorganic selenium commonly exploits native nutrient-transport systems, whereas the resulting intracellular exposure is strongly shaped by ion competition and cellular physiology. In this review, cellular selenium loading refers conceptually to the metabolically accessible selenium presented to intracellular transformation pathways. It is an integrative physiological concept rather than a single standardized analytical measurement and should be distinguished from total biomass-associated selenium.

3. Intracellular Metabolism

Once selenium becomes metabolically accessible, reduction alters its oxidation state, and assimilation directs part of the reduced selenium toward cellular biosynthesis. These processes overlap but are not equivalent. Reduced selenium can subsequently enter organic selenium synthesis, elemental selenium formation, methylation, intracellular sequestration, or other stress-associated routes. Their relative contribution depends on the physiological function of reduction and on the metabolic resources available to process selenium.

The term selenide-related reduced intermediates is used here for highly reduced selenium species downstream of Se(IV), including chemical forms associated with $\text{H}_2\text{Se}/\text{HSe}^-$ and thiol-bound selenium. Their intracellular identity varies with pH, thiol availability, redox state, and cellular environment. They are therefore treated as a functional intermediate pool rather than a universally conserved freely diffusible metabolite (Figure 3).

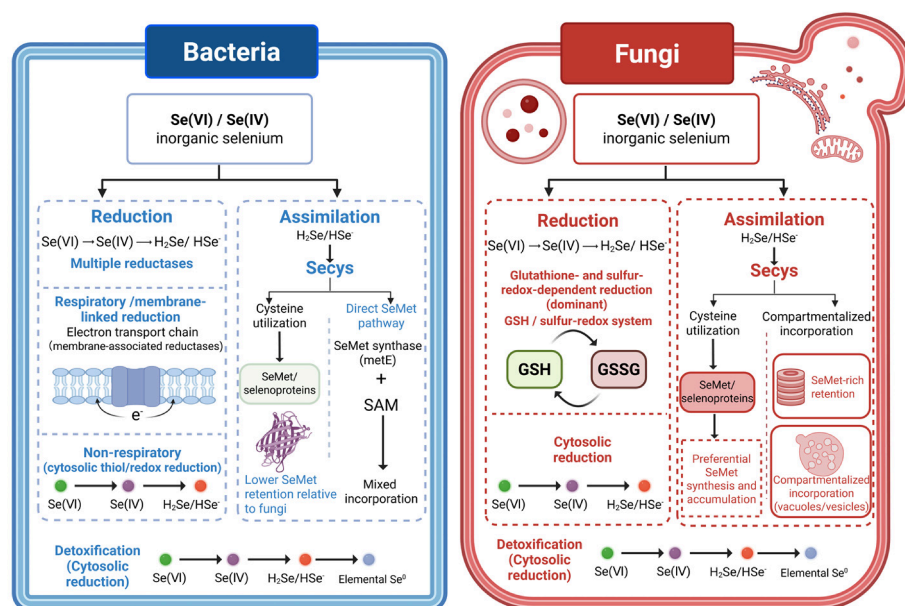


Figure 3. Comparative overview of selenium reduction and assimilation in bacteria and fungi.

3.1. Selenium Reduction

3.1.1. Respiratory Reduction

Respiratory selenium reduction occurs in specialized microorganisms that use selenium oxyanions in anaerobic electron transport. A well-characterized example is the periplasmic selenate reductase SerABC of *Thauera selenatis*, which catalyzes reduction of Se(VI) to Se(IV) during selenate respiration [19,36,37]. SerA contains the catalytic molybdenum center, SerB contains iron-sulfur centers involved in electron transfer, and SerC anchors the complex to the membrane. Biochemical characterization combined with a defined respiratory function gives this mechanism strong causal support.

Other bacterial reductases and electron-transfer components can participate in selenium reduction without functioning as dedicated selenium-respiratory systems. Nitrate-reductase-related enzymes [38,39], thioredoxin-associated proteins [40,41], and extracellular electron-transfer components can contribute under different physiological conditions. In *Shewanella oneidensis* MR-1, electron shuttles such as anthraquinone-2,6-disulfonate (AQDS) and riboflavin redirect Se(IV) reduction toward an extracellular route that depends strongly on the outer-membrane cytochromes OmcA and MtrC while bypassing the periplasmic FccA-associated route [42]. These mechanisms are therefore condition-dependent and should not be generalized across taxa.

This distinction is important for food microbiology. Selenium-respiring and extracellular-electron-transfer bacteria provide mechanistic reference systems for reductase chemistry and spatial electron transfer, while most food-associated aerobic or fermentative bacteria are better described in terms of non-respiratory selenium transformation, redox adaptation, and tolerance [34,40].

3.1.2. Detoxification-Associated Reduction

In many food-associated bacteria and fungi, Se(IV) reduction is integrated with redox homeostasis and selenium tolerance. Reduced glutathione (GSH), thioredoxin-related systems, NAD(P)H-dependent oxidoreductases, and reducing biomolecules participate in selenium transformation [40,43]. In GSH-dependent chemistry, Se(IV) can form selenodiglutathione (GS₂SeSG) and related thiol-associated intermediates, which can subsequently be redistributed toward lower-valence selenium species or Se(0) [20].

These reactions consume reducing equivalents and can perturb cellular redox balance. Selenium-associated oxidative stress can arise from reactive selenium intermediates, depletion of cellular reductants, and redox cycling [20,44]. In *S. cerevisiae*, selenium exposure alters glutathione homeostasis and central carbon metabolism, consistent with an increased requirement for cellular reducing power [45]. Thiol-dependent conversion can contribute to tolerance, while accumulation of highly reduced intermediates can also increase toxicity under particular conditions [46].

Food-associated bacteria recruit similarly complex redox networks. In *Lactiplantibacillus plantarum* CXG4, thioredoxin- and short-chain dehydrogenase/reductase-related proteins have been associated with Se(IV) transformation [40]. Reduced functional groups in extracellular polymeric substances can also participate in Se(IV) reduction or stabilization of selenium-containing particles [43].

Recent studies strengthen this network-level interpretation. Integrated multi-omics analyses of *Serratia marcescens* HBQT linked Se(IV) transformation with thioredoxin-associated processes, sulfur assimilation, and NADH/NADPH regeneration [16]. In *Ligilactobacillus salivarius* DACN818, Se(IV) conversion and SeNP formation were accompanied by changes in sulfur/glutathione metabolism, amino acid metabolism, transport, and energy metabolism [13]. Non-respiratory selenium reduction is therefore frequently embedded within broader metabolic adaptation.

3.1.3. Differences Between Bacteria and Fungi

The most informative bacterial–fungal differences concern the physiological role, energetic context, and cellular organization of selenium reduction. Selected selenium-respiring bacteria can couple oxyanion reduction to anaerobic electron transport and energy conservation [47,48]. Most food-associated bacteria instead use selenium reduction as part of redox adaptation, tolerance, or selenium transformation [34,40].

Fungal selenium reduction is commonly associated with GSH-dependent redox buffering, sulfur metabolism, NADPH demand, and intracellular compartmentalization [44,49,50]. Persistent selenium exposure in *S. cerevisiae* can disturb glutathione balance and central carbon metabolism [45], while vacuolar and vesicle-associated processes provide additional routes for sequestration and redistribution.

Cellular architecture influences both where reduction occurs and how much metabolic investment is required. Depending on the taxon, bacterial reduction may occur in the cytoplasm, periplasm, cell envelope, or extracellular electron-transfer system. Fungi lack a bacterial-type periplasm and possess extensive vacuolar and endomembrane organization, which can reduce cytoplasmic exposure to reactive selenium and redistribute selenium among intracellular compartments.

These differences represent recurring taxon-associated tendencies rather than fixed bacterial–fungal boundaries. The degree to which selenium reduction is coupled to energy conservation, redox buffering, and cellular compartmentalization provides a more informative comparative framework than a simple taxonomic dichotomy.

3.2. Assimilatory Metabolism

3.2.1. Coupling with Sulfur and Redox Metabolism

Assimilatory selenium metabolism incorporates selenium into organic compounds and cellular biomolecules. The relevant reactions overlap extensively with sulfur metabolism because enzymes participating in sulfate activation, sulfur reduction, cysteine biosynthesis, and methionine metabolism can accept selenium analogs [51,52]. Selenium assimilation is therefore embedded within pre-existing sulfur and redox networks.

When Se(VI) is supplied, activation and reduction can proceed through sulfate-assimilation-related reactions before selenium reaches Se(IV) and more reduced intermediates [20,51]. Direct supplementation with Se(IV), which is common in selenium-enrichment studies, bypasses part of this upstream sequence. Selenium substrate identity therefore changes the pathway entry point and influences interpretation of conversion efficiency.

In bacteria, thioredoxin-associated reactions, NAD(P)H-dependent processes, sulfur metabolism, and amino acid biosynthesis can contribute to organic selenium formation [51–53]. Fungal assimilation similarly recruits ATP sulfurylase, glutathione, thioredoxin, sulfate-reduction-related enzymes, and NADPH-dependent metabolism [20,44,54]. In *Monascus ruber* M7, expression of sulfate-reduction-related genes is associated with formation of reduced selenium products [54], supporting recruitment of sulfur-assimilation machinery during selenium transformation.

Sulfur availability can influence selenium assimilation in multiple ways. Sulfur metabolism supplies enzymes, reducing equivalents, and biosynthetic precursors required for selenium incorporation, while sulfate and sulfur-containing metabolites can also compete with selenium during uptake or shared metabolic reactions. The effect of sulfur supplementation therefore depends on selenium substrate, nutrient background, exposure level, and strain physiology.

3.2.2. Formation of SeMet and SeCys

Selenomethionine (SeMet) and selenocysteine (SeCys) are major organic selenium products, but their biosynthetic origins and biological meanings differ.

SeMet formation recruits methionine-biosynthesis-related reactions. In selected bacteria, reduced selenium intermediates can enter reactions involving O-acetylhomoserine or related sulfur-acceptor substrates and subsequently form SeMet-related products [51]. In *L. plantarum* CXG4, methionine sulfoxide reductase A has been associated with reduction of oxidized SeMet, suggesting a potential salvage role [40]. In yeasts, SeMet can be incorporated nonspecifically in place of methionine during protein synthesis, producing an important retained selenium pool in selenium-enriched biomass [21,55].

The proportion of SeMet varies substantially with strain, selenium source and dose, sulfur availability, growth phase, and analytical method [21,55]. Siderophore-assisted cultivation of *S. cerevisiae* increased selenium accumulation and yielded a measured selenoamino acid pool strongly enriched in SeMet [11]. Such process-level evidence demonstrates that microbial physiology can shift both selenium accumulation and the chemical composition of retained organic selenium.

SeCys requires a distinction between metabolic formation and genetically encoded incorporation. Sulfur-metabolism enzymes can generate free or metabolite-associated SeCys-related compounds by accepting selenium analogs. In contrast, insertion of genet-

ically encoded SeCys into selenoproteins requires specialized Sec-utilization machinery, including tRNA^{Sec}, selenium-donor synthesis, SeCys synthesis, SelB, and the appropriate insertion sequence [51,56]. Such machinery occurs in selected bacteria but is absent from most food-related yeasts and filamentous fungi. Early-diverging fungal lineages provide documented exceptions [57,58]. Specific bacterial examples also indicate that SeCys formation can recruit sulfur-metabolic enzymes outside the canonical SelA/SelD route [59,60].

Accordingly, detection of SeCys after hydrolysis of selenium-enriched fungal biomass should be interpreted through species-resolved selenium analysis. The measured pool can include free metabolites, sulfur-pathway products, and protein-associated selenium released during sample processing [55]. Distinguishing these pools is important when mechanistic conclusions are linked to nutritional or functional properties.

3.2.3. Bacterial–Fungal Differences

Bacterial and fungal selenium assimilation differ in both biosynthetic organization and the predominant forms of retained selenium. Selected bacteria possess canonical Sec-utilization machinery and can generate genetically encoded selenoproteins [51,56]. The relative proportions of SeMet-, SeCys-, and other organic selenium pools vary substantially among bacterial species and strains [59,61]. Food-associated bacteria can also distribute considerable selenium into Se(0)/SeNPs, particularly when reductive stress responses become prominent [12,15,61].

Most food-related yeasts and filamentous fungi lack canonical Sec-insertion machinery, whereas SeMet-rich protein retention is a recurring feature of selenium-enriched yeasts [20,21,55]. Fungal assimilation also occurs in a cellular context characterized by strong GSH/NADPH involvement and extensive vacuolar or endomembrane compartmentalization. These properties influence the balance between biosynthetic incorporation and intracellular sequestration.

The bacterial–fungal distinction in assimilation is therefore more informative when expressed through the relative importance of canonical Sec utilization, SeMet-rich protein retention, redox investment, and compartmentalization. Both groups can form organic selenium, but the dominant retained pools and the cellular processes supporting them differ among taxa and strains.

3.2.4. Selenium Metabolic Partitioning

The final selenium profile is determined not only by selenium uptake but by the balance between cellular selenium exposure and the metabolic capacity available to process that selenium. The relative distribution of selenium among organic, particulate, methylated, and sequestration-associated pools depends on cellular selenium exposure together with the metabolic capacity available to process that exposure. GSH/thioredoxin buffering, NAD(P)H regeneration, sulfur assimilation, biosynthetic precursor supply, biomass formation, oxygen status, and growth phase all contribute to this capacity [13,45,62].

When selenium exposure approaches or exceeds the redox and biosynthetic capacity of a strain, stress-associated reduction, particle formation, sequestration, and loss pathways can become more prominent. Under tolerated exposure with adequate reducing power and sulfur-assimilation capacity, a greater proportion of selenium may enter organic pools. The response to sulfur or cysteine supplementation can change with nutritional background, indicating that individual environmental factors do not impose a universally fixed direction of selenium allocation [45].

Current evidence therefore supports a conditional relationship between cellular selenium exposure and metabolic processing capacity. Selenium partitioning reflects competi-

tion among processes with different requirements for reducing power, sulfur metabolism, biosynthetic precursors, and cellular compartments. Their relative contribution differs between bacteria and fungi and among strains within each group. Quantitative, species-resolved selenium-flux measurements are needed to convert this qualitative relationship into predictive allocation models. Thus, selenium partitioning represents a dynamic allocation process governed by competition among assimilation, particulate formation, methylation, sequestration, and loss pathways. Their relationship to branch selection is illustrated in Figure 4.

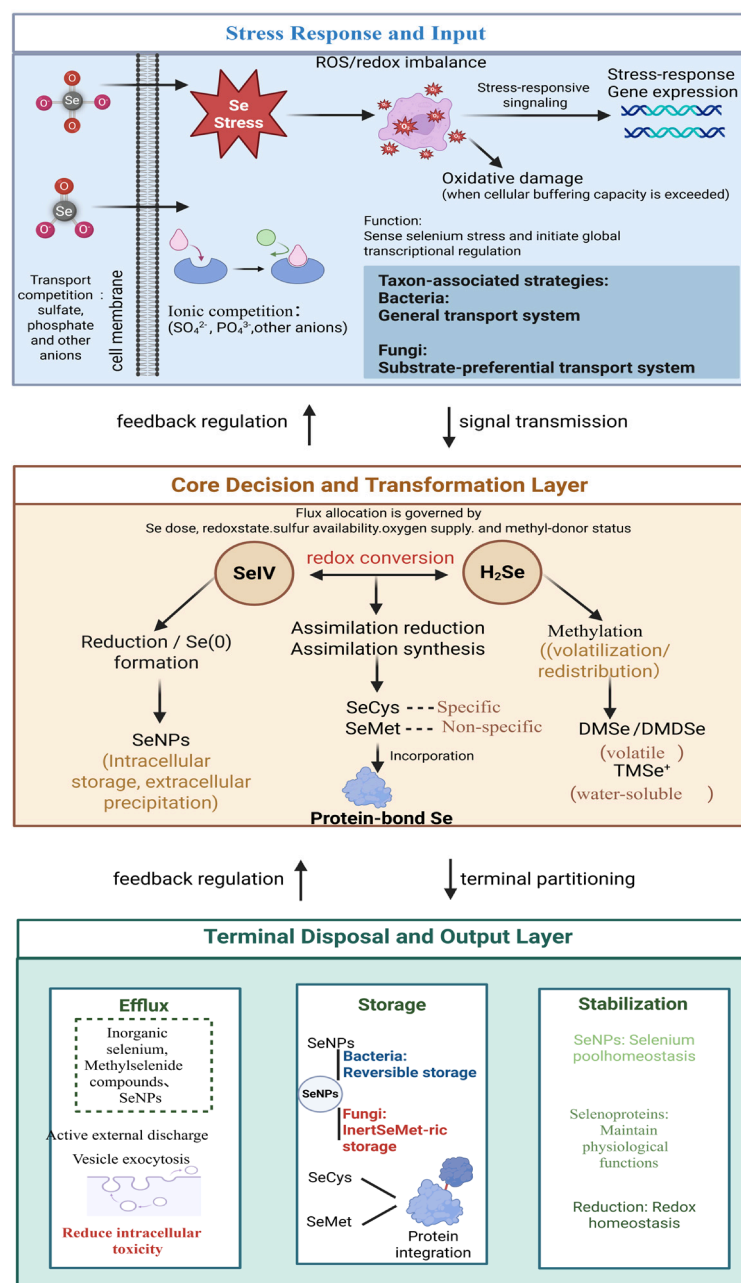


Figure 4. Conceptual branch-node model for selenium partitioning around Se(IV) and $\text{H}_2\text{Se}/\text{HSe}^-$ -related intermediates. Note. Redox perturbation and oxidative stress are positioned downstream of reactive selenium exposure. Arrows summarize condition-dependent tendencies rather than universal quantitative fluxes.

4. Selenium Methylation

Microbial selenium methylation converts reduced inorganic selenium or organic selenium metabolites into low-molecular-mass methylated species. Some products, including dimethyl selenide (DMSe) and dimethyl diselenide (DMDSe), are volatile and can leave microbial biomass or culture systems [63–65]. Other methylated selenium species remain nonvolatile. Selenium methylation should therefore be considered a process of selenium redistribution among chemical pools rather than a synonym for selenium volatilization (Figure 5).

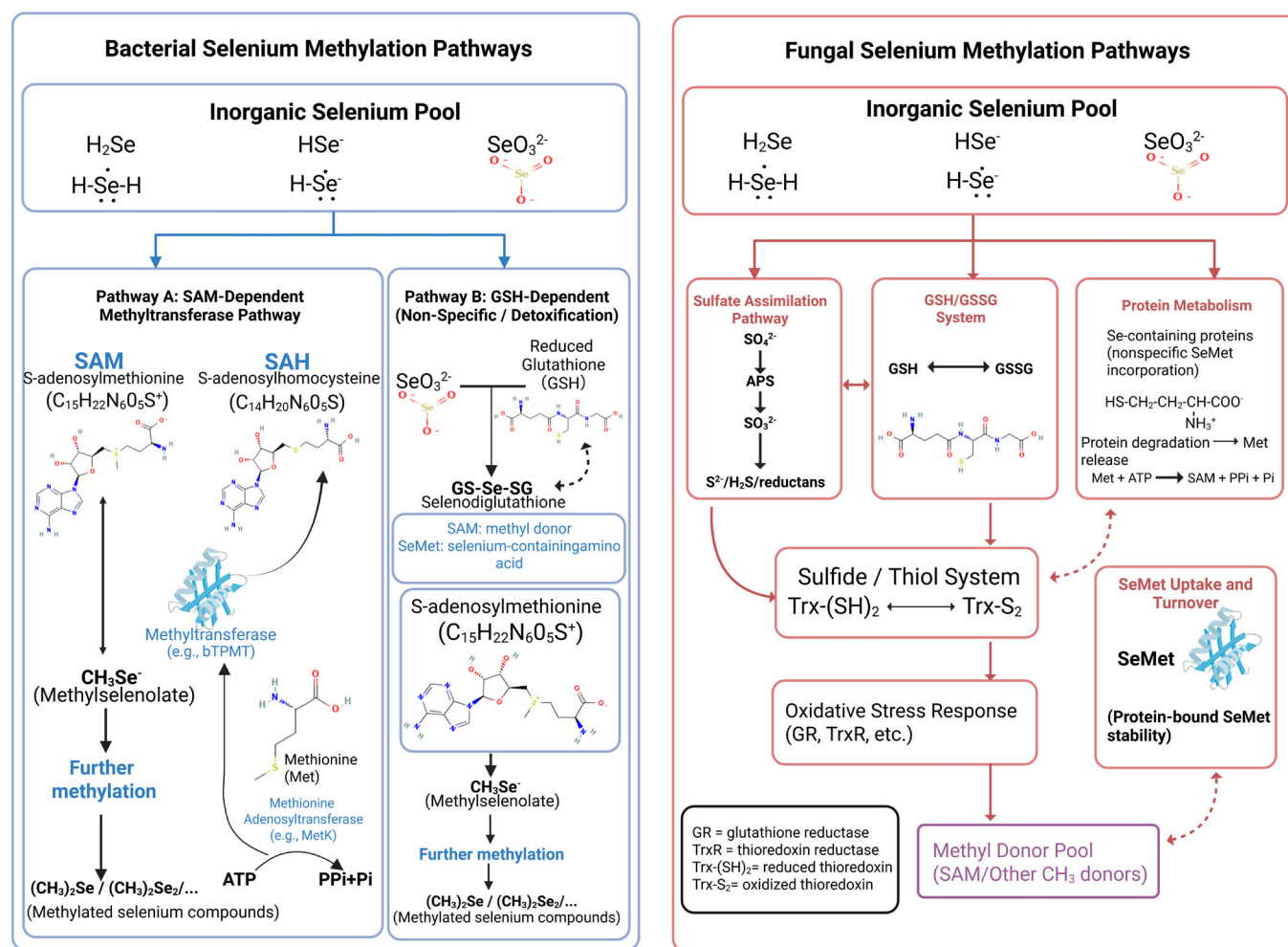


Figure 5. Comparative selenium methylation pathways in bacteria and fungi. Note. The arrow direction indicates the metabolic flow, and the dashed lines imply that there may be many unknown metabolic pathways between them.

4.1. Methylation Routes and Products

4.1.1. Methylation of Reduced Inorganic Selenium

Selenium oxyanions generally undergo reduction or metabolic conversion before formation of methylated products. Se(VI) first enters reductive pathways, while Se(IV) can undergo thiol- and redox-associated conversion toward more reduced intermediates. The identity and sequence of these intermediates vary among organisms, making microbial methylation more appropriately represented as convergent metabolic reactions than as one universally conserved linear pathway.

Direct functional evidence for a defined methyltransferase mechanism is available in bacteria. Expression of a bacterial thiopurine methyltransferase gene in *E. coli* enabled

formation of methylated selenium products from selenite and selected selenium-containing substrates [65,66]. These experiments provide strong evidence for bTPMT-mediated selenium methylation in the studied systems and establish specific methyltransferase activity as one bacterial route to selenium methylation.

Selenium methylation can also arise through substrate-promiscuous reactions associated with sulfur metabolism. Studies in *Pseudomonas tolaasii* showed that sulfur-amino acid availability alters selenium volatilization and the distribution of methylated selenium products [67,68]. These observations support metabolic coupling between selenium and sulfur pathways and show that sulfur status can redirect selenium among volatile and nonvolatile pools.

DMSe and DMDSe should consequently be regarded as related methylated products whose formation depends on reduced selenium availability, methyl-transfer reactions, redox conditions, and microbial background. Their occurrence does not imply an identical sequence of biochemical steps in all microorganisms (Figure 5).

4.1.2. Methylation of Organic Selenium Precursors

Organic selenium compounds can also supply substrates or intermediates for methylated selenium formation. Bacterial methyltransferase systems can act on selected selenium-containing organic substrates in addition to inorganic selenium [65,66]. Organic selenium may enter methylation after cleavage or metabolic remodeling of selenium-containing amino acids, generating lower-molecular-mass intermediates available for further methyl transfer.

SeCys-related compounds can be converted through β -lyase-like or other sulfur-metabolism-associated reactions. Their relative contribution depends on selenium substrate and microbial background. SeMet in selenium-enriched yeasts is frequently retained within proteins and is therefore comparatively stable, although metabolic turnover can eventually return part of this selenium to low-molecular-mass pools.

Organic selenium methylation can therefore be viewed as secondary redistribution of selenium that has already entered biosynthetic metabolism. Direct substrate tracing and species-resolved analysis provide the clearest basis for determining how strongly individual organic selenium pools contribute to methylation (Figure 5).

4.2. Taxon-Dependent Methylation

4.2.1. Selenium Methylation in Bacteria

Bacterial selenium methylation includes several comparatively well-resolved biochemical examples. bTPMT establishes a direct link between a defined methyltransferase and the formation of methylated selenium products [65,66]. This mechanism demonstrates that specific enzyme activities can contribute to selenium methylation.

P. tolaasii illustrates a different mode in which selenium methylation is strongly integrated with sulfur metabolism [67,68]. Altering sulfur-amino acid availability changes both selenium volatilization and the relative distribution of methylated products. This system supports a broader role for sulfur-metabolic substrate promiscuity in bacterial selenium methylation.

These observations indicate that bacterial methylation can arise through more than one biochemical solution. Specific methyltransferases and broader sulfur-metabolic reactions can both contribute, and their relative importance is organism- and condition-dependent.

4.2.2. Selenium Methylation in Fungi

Fungi also form methylated selenium, although mechanistic resolution is more frequently available at the pathway and metabolic-network levels. In *Ganoderma lucidum*, selenium exposure and methylated selenium formation have been associated with changes in thioredoxin-related proteins, glutathione reductase, methionine metabolism, and sulfur-amino acid-related processes [50]. The combined evidence supports coordinated involvement of sulfur and redox metabolism in fungal methylation and identifies candidate processes for targeted validation.

Other fungal studies indicate substantial effects of selenium substrate, dose, growth phase, and culture conditions on methylated selenium formation. Methylation in fungi therefore occurs within a wider metabolic background involving sulfur assimilation, amino acid metabolism, redox buffering, and intracellular organization.

The currently visible bacterial–fungal difference is thus partly a difference in mechanistic resolution. Selected bacterial systems have been resolved to specific methyltransferase activities, while fungal methylation is more often supported by coordinated pathways, omics, speciation, and physiological evidence. Both groups nevertheless show substantial species- and strain-level variation.

4.3. Regulation and Metabolic Consequences of Methylation

Selenium species and dose, sulfur and sulfur-amino acid status, methyl-donor metabolism, redox conditions, oxygen availability, carbon metabolism, and growth phase can alter the amount and composition of methylated selenium [50,67,68].

Sulfur metabolism is particularly influential because sulfur compounds can compete with selenium while sulfur-metabolic enzymes can also accept selenium analogs. The direction and magnitude of the response depend on both the specific sulfur compound and the broader nutritional background. Changes observed following sulfur-amino acid supplementation in *P. tolaasii* illustrate this condition-dependent redistribution [67,68].

Methylation can operate concurrently with other selenium transformations. In *G. lucidum*, methylated selenium formation occurs within a wider Se(IV)-responsive metabolic network that also includes reduction and particulate selenium formation [50]. Methylation therefore competes with assimilatory retention, particle formation, and sequestration for selenium precursors and metabolic resources.

A recurring relationship emerges from these studies. Selenium methylation is shaped by the availability of reduced selenium intermediates together with sulfur and methyl-donor metabolism, while physiological state determines its quantitative contribution. Importantly, methylation does not necessarily result in volatilization. DMSe and DMDSe formation transfers selenium out of retained microbial pools, whereas nonvolatile methylated selenium can remain in intracellular or extracellular soluble fractions.

This distinction has direct implications for selenium mass balance. Systems with appreciable volatile methylation cannot be fully characterized by biomass selenium and residual inorganic selenium alone. Volatile loss, nonvolatile methylated selenium, particulate selenium, and retained organic selenium represent distinct outputs of microbial selenium metabolism.

5. Terminal Selenium Fate

After uptake, reduction, assimilation, and methylation, the remaining nonvolatile selenium is distributed among soluble intracellular pools, intracellular compartments, cell-envelope-associated material, particulate selenium, retained organic selenium, and extracellular pools. Terminal selenium fate therefore has two complementary dimensions: chemical identity and spatial localization. Similar chemical species can have different

physiological meanings depending on whether they occur in the cytoplasm, vacuole, periplasm, cell envelope, cell surface, or extracellular environment.

This distinction is important because selenium recovered with harvested biomass does not necessarily represent intracellularly retained selenium. It can include protein-bound organic selenium, intracellular SeNPs, compartmentalized selenium conjugates, and cell-surface-associated particles. Conversely, extracellular selenium can originate from direct efflux, direct extracellular reduction, or intracellular transformation followed by release.

5.1. Redistribution of Soluble Selenium

5.1.1. Direct Efflux

Direct efflux can decrease cytoplasmic exposure to soluble selenium species and contribute to selenium tolerance. In *S. cerevisiae*, the plasma-membrane sulfite transporter Ssu1 contributes to selenite efflux and resistance, providing direct genetic support for an export phenotype [69]. This mechanism illustrates how transport systems evolved for sulfur-containing substrates can influence selenium homeostasis through substrate promiscuity.

Reduced intracellular selenium accumulation can also result from decreased uptake, increased intracellular conversion, sequestration, altered growth, or surface association. Directional transport assays and compartment-resolved measurements therefore provide the strongest basis for distinguishing true efflux from other causes of reduced cellular accumulation.

In bacterial systems, sulfate-, phosphate-, ABC-, and other anion-associated transport processes can alter selenium homeostasis [26,32], but their contribution to export varies among organisms. These systems are best viewed as candidate components of selenium homeostasis when directional transport has not been directly resolved.

5.1.2. Intracellular Sequestration

Intracellular sequestration lowers cytoplasmic exposure to reactive selenium while retaining selenium within the cell. In *S. cerevisiae*, vacuolar transport involving Ycf1p contributes to sequestration of glutathione-associated selenium species [49]. This process reduces cytoplasmic selenium pressure without necessarily decreasing total cellular selenium.

Efflux and intracellular sequestration can therefore produce similar improvements in tolerance while generating fundamentally different selenium retention profiles. A microorganism can maintain high biomass selenium while reducing cytoplasmic exposure through compartmentalization.

Fungal vacuolar and endomembrane systems provide particularly extensive opportunities for such redistribution. Vesicle trafficking, vacuolar storage, and other compartment-associated processes have been implicated in fungal selenium tolerance and selenium particle handling [49,70,71]. Their contribution varies among species and culture conditions.

5.2. Particulate Selenium Formation

5.2.1. Extracellular Reduction and Post-Formation Export

Extracellular Se(0) can arise through mechanistically distinct routes. In *Shewanella oneidensis* MR-1, addition of electron shuttles such as AQDS or riboflavin can redirect Se(IV) reduction toward an extracellular pathway that depends strongly on the outer-membrane cytochromes OmcA and MtrC, bypassing the periplasmic FccA-associated route and promoting extracellular Se(0) nanoparticle formation [42]. In another *Shewanella* system, secreted riboflavin likewise facilitates extracellular electron transfer to Se(IV) [72].

Extracellular particulate selenium can therefore form directly without prior intracellular particle assembly.

A separate route involves intracellular formation followed by release. Earlier bacterial and yeast studies reported selenium particles in intracellular and extracellular fractions [70,71,73], but the initial site of particle formation was often difficult to determine. Recent work in *E. coli* provided substantially greater mechanistic resolution [18]. Extracellular SeNPs contained a Se(0) core associated with membrane-derived material, while disruption of outer-envelope components, including OmpC or TolA, impaired particle export and increased intracellular particle accumulation without abolishing Se(0) formation. Particle synthesis and particle export can therefore represent experimentally separable steps.

Extracellular detection of SeNPs alone cannot determine their site of biosynthesis. Mechanistic interpretation requires distinction among direct extracellular reduction, intracellular formation followed by export, cell-surface deposition, and redistribution caused by cell disruption or sample processing.

SeNP formation involves more than reduction of Se(IV) to Se(0). Particle size, aggregation state, crystallinity, localization, and biomolecular coating influence physicochemical stability and biological interactions [71,74]. Biogenic SeNP formation should therefore be considered a coupled process of selenium redox transformation and material assembly.

5.2.2. Biomolecular Stabilization of SeNPs

Bacterial SeNPs have been observed in the cytoplasm, periplasm, cell envelope, and extracellular environment [73,75,76]. Recent food-relevant studies extend this evidence. *Pediococcus acidilactici* JD-21 produced protein- and polysaccharide-associated SeNPs, accompanied by selenium-responsive transcriptomic remodeling [12]. *Ligilactobacillus salivarius* DACN818 produced predominantly amorphous SeNPs coated with proteins and polysaccharides, while multi-omics analyses associated particle formation with sulfur/glutathione metabolism, amino acid metabolism, transport, and energy metabolism [13]. Genetic and mutagenesis-based work in *Stenotrophomonas maltophilia* further illustrates the value of resolving the cellular determinants of SeNP synthesis [14].

Fungal particulate selenium frequently occurs in association with intracellular compartments and biomolecular interfaces. Selenium/protein nanoparticles have been observed in vesicle-like structures and extracellular fractions of *S. cerevisiae* under microaerophilic conditions [70]. Other fungi show intracellular, cell-wall-associated, or extracellular particulate selenium [71,77,78].

Proteins, polysaccharides, lipids, and other cellular components [12,18] can modify SeNP nucleation, aggregation, colloidal stability, and surface reactivity [43,74]. These physicochemical properties require direct characterization. Biomolecular coating or improved aqueous dispersion alone does not establish enhanced bioavailability or reduced toxicity.

Particulate Se(0) frequently represents a relatively low-reactivity selenium pool under stress, but particle formation need not constitute permanent terminal storage. Its persistence, remobilization, and metabolic accessibility are species- and condition-dependent. Reported bacterial and fungal SeNP localization and biomolecular stabilization are summarized in Figure 6.

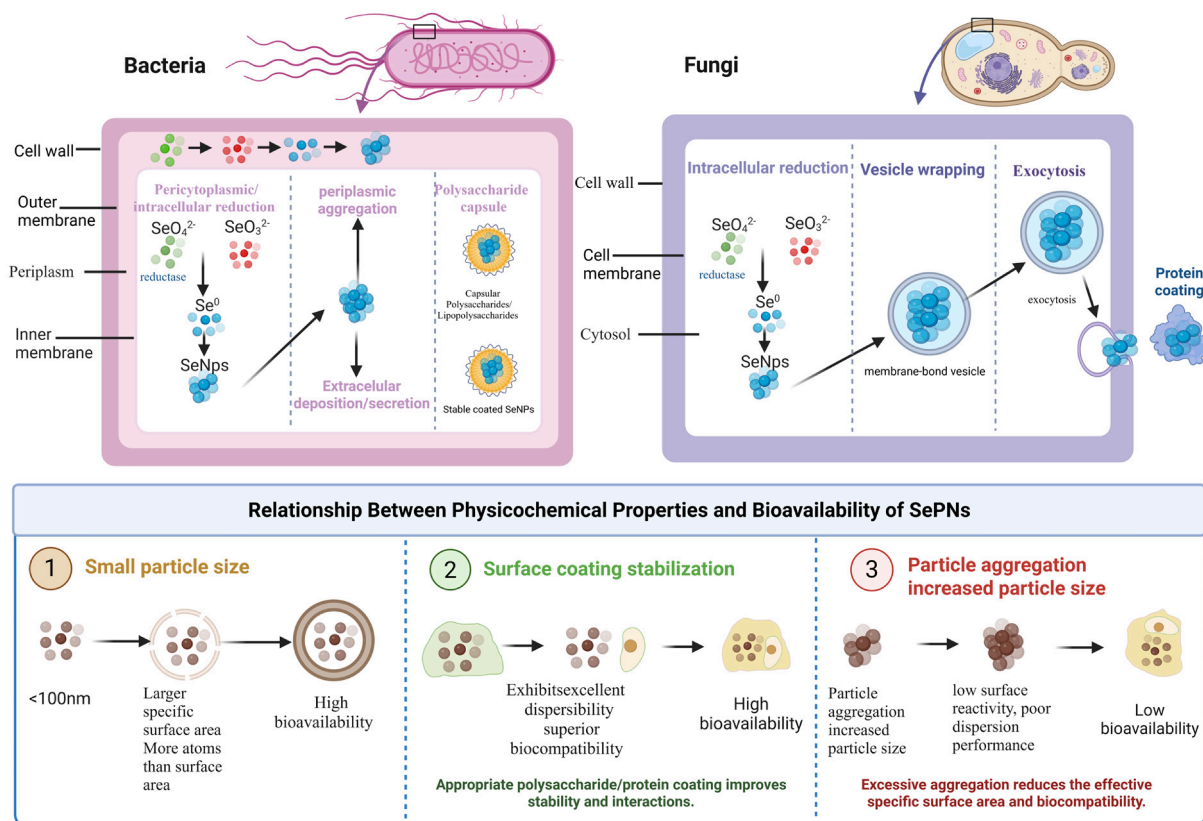


Figure 6. Reported localization, extracellular deposition, and biomolecular stabilization of microbial selenium nanoparticles (SeNPs). Note: Particle localization and biomolecular association can influence physicochemical behavior, whereas bioavailability and safety require direct experimental evaluation.

5.3. Organic Selenium Retention in Microbial Biomass

Organic selenium retention represents a terminal outcome distinct from particulate sequestration. Once selenium enters amino acid and protein metabolism, part of it can remain associated with cellular biomolecules after microbial growth and processing.

Selenium-enriched yeasts commonly retain substantial selenium in SeMet-containing proteins because SeMet can substitute for methionine during protein synthesis [20,21]. The retained fraction depends strongly on strain, selenium source and dose, sulfur nutrition, growth phase, and analytical method. Siderophore-assisted cultivation of *S. cerevisiae* increased cellular selenium accumulation and favored SeMet within the measured selenoamino acid pool [11], demonstrating that microbial physiological state and cultivation design can modify the chemical composition of retained selenium.

Organic selenium retention in bacteria is more heterogeneous. Food-associated lactic acid bacteria can contain SeMet-, SeCys-, and other organic selenium pools whose relative abundance varies among strains and culture conditions [40,59,61]. Genetically encoded SeCys and nonspecific SeMet incorporation represent mechanistically distinct pools and should be distinguished whenever species-resolved information is available.

Direct selenium speciation provides the strongest basis for defining organic selenium retention. Estimation by subtracting measured inorganic selenium from total selenium can also incorporate unmeasured particulate selenium, surface-associated selenium, unidentified compounds, and analytical recovery differences. Organic selenium should therefore be resolved analytically rather than treated as a residual fraction.

5.4. Differences in Terminal Selenium Handling Between Bacteria and Fungi

Bacteria and fungi show recurring differences in the spatial organization of terminal selenium pools. Bacterial selenium can occur in cytoplasmic, periplasmic, cell-envelope-associated, and extracellular compartments. This spatial diversity is particularly evident in taxa capable of periplasmic reduction, extracellular electron transfer, or particle export [18,41,73].

Fungal terminal selenium handling generally shows more prominent intracellular compartmentalization. Vacuolar sequestration, endomembrane trafficking, and vesicle-associated storage or release can decrease cytoplasmic selenium exposure [70,71]. Selenium-enriched yeasts additionally retain substantial selenium in SeMet-containing proteins [11,20,21]. Protein-associated organic selenium and intracellular compartmentalization therefore represent recurring features of many fungal enrichment systems.

These characteristics are tendencies associated with cellular architecture and metabolic specialization rather than mutually exclusive taxonomic outcomes. Bacteria can retain substantial organic selenium, and fungi can form and release SeNPs. Strain background and environmental conditions remain important modifiers.

Nevertheless, a useful comparative relationship emerges. Bacterial terminal selenium handling more frequently involves the periplasm, cell envelope, and extracellular interface, whereas fungal systems more often emphasize intracellular compartmentalization and biomolecular retention. This distinction is most informative when chemical speciation and direct spatial localization are available simultaneously (Table 1).

5.5. Chemical and Spatial Characterization of Terminal Selenium Pools

Chemical speciation and spatial localization provide complementary information on terminal selenium fate. Chemical analysis distinguishes organic selenium, soluble inorganic or conjugated species, and particulate Se(0), while spatial analysis determines whether these pools reside in the cytoplasm, intracellular compartments, cell envelope, biomass surface, or extracellular environment.

Either dimension alone can be misleading. Extracellular Se(0) can originate from direct extracellular reduction or intracellular formation followed by export [18,41,72]. Selenium recovered with microbial biomass can include SeMet-containing proteins, intracellular SeNPs, vacuolar selenium conjugates, and particles associated with the cell surface. Similar total selenium concentrations can therefore represent markedly different cellular processes and terminal selenium pools.

A recurring limitation of current studies is that selenium accumulation or dominant chemical species are often characterized without resolving cellular localization. Combining species-resolved selenium analysis with cell fractionation, imaging, particle characterization, and selenium mass balance offers greater mechanistic resolution than total selenium or a simple organic/inorganic classification.

This chemical-spatial view provides the final mechanistic bridge to the next level of synthesis. The important question is no longer only which pathway is active, but what integrated selenium-transformation characteristic emerges from the combined operation of uptake, redox metabolism, assimilation, methylation, sequestration, and export in a given microorganism.

Table 1. Comparative tendencies in selenium handling by bacteria and fungi. These are recurring tendencies rather than fixed taxonomic rules.

Dimension	Bacteria	Fungi
Cellular organization	Cytoplasm, periplasm, cell envelope, and extracellular interfaces can all contribute to selenium handling.	Vacuoles, endomembranes, and vesicles provide prominent intracellular sequestration and trafficking capacity.
Uptake	Commonly recruits sulfate-, phosphate-, or other anion-related transport systems; direct selenium specificity is demonstrated only in selected systems.	Phosphate-, sulfate-, carboxylate-, ABC/MFS/SLC-related systems have been implicated; strongest direct evidence is concentrated in <i>S. cerevisiae</i> .
Reduction and energy coupling	Reduction can be cytoplasmic, periplasmic, or extracellular; selected selenium-respiring taxa couple oxanion reduction to anaerobic energy conservation.	Reduction is generally non-respiratory and more closely integrated with GSH/NADPH-dependent redox buffering and compartmentalization.
Redox buffering	Thioredoxin, glutathione, NAD(P)H-dependent enzymes, and stress networks can support tolerance and reduction.	GSH/thioredoxin systems and NADPH supply are often major components of selenium stress adaptation.
Assimilation and Sec utilization	SeMet- and SeCys-related pools vary by species; canonical Sec-utilization machinery occurs in selected bacteria.	SeMet-rich protein retention is common in selenium-enriched yeasts; most food-related fungi lack canonical Sec-insertion machinery.
Methylation	Direct bTPMT evidence exists in selected bacteria; sulfur-metabolic promiscuity can also contribute.	Methylation is supported mainly by pathway-, omics-, speciation-, and physiology-level evidence; direct enzyme resolution is more limited.
Efflux and sequestration	Direct transport effects, cell-envelope processes, extracellular reduction, and particle export can all contribute depending on taxon.	Plasma-membrane transport, vacuolar sequestration, and vesicle-associated release are recurring mechanisms.
SeNP localization	Cytoplasmic, periplasmic, envelope-associated, cell-surface, and extracellular SeNPs are reported.	Intracellular, vacuolar/vesicular, cell-wall-associated, and extracellular particulate selenium are reported.
Organic selenium retention	Strain-dependent mixtures of SeMet, SeCys-related compounds, proteins, and other organic pools.	SeMet-containing proteins can constitute a major retained pool in selenium-enriched yeasts.
Evidence profile	Strong direct evidence exists for respiratory reductases and selected transport/export systems, but many food-associated bacterial mechanisms remain multi-omics-supported.	Direct evidence is strongest in <i>S. cerevisiae</i> ; many non-Saccharomyces mechanisms remain pathway-associated.
Integrated tendency	Greater diversity of periplasmic, envelope, and extracellular handling is repeatedly observed in selected taxa.	Greater emphasis on intracellular compartmentalization and biomolecular retention is repeatedly observed in many systems.

6. Selenium Transformation Characteristics and Engineering Perspectives

Together, the mechanisms described above generate strain-specific differences in selenium accumulation, organic selenium retention, particle formation, methylation, intracellular sequestration, and extracellular redistribution. Integrating these processes at the whole-cell level provides a basis for comparing microbial selenium-transformation characteristics and for relating them to strain selection, application matching, and microbial engineering.

6.1. Integrated Characteristics of Selenium Transformation

Microbial selenium-transformation characteristics arise from the combined contributions of selenium uptake, redox processing, sulfur and amino acid metabolism, methylation, intracellular compartmentalization, particle formation, and export. Differences in these processes can generate markedly different selenium outcomes even among strains exposed to similar selenium concentrations. Stronger assimilatory and biosynthetic capacity may favor organic selenium retention, whereas enhanced reductive processing can increase SeNP formation or other stress-associated selenium pools.

These characteristics are better described as a selenium-transformation profile than as fixed or mutually exclusive phenotypes. The relative contribution of each process can shift with selenium dose, nutrient status, oxygen availability, and growth phase. Consequently, total selenium alone provides limited information on microbial selenium physiology because similar accumulation can correspond to substantially different chemical species and cellular locations.

At an integrated level, bacteria and fungi also show recurring tendencies. Bacterial selenium handling more frequently involves diverse cytoplasmic, periplasmic, cell-envelope, and extracellular processes, whereas fungal systems often show stronger redox buffering, intracellular compartmentalization, and SeMet-rich retention. These differences remain strain- and condition-dependent and should therefore be interpreted as comparative tendencies rather than fixed taxonomic rules.

6.2. Application Relevance of Selenium-Transformation Characteristics

The practical value of selenium-transforming microorganisms depends on whether their selenium-transformation characteristics match the intended application. Selenium-enriched *Saccharomyces cerevisiae* combines nutrient-dependent selenium uptake [11,25], sulfur/redox metabolism, intracellular retention, and efficient SeMet incorporation [20,21], making organic selenium retention an important characteristic of yeast-based enrichment systems. Food-associated lactic acid bacteria can display a broader combination of Se(IV) reduction [40,79,80], organic selenium formation [40,61,80], SeNP production [12,13,81], redox adaptation [13,79], and particle stabilization [12,13].

In more complex fermentation systems, the final selenium composition reflects interactions among strain characteristics, microbial community structure, substrate matrix, and cultivation conditions. Mechanistic interpretation therefore requires selenium speciation to be considered together with strain identity and cellular or extracellular localization. Application scenarios are most useful when they demonstrate how microbial physiological differences generate distinct selenium outputs rather than when strains are evaluated only by total selenium enrichment.

6.3. Evidence-Guided Engineering and Research Priorities

6.3.1. Engineering Microbial Selenium Transformation

Engineering strategies should be designed around defined selenium-transformation outcomes rather than maximum selenium accumulation. Potential intervention points include transport systems controlling cellular selenium loading, GSH/thioredoxin and NAD(P)H-dependent redox networks, sulfur and methionine metabolism influencing organic selenium formation, methylation pathways affecting selenium redistribution, and cellular processes involved in SeNP formation, stabilization, and export. Because these processes are interconnected, engineering effects should be evaluated using selenium speciation and cellular localization in addition to growth or total selenium.

Target selection should follow the evidence hierarchy used throughout this review. Mechanisms supported by Level I evidence, including targeted genetic perturbation, complementation, substrate-specific transport, or biochemical validation, provide the strongest candidates for engineering after strain-specific confirmation. Level II and Level III findings remain valuable for identifying candidate intervention points but are better used to guide focused functional validation before causal engineering is attempted. Representative mechanistic systems and their evidence boundaries are summarized in Table 2.

Table 2. Representative genes, proteins, and molecular systems relevant to microbial selenium transformation and their evidence boundaries.

Functional Category	Representative System	Mechanistic Role and Taxon Context	Evidence Level or Boundary	Reference
Transport	<i>CysPUWA</i> /sulfate-permease systems	Sulfur-oxyanion transport can permit Se(VI) entry through substrate overlap; generality varies among taxa.	Direct overlap evidence exists in <i>E. coli</i> ; selenium specificity should not be generalized to all homologs.	[4,23,27]
Transport	<i>Pho84p/Pho87p</i>	Major phosphate-transport contribution to Se(IV) uptake in <i>S. cerevisiae</i> , with phosphate competition.	Level I for the cited <i>S. cerevisiae</i> uptake mechanism.	[25]
Transport	<i>AqpZ/NhaA</i>	Genetically implicated in Se(IV) uptake/homeostasis in <i>R. aquatilis</i> HX2.	Level I for phenotype involvement; detailed substrate kinetics remain system-specific.	[28]
Efflux	<i>Ssu1</i>	Plasma-membrane sulfite pump contributes to selenite efflux and tolerance in <i>S. cerevisiae</i> .	Level I for selenite efflux/tolerance in the cited yeast system.	[69]
Respiratory reduction	<i>SerABC/SrdBCA</i>	Respiratory selenate reductase systems in specialized bacteria.	Level I biochemical/physiological evidence in selenium-respiring bacteria.	[19,36,37,48]

Table 2. Cont.

Functional Category	Representative System	Mechanistic Role and Taxon Context	Evidence Level or Boundary	Reference
Extracellular reduction	<i>MtrC/OmcA</i> and electron shuttles	Electron shuttles can redirect Se(IV) reduction toward an OmcA/MtrC-dependent extracellular route in <i>S. oneidensis</i> MR-1; secreted riboflavin can also facilitate extracellular electron transfer in another <i>Shewanella</i> system.	Direct experimental evidence in defined <i>Shewanella</i> systems; strongly condition-dependent and not a universal Se(IV)-reduction route.	[42,72]
Redox processing	GSH/Trx/SDR-related systems	Support selenium reduction, redox buffering, and stress adaptation in multiple bacteria and fungi.	Level II as a general network-level synthesis; individual components reach stronger evidence in selected systems.	[13,16,20,43,44]
Intracellular sequestration	<i>Ycf1p</i>	Vacuolar transport of glutathione-associated selenium species in <i>S. cerevisiae</i> .	Level I for GSSeSG transport in the cited yeast system.	[49]
Organic Se synthesis	<i>CysK</i> /cysteine-synthase-related enzymes	Can contribute to SeCys-related formation through sulfur-metabolic reactions in selected bacteria.	Functional evidence exists in selected systems; contribution is strain-dependent.	[40,60]
Organic Se retention	Methionine-biosynthesis enzymes/SeMet incorporation	Support SeMet formation and protein-associated retention; SeMet incorporation can occur nonspecifically during translation.	Biochemical/pathway support is strong; quantitative flux contribution varies by strain and condition.	[20,21,40]
Methylation	bTPMT	Catalyzes methylation of inorganic and organic selenium substrates in defined bacterial systems.	Level I for the cited bTPMT-mediated methylation mechanism.	[65,66]
SeNP export	<i>OmpC/TolA</i>	Outer-envelope components are functionally linked to export of membrane-enveloped SeNPs after intracellular formation in <i>E. coli</i> .	Level I for selected export components in the cited <i>E. coli</i> system.	[18]
Regulation	<i>OxyR/CysB/Yap1/Met4</i>	Coordinate oxidative-stress or sulfur-metabolism responses that influence selenium handling.	Established stress/sulfur regulatory functions; they should not be described as universal selenium-specific sensors.	[4,44,45,55]

6.3.2. Key Microbiological Questions

Future work should focus on a limited number of unresolved microbiological questions, particularly the substrate specificity and directionality of selenium transport, quantitative flux among organic selenium, SeNPs, methylated selenium, and extracellular pools, and the extent to which bacterial–fungal differences in selenium handling remain consistent across strains and cultivation conditions. Greater emphasis is also needed on transferring mechanisms established in model or environmental microorganisms to food-relevant yeasts, lactic acid bacteria, *Bacillus*, and filamentous fungi. Integrating targeted genetics, selenium speciation, spatial localization, and quantitative flux analysis will be critical for moving the field from descriptive selenium accumulation toward predictive and mechanism-guided microbial selenium biotransformation. Representative recent studies illustrating improved evidence resolution are summarized in Table 3.

Table 3. Representative recent studies illustrating advances in evidence resolution and microbial selenium transformation.

Year	Microorganism or System	Main Mechanistic Advance	Evidence Level and Boundary	Reference
2023	<i>Rahnella aquatilis</i> HX2	<i>AqpZ</i> and <i>NhaA</i> were genetically implicated in Se(IV) uptake/homeostasis.	Level I for phenotype involvement; mechanistic reference bacterium.	[28]
2023	<i>Saccharomyces cerevisiae</i>	Adaptive evolution and gene validation identified Ssu1-mediated selenite efflux and tolerance.	Level I; food-associated model yeast.	[69]
2023	<i>Lactobacillus casei</i> ATCC 393	Proteomics linked membrane, redox, and stress systems with Se(IV) reduction and SeNP formation.	Level II; food-grade/probiotic context.	[34]
2024	<i>Aureobasidium melanogenum</i> I15	Multi-pathway redox processes were associated with Se(IV) reduction and intra-/extracellular SeNP biogenesis.	Level II overall; fungal mechanistic reference.	[24]
2024	<i>Pichia kudriavzevii</i>	Integrated omics linked transport, sulfur metabolism, redox responses, and selenium transformation.	Level II; food-associated yeast requiring strain-level safety interpretation.	[31]
2025	<i>Lactiplantibacillus plantarum</i> CXG4	Selenium was partitioned into SeNPs and organic pools with Trx/SDR-related processes implicated.	Level II; food-associated bacterium with species-resolved selenium endpoints.	[40]
2025	Fermented goat-milk system	Proteomic/metabolomic evidence linked GST-associated responses with selenium uptake, reduction, and organification.	Level II; food-fermentation system.	[80]

Table 3. Cont.

Year	Microorganism or System	Main Mechanistic Advance	Evidence Level and Boundary	Reference
2026	<i>Saccharomyces cerevisiae</i>	Siderophore-assisted cultivation increased selenium uptake/tolerance and favored SeMet within the measured selenoamino-acid pool.	Level II for the process-to-speciation relationship.	[11]
2026	<i>Pediococcus acidilactici</i> JD-21	Food-grade strain reduced Se(IV), produced protein/polysaccharide-associated SeNPs, and showed Se-responsive transcriptional remodeling.	Level II; directly food-relevant LAB system.	[12]
2026	<i>Paenibacillus polymyxa</i> P10	Se(IV) bioconversion to SeNPs was linked to metabolic adaptation and enzyme-associated processes.	Level II overall; mechanistic contribution is claim-specific.	[15]
2026	<i>Serratia marcescens</i> HBQT	Multi-omics and functional assays linked selenium detoxification with thioredoxin-related reduction, sulfur assimilation, and NADH/NADPH regeneration.	Level II overall with stronger evidence for selected tested components; mechanistic reference bacterium.	[16]
2026	<i>Ligilactobacillus salivarius</i> DACN818	Biomolecule-coated SeNP formation was associated with sulfur/glutathione, amino acid, transport, and energy metabolism.	Level II; food-related LAB.	[13]
2026	<i>Escherichia coli</i>	Outer-envelope components were functionally linked to export of membrane-enveloped SeNPs after intracellular formation.	Level I for selected export components; mechanistic reference bacterium.	[18]
2026	<i>Priestia aryabhattai</i> YL286	Se(IV) reduction and SeNP formation were accompanied by coordinated carbon, glutathione, sulfur/selenium, and stress responses.	Level II; environmental reference supporting integrated stress-adaptation patterns.	[17]

7. Conclusions

Microbial selenium biotransformation is governed by the coordinated interaction of selenium uptake, intracellular processing, metabolic partitioning, and terminal redistribution. Inorganic selenium commonly enters cells through pre-existing nutrient-transport systems, while the resulting cellular selenium loading determines the selenium exposure presented

to downstream metabolism. The available evidence indicates that selenium partitioning is shaped by the balance between this exposure and cellular redox, sulfur-metabolic, biosynthetic, and compartmental capacities. This relationship provides a physiological basis for understanding why similar selenium exposure can generate markedly different terminal selenium pools among microorganisms. The major contribution of this review is the shift from pathway-centered description toward capacity-dependent selenium partitioning analysis.

The comparative analysis of bacteria and fungi further shows that cross-taxon comparison is valuable because it separates broadly shared principles of selenium transformation from taxon- and strain-associated tendencies. Bacteria exhibit greater diversity in cytoplasmic, periplasmic, cell-envelope, and extracellular selenium handling, and selected taxa can couple selenium reduction to electron transfer or energy conservation. Fungal systems more frequently emphasize glutathione-dependent redox buffering, intracellular compartmentalization, and SeMet-rich retention. These differences are not absolute taxonomic rules, but they reveal how cellular architecture, energetic organization, and metabolic resource allocation can bias selenium toward distinct terminal outcomes. Cross-taxon comparison therefore provides more than a descriptive contrast. It helps identify which physiological determinants are likely to be broadly transferable, which mechanisms require taxon-specific validation, and which apparent differences may reflect unequal mechanistic resolution rather than true biological divergence.

These insights have direct implications for both research and application. Microorganisms intended for selenium enrichment can be selected according to the desired selenium-transformation profile, such as enhanced organic selenium retention, controlled SeNP formation, reduced volatile loss, or defined intracellular/extracellular selenium distribution, rather than by total selenium accumulation alone. The same comparative framework can also guide cultivation design by linking process variables to the dominant physiological constraints of different microbial groups and can prioritize engineering targets according to evidence strength. Future progress will therefore depend on combining selenium speciation, spatial localization, quantitative flux analysis, and direct functional validation to move from empirical strain screening toward mechanism-guided selection and control of microbial selenium biotransformation. This approach provides a stronger foundation for selenium-enriched yeast, food-associated bacteria, microbial SeNP production, and other selenium-biotransformation systems in which the identity, retention, and location of selenium are as important as its total concentration.

Author Contributions: Y.D.: Conceptualization, literature search and systematic analysis, and original draft writing. Q.S.: Conceptualization, literature retrieval and classification, and drawing pictures. Y.J.: Manuscript revision, visualization design, and reference collation. B.F.: Manuscript editing, visualization production, and content supplementation. X.L.: Project supervision, framework revision, manuscript review, and final approval. D.L.: Project supervision, research design optimization, critical revision, and final approval. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: No new data were created or analyzed in this study. Data sharing is not applicable to this article.

Acknowledgments: During manuscript preparation, ChatGPT (G5.5) was used for English language polishing, format checking, and figure beautification. The authors have reviewed and edited the output and take full responsibility for the content of this publication.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Sun, Y.; Wang, Z.; Gong, P.; Yao, W.; Ba, Q.; Wang, H. Review on the health-promoting effect of adequate selenium status. *Front. Nutr.* **2023**, *10*, 1136458. [[CrossRef](#)] [[PubMed](#)]
2. Yang, H.; Yang, X.; Ning, Z.; Kwon, S.Y.; Li, M.-L.; Tack, F.M.G.; Kwon, E.E.; Rinklebe, J.; Yin, R. The beneficial and hazardous effects of selenium on the health of the soil-plant-human system: An overview. *J. Hazard. Mater.* **2022**, *422*, 126876. [[CrossRef](#)] [[PubMed](#)]
3. Bai, S.; Zhang, M.; Tang, S.; Li, M.; Wu, R.; Wan, S.; Chen, L.; Wei, X.; Feng, S. Effects and Impact of Selenium on Human Health, A Review. *Molecules* **2025**, *30*, 50. [[CrossRef](#)] [[PubMed](#)]
4. Wang, D.; Rensing, C.; Zheng, S. Microbial reduction and resistance to selenium: Mechanisms, applications and prospects. *J. Hazard. Mater.* **2022**, *421*, 126684. [[CrossRef](#)] [[PubMed](#)]
5. Luo, L.; Hou, X.; Yi, D.; Deng, G.; Wang, Z.; Peng, M. Selenium-Enriched Microorganisms: Metabolism, Production, and Applications. *Microorganisms* **2025**, *13*, 1849. [[CrossRef](#)] [[PubMed](#)]
6. Ma, Q.; Xu, X.; An, K.; Cai, J.; Meng, L. Sensory quality and metabolite dynamics in an organic selenium-enriched milk fermented by *Geotrichum candidum*. *Food Res. Int.* **2025**, *202*, 115672. [[CrossRef](#)] [[PubMed](#)]
7. Gaglio, R.; Pescuma, M.; Madrid-Albarrán, Y.; Franciosi, E.; Moschetti, G.; Francesca, N.; Mozzi, F.; Settanni, L. Selenium bio-enrichment of Mediterranean fruit juices through lactic acid fermentation. *Int. J. Food Microbiol.* **2021**, *354*, 109248. [[CrossRef](#)] [[PubMed](#)]
8. Larsen, E.H.; Hansen, M.; Paulin, H.; Moesgaard, S.; Reid, M.; Rayman, M. Speciation and bioavailability of selenium in yeast-based intervention agents used in cancer chemoprevention studies. *J. AOAC Int.* **2004**, *87*, 225–232. [[CrossRef](#)]
9. Zhou, J.; Obianwuna, U.E.; Zhang, L.; Liu, Y.; Zhang, H.; Qiu, K.; Wang, J.; Qi, G.; Wu, S. Comparative effects of selenium-enriched lactobacilli and selenium-enriched yeast on performance, egg selenium enrichment, antioxidant capacity, and ileal microbiota in laying hens. *J. Anim. Sci. Biotechnol.* **2025**, *16*, 27. [[CrossRef](#)] [[PubMed](#)]
10. Wells, M.; Stolz, J.F. Microbial selenium metabolism: A brief history, biogeochemistry and ecophysiology. *FEMS Microbiol. Ecol.* **2020**, *96*, fiae209. [[CrossRef](#)] [[PubMed](#)]
11. Du, W.-T.; Wei, Y.-R.; Zhao, X.; Gou, Q.-Q.; Ali, O.H.; Wang, W.-D.; Xu, J.-N.; Feng, Z.-P.; Zhang, X.-G. Efficient biosynthesis of selenium-enriched *Saccharomyces cerevisiae* via siderophore-assisted selenite uptake and biotransformation. *Bioresour. Technol.* **2026**, *445*, 134145. [[CrossRef](#)] [[PubMed](#)]
12. Fan, S.; Li, J.; Zhao, X.; He, Y.; Li, Z.; Wang, Z.; Gao, C.; Ma, Y.; Li, J.; Chen, X.; et al. Biogenic selenium nanoparticles from food-grade *Pediococcus acidilactici* JD-21: Selenite bioreduction, enhanced probiotic traits, and antioxidant protection. *Foods* **2026**, *15*, 2440. [[CrossRef](#)] [[PubMed](#)]
13. Guo, Q.; Zhou, H.; Huang, D.; Xiao, Q.; Wang, J.; Suo, H.; Chen, X. Biosynthesis of selenium nanoparticles by *Ligilactobacillus salivarius* DACN818: Characterization and mechanism. *J. Agric. Food Chem.* **2026**, *74*, 15126–15137. [[CrossRef](#)] [[PubMed](#)]
14. Wan, F.; Wang, Y.; Wang, X.; Xue, H.; Hang, Y.; Pei, C.; Lu, Y. Selenium nanoparticle synthesis in *Stenotrophomonas maltophilia*: Mutagenesis and molecular mechanisms. *Biochimie* **2026**, *249*, 118–126. [[CrossRef](#)] [[PubMed](#)]
15. Zhou, J.; Sang, C.; Liu, Z.; Li, W.; Sun, Y.; Zhang, J.; Wang, S.; Zeng, X. Bioconversion of selenite to selenium nanoparticles by *Paenibacillus polymyxa* P10: Metabolic basis and potential for wastewater treatment. *Appl. Environ. Microbiol.* **2026**, *92*, e0070426. [[CrossRef](#)] [[PubMed](#)]
16. Zhang, Y.; Lin, J.; He, M.; Li, S.; Liu, Y.; Feng, H.; Geng, Y.; Li, T.; Zhang, L.; Xia, J.; et al. Integrated multi-omics analysis reveals mechanism of metabolic reprogramming enabling bacterial selenite detoxification and selenium nanoparticles biogenesis by *Serratia marcescens* HBQT. *Bioresour. Technol.* **2026**, *456*, 134925. [[CrossRef](#)] [[PubMed](#)]
17. Jing, L.; Hu, C.; Yang, M.; Dang, Y.; Jia, Y.; Hong, J. Selenite tolerance, reduction performance and biogenic selenium nanoparticle biosynthesis by *Priestia aryabhattai* YL286 isolated from the wheat phyllosphere. *Int. Microbiol.* **2026**. *Epub ahead of printing.* [[CrossRef](#)] [[PubMed](#)]
18. Ochi, A.; Shibamoto, K.; Toyotake, Y.; Fujioka, D.; Yokoyama, F.; Okanishi, H.; Imai, T.; Fujita, D.; Aono, R.; Inoue, M.; et al. Biosynthesis and export of membrane-enveloped selenium nanoparticles by *Escherichia coli*. *Environ. Sci. Technol.* **2026**, *60*, 4213–4227. [[CrossRef](#)] [[PubMed](#)]
19. Nancharaiyah, Y.V.; Lens, P.N.L. Ecology and biotechnology of selenium-respiring bacteria. *Microbiol. Mol. Biol. Rev.* **2015**, *79*, 61–80. [[CrossRef](#)] [[PubMed](#)]
20. Kieliszek, M.; Blazejak, S.; Gientka, I.; Bzducha-Wróbel, A. Accumulation and metabolism of selenium by yeast cells. *Appl. Microbiol. Biotechnol.* **2015**, *99*, 5373–5382. [[CrossRef](#)] [[PubMed](#)]
21. Wang, H.; Yang, S.; Chen, Y.; Wang, Z.; Yuan, Y.; Yue, T. Comprehensive distribution and species of selenium in Se-enriched *Pichia kudriavzevii* 1845. *Food Chem.* **2024**, *438*, 137966. [[CrossRef](#)] [[PubMed](#)]

22. Sabuda, M.C.; Mejia, J.; Wedal, M.; Kuester, B.; Xu, T.; Santelli, C.M. The effect of organic carbon form and concentration on fungal selenite reduction. *Appl. Geochem.* **2022**, *136*, 105163. [[CrossRef](#)]
23. Eswayah, A.S.; Smith, T.J.; Gardiner, P.H.E. Microbial transformations of selenium species of relevance to bioremediation. *Appl. Environ. Microbiol.* **2016**, *82*, 4848–4859. [[CrossRef](#)] [[PubMed](#)]
24. Xue, S.-J.; Zhang, X.-T.; Li, X.-C.; Zhao, F.-Y.; Shu, X.; Jiang, W.-W.; Zhang, J.-Y. Multi-pathways-mediated mechanisms of selenite reduction and elemental selenium nanoparticles biogenesis in the yeast-like fungus *Aureobasidium melanogenum* I15. *J. Hazard. Mater.* **2024**, *470*, 134204. [[CrossRef](#)] [[PubMed](#)]
25. Lazard, M.; Blanquet, S.; Fisicaro, P.; Labarraque, G.; Plateau, P. Uptake of selenite by *Saccharomyces cerevisiae* involves the high and low affinity orthophosphate transporters. *J. Biol. Chem.* **2010**, *285*, 32029–32037. [[CrossRef](#)] [[PubMed](#)]
26. Lindblow-Kull, C.; Kull, F.J.; Shrift, A. Single transporter for sulfate, selenate, and selenite in *Escherichia coli* K-12. *J. Bacteriol.* **1985**, *163*, 1267–1269. [[CrossRef](#)] [[PubMed](#)]
27. Sirko, A.; Zatyka, M.; Sadowy, E.; Hulanicka, D. Sulfate and thiosulfate transport in *Escherichia coli* K-12: Evidence for a functional overlapping of sulfate- and thiosulfate-binding proteins. *J. Bacteriol.* **1995**, *177*, 4134–4136. [[CrossRef](#)] [[PubMed](#)]
28. Xu, Q.; Zhang, S.; Ren, J.; Li, K.; Li, J.; Guo, Y. Uptake of Selenite by *Rahnella aquatilis* HX2 Involves the Aquaporin AqpZ and Na⁺/H⁺ Antiporter NhaA. *Environ. Sci. Technol.* **2023**, *57*, 2371–2379. [[CrossRef](#)] [[PubMed](#)]
29. van der Ploeg, J.R.; Iwanicka-Nowicka, R.; Kertesz, M.A.; Leisinger, T.; Hryniewicz, M.M. Involvement of CysB and Cbl regulatory proteins in expression of the tauABCD operon and other sulfate starvation-inducible genes in *Escherichia coli*. *J. Bacteriol.* **1997**, *179*, 7671–7678. [[CrossRef](#)] [[PubMed](#)]
30. Jia, H.L.; Huang, S.W.; Cheng, S.; Zhang, X.W.; Chen, X.; Zhang, Y.S.; Wang, J.; Wu, L.F. Novel mechanisms of selenite reduction in *Bacillus subtilis* 168: Confirmation of multiple-pathway mediated remediation based on transcriptome analysis. *J. Hazard. Mater.* **2022**, *433*, 128834. [[CrossRef](#)] [[PubMed](#)]
31. Wang, H.; Chen, Y.; Wang, Z.; Yuan, Y.; Yue, T. Integrated analysis of transcriptome, proteome and non-targeted metabolome for exploring the mechanism of selenium biotransformation in *Pichia kudriavzevii*. *Food Biosci.* **2024**, *61*, 104958. [[CrossRef](#)]
32. Ullah, A.; Yin, X.; Naveed, M.; Aslam, S.; Chan, M.W.H.; Bo, S.; Wang, F.H.; Xu, B.; Xu, B.C.; Yu, Z. Study of selenium enrichment metabolomics in *Bacillus subtilis* BSN313 via transcriptome analysis. *Biotechnol. Appl. Biochem.* **2024**, *71*, 609–626. [[CrossRef](#)] [[PubMed](#)]
33. Gao, L.; Li, X.; Li, Y.; Zhang, Z.; Wang, J.; Xu, C.; Wu, X. Biochemical characterization, biosynthesis mechanism, and functional evaluation of selenium-enriched *Aspergillus oryzae* A02. *Int. J. Biol. Macromol.* **2024**, *275*, 133714. [[CrossRef](#)] [[PubMed](#)]
34. Qiao, L.; Dou, X.A.; Song, X.F.; Chang, J.J.; Zeng, X.A.; Zhu, L.X.; Xu, C.L. Selenite bioremediation by food-grade probiotic *Lactobacillus casei* ATCC 393: Insights from Proteomics Analysis. *Microbiol. Spectr.* **2023**, *11*, e0065923. [[CrossRef](#)] [[PubMed](#)]
35. Hao, W.H.; Li, Y.; Guo, H.L.; Chen, J.; Pi, F.W. Co-metabolism of Na⁺/K⁺ ion regulated physiological enhancement on selenium-accumulation in *Saccharomyces* yeasts. *J. Sci. Food Agric.* **2024**, *104*, 4136–4144. [[CrossRef](#)] [[PubMed](#)]
36. Macy, J.M.; Rech, S.; Auling, G.; Dorsch, M.; Stackebrandt, E.; Sly, L.I. *Thauera selenatis* gen. nov., sp. nov., a member of the beta subclass of Proteobacteria with a novel type of anaerobic respiration. *Int. J. Syst. Bacteriol.* **1993**, *43*, 135–142. [[CrossRef](#)] [[PubMed](#)]
37. Schröder, I.; Rech, S.; Krafft, T.; Macy, J.M. Purification and characterization of the selenate reductase from *Thauera selenatis*. *J. Biol. Chem.* **1997**, *272*, 23765–23768. [[CrossRef](#)] [[PubMed](#)]
38. Tan, Y.; Wang, Y.; Wang, Y.; Xu, D.; Huang, Y.; Wang, D.; Wang, G.; Rensing, C.; Zheng, S. Novel mechanisms of selenate and selenite reduction in the obligate aerobic bacterium *Comamonas testosteroni* S44. *J. Hazard. Mater.* **2018**, *359*, 129–138. [[CrossRef](#)] [[PubMed](#)]
39. Zheng, S.X.; Su, J.; Wang, L.; Yao, R.; Wang, D.; Deng, Y.J.; Wang, R.; Wang, G.J.; Rensing, C. Selenite reduction by the obligate aerobic bacterium *Comamonas testosteroni* S44 isolated from a metal-contaminated soil. *BMC Microbiol.* **2014**, *14*, 204. [[CrossRef](#)] [[PubMed](#)]
40. Li, Y.; Wang, T.; Liu, D.; Zhang, C.; Wu, W.; Yi, H.; Zhang, J. Biotransformation of inorganic selenium into selenium nanoparticles and organic selenium by *Lactiplantibacillus plantarum* CXG4. *Food Biosci.* **2025**, *65*, 106060. [[CrossRef](#)]
41. Xiao, H.; Tan, J.; Li, M.; Yuan, Z.; Zhou, H. The mechanism of Se(IV) multisystem resistance in *Stenotrophomonas* sp. EGS12 and its prospect in selenium-contaminated environment remediation. *J. Hazard. Mater.* **2023**, *452*, 131358. [[CrossRef](#)] [[PubMed](#)]
42. Zhang, X.; Fan, W.-Y.; Yao, M.-C.; Yang, C.-W.; Sheng, G.-P. Redox state of microbial extracellular polymeric substances regulates reduction of selenite to elemental selenium accompanying with enhancing microbial detoxification in aquatic environments. *Water Res.* **2020**, *172*, 115538. [[CrossRef](#)] [[PubMed](#)]
43. Xia, Z.C.; Cheng, Y.Y.; Kong, W.Q.; Shi, X.Y.; Yang, T.; Wang, M.Y.; Huang, F.; Wu, C. Electron shuttles alter selenite reduction pathway and redistribute formed Se(0) nanoparticles. *Process Biochem.* **2016**, *51*, 408–413. [[CrossRef](#)]
44. Zhang, G.; Yao, X.; Wang, C.; Wang, D.; Wei, G. Transcriptome analysis reveals the mechanism underlying improved glutathione biosynthesis and secretion in *Candida utilis* during selenium enrichment. *J. Biotechnol.* **2019**, *304*, 89–96. [[CrossRef](#)] [[PubMed](#)]
45. Mapelli, V.; Hillestrom, P.R.; Patil, K.; Larsen, E.H.; Olsson, L. The interplay between sulphur and selenium metabolism influences the intracellular redox balance in *Saccharomyces cerevisiae*. *FEMS Yeast Res.* **2012**, *12*, 20–32. [[CrossRef](#)] [[PubMed](#)]

46. Tarze, A.; Dauplais, M.; Grigoras, I.; Lazard, M.; Ha-Duong, N.-T.; Barbier, F.; Blanquet, S.; Plateau, P. Extracellular Production of Hydrogen Selenide Accounts for Thiol-assisted Toxicity of Selenite against *Saccharomyces cerevisiae*. *J. Biol. Chem.* **2007**, *282*, 8759–8767. [[CrossRef](#)] [[PubMed](#)]
47. Macy, J.M.; Lawson, S. Cell yield (YM) of *Thauera selenatis* grown anaerobically with acetate plus selenate or nitrate. *Arch. Microbiol.* **1993**, *160*, 295–298. [[CrossRef](#)]
48. Kuroda, M.; Yamashita, M.; Miwa, E.; Imao, K.; Fujimoto, N.; Ono, H.; Nagano, K.; Sei, K.; Ike, M. Molecular Cloning and Characterization of the *srdBCA* operon, encoding the respiratory selenate reductase complex, from the selenate-reducing bacterium *Bacillus selenatarsenatis* SF-1. *J. Bacteriol.* **2011**, *193*, 2141–2148. [[CrossRef](#)] [[PubMed](#)]
49. Lazard, M.; Ha-Duong, N.T.; Mounié, S.; Perrin, R.; Plateau, P.; Blanquet, S. Selenodiglutathione uptake by the *Saccharomyces cerevisiae* vacuolar ATP-binding cassette transporter Ycf1p. *FEBS J.* **2011**, *278*, 4112–4121. [[CrossRef](#)] [[PubMed](#)]
50. Xu, M.M.; Zhu, S.; Wang, Q.; Chen, L.; Li, Y.R.; Xu, S.; Gu, Z.H.; Shi, G.Y.; Ding, Z.Y. Pivotal biological processes and proteins for selenite reduction and methylation in *Ganoderma lucidum*. *J. Hazard. Mater.* **2023**, *444*, 130409. [[CrossRef](#)] [[PubMed](#)]
51. Zhang, Y.; Jin, J.; Huang, B.; Ying, H.; He, J.; Jiang, L. Selenium metabolism and selenoproteins in Prokaryotes: A bioinformatics perspective. *Biomolecules* **2022**, *12*, 917. [[CrossRef](#)] [[PubMed](#)]
52. Kayrouz, C.M.; Huang, J.; Hauser, N.; Seyedsayamdost, M.R. Biosynthesis of selenium-containing small molecules in diverse microorganisms. *Nature* **2022**, *610*, 199–204. [[CrossRef](#)] [[PubMed](#)]
53. Xu, Y.; Wu, S.; Wang, P.; Wei, L.; Li, H. Label-free quantitative proteomic analysis of the mechanism of salt stress promoting selenium enrichment in *Lactobacillus rhamnosus*. *J. Proteom.* **2022**, *265*, 104663. [[CrossRef](#)] [[PubMed](#)]
54. Zhu, L.; Long, P.; Hu, M.; Wang, L.; Shao, Y.; Cheng, S.; Dong, X.; He, Y. Insight into selenium biofortification and the selenite metabolic mechanism of *Monascus ruber* M7. *Food Chem.* **2024**, *455*, 139740. [[CrossRef](#)] [[PubMed](#)]
55. LeBlanc, K.L.; Mester, Z. Compilation of selenium metabolite data in selenized yeasts. *Metallomics* **2021**, *13*, mfab031. [[CrossRef](#)] [[PubMed](#)]
56. Funkner, K.; Poehlein, A.; Jehmlich, N.; Egelkamp, R.; Daniel, R.; von Bergen, M.; Rother, M. Proteomic and transcriptomic analysis of selenium utilization in *Methanococcus maripaludis*. *mSystems* **2024**, *9*, e0133823. [[CrossRef](#)] [[PubMed](#)]
57. Mariotti, M.; Salinas, G.; Gabaldón, T.; Gladyshev, V.N. Utilization of selenocysteine in early-branching fungal phyla. *Nat. Microbiol.* **2019**, *4*, 759–765. [[CrossRef](#)] [[PubMed](#)]
58. Yang, H.M.; Wang, Y. From fragmentation to resolution: High-fidelity genome assembly of *Zancudomyces culisetae* through comparative insights from PacBio, Nanopore, and Illumina sequencing. *G3 Genes Genomes Genet.* **2025**, *15*, jkaf204. [[CrossRef](#)] [[PubMed](#)]
59. Castañeda-Ovando, A.; Segovia-Cruz, J.A.; Flores-Aguilar, J.F.; Rodríguez-Serrano, G.M.; Salazar-Pereda, V.; Ramírez-Godínez, J.; Contreras-López, E.; Jaimez-Ordaz, J.; González-Olivares, L.G. Serine-enriched minimal medium enhances conversion of selenium into selenocysteine by *Streptococcus thermophilus*. *J. Dairy Sci.* **2019**, *102*, 6781–6789. [[CrossRef](#)] [[PubMed](#)]
60. Escobar-Ramírez, M.C.; Rodríguez-Serrano, G.M.; Zúñiga-León, E.; García-Montes, M.A.; Pérez-Escalante, E.; González-Olivares, L.G. Selenocysteine formation by *Enterococcus faecium* ABMC-05 follows a mechanism that is not dependent on genes *sclA* and *sclD* but on gene *cysK*. *Fermentation* **2023**, *9*, 684. [[CrossRef](#)]
61. Sun, Y.; Wang, H.; Zhou, L.; Chang, M.; Yue, T.; Yuan, Y.; Shi, Y. Distribution characteristics of organic selenium in Se-enriched *Lactobacillus* (*Lactobacillus paracasei*). *LWT—Food Sci. Technol.* **2022**, *165*, 113699. [[CrossRef](#)]
62. Bertels, L.K.; Murillo, L.F.; Heinisch, J.J. The pentose phosphate pathway in yeasts—more than a poor cousin of glycolysis. *Biomolecules* **2021**, *11*, 725. [[CrossRef](#)] [[PubMed](#)]
63. Reamer, D.C.; Zoller, W.H. Selenium biomethylation products from soil and sewage sludge. *Science* **1980**, *208*, 500–502. [[CrossRef](#)] [[PubMed](#)]
64. Ruiz-Fresneda, M.A.; Eswayah, A.S.; Romero-González, M.; Gardiner, P.H.E.; Solari, P.L.; Merroun, M.L. Chemical and structural characterization of SeIV biotransformations by *Stenotrophomonas bentonitica* into Se0 nanostructures and volatiles Se species. *Environ. Sci. Nano* **2020**, *7*, 2140–2155. [[CrossRef](#)]
65. Ranjard, L.; Prigent-Combaret, C.; Nazaret, S.; Cournoyer, B. Methylation of inorganic and organic selenium by the bacterial thiopurine methyltransferase. *J. Bacteriol.* **2002**, *184*, 3146–3149. [[CrossRef](#)] [[PubMed](#)]
66. Ranjard, L.; Nazaret, S.; Cournoyer, B. Freshwater bacteria can methylate selenium through the thiopurine methyltransferase pathway. *Appl. Environ. Microbiol.* **2003**, *69*, 3784–3790. [[CrossRef](#)] [[PubMed](#)]
67. Liu, Y.; Hedwig, S.; Schäffer, A.; Lenz, M.; Martinez, M. Sulfur amino acid status controls selenium methylation in *Pseudomonas tolaasii*: Identification of a novel metabolite from promiscuous enzyme reactions. *Appl. Environ. Microbiol.* **2021**, *87*, e0010421. [[CrossRef](#)] [[PubMed](#)]
68. Liu, Y.; Schäffer, A.; Martinez, M.; Lenz, M. Environmental selenium volatilization is possibly conferred by promiscuous reactions of the sulfur metabolism. *Chemosphere* **2023**, *345*, 140548. [[CrossRef](#)] [[PubMed](#)]

69. Gong, A.; Liu, W.Y.; Lin, Y.L.; Huang, L.L.; Xie, Z.X. Adaptive laboratory evolution reveals the selenium efflux process to improve selenium tolerance mediated by the membrane sulfite pump in *Saccharomyces cerevisiae*. *Microbiol. Spectr.* **2023**, *11*, e0132623. [[CrossRef](#)] [[PubMed](#)]
70. Zhang, L.; Li, D.P.; Gao, P. Expulsion of selenium/protein nanoparticles through vesicle-like structures by *Saccharomyces cerevisiae* under microaerophilic environment. *World J. Microbiol. Biotechnol.* **2012**, *28*, 3381–3386. [[CrossRef](#)] [[PubMed](#)]
71. Liang, X.J.; Perez, M.; Nwoko, K.C.; Egbers, P.; Feldmann, J.; Csetenyi, L.; Gadd, G.M. Fungal formation of selenium and tellurium nanoparticles. *Appl. Microbiol. Biotechnol.* **2019**, *103*, 7241–7259. [[CrossRef](#)] [[PubMed](#)]
72. Cheng, M.M.; Zhang, H.K.; Li, Y.; Chen, W.H. Riboflavin secreted by *Shewanella* sp. FDL-2 facilitates its reduction of Se(IV) and Te(IV) by promoting electron transfer. *RSC Adv.* **2023**, *13*, 34445–34454. [[CrossRef](#)] [[PubMed](#)]
73. Butler, C.S.; Debieux, C.M.; Dridge, E.J.; Splatt, P.; Wright, M. Biomineralization of selenium by the selenate-respiring bacterium *Thauera selenatis*. *Biochem. Soc. Trans.* **2012**, *40*, 1239–1243. [[CrossRef](#)] [[PubMed](#)]
74. Tugarova, A.V.; Kamnev, A.A. Proteins in microbial synthesis of selenium nanoparticles. *Talanta* **2017**, *174*, 539–547. [[CrossRef](#)] [[PubMed](#)]
75. Li, R.X.; Chen, W.Q.; Huang, S.Y.; Jiang, D.H.; Zhu, Z.J.; Li, C.; Huang, X.J. Three bacterial strains efficiently reduce selenite to selenium nanoparticles in cell membranes. *BMC Microbiol.* **2025**, *25*, 564. [[CrossRef](#)] [[PubMed](#)]
76. Oremland Ronald, S.; Herbel Mitchell, J.; Blum Jodi, S.; Langley, S.; Beveridge Terry, J.; Ajayan Pulickel, M.; Sutto, T.; Ellis Amanda, V.; Curran, S. Structural and spectral features of selenium nanospheres produced by se-respiring bacteria. *Appl. Environ. Microbiol.* **2004**, *70*, 52–60. [[CrossRef](#)] [[PubMed](#)]
77. Negi, B.B.; Sinharoy, A.; Pakshirajan, K. Selenite removal from wastewater using fungal pelleted airlift bioreactor. *Environ. Sci. Pollut. Res.* **2020**, *27*, 992–1003. [[CrossRef](#)] [[PubMed](#)]
78. Sinharoy, A.; Lens, P.N.L. Selenite and tellurite reduction by *Aspergillus niger* fungal pellets using lignocellulosic hydrolysate. *J. Hazard. Mater.* **2022**, *437*, 129333. [[CrossRef](#)] [[PubMed](#)]
79. Wang, L.; Ju, J.; Xie, H.; Qiao, F.; Luo, Q.; Zhou, L. Comparative study on growth and metabolomic profiles of six *Lactobacilli* strains by sodium selenite. *Microorganisms* **2024**, *12*, 1937. [[CrossRef](#)] [[PubMed](#)]
80. Guo, A.; Jia, W. Metabolomics and proteomics analysis elucidate the regulation of selenium uptake and metabolism by selenite via glutathione S-transferase in fermented goat milk. *Food Chem.* **2025**, *491*, 145328. [[CrossRef](#)] [[PubMed](#)]
81. Lei, X.; Peng, Y.; Li, Y.; Chen, Q.; Shen, Z.; Yin, W.; Lemiasheuski, V.; Xu, S.; He, J. Effects of selenium nanoparticles produced by *Lactobacillus acidophilus* HN23 on lipid deposition in WRL68 cells. *Bioorganic Chem.* **2024**, *145*, 107165. [[CrossRef](#)] [[PubMed](#)]

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