

Developments in the study and applications of bacterial transformations of selenium species

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Developments in the Study and Applications of Bacterial Transformations of Selenium Species

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3 1 Developments in the Study and Applications of **Bacterial** Transformations of Selenium

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21 Abstract

22 Microbial bio-transformations of the essential trace element selenium are now
23 recognised to occur among a wide variety of microorganisms. These transformations
24 are used to convert the element into its assimilated form of selenocysteine, which is at
25 the active centre of a number of key enzymes, **and to produce selenium nanoparticles,**
26 **quantum dots, metal selenides and methylated selenium species that are indispensable**
27 **for biotechnological and bioremediation applications.** The focus of this review is to
28 present the state-of-the-art of all aspects of the investigations into the bacterial
29 transformations of selenium species, and to consider the characterization and
30 **biotechnological uses of these transformations and their products.**

31 Keywords

32 selenium species, **bacterial** selenium bio-transformation, selenium nanoparticles,
33 selenides, selenium-containing quantum dots, methylated selenium species

34 Introduction

35 The phylogenetical diversity and distribution of **bacterial** Se bio-transformations are
36 now recognised to be widespread. (1, 2) A variety of methods and techniques have been
37 used in a bid to elucidate the different mechanisms that are involved in the microbial
38 transformation of selenium species. The emphasis in most studies has been to
39 demonstrate that selenite or selenate is transformed by the bacterium or bacterial
40 consortia. Invariably, the products from such reactions are selenium nanoparticles
41 (SeNPs), metal selenide **and** quantum dots (3), or the methylated selenium species
42 **concomitantly produced** in the headspace and solution medium. (4-6) In other
43 investigations, the focus was to localize where the biotransformation reactions are
44 occurring in the cells (see **Scheme 1**). The experiments were conducted assuming that
45 the detected selenium species are produced solely by the biochemical reactions that take
46 place in the microorganisms under the incubation conditions. However, this may be a
47 simplified interpretation of what is likely to be occurring. Until recently, complex
48 interactions between bacterium cells forming biofilms, and the probability of abiotic
49 reactions involving selenium-containing reactants generated by the biotic processes
50 have been given scant attention. (4, 7, 8)

51 The aim of this review is to critically appraise information from recent literature on the
52 microbial transformations of selenium species, their characterization, and to examine
53 the developments and potential biotechnological uses of **bacterial** inspired selenium-
54 containing products **and related processes.**

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58 Outline of mechanisms of bacterial transformation of selenium species

59 Over the last decade, to the best of our knowledge, there have been no reports of the
60 direct oxidation of reduced selenium compounds by microorganisms. Solubilization of
61 elemental selenium (Se^0) can be mediated by microbial release of reactive sulfur
62 compounds such as sulfite (SO_3^{2-}), sulfide (S^{2-}) and thiosulfate ($\text{S}_2\text{O}_3^{2-}$) via the
63 formation of soluble selenosulfur complexes, as has recently been reported by Goff et
64 al. for a *Bacillus* sp., presenting an example of “bio-induced” chemical weathering of
65 Se^0 . (9) Thus from the applied microbiology and biotechnology view point the
66 reduction reactions of selenium oxyanions producing Se^0 or selenides Se^{2-} , which
67 ultimately form nanostructures, and volatile selenium species, are of particular interest.

68 The oxyanion, selenate (SeO_4^{2-}) can be reduced by microorganisms during the course
69 of anaerobic respiration, where it acts as the ultimate electron acceptor, and the process
70 is mediated by selenate reductases. This has been shown for bacteria such as *Salmonella*
71 *enterica* (10) and *E. coli*. (11) For *Thauera selenatis*, its selenate reductase was shown
72 to be very similar to thermostable nitrate reductases (pNAR) found in
73 hyperthermophilic archaea. (12) Other anaerobic methane-oxidizing bacteria have been
74 recently shown to be capable of coupling methane oxidation to selenate reduction (13),
75 suggesting a possible link between the biogeochemical cycles of selenium and methane.
76 Subedi et al. have reported the simultaneous selenate reduction and denitrification by a
77 consortium of bacteria from a mine-impacted natural marsh sediment. (14) Tan and co-
78 workers have demonstrated a competitive reduction between SeO_4^{2-} and structurally
79 similar sulfate (SO_4^{2-}) for the obligate aerobic bacterium *Comamonas testosterone*.
80 When the genes responsible for the reduction of SO_4^{2-} ions are deleted, the reduction of
81 SeO_4^{2-} ions to red Se^0 was not observed indicating that the reduction of selenate was
82 catalysed by enzymes of the sulfate reduction pathway. (15)

83 The pathways of the more common SeO_3^{2-} reduction by different microorganisms
84 include: (i) the so-called Painter-type reactions involving thiol groups (16); (ii)
85 processes involving the thioredoxin – thioredoxin reductase system; (iii) siderophore-
86 mediated reduction; (iv) sulfide-mediated reduction, and (v) dissimilatory reduction.
87 Details of these mechanisms can be found in (1). According to Rauschenbach et al. (17)
88 selenite reductases have not been characterized thus far, and investigators have failed to
89 identify any for *Desulfurispirillum indicum* strain S5, a novel obligate anaerobe
90 belonging to the phylum *Chrysiogenetes*, a dissimilatory selenate-, selenite-, arsenate-,
91 nitrate- and nitrite-reducing bacterium. For *Rhizobium selenitireducens*, besides nitrite
92 reductase involved in SeO_3^{2-} reduction, another protein showing selenate reductase
93 activity was characterized. (18) It was shown to be a member of a protein family
94 termed old-yellow-enzymes (OYE); the latter are often involved in protecting cells
95 from oxidative stress and are generally active on a wide variety of substrates.
96 Furthermore, a novel aerobic selenite reductase (CsrF) was identified in *Alishewanella*

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3 97 sp. WH16-1, a facultative anaerobic bacterium isolated from mining soil capable of
4 98 reducing SeO_3^{2-} to Se^0 nanoparticles as well as chromate (VI). (19) Recently, a selenite
5 99 reductase in *Bacillus selenitireducens* specific for SeO_3^{2-} but not SeO_4^{2-} , AsO_4^{3-} or
6 100 $\text{S}_2\text{O}_3^{2-}$ has been identified. (20)
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9 101 **A generalized scheme of the biotransformation of selenium compounds in a bacterial**
10 102 **cell is shown in Scheme 1.** Selenite is reduced to Se^0 mainly in reactions involving
11 103 thiol-containing molecules and various oxidoreductases, while other proteins may also
12 104 be involved in the reduction of both oxyanions. (16) Selenium oxyanions reduction
13 105 results in the formation of amorphous red and other allotropic Se forms. The formation
14 106 of intra- or extracellular SeNPs has been shown for the commonly studied *T. selenatis*
15 107 (21); the plant-growth-promoting rhizobacterium *Azospirillum brasilense*, (16)
16 108 methane-oxidising bacteria *Methylococcus capsulatus* and *Methylosinus trichosporus*
17 109 (22) and many others. Information on the types of microorganisms (bacteria and fungi)
18 110 involved in the reduction of selenium oxyanions has been published. (1-3, 23)
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23 111 Volatile methylated species have been identified during Se biotransformation and these
24 112 include: dimethyl selenide ($\text{CH}_3\text{-Se-CH}_3$), dimethyl diselenide ($\text{CH}_3\text{-Se-Se-CH}_3$) and
25 113 dimethyl selenenyl sulfide ($\text{CH}_3\text{-Se-S-CH}_3$). (24) Interestingly, while the methane-
26 114 oxidizing bacterium *Methylosinus trichosporium* was found to produce dimethyl
27 115 diselenide and dimethyl selenenyl sulfide only, another methane-oxidizing bacterium,
28 116 *Methylococcus capsulatus*, produced five volatile Se-containing substances. Besides the
29 117 three dimethylated forms mentioned above, methyl selenol ($\text{CH}_3\text{-Se-H}$) and
30 118 methylselenoacetate ($\text{CH}_3\text{-Se-C(=O)CH}_3$) were detected in the headspace (22).
31 119 Reduction of organic forms of Se can result in the formation of volatile and highly toxic
32 120 H_2Se , although ultimate microbial dissimilatory reduction of selenium species to
33 121 selenides is limited in environmental microorganisms. (25)
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39 122 Selenium oxyanions reduction mechanisms have been relatively well studied and
40 123 reported in a number of articles and reviews (see for example: (1, 2, 16)). However, the
41 124 formation of SeNPs (i.e., their assembly from precursors), and the factors regulating
42 125 this process are yet to be elucidated. Processes for SeNPs formation inside cells with
43 126 their subsequent release, as well as the removal of Se^0 precursors after the intracellular
44 127 reduction of selenium oxyanions may involve unknown transport systems. (26-30)
45 128 Tugarova et al. (31, 32), have shown that proton-dependent transport is involved in
46 129 SeO_3^{2-} reduction. Inhibition of proton-dependent transport resulted in Se^0 accumulated
47 130 as intracellular crystallites without formation of extracellular SeNPs. (32)
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51 131 It has been proposed that SeNPs formation can proceed via Ostwald ripening. (26-27)
52 132 **However, biogenic SeNPs in contrast to chemically synthesized ones** are always capped
53 133 by various biomacromolecules, mainly proteins, polysaccharides and lipids (see for
54 134 example (16,31,33-36), indicating that SeNPs formation is more complex than the
55 135 Ostwald ripening process would suggest. A recent proposal is that the precursor for the
56 136 Se^0 formation in methane-oxidizing bacteria is methyl selenol, and that the semi-
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3 137 volatile methylated Se species polymerise to form particulate selenium allotropes (4).
4 138 Lampis et al. proposed a possible biosynthetic mechanism of selenite reduction with the
5 139 formation of SeNPs by the bacterium *Stenotrophomonas maltophilia*. They also
6 140 identified an alcohol dehydrogenase homologue, possibly associated both with the
7 141 biogenic synthesis of SeNPs and also involved in their stabilization. (27)

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10 142 Cell-surface-bound SeNPs formation **may have another role in addition to**
11 **detoxification** and that is to protect the microbial cells from high level of harmful
12 143 effects of UV radiation via light absorption and/or scattering. Similar action of
13 144 intracellular granules of polyhydroxyalkanoates (PHA; carbon and energy storage
14 145 materials biosynthesized and accumulated by many prokaryotes) have been reported
15 146 recently. (37, 38) Noteworthy is that both biogenic SeNPs (see (22, 32, 39, 40)) and
16 147 chemically synthesized analogues (41, 42) **have similar optical spectra of their aqueous**
17 148 **suspensions, including their absorption in the UV region.** Understanding the processes
18 149 involved in the synthesis of SeNPs could be useful in the study of the biogeochemical
19 150 origins of individual selenium -containing mineral deposits. Indeed, study of the genetic
20 151 bases and diversity of the reduction processes will no doubt result in predictable and
21 152 efficient production of useful industrial materials. These aspects are discussed below.
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23 154 **Diversity and distribution of selenium transforming organisms (gene analysis and** 24 155 **culture-independent metagenomics)**

25 156 The study of the diversity and speciation of selenium transforming microorganisms and
26 157 communities by means of the metagenomic approach using high throughput sequencing
27 158 analyses has been poorly represented when compared to studies based on culture
28 159 dependent methods. In a majority of investigations, the focus was on highly speciated
29 160 microbial cenoses inside specific conditioned environments, such as Se-amended
30 161 bioreactors intended for the biosynthesis of valuable end-products, or in granular sludge
31 162 from wastewater treatment plants. However, sparse information is available on the
32 163 assessment of microbial communities in soil or plant rhizosphere.

33 164 Bai and co-workers reported changes in the microbial community structure found in a
34 165 bioreactor designed for the oxidation of methane coupled to selenite reduction by
35 166 bacteria. (43) There was a remarkable shift in the makeup of the denitrifying anaerobic
36 167 methane oxidation (DAMO) community when selenite replaced nitrate as the electron
37 168 acceptor after prolonged nitrate reduction. Alpha-, Beta- and Gammaproteobacteria as
38 169 well as Igavibacteria increased in the presence of selenite, whereas Methanomicrobia
39 170 and Nitrospira significantly decreased when compared to the composition of the
40 171 community in the presence of nitrate. At genus level, *Methylococcus*, *Lautropia*,
41 172 *Verribacter* and *Denitratisoma* – all belonging to Beta- and Gammaproteobacteria –
42 173 were the most abundant in the presence of SeO_3^{2-} .

43 174 A metagenomic approach was also chosen in order to understand the composition of the
44 175 microbial community selected after exposure to SeO_3^{2-} in anaerobic granular sludge
45 176 from a fullscale reactor treating brewery wastewater. (44) High-throughput sequencing

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3 177 of 16S rRNA gene showed that Negativicutes, Gammaproteobacteria and Clostridia
4 178 were the most abundant classes in SeO_3^{2-} reducing microbial aggregates, with
5 179 *Veillonellaceae* (ca. 20%) and *Pseudomonadaceae* (ca.10%) as the main families
6 180 represented.

9 181 High-resolution phylogenetic analysis of anoxic contaminated soil amended with
10 182 selenate revealed that the relative frequency of an operational taxonomic unit (OTU)
11 183 from the genus *Dechloromonas* increased markedly from 0.2% to 36%. Multiple OTUs
12 184 representing less abundant microorganisms from the *Rhodocyclaceae* and
13 185 *Comamonadaceae* showed significant increases as well. (45) In a study of the
14 186 rhizomicrobiome of Se hyperaccumulator and non-hyperaccumulator plants grown on
15 187 seleniferous soil, Cochran and co-workers investigated the effect of selenium-
16 188 hyperaccumulator plants on the diversity and composition of rhizosphere microbiomes.
17 189 They found higher diversity of the OTUs in the rhizosphere of hyperaccumulator plants
18 190 when compared to non-accumulators and the bulk soil.(46)The microbiome of the
19 191 seleniferous soil was composed of taxa belonging mainly to *Crenarchaeota* (Archea),
20 192 *Acidobacteria* and *Actinobacteria*, in contrast to hyperaccumulator plant rhizospheres in
21 193 which *Acidobacteria*, *Crenarchaeota* (Archea) and *Proteobacteria* were dominant.

22 194 There are few examples of the exploitation of mixed microbial cultures for selenium
23 195 species biotransformation. A consortium of four selenium tolerant rhizosphere aerobic
24 196 bacteria belonging to *Bacillus* spp. was used to remove the element from Se enriched
25 197 natural soils. (47) The strains were isolated from Se contaminated soils in the region of
26 198 Punjab, India, by culture enrichment, and the consortium developed was tested on
27 199 SeO_3^{2-} or SeO_4^{2-} spiked soils. While complete removal of Se was observed in SeO_3^{2-}
28 200 augmented soils, 72% removal was recorded for the SeO_4^{2-} contaminated soils after 120
29 201 days. A methanogenic granular sludge from a bioreactor used for the treatment of paper
30 202 waste streams has been shown to produce selenium sulfide (SeS_2) in a new process to
31 203 recover Se from SeO_4^{2-} and SeO_3^{2-} polluted streams, where the former is reduced first to
32 204 the latter which in turn reacts with sulfide to form SeS_2 . (48) (See also the discussion on
33 205 biofilms below.)

34 206 The recent reduction in the cost of high throughput sequencing analyses will allow the
35 207 accumulation of a wide range and variety of sequencing data of microbial communities
36 208 involved in selenium transformation in different environmental matrices. The
37 209 information will enable better understanding of the biogeochemical cycle of selenium in
38 210 the environment and will probably furnish interesting information on the microbial
39 211 species involved in the biotransformation of the element. At the same time, the
40 212 information would be useful in identifying appropriate cultural conditions to apply in
41 213 order to obtain new microbial isolates in axenic cultures for biotechnological
42 214 exploitation.

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53 215 **The role of biofilms in the biotransformation of selenium species**

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3 216 Selenium biotransformation has been extensively described for planktonic cells;
4 217 however, in the environment, microorganisms are commonly found as biofilms (49)
5 218 where resistance to toxic metals is up to 600 times higher than in planktonic forms. (50)
6 219 Moreover, bacteria at any stage of biofilm development are generally believed to be
7 220 physiologically distinct from those in the planktonic state. (51)

10 221 As with planktonic cells, selenium also undergoes biotransformation into less
11 222 bioavailable species in biofilms. (8, 52,53) The presence of Se altered the microbial
12 223 diversity and induced structural changes in the biofilms. (8,53,54) Yang et al. (53)
13 224 observed that a multispecies biofilm consisting of selenium-resistant *Rhodococcus* sp.,
14 225 *Pseudomonas* sp., *Bacillus* sp. and *Arthrobacter* sp., incubated aerobically in the
15 226 presence of selenate or selenite transformed the selenium oxyanions into SeNPs, with
16 227 SeO_3^{2-} more readily reduced than SeO_4^{2-} . The results showed that specific regional
17 228 communities within the biofilms were responsible for selenium detoxification, as
18 229 indicated by the localised distribution of reduced selenium species within the biofilm
19 230 structure. The formation of SeNPs (size range 50–700 nm) was observed inside the
20 231 bacterial cells and also shown to be associated with proteins and polysaccharides from
21 232 the **extracellular polymeric substances (EPS)**. **Bioaccumulation of Se** has also been
22 233 observed in more complex, heterogeneous biofilms containing not only bacteria, but
23 234 also diatoms and filamentous algae. Interestingly, in the more heterogeneous biofilm
24 235 community, Se partitioned differently into the various components of the biofilm, with
25 236 diatoms containing approximately two-thirds of the Se. Also, density-separated algae
26 237 fractions from the biofilms showed that the concentration of Se was significantly higher
27 238 in the fraction not containing filamentous green algae compared to the filamentous
28 239 green algal fraction. (55)

30 240 The immobilization of selenium has also been observed under anaerobic conditions. A
31 241 recent study by Tan et al. (8), using biofilms from an anaerobic sludge inoculum in the
32 242 presence of SeO_4^{2-} , revealed that colloidal SeNPs were formed by microbial reduction
33 243 within the biofilm matrix, and retained in the biofilm system. The study also addressed
34 244 how the biofilm structure was affected, not only by the presence of SeO_4^{2-} , but also by
35 245 the presence of other electron acceptors such as NO_3^- and SO_4^{2-} . Relatively thin and
36 246 compact biofilms were formed in the presence of SeO_4^{2-} alone, while thicker biofilms
37 247 occurred in the presence of NO_3^- or SO_4^{2-} . The thicker biofilms in the presence of NO_3^-
38 248 or SO_4^{2-} revealed gas pockets within the biofilm matrix, likely to be due to the
39 249 microbial production of gases. With respect to Se removal, the presence of NO_3^- did not
40 250 have a stimulating effect showing similar removal efficiency to that grown in the
41 251 presence of SeO_4^{2-} only. In contrast, the presence of SO_4^{2-} showed higher removal
42 252 efficiencies and greater biomass growth when compared to SO_4^{2-} free treatments. A
43 253 possible explanation for the increase in Se removal in the presence of SO_4^{2-} could be
44 254 related to abiotic reactions possibly occurring between Se-containing species and S
45 255 compounds within the biofilm matrix. (8, 56)

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3 256 In biofilm-mediated biotransformation the biogenic elemental Se formed is retained in
4 257 the biofilm matrix. In contrast, when using planktonic cultures, one major drawback is
5 258 that the biogenic Se⁰ remains in suspension as SeNPs for prolonged periods. (57-59)
6 259 Under these conditions, further treatment such as electrocoagulation or precipitation is
7 260 required to remove the SeNPs. (1,60, 61) The study of biofilms has provided evidence
8 261 that selenium is immobilised in the biofilm matrix, thus modifying both its stability and
9 262 bioavailability in the environment. (53) **In addition, biofilms are to be preferred for**
10 263 **effective and reliable biotransformation and sequestration of selenium.**

11 264 Since diet is the primary route of Se exposure and uptake in vertebrates, Se
12 265 bioaccumulation in biofilms, as the base of the food chain, could serve as the primary
13 266 food source for benthic invertebrates and higher trophic organisms. (62) Moreover,
14 267 differences in the proportions of bacteria, filamentous algae and/or diatoms in naturally
15 268 occurring biofilms could lead to variations in Se accumulation in these ecosystems, as
16 269 observed by Arnold et al. (55) Depending on how Se partitions between these various
17 270 components, Se exposure via ingestion by higher organisms could vary, because these
18 271 organisms may preferentially feed on specific biofilm components and, thus, be
19 272 exposed to different concentrations of Se. (55,62) The use of biofilms for Se
20 273 sequestration represents an important and viable means of Se-laden wastewater
21 274 treatment and bioremediation of selenium-contaminated areas such as mine-impacted
22 275 sites. (52, 53, 63)

23 276 Selenium immobilisation by biofilms is a complex phenomenon and has distinct
24 277 dynamics and controlling factors. The composition of the microbial communities is a
25 278 major determining factor in Se uptake and biotransformation by biofilms, and therefore
26 279 the behaviour of each would be different. While Yang et al. (53) used a multispecies
27 280 biofilm consisting of selenium-resistant bacteria, and Tan et al. (64) studied inocula
28 281 from a reactor treating Se-laden wastewater, other biofilm communities may be
29 282 severely affected by the presence of Se. Recently it was shown how SeNPs disrupted
30 283 the quorum sensing signalling system of *Pseudomonas aeruginosa*, provoking a
31 284 reduction of 80% in the volume of the bacterial biofilm, and demonstrating the potential
32 285 use of SeNPs as effective antibacterial agents. (65) Physicochemical and environmental
33 286 factors affect the growth of EPS-producing cells, influence the structure and
34 287 composition of the biofilm matrix, and its role in Se uptake. (66) As described by Tan et
35 288 al., (64) the presence of other electron acceptors (or, in general, other reducing or
36 289 oxidizing species) may also affect the efficiency of Se uptake by biofilms. Aerobic or
37 290 anaerobic conditions, maturity of the biofilm, duration of the interactions are
38 291 parameters which determine the extent of Se uptake and thus biotransformation.
39 292 Therefore, close monitoring and regulation of the experimental conditions is
40 293 recommended in order to yield maximum Se removal. (66)

41 294 It is envisaged that the use of multispecies biofilms rather than isolated planktonic
42 295 microorganisms for the remediation of Se-compounds in water reservoirs, the
43 296 development of more efficient biofilm-based reactors (8,64, 67,68), the use of such

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3 297 bioreactors for selenium removal from wastewater (69) and the exploitation of the
4 298 biofilm microbes for the manufacture of biogenic Se nanospheres and nanorods will be
5 299 the focus of future research. (69, 70) **It is still unclear how biofilms are affected or**
6 300 **modified in response to the stress caused by exposure to high levels of Se oxyanions,**
7 301 **and what effects these changes have on the metabolic pathways of the element.** In
8 302 addition, the effects of the presence of selenium resistant microorganisms on the
9 303 composition and overall behaviour of a mixed culture are poorly understood. More
10 304 importantly, the impact on molecular level mechanisms describing quorum sensing
11 305 signalling processes of transcription and translation of enzyme genes are yet to be
12 306 elucidated. Studies aimed at reducing the knowledge gaps and to expand our
13 307 understanding of the natural microbial interactions, dynamics and ecology in these
14 308 bacterial communities, will greatly enhance the advantages of the use of biofilms for the
15 309 biotransformation and immobilization of selenium. Developments in the knowledge
16 310 underpinning the behaviour of biofilms will lead to the production of engineered
17 311 synthetic microbial consortia with increased robustness, featuring communities able to
18 312 compartmentalize functions, with simultaneous execution of multiple tasks and
19 313 metabolic division-of-labour. (71)

26 314 **Multidisciplinary approach for the characterization of selenium speciation in** 27 315 **bacterial transformations**

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30 316 Over the years, a suite of complementary microscopic, spectroscopic, chromatography-
31 317 mass spectrometric and synchrotron-based techniques have emerged for the
32 318 characterization of the physical (size, morphology, structure, crystallography, etc.) and
33 319 chemical (oxidation state, elemental composition, local coordination, chemical
34 320 speciation, etc.) properties of selenium biotransformation products (22, 31-34, 72-75).
35 321 A list of the techniques and the information they provide are summarized in Table 1.

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39 322 **The characterization of Se-containing particulates by Raman spectroscopy and Raman**
40 323 **microscopy have been used to determine their size, morphology (76, 77), and to obtain**
41 324 **structural data. (4, 22, 31, 32)** Raman spectroscopic measurements can be used to
42 325 differentiate between the various Se allotropes. The Se–Se stretching vibration mode in
43 326 Raman spectra can be used to identify the structure of Se. Amorphous SeNPs exhibit a
44 327 broadened Se–Se band at $\sim 250\text{ cm}^{-1}$ as reported for SeNPs biosynthesized by
45 328 azospirilla. (31, 32) Raman peaks corresponding to the symmetric stretching mode of
46 329 trigonal Se occurs at 234 cm^{-1} , (72) the corresponding peak for monoclinic Se is located
47 330 at 264 cm^{-1} , (78) while covalently bound sulfur can be revealed by the Se–S band
48 331 around $352\text{--}377\text{ cm}^{-1}$. (32, 73)

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53 332 The nature of the organic matter (lipids, proteins, polysaccharides) associated with
54 333 biogenic SeNPs has been investigated by infrared (IR) spectroscopy. (4, 22, 31, 34) IR
55 334 spectroscopy has enabled the identification of the presence of polymeric materials
56 335 surrounding the NPs and **demonstrated** their role in increasing the thermodynamic
57 336 stability of biogenic SeNPs. (33) Amorphous Se (a-Se) is thermodynamically unstable

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3 337 and undergoes transformation to trigonal Se at increased temperatures. Monoclinic Se
4 338 (m-Se) is metastable and could also eventually undergo conversion to the trigonal form
5 339 (t-Se). (79) Transformation of SeNPs from monoclinic nanospheres to t-Se nanorods by
6 340 the cells of *Pseudomonas alcaliphila* was revealed by the use of a combination of TEM
7 341 and Raman spectroscopy. (74) Ho et al. (80) described the process of transformation of
8 342 a-Se nanospheres produced by *Shewanella* to t-Se nanostructures (e.g. nanowires,
9 343 nanoribbons, nanorods, etc.) where organic solvents such as DMSO play a major role.
10 344 In addition, the anaerobic biotransformation of a-Se nanospheres to t-Se nanorods has
11 345 been shown for microbial granular activated sludge **at a high temperature (55 °C)**. (75)
12 346 Results from time-dependent SeNP experiments have shown that the cells of the strain
13 347 *Stenotrophomonas bentonitica* and their proteins are able to transform amorphous Se⁰
14 348 nanospheres to one-dimensional (1D) t-Se nanostructures (hexagons, polygons and
15 349 nanowires) under mesophilic conditions.

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21 350 Recently, modern spectroscopic and imaging techniques based on synchrotron radiation
22 351 have been used to investigate the biotransformation of selenium by multispecies
23 352 biofilms avoiding damage to the sensitive samples. (53) Information from the Se K-
24 353 edge EXAFS analysis was used to demonstrate the ability of the biofilm to reduce
25 354 selenite to SeNPs. In addition, nanoscale Se L_{III} edge Scanning Transmission X-ray
26 355 Microscopy (STXM) showed the co-localization of elemental Se with microbial cells,
27 356 **EPS** and lipids using the carbon K-edge. Structural and chemical data from the reaction
28 357 products can be used to investigate Se biotransformation mechanisms (oxidation,
29 358 reduction, etc.), to study the stability of the products and to inform the development of
30 359 strategies for Se remediation.

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35 360 Beside measurements on the bacterial material, samples from the headspace and
36 361 medium should be included as a matter of course. The information produced by these
37 362 measurements will serve to fill in the gaps in our understanding of the metabolic and
38 363 non-metabolic processes that are involved in the biotransformation of selenium-
39 364 containing species. Recently, Eswayah et al. have shown that it is possible using
40 365 sorptive extraction followed by thermal desorption-gas chromatography-mass
41 366 spectrometry (TD-GC-MS) to investigate both the volatile and semi-volatile selenium
42 367 species produced during the biotransformation steps, and based on their findings have
43 368 proposed the mechanisms for the formation of SeNPs. (4)

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48 369 All the above mentioned bulk spectroscopic and microscopic techniques are useful for
49 370 the investigation of the chemical speciation and physicochemical properties of biogenic
50 371 SeNPs. However, the heterogeneity that exists in SeNPs generated by complex
51 372 biological systems (e.g. biofilms, granular activated sludge, microbial consortia) often
52 373 makes it difficult to interpret chemical speciation and structure data by means of bulk
53 374 techniques such as EXAFS spectroscopy. In recent years, the development of
54 375 microscopic resolved synchrotron radiation using micro- or nano-focused based
55 376 techniques (for example: micro (μ)EXAFS/XANES, μ XRD, μ infrared spectroscopy,
56 377 etc.) has created new opportunities for the investigation of the speciation and spatial

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3 378 heterogeneity of the chemical elements associated with the selenium species (see, e.g.
4 379 (81,82) for detailed discussion of some of these techniques). Other techniques which
5 380 could provide information on the distribution of selenium species in bacteria include
6 381 laser ablation-inductively coupled plasma-mass spectrometry and matrix assisted laser
7 382 desorption ionisation-MS which can be used to localize and identify selenium-
8 383 containing species and biomolecules associated with the selenium particulates,
9 384 respectively.

13 385 Both the quantitative and qualitative distribution of the different Se species, and
14 386 structures within complex biological/environmental samples can now be studied. The
15 387 information from *in-situ* kinetic and thermodynamic properties of the
16 388 biotransformations of SeNPs using synchrotron based techniques would provide the
17 389 basis for comprehensive understanding of the processes which control the size and
18 390 structure of the selenium-containing particulates. It is particularly so, since their
19 391 environmental stability and industrial applications are intimately linked to their
20 392 structural characteristics.

24 393 **Bioremediation of selenium contamination**

26 394 Remediation technologies involving microorganisms (bioremediation) offer an
27 395 environment-friendly approach for the clean-up of pollution. (2, 8, 52, 83-85)
28 396 Bioremediation of selenium in various environmental niches results in the reduction of
29 397 selenium oxyanions and precipitation of solid Se⁰ (SeNPs), together with the formation
30 398 of volatile methylated selenium compounds (2, 22, 24, 25) thus reducing the total Se
31 399 burden in the immediate vicinity of the pollution source.

35 400 In an approach developed by Barlow et al. (86) the selenite-reducing bacteria (*Bacillus*
36 401 *subtilis*) were encapsulated in semi-permeable biodegradable polymeric membranes
37 402 (polymersomes) to rapidly reduce dissolved SeO₃²⁻. The bacteria remained viable
38 403 throughout the synthesis of the polymersomes followed by proliferation when the
39 404 incubation temperature was raised to 37 °C, with rapid formation of biofilms and the
40 405 conversion of soluble selenite (3 mM) to individual and clustered spherical SeNPs
41 406 (~200–350 nm). The SeNPs remained entrapped in the membrane and as a result they
42 407 were easily retrieved from the solution.

46 408 A new *Cronobacter* sp. isolated and enriched from domestic waste water was found to
47 409 grow heterotrophically, using organic substrates such as acetate, lactate, propionate or
48 410 butyrate as the electron donor, and to reduce selenite to SeNPs under microaerobic
49 411 conditions. (87) The latter conditions were favourable for its growth and resulted in
50 412 several-fold increased SeO₃²⁻ removal when lactate was used as the electron donor. In a
51 413 different study, a UASB reactor was successfully used for ex situ bioremediation, where
52 414 Se-rich soil was leached with water, followed by treatment of the leachate in which
53 415 90% of the Se was removed at a rate of ca. 44 µg Se per gram of granular sludge. (88)
54 416 It has been shown that it is possible to remove selenite (20–100 mg L⁻¹) from high-
55 417 salinity (70 g·L⁻¹) artificial waste water with removal efficiency of up to 98% using

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3 418 aerobic sequencing batch reactors with activated sludge derived from a municipal
4 419 wastewater treatment plant. (89) Mass balance analysis showed that bio-volatilization
5 420 was the main route of selenium removal. A similar sequencing batch reactor with
6 421 activated sludge under oxygen-limiting conditions has been successfully used to
7 422 reductively remove up to 98% SeO_4^{2-} (1 mM) from waste water in the presence of 3%
8 423 NaCl, with most of selenium accumulating in the sludge as micrometer-sized particles.
9 424 (90)

13 425 Recently, biofilm of selenate-reducing bacteria was utilized in a model of a membrane
14 426 biofilm reactor with H_2 as the electron donor, for simultaneous reduction and removal
15 427 of SeO_4^{2-} (maximum removal efficiency up to ca. 50–61% depending on the conditions
16 428 applied) and nitrate (up to 97–99.9%) from aqueous solutions.(91) It is generally
17 429 accepted that microorganisms isolated from selenium-contaminated environments are
18 430 more tolerant of Se compounds, and therefore more suited for selenium bioremediation.
19 431 An example is the use of two *Lysinibacillus* spp. (*L. xylanilyticus* and *L. macrolides*)
20 432 isolated from a Se-rich soil and shown to be capable of using both SeO_4^{2-} and SeO_3^{2-} as
21 433 electron acceptors to produce Se^0 nanospheres (80–200 nm). (92)

26 434 The reduction of selenite to Se^{2-} by *E. coli* resulting in the formation of insoluble and
27 435 thus much less toxic metal selenides, makes selenite-reducing microorganisms possible
28 436 candidates for bioremediation of not only selenium-polluted lands, but also when
29 437 mercury is present. (93) Mercury immobilization (Hg^0 is formed when Hg^{2+} is reduced)
30 438 by biogenic SeNPs can be improved in the presence of soil-borne dissolved organic
31 439 matter (DOM). DOM enhances the stability of the SeNPs resulting in up to 99% Hg
32 440 immobilization. (94) The extent to which toxic methylmercury is formed in the
33 441 presence of methylated selenium species and their effect on plant growth is of interest.
34 442 (95)

38 443 Soil bacteria with phytostimulating properties and tolerance for selenium oxyanions can
39 444 be used for the dual purpose of soil bioremediation and the promotion of plant growth.
40 445 Several strains of bacteria of the widely studied genus *Azospirillum*, many of which
41 446 display plant-growth-promoting traits, have been shown to be relatively tolerant to
42 447 SeO_3^{2-} and to efficiently reduce it to SeNPs (31,32, 34, 35, 96, 97) and also to
43 448 selenium–sulfur mixed NPs ($\text{Se}_{8-n}\text{S}_n$) in the presence of both selenite and high
44 449 concentrations of sulfate ($\sim 0.8 \text{ g L}^{-1}$). (73) Recently, a *Herbaspirillum* sp., a plant-
45 450 growth-promoting endophyte specific to the tea plant *Camellia sinensis* (L.), has been
46 451 shown to be capable of reducing selenate (via selenite) to SeNPs in culture medium.
47 452 Indeed, more than two-fold higher Se content was found in the plant leaves grown on
48 453 selenate-spiked soil compared to the control plants. (36) The combined utilization of
49 454 selenium oxyanion conversions to Se^0 and possibly other Se species that are relatively
50 455 non-toxic and bioavailable to plants in addition to their plant growth-promotion traits
51 456 are definitely of potential agricultural and agrobiotechnological significance.

58 457 **Bacterial transformations in the production of biotechnologically useful products**

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3 458 Examples of biotechnologically useful selenium-containing products are summarized
4 459 in Table 2. (29,30,32,40,48,73,77,87,99,100–116)

6 460 Se²⁻ ions can form largely insoluble metal selenides in the presence of appropriate
7 461 heavy metal species, such as Hg²⁺, Cd²⁺, Cu⁺ or Cu²⁺, etc. Microorganisms such as
8 462 *Pseudomonas aeruginosa*, *Bacillus subtilis* and *Saccharomyces cerevisiae* have been
9 463 shown to reduce SeO₃²⁻ in the presence of the corresponding cations to form cadmium
10 464 and zinc selenides (98–101). Incubation of the plant pathogenic fungus
11 465 *Helminthosporium solani* in aqueous solution with CdCl₂ and SeCl₄ has been shown to
12 466 produce small nanospheres of CdSe. (102) The Gram-negative bacterium *Pantoea*
13 467 *agglomerans* was found to form Cu²⁺- and Cu⁺-containing black nanocrystallites (Cu₂-
14 468 xSe) in the presence of Cu²⁺-EDTA and SeO₃²⁻, (103) exhibiting the ability to
15 469 simultaneously reduce copper(II) to copper(I) and SeO₃²⁻ to Se²⁻.

16 470 The first complete genome data have been recently reported for *B. cereus* (strain CC-1
17 471 isolated from marine sediments), a selenite/selenate-reducing and metal selenide-
18 472 producing bacterium. (104) The putative genes involved in selenate/selenite reduction
19 473 as well as in salt and metal resistance were identified, and the bacterium was shown to
20 474 be capable of producing SeNPs (in the absence of heavy metal ions) or
21 475 photoluminescent Bi₂Se₃, PbSe and Ag₂Se NPs when Bi³⁺, Pb²⁺ or Ag⁺ nitrates,
22 476 respectively, are present. The addition of 5 mM glutathione (GSH) significantly
23 477 inhibited the formation of cell-bound Bi₂Se₃ nanosheet-like particles and instead SeNPs
24 478 were formed. (105) Hence it was proposed that specific enzymes, instead of thiols, were
25 479 responsible for the formation of metal selenides in this bacterium. In contrast,
26 480 *Lysinibacillus* sp. was found to synthesize both extra- and intracellular Bi₂Se₃
27 481 nanosheets, formation of which was faster when 5 mM GSH was added indicating the
28 482 existence of different mechanisms of biogenic nano-Bi₂Se₃ formation. (105)

29 483 Recently, there have been reports on the applications of microbial synthesized Se-
30 484 containing NPs in chemotherapy, drug delivery, as well as in cancer diagnostics,
31 485 prevention and treatment. (117–118) Biogenic SeNPs have been shown to exhibit
32 486 antioxidant and anti-tumour activity, immunostimulatory and anti-inflammatory
33 487 effects in animal models (106); for recent reviews, see (118,119–121). Investigations
34 488 into the antimicrobial and antibiofilm activities of microbial synthesized SeNPs have
35 489 shown that the surface bioorganic layers characteristic of biogenic nanostructures play
36 490 important roles in their biochemical behaviour. (122)

491 **Bacterial selenoproteins and selenoproteomes**

492 **Although the focus of this review has been on the visible changes in the chemical**
493 **speciation of selenium species in the presence of bacteria, and the uses of the products**
494 **of the biotransformation reactions, it is important to note that selenium is an essential**
495 **element for bacteria. It is incorporated in a variety of prokaryotic selenoproteins,**
496 **which are involved in biochemical redox functions. The mechanism and the genes**
497 **responsible for the synthesis and insertion of selenocysteine, the amino acid at the**

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3 498 active centre of these proteins, have been described.(123-126) The unique genetic
4 499 signature of this mechanism has provided researchers with the information that has
5 500 enabled them to easily establish if a particular bacterium has the ability to synthesize
6 501 selenoproteins from the examination of its complete sequenced genome.(127-129)
7 502 Over 70 prokaryotic selenoprotein families have so far been identified but the
8 503 biochemical roles of some are yet to be elucidated.(130) The variety of the
9 504 selenoproteomes in each bacterium presents clues as to the extent to which it utilizes
10 505 the element in its metabolism and its ability to tolerate exposure to high levels of
11 506 selenium species. The deployment of the genomic approach for the screening and
12 507 selection of suitable selenium-tolerant bacteria and to the study of selenium-rich
13 508 environmental niches will yield information on how bacteria have evolved to use the
14 509 element. In addition, it is probable that bacteria with the desirable characteristics,
15 510 which can be harnessed to produce useful biotechnological products, will be
16 511 identified.

512 **Concluding remarks and future directions**

513 The complexity of bacterial biotransformation of selenium species has only recently
514 began to emerge. It is now clear that selenium biotransformation is widespread in
515 diverse prokaryotes, some anaerobes, and certain clostridial species, while the focus
516 of current research has been on planktonic microorganisms and their ability to convert
517 selenium species to reduced selenium anions, elemental selenium, metal-selenide and
518 quantum dots, methylated volatile and semi-volatile compounds. A holistic approach
519 is therefore now required in order to gain a better understanding of the types of
520 reactions that are not only occurring on the surfaces and inside bacterial cells but also
521 in the culture medium and to characterize the products of such reactions. There have
522 been few studies which replicate the conditions in selenium-rich environmental niches
523 in which the microorganisms thrive by interacting with each other to form biofilms,
524 and utilize selenium oxyanions in order to conserve energy. The application of
525 functional gene analysis and metagenomics to the study of these microbial niches will
526 provide a better understanding of how selenium biogeochemical cycle interacts with
527 those of other elements leading to the identification of the key factors which
528 influence, determine and underpin selenium biotransformation. These developments
529 will enable the discovery and introduction of innovative biotechnological applications
530 of the products thereof.

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532 **Compliance with Standards**

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3 536 **Ethical approval**
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5 537 This article does not contain any studies with human participants or animals
6 538 performed by any of the authors.
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Table 1

Microscopic and spectroscopic techniques used to investigate the speciation of selenium and the structure of SeNPs produced by microorganisms

Technique	Information provided
X-ray Absorption Spectroscopy, XAS: (X-ray Absorption Near Edge Structure, XANES*; Extended X-Ray Absorption Fine Structure, EXAFS**)	Element specific technique Determination of local coordination of Se: *Oxidation state; VI, IV, 0, -II **Structural parameters of biogenic Se species: number and chemical identities of near neighbours atoms and the average interatomic distances up to 5-6 Å.
X-ray Photoelectron Spectroscopy	Surface chemistry of purified biogenic SeNPs (oxidation state, nature of functional groups of organic matter adsorbed to SeNPs surfaces, etc.) Elemental composition of surface-bound Se NPs of whole cells (outermost 10 nm of the cell wall)
X-Ray Diffraction	Determination of size and phase of SeNPs (amorphous, monoclinic, trigonal)
Infrared Spectroscopy	Compositional data: nature of organic matter (lipids, proteins, polysaccharides) associated with biogenic SeNPs Monitoring molecular-level changes in the structure and composition of cellular macrocomponents involved in the interactions with SeNPs.
Raman Spectroscopy	Sensitive to differences in various allotropic changes (amorphous, monoclinic, trigonal) and crystallinity of Se in SeNPs Composition of SeNPs (presence of Se-S, etc.)
Scanning Transmission Electron Microscopy (STEM) coupled with a High Angle Annular Dark-Field (HAADF)	Cellular localization of the biogenic SeNPs Elemental composition (S, Se, P, etc.) Crystallographic properties of the SeNPs
Variable Pressure Field Emission Scanning Electron Microscope (VP-FESEM)	Determination of size and chemical composition of SeNPs (interactions with organic matter including proteins, EPS, etc.)
Dynamic light scattering and zeta potential analysis	Particle size and surface charge

Table 2

Biotechnologically useful selenium-containing nano-sized products of microbial origin and conditions of their biogenic synthesis*

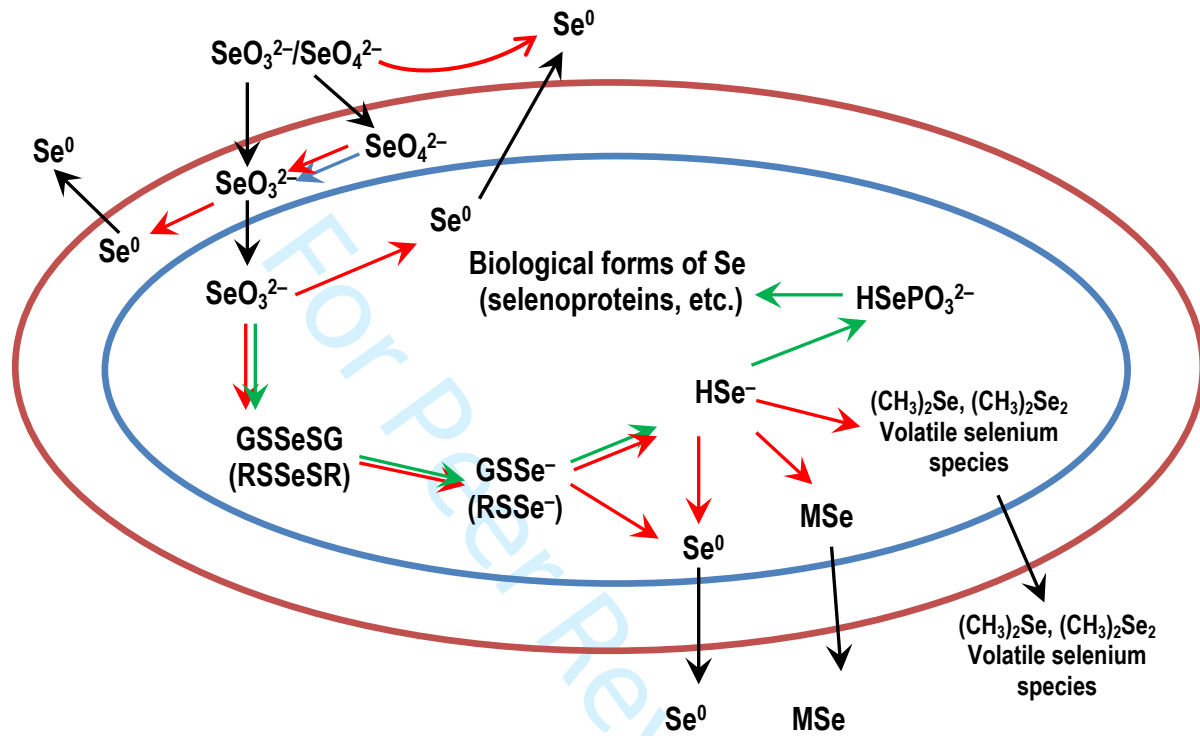
Composition	Micro-organisms	Electron donors (medium) / electron acceptors	Conditions	Localisation, properties, morphology, size	Notes	References
Se ⁰	<i>Cronobacter</i> sp.	Acetate, lactate, propionate or butyrate / selenite	Microaerobic	Extracellular (aggregates)	Selenite bioreduction rates 0.10–0.24 mM·d ⁻¹	(87)
Se ⁰	<i>Cronobacter</i> sp.	Graphite felt electrode / selenite	Anaerobic electrotrophic bioreduction (at –0.3 V vs. SHE)	NPs (50 to 300 nm) attached to the electrode	Selenite bioelectroreduction rate 0.03 mM·d ⁻¹	(87)
Se ⁰	<i>Pseudomonas putida</i>	LB broth / selenite	Aerobic	Extracellular spherical NPs and aggregates (100–500 nm)	High selenite bioreduction rate (0.444 mM·h ⁻¹)	(107)
Se ⁰	<i>Pseudomonas aeruginosa</i>	Peptone nutrient broth / selenite	Aerobic	Extracellular (cell surface-bound), spherical, amorphous (~47–165 nm; average size ~96 nm)	Covered with a bioorganic layer (NPs characterised by a range of instrumental techniques)	(77)
Se ⁰	<i>Tetrahymena thermophila</i>	Proteose peptone medium / selenite	Aerobic	Intracellular amorphous spherical (50–500 nm), with irregular NPs	Covered with a bioorganic layer (including proteins); NPs characterised by a range of instrumental techniques)	(108)
Se ⁰	<i>Staphylococcus carnosus</i>	LB culture medium / selenite	Aerobic	Intracellular (isolated by cell disruption and separated); spherical (average sizes ~440–525 nm)	Associated with proteins. NPs showed considerable anti-nematode and antimicrobial activities	(109)
Se ⁰	A microbial community of anaerobic sludge	Lactic acid / selenate; selenium sulphide (SeS ₂)	Anaerobic bioreduction of selenate or SeS ₂ (precipitated during reduction of selenite by sulphide)	Amorphous nanospheres; hexagonal acicular crystallites (not attached to biomass)	Higher pH and temperatures are favourable for obtaining crystals (without a bioorganic 'coating')	(40,48)
Se ⁰	<i>Escherichia coli</i> (weakly virulent α-hemolytic)	Culture broth / selenite	Aerobic	Intracellular spherical or ovoid NPs; 30–120 nm	Promising as an adjuvant (for the immunisation of livestock and poultry against	(110)

	strain B-5)				colibacillosis)	
Se ⁰	<i>Escherichia coli</i> (selenite reductase CsrF overexpressing strain)	LB culture medium / selenite	Aerobic	Intra- and extracellular irregular nanospheres (60–105 nm)	Covered with a bioorganic layer. High potential for adsorption and removal of dyes	(111)
Se ⁰	<i>Lactobacillus casei</i>	MRS culture broth (Sigma) / selenite	Anaerobic	Intracellular spherical NPs; 50–80 nm	Promising as a probiotic	(106)
Se ⁰	<i>Azospirillum brasilense</i>	Autotrophic (in physiological solution) / selenite	Microaerobic	Extracellular, spherical (~50–100 nm), amorphous	Covered with a bioorganic layer	(32)
Se _{8-n} S _n	<i>Azospirillum brasilense</i>	Malate-containing salt medium + 1 g·L ⁻¹ (NH ₄) ₂ SO ₄ / selenite	Aerobic (selenite reduction in the presence of an increased concentration of sulphates)	Extracellular, spherical (~400 nm), amorphous	Covered with a bioorganic layer (NPs characterised by a range of instrumental techniques)	(73)
Se ⁰	<i>Mariannaea</i> sp.	Modified Martin medium with 1 g·L ⁻¹ glucose / SeO ₂	Aerobic (at varying SeO ₂ concentrations and pH 5–12)	Intracellular (~45 nm) or extracellular (~212 nm) crystalline spherical NPs	Extracellular localisation of NPs at alkaline pH. NPs associated with proteins	(30)
Se ⁰ , Se ⁰ -Te ⁰	Microbial community of methanogenic granular sludge	Anaerobic granular sludge (with lactate) / selenite + tellurite	Anaerobic (simultaneous reduction of selenite and tellurite)	EPS-entrapped crystalline Se ⁰ , Te ⁰ and mixed Se ⁰ -Te ⁰ irregular anisotropic nanostructures	First demonstration of mixed Se ⁰ -Te ⁰ NPs formed by anaerobic microorganisms	(112)
CdSe	<i>Veillonella atypica</i>	H ₂ / selenite (with 0.1 mM AQDS as an electron shuttling compound)	Anaerobic (with further filtering the Se ²⁻ -containing culture and adding Cd ^{II} -GSH solution)	Fluorescent QDs; 2.3–3.6 (± 1.2) nm	Associated with a range of proteins and GSH as a capping agent	(100)
CdSe	<i>Helminthosporium solani</i>	Incubation in aqueous solution of CdCl ₂ / SeCl ₄	Aerobic (ambient conditions)	Extracellular monodisperse spheres (QDs; mean diameter 5.5 ± 2 nm)	Characterised by a range of instrumental techniques	(102)
CdS _{0.5} Se _{0.5}	<i>Staphylococcus aureus</i>	GSH / selenite	Aerobic; intracellular reduction (further interaction with Cd ²⁺)	Intracellular uniform monodisperse nanocrystals (1.8 ± 0.5 nm; fluorescent QDs)	Low crystallinity; possible presence of a capping protein/peptide layer	(113)
CdSe	<i>Bacillus subtilis</i>	LB culture medium / selenite	Aerobic; intracellular reduction (further	Blocks of intracellular nanocrystals with angular shape	No isolation and chemical analysis of CdSe was performed	(99)

			interaction with Cd ²⁺)	(fluorescent QDs)		
CdSe	<i>Saccharomyces cerevisiae</i>	Sterilised yeast extract peptone medium / selenite	Aerobic; Se ^{IV} -exposed cells (in fresh medium) added to CdCl ₂ solution	Intracellular QDs (isolated by cell lysis and homogenisation with further separation); ~2.8 nm	Biosynthetic protocol optimized by concentrations and times of exposure	(101)
CdSe	<i>Shewanella oneidensis</i>	LB medium / selenite	Anaerobic (incubation with selenite followed by CdCl ₂ addition)	Intracellular high-purity uniform fluorescent QDs (~3.3 ± 0.6 nm)	Highest CdSe bioproduction rates. (Extracellular Se ⁰ NPs also obtained)	(29)
CdSe; CdSe/CdS	A methanogenic microbial consortium	Anaerobic granular sludge (with lactate) / selenite	Anaerobic (selenite reduction in the presence of Cd ²⁺ -NTA complex)	Extracellular fluorescent CdSe and CdSe/CdS core-shell NPs (10–190 nm)	CdSe NPs capped by extracellular polymeric substances (contain impurities of Se ⁰ NPs)	(114)
CdSe	<i>Pseudomonas stutzeri</i>	GSH / selenite	Aerobic (selenite reduction in the presence of Cd ²⁺)	Intracellular fluorescent QDs (isolated by cell disruption and separated); < 10 nm	Covered with a bioorganic layer (QDs characterised by a range of instrumental techniques)	(115)
CdS _{1-x} Se _x	<i>Tetrahymena pyriformis</i>	Proteose peptone medium / selenite	Aerobic (incubation with selenite followed by CdCl ₂ addition)	Intracellular fluorescent QDs (isolated by cell lysis and disruption, separated and purified); 8.3 ± 0.8 nm	Optimised biosynthetic protocol; QDs characterised by a range of instrumental techniques	(116)
Cu _{2-x} Se	<i>Pantoea agglomerans</i>	Glucose-containing salt medium (with EDTA-Cu ²⁺) / selenite	Anaerobic	Extracellular uniform crystallites (~80 nm)	Capped by proteins (NPs characterised by a range of instrumental techniques)	(103)
Bi ₂ Se ₃	<i>Lysinibacillus sp.</i>	Tryptic soy broth / selenite	Aerobic (selenite reduction in the presence of Bi ³⁺ nitrate)	Extracellular (also intracellular) crystalline nanosheets (~60 nm; average thickness 5–6 nm)	Covered with a bioorganic layer (proteins). Promising for photothermal therapy against cancer cells	(105)
Se ⁰ , Bi ₂ Se ₃ , PbSe, Ag ₂ Se	<i>Bacillus cereus</i>	Tryptic soy broth / selenite	Aerobic (selenite reduction to Se ⁰ or, in the presence of either of metal ions, to metal selenides)	Extra- and intracellular trigonal Se ⁰ NPs (without metal ions); extracellular crystalline photoluminescent PbSe and Ag ₂ Se, cell-bound Bi ₂ Se ₃ (~10–50 nm)	Adding 1% PVP to the culture medium changed the size and morphology of Bi ₂ Se ₃ and PbSe NPs	(104)

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3 * Abbreviations: AQDS, anthraquinone-2,6-disulphonate ; EPS, extracellular polymeric
4 substances; GSH, reduced glutathione; LB, liquid Luria-Bertani broth; NPs, nanoparticles;
5 NTA, nitrilotriacetic acid; PVP, polyvinyl pyrrolidone; QDs, quantum dots; SHE, standard
6 hydrogen electrode
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Arrows indicate different processes:

- Anaerobic respiration
- Detoxification
- Assimilation
- Transport

G – glutathione;

R = thiol-containing proteins such as thioredoxin, bacillithiol;

M = metal (Cd, Cu, Pb, Hg).