

Review Article

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## Potential of Genetically Engineered Strains to Enhance Concrete Strength: A Review

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### Abstract

The gradual development of microcracks reduces concrete's durability. Their appearance reduces performance properties, including water resistance, frost resistance, and strength. One promising approach to lowering microcrack development is the use of spore-forming bacteria that can precipitate calcium carbonate in the environment. When water enters concrete cracks, bacterial spores germinate and initiate mineralization, facilitating partial restoration of the material's structure. The first experiments on producing bioconcrete were conducted in the mid-2000s and demonstrated that bacteria can form calcite particles up to 100  $\mu\text{m}$  in size and seal microcracks. Concrete has a limited capacity for self-healing through atmospheric carbonation, in which  $\text{CO}_2$  reacts with calcium hydroxide to form calcite; however, this process is slow and unpredictable. In most biotechnological systems,  $\text{CaCO}_3$  precipitation is enhanced by the enzymatic hydrolysis of urea, catalyzed by the enzyme urease. In addition to the urease pathway, alternative mechanisms for urea degradation to form carbonates are also known. For example, the amidolyase pathway, in which allophanate is formed from urea, and in a subsequent reaction, allophanate hydrolase decomposes it to ammonia and bicarbonate. Furthermore, in microcracks with elevated  $\text{CO}_2$  content, bicarbonate can be produced by carbonic anhydrase. However, in the surface layers of concrete exposed to the atmosphere, this approach is apparently impossible due to the reverse reaction, as the dehydration of bicarbonate to  $\text{CO}_2$ , which will escape into the atmosphere. This publication hypothesizes that combining urease and carbonic anhydrase may yield better results in concrete stabilization. Both enzymatic reactions produce hydrocarbonates, but  $\text{CO}_2$ , the product of the first reaction, becomes the substrate for the second. The creation of new genetically engineered strains with genes encoding enzymatic systems based on the described pathways can increase the efficiency of mineralization and improve the performance properties of bioconcrete.



# 1 Introduction

Systematic research into engineered self-healing concrete and other materials gained momentum at the beginning of the 2000s, driven by advances in biological and chemical healing agents, and expanded rapidly in the 2010s [1]. Reviews [2] and [3] indicate that self-healing concrete seals internal damage, such as cracks, without the need for external repair. Review [4] examines autonomous self-healing technology based on biological mechanisms for crack closure. The review process encompassed four phases: examination of global prior research, ecological and economic evaluations, consideration of future directions and benefits, and conclusions. This analysis incorporated 257 publications sourced from approximately 10 international databases [4].

A comparable technique applied encapsulated rejuvenators for in-situ healing of asphalt concrete pavement [5] and cement concrete pavements [6] to improve intrinsic self-repair capacity. Encapsulated rejuvenators proved viable for asphalt repair, raising healing temperature and duration to achieve up to 80% healing efficiency [7]. A study developed self-healing concrete incorporating low-calcium fly ash and partial replacement with recycled aggregate, which reduced overall strength [7].

Accumulated data from self-healing concrete research now supports the application of machine learning techniques to forecast material properties [8], [9], [10], [11] and optimize designs, complemented by fractal analysis methods [12]. An attempt to develop cyber-physical modeling and prediction of self-healing processes dynamics in bioconcrete [13] seems interesting, but attempts to validate such models have not yet been made.

Bio-based bacterial self-healing concrete is an alternative to conventional concrete in the construction industry [14], [15], [16], [17], [18], [19]. The bibliometric overview of 2025 [20] covers 150 references. Ongoing research targets resilient bacterial strains and spores that endure concrete's alkaline environment, tackling challenges like production costs, long-term viability, and environmental impact, while genetic engineering and smart tech enhance their efficiency [21], [17], [18].

Microbially induced calcium carbonate precipitation (MICP) has emerged as an essential biomineralization process with wide-ranging applications, including space exploration. The possibility of using local resources to construct extraterrestrial bases through microbial-induced carbonate precipitation on the Moon and Mars was reviewed [22] as an ambitious project and as one of the most unusual applications of biomineralization.

An experimental study [23] evaluates how different calcite-to-sand ratios affect mechanical properties and microstructure in self-healing concrete, utilizing *Hay Bacillus* to trigger calcite formation. Results from identifying *Bacillus subtilis* [24] as the most effective bacterial strain, with a 3% concentration enhancing beam load-bearing capacity by 20.2%. *Bacillus cohnii*, *Bacillus halodurans*, and *Bacillus pseudofirmus* enhance their performance properties, including strength and service life, in bioconcrete [25].

Further development of self-healing concrete, also known as bioconcrete, requires intensive microbiological research before it can proceed [26]. Microorganisms from ancient unique structures [13] can serve as a basis for the search for rational bacterial strains for bioconcrete.

The review [27] aimed to reduce the cost of microbial growth media for microbially induced calcium carbonate precipitation, the utilization of plant extractives as enzyme substitutes in enzyme-induced carbonate precipitation, the substitution of urea with urine as a low-cost source of nitrogen, the exploration of affordable alternatives to calcium ions, and the valorization of ammonia or ammonium byproducts, and other pathways.

Due to the aggressive environment of concrete mixes, spore-forming bacteria that can survive these conditions are most often used. The main property of these strains is their ability to initiate calcium carbonate mineralization in microcracks that form in concrete when water penetrates them. Bacteria with urease activity are primarily used for this purpose [28]. Urease catalyzes the hydrolysis of urea to form carbon dioxide, which, after exiting the cell, promotes the precipitation of calcium carbonate in an aqueous environment [29].

The use of genetic engineering methods to develop an actual self-healing biological agent appears promising. The bioremediase-like gene of a thermophilic anaerobic bacterium, BKH2 (GenBank accession no. KP231522), was thus transferred to the *Bacillus* strain to develop a self-healing agent [30]. The transposon mutagenesis method was employed to modify the genes of *B. halodurans* and create a mutant bacterial strain with higher efficiency of calcium carbonate productivity by catalyzing the combination of carbonate and calcium ion [31]



Although culturable bacterial strains with high urease activity already exist, carbonate formation can be improved by enhancing urease activity through the addition of accessory proteins or by using alternative urea-hydrolysis pathways. This work aimed to review bacterial metabolic pathways and enzymes used for biomineralization [32], as well as other promising enzymes that could accelerate existing pathways or exploit alternative principles of calcium carbonate precipitation.

## 2 Literature Search Methods

A systematic literature search was conducted to identify relevant studies on bioconcrete, bacterial biomineralization, and enzymatic pathways for calcium carbonate precipitation. The search encompassed multiple bibliographic databases, including Scopus and PubMed, to ensure comprehensive coverage of interdisciplinary fields such as biotechnology, materials science, and civil engineering. The time frame for the search was limited to publications from 1995 onward, marking the year in which the crystal structure of the urea transporter protein (UT) was first determined [36], providing foundational insights into urea transport mechanisms relevant to this review. The search was updated through December 2025 to incorporate the most recent advancements.

Keywords and phrases were selected based on core concepts from the field, including "bioconcrete," "self-healing concrete," "calcium carbonate precipitation," "urease," "urea amidolyase," "carbonic anhydrase," "*Bacillus subtilis*," "*Sporosarcina pasteurii*," "bacterial biomineralization," "genetically engineered bacteria," "microcrack repair," and "enzymatic mineralization." Boolean operators and advanced search techniques were employed to refine results. For example, in Scopus, queries such as

TITLE-ABS-KEY ((bioconcrete OR "self-healing concrete" AND bacteria AND (urease OR amidolyase OR "carbonic anhydrase")) AND PUBYEAR > 1994

were used to target studies on bacterial enhancements in concrete. Another example query focused on alternative pathways:

TITLE-ABS-KEY ((urease OR "urea hydrolysis" OR amidolyase OR "allophanate hydrolase" OR "carbonic anhydrase") AND "calcium carbonate" AND (concrete OR cement)) AND PUBYEAR > 1994.

The initial search yielded approximately 1,200 unique records after deduplication using tools like Zotero. These were screened based on title and abstract relevance, with full-text reviews conducted for 250 articles that met inclusion criteria (e.g., empirical studies or reviews of bacterial enzymatic systems for concrete applications). To map research connections and identify clusters of related work, the bibliographic data (including keywords, citations, and authors) were analyzed and visualized using VOSviewer software (version 1.6.20). This tool generated network maps of keyword co-occurrence and citation networks, highlighting thematic clusters such as urease-dominated biomineralization and emerging amidolyase pathways, thereby illustrating the evolution and interconnections within the field.

## 3 Literature Review

### 3.1 Genes encoding urease and accessory proteins

The primary method for producing calcite is the release of carbon dioxide in an aqueous environment during the enzymatic breakdown of urea by urease, as reviewed in [32], [33], [39], and [35]. Bacterial urease is a nickel-containing enzyme consisting of three subunits: UreA, UreB, and UreC. UreC contains a catalytic center containing two ions  $\text{Ni}^{2+}$ , without which the enzyme is inactive [36], [37], [43], and [39].

For the correct assembly of the urease complex, chaperones are used, namely the proteins UreD, UreE, UreF, and UreG [29],[40], [41]. These accessory proteins form a complex that facilitates  $\text{Ni}^{2+}$  insertion into the dinuclear active site of UreC, preventing the toxic release of free nickel in the cell. UreE acts as a metallochaperone, UreG as a GTPase, UreF as a regulator, and UreD (or UreH ortholog) as a scaffold [36], [42], [43]. It is believed that UreD first binds to apo-urease and forms an initial complex, which is subsequently joined by UreF, UreG, and the nickel-binding metallochaperone UreE, which carries nickel ions [41], [44], [45].

UreG's GTP hydrolysis induces a conformational shift (e.g., dimer dissociation), enabling  $\text{Ni}^{2+}$  release from UreE-bound complexes and transfer through a tunnel-like path in the accessory complex to UreC. This transfer couples energy from hydrolysis to metal insertion [36], [41], [44], [45], [46]. The



maturation process involves sequential or modular assembly of accessory proteins onto apo-urease (the inactive form lacking nickel), starting with UreD (or UreH) as a scaffold that induces conformational changes, followed by UreF recruitment to form UreDF, and then UreG to complete the UreDFG preactivation complex. This order is evidenced by affinity pull-downs, cross-linking, and structural analyses showing UreD's initial interaction prepares the enzyme for subsequent bindings, [41], [47], [48]. The article [45] states that UreD and UreF can form a UreFD complex, which can then recruit UreG to form a UreGFD complex, and interactions start with UreD-apo-urease. The research [49] confirms that UreH [UreD] and UreF form an initial complex with apo-urease before UreG joins. Early evidence for UreD-UreF-UreG-apo-urease complex formation, implying sequential assembly, was published in [50].

UreE, a nickel-specific metallochaperone, interacts with the preformed UreDFG-apo-urease complex to deliver Ni<sup>2+</sup> ions, often as the final step before insertion. It binds Ni<sup>2+</sup> at sites such as His-rich regions or C-terminal motifs and transfers it via protein-protein interactions, without being essential for complex formation but rather facilitating maturation [51], [52].

UreG, a SIMIBI-class GTPase, binds GTP, undergoes hydrolysis-induced conformational changes (e.g., switch I/II regions and dimer-monomer transitions), and couples this to Ni<sup>2+</sup> release from UreE/UreG, channeling it through the accessory complex to UreC's dinuclear site. This coupling prevents premature Ni release and ensures fidelity [53].

The study [54] elucidates the structure and the regulatory mechanism of urease gene expression in *S. pasteurii* under different culture conditions were studied using transcriptome sequencing. The results revealed a urease biosynthesis *S. pasteurii* is determined by two operons. Operon-1 containing *ureA*, *ureB*, *ureC*, *ureE*, and *ureF* genes, and operon-2 containing *ureG* and *ureD* genes.

The study [55] investigated urease activity in a newly isolated strain, YX-3 of *Shingobacterium thalpoophilum*, which exhibits the ability to precipitate calcium carbonate. Genome sequencing revealed the presence of the structural genes *ureA*, *ureB*, and *ureC*, along with the auxiliary genes *ureD*, *ureE*, *ureF*, and *ureG*. Reverse Transcription Quantitative Polymerase Chain Reaction analysis showed that the addition of NiCl<sub>2</sub> resulted in a significant up-regulation of *ureC* expression. His267, His294, and Gly325 in the UreC domain were further demonstrated to coordinate simultaneously with nickel ions and urea through homology modeling and molecular docking.

However, strains used in practice that can synthesize urease may lack chaperone genes *ureD*, *ureE*, *ureF*, *ureG*, and *ureD*. For example, in *B. subtilis*, the genome contains only the genes for the primary urease enzyme, *ureABC*. Still, these genes are fewer than in organisms with a complete genes set, indicating the presence of alternative pathways for urease maturation [40].

One of the bottlenecks in increasing urease activity is the rate of urea transport across the membrane. Several kinetic and physiological studies indicate that urease activity may be limited by the transport of urea across the cell membrane [56], [57].

Therefore, to increase urease activity, urea transporters should be used. Bacteria have several types of transport systems for pumping urea into the cell. These include Urel as a proton-dependent channel from the bacterium *Helicobacter pylori*. It helps bacteria survive in acidic conditions (pH 4-6) but is inactive in the alkaline environment of concrete mix (pH 11-14), so it has no practical value for bioconcrete pH [58], [59]. More promising proteins for creating strains with increased urease activity are membrane transporters of the UT (urea transporter) family, which facilitate the diffusion of urea through the cell membrane without energy expenditure [60], [61], [62]. Hereafter, these proteins are referred to as UT [70], since the bacterial channels of this class lack nomenclature; for example, the urea transporter Yut has been described in *Yersinia pseudotuberculosis* [61], [63]. Active systems for transporting urea across the membrane have also been identified in bacterial cells, for example, the UrtABC urea transporter [60], [63], which requires ATP for function and may reduce the cell's urease potential.

Functional characterization of bacterial UTs, such as ApUT from *Actinobacillus pleuropneumoniae*, demonstrates saturable urea flux that is inhibited by compounds such as phloretin, underscoring their potential to enhance intracellular urea availability.

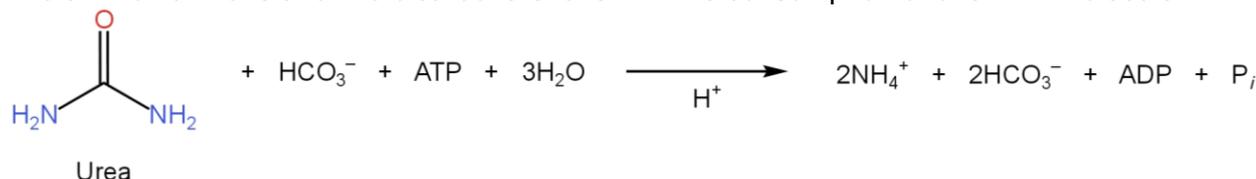
Further research on UT structures has provided insights into permeation mechanisms, including cryo-EM structures of human and zebrafish UTs that reveal trimeric assemblies and selective urea-binding sites, which could inform the engineering of bacterial variants for bioconcrete applications [64], [65], [66]. Evolutionary studies suggest that UTs in vertebrates evolved to adapt to urea concentration gradients, a principle that might be leveraged in bacteria to optimize mineralization in concrete [67]. Molecular dynamics simulations of UTs indicate conformational changes during urea transport, facilitating efficient diffusion without energy input [68]. In colonic models, UT-B transporters mediate urea movement to support symbiotic bacteria, highlighting a role in nitrogen salvaging that parallels potential





Widespread annotation corrections indicate that many bacterial proteins labeled as ureases are actually urea carboxylases, expanding the known distribution of this pathway [81]. Prokaryotic urea carboxylase from sources like *Kluyvera intermedia* lacks the AH domain but retains high activity, suggesting potential for hybrid systems [83]. Single-particle cryo-EM of urea amidolyase shows hexameric organization, enhancing catalytic efficiency in microbial urea degradation [85]. Allophanate hydrolase from *O. sagaranensis* generates ammonia, adjacent to UC genes, forming an ATP-dependent alternative pathway [83]. Crystal structures of UC provide mechanistic insights into biotin-mediated carboxylation, a crucial step in the production of bicarbonate in bioconcrete [86]. Structures of AH from *Granulibacter bethesdensis* reveal substrate binding sites, aiding in understanding hydrolysis yields [87]. In cyanuric acid metabolism, AH functions independently of urease, highlighting the versatility of urea catabolism in bacteria [88]. Evolutionary analyses show that fungi exhibit fusion events, but bacterial forms remain separate, offering flexibility for genetic engineering [89].

In summary, the amidolyase pathway converts one urea molecule and one bicarbonate ion into two ammonium ions and two bicarbonate ions with the consumption of one ATP molecule:



Thus, the amidolyase pathway is an ATP- and biotin-dependent alternative to urease hydrolysis of urea. This process is self-sustaining with a sufficient urea supply, as the bicarbonate ion required for urea carboxylase is generated by the hydrolysis of allophanate [85].

### 3.4 Survival of bacteria in concrete

One of the main problems is survival in concrete, starting with hydration of the concrete when the pH reaches 12-13. Survivability in concrete is also affected by the chemical composition and the tensile stress that occurs when mixing concrete. It has been shown that spore viability in concrete can be as low as 1% after 9 days of incorporation into concrete [90]. To increase the bacterial titer, preparations containing mainly bacterial spores in concrete are used. In addition, various carriers are used, such as diatomaceous earth [91],[92], expanded clay [93], perlite [94] and hydrogel [95]. Which can increase the lifespan of bacteria in concrete by an order of magnitude [95], [96], [97], [98]. Standard tests are used to compare the effectiveness of different self-healing concrete systems [99], [100].

The survival of bacteria can also be negatively affected by increased consumption of ATP, as in the amidolyase pathway, due to the poor environment. Bacteria may simply not have time to seal the cracks. To solve this problem, it may be necessary to increase the concentration of spores in the concrete, which will increase the cost.

For urease to work, nickel ions are required, which are toxic to bacteria. To reduce the toxicity of nickel, it can be added in the form of slightly soluble, bioavailable salts, which will reduce toxicity.

## 4 Conclusions

In this article, methods are proposed to increase urease activity in strains already used for bioconcrete production. Also, the possibility of developing strains containing the proposed genes in different combinations is explored to find an optimal gene combination for increasing carbonate production. A combination of enzymes such as urease and carbonic anhydrase or the amidolyase pathway in combination with carbonic anhydrase, may be particularly promising. Expressing carbonic anhydrase externally to fix the resulting carbon dioxide was also proposed to enhance mineralization. Recent breakthroughs in bacteria-powered self-healing concrete emphasize genetic modifications to enhance spore viability and calcite deposition, addressing challenges such as bacterial survival in harsh concrete matrices [30], [31].

The use of genetically engineered strains that produce urease, carbonic anhydrase, and other enzymes involved in the biomineralization process represents a promising approach to improving concrete durability. Combining these enzymes in a single strain can accelerate calcium carbonate precipitation and enhance the efficiency of microcrack repair. Based on existing research and the mechanisms described in this article, such as the urease and amidolyase pathways, these mechanisms may enable further improvements in bioconcrete properties. Advances in microbial self-healing concrete using engineered bacteria show up to 50% better crack closure rates, with synthetic biology tools



optimizing enzyme expression [21]. Characteristics of rubberized concrete with bacteria such as *S. pasteurii* demonstrate enhanced mechanical properties through genetic that increase output [21]. Genetically modified *B. subtilis* strains yield self-healing bioconcrete with improved compressive strength, as shown in mortar specimens [101]. Engineered microbial strategies in low-carbon concrete incorporate Bacillus-based encapsulation and genetic enhancements for alkaline resistance [102].

In the future, it is also necessary to explore the potential applications of these approaches to real building materials and their adaptation to optimal concrete conditions, such as alkaline pH. The development of effective genetically engineered strains that incorporate a complex of enzymes to enhance mineralization and restore concrete will reduce environmental impact. Bio-based bacterial concrete reviews highlight *Sporosarcina* spp. for sustainable infrastructure, with genetic engineering advancing crack-sealing technologies [103]. Tailored strains with improved calcite production via synthetic biology promise reduced environmental impact [75].

Thus, bioconcrete improved with urease, carbonic anhydrase, and amidolyase can play an essential role in creating new materials that are not only stronger and more durable but also more environmentally protective through biocarbonization and carbon dioxide fixation.

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## 6 Conflict of Interests

The authors declare no conflict of interest.

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