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Transformative Microbes to Reduce the Presence of Toxic Mercury in Wastewater and Dental Applications

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Introduction

Elemental mercury (Hg^0) is a naturally occurring, silvery, and volatile metal that remains liquid at room temperature. It is typically found bound in mineral deposits and salts but can also be released from natural sources such as volcanic activity and geothermal vents. Mercury exists in multiple chemical forms and is a significant environmental contaminant due to its toxicity, persistence, and bio accumulative behavior. In its elemental form, Hg^0 is used in thermometers, electrical switches, and dental amalgams.

Though less toxic than its inorganic salts, elemental mercury can transform into more hazardous compounds by combining with halogens, oxygen, or sulfur—forming species commonly present in soils and rocks [1]. These inorganic salts are released geologically through volcanic emissions and the weathering of cinnabar (HgS), a major mercury ore. Human activities such as coal combustion, mining, septic effluents, and dental practices further increase environmental mercury levels. These emissions contaminate air, soil, and water, interfering with metabolic processes in exposed organisms [2]. Since the Industrial Revolution, atmospheric mercury concentrations have increased tenfold, with widespread accumulation in sediments.

Under anoxic conditions, inorganic mercury (Hg^{2+}) undergoes microbial methylation by anaerobic bacteria, which attach a methyl group ($-\text{CH}_3$) to produce methylmercury (CH_3Hg^+) [3,4]. This process is enhanced by organic substrates and sulfur compounds. Methylmercury is lipophilic and bioaccumulates efficiently through aquatic food webs, leading to high concentrations in predatory species and human consumers, primarily through fish and shellfish [5].

Highly neurotoxic, methylmercury crosses the blood-brain barrier and placenta, where it binds to proteins and disrupts neural development. Prenatal and early-life exposures are associated with birth defects, reduced intelligence, cognitive impairments, and motor dysfunction [6]. It may also be transferred to infants via breast milk, though to a lesser extent.

Microbial demethylation plays a key role in mercury detoxification. Both aerobic and anaerobic bacteria use enzymatic pathways, encoded by the mer operon, to convert methylmercury into less toxic inorganic forms and inert Hg^0 [7-9]. Engineered microbial consortia expressing mer genes—delivered through aspirated fluids, biofilms, immobilized gels, or biomass—offer promising bioremediation solutions for contaminated environments such as wastewater, dental systems, and soils. These approaches maintain enzymatic activity, including organic degradation, while mitigating mercury toxicity.

This paper explores mercury and its sources, microbial transformations, and emerging technologies for sustainable remediation.

Mercury Sources and Environmental Pathways

Mercury is an environmentally persistent element that does not readily undergo degradation [10]. Anthropogenic mercury emissions significantly augment natural background levels, resulting in widespread environmental dispersal and elevated health risks. These sources include coal-fired power plants, septic systems, dental office wastewater, mining effluents, and industrial discharges [11,12]. Once introduced to an aquatic system, mercury undergoes biogeochemical cycling, including microbial methylation to form methylmercury, which is highly soluble and bioavailable [13,14]. This compound bioaccumulates and biomagnifies through food chains, with apex predators such as tuna and swordfish exhibiting the highest mercury concentrations [15].

Coal Combustion

Coal-fired power generation remains the predominant source of anthropogenic mercury emissions both globally and within the United States [16]. Mercury released from coal combustion enters the environment through coal ash residues, flue gas emissions, and airborne particulates. Despite the implementation of pollution control technologies, mercury emissions persist at significant levels in many facilities. Modernization efforts involve the adoption

of advanced emission control systems that can reduce mercury output; however, these technologies are often complex and have limited penetration across aging power plants in North America.

Septic Systems

Dental amalgams, comprised of approximately 50% elemental mercury combined with metals such as silver, tin, and copper, undergo degradation within the oral cavity. Oral bacteria, most notably *Streptococcus mutans*, produce acidic byproducts and hydrogen sulfide (H_2S), both of which contribute to the corrosion of amalgam fillings. These microbial processes facilitate the release of mercury as elemental and inorganic forms. Furthermore, bacterial enzymatic activity may promote the methylation of mercury, converting it into methylmercury.

Mercury release is exacerbated by common oral activities, including chewing, brushing, teeth grinding, and exposure to saliva and acidic foods [17]. Elemental mercury vapor is readily inhaled and absorbed into the circulatory system, while other mercury species are ingested, pass through the digestive tract, and excreted via urine and feces [18]. Studies indicate that individuals with multiple amalgam restorations exhibit urinary mercury levels 2 to 12 times higher than those without such fillings. Although individual households produce minimal mercury contributions from dental amalgams to municipal sewage, cumulative inputs from multiple sources can lead to significant localized mercury accumulation. In septic systems, mercury binds to organic matter within sludge and can persist for extended periods. Anaerobic conditions, typical of septic tanks and leach fields, promote microbial conversion of inorganic mercury into methylmercury. Elevated mercury concentrations have been documented in septic sludge linked to dental sources [19,20]. Environmental risks escalate when mercury-laden sludge is mishandled or when septic effluents are discharged to surface waters, facilitating aquatic bioaccumulation. Rural areas relying on private wells and household septic systems are particularly vulnerable due to limited heavy metal filtration capacity. While per-household mercury loads may be small, long-term accumulation poses substantial environmental and public health threats, especially in sensitive or inadequately monitored regions.

Similarly, marine septic systems can discharge mercury into aquatic environments through waste from human excretion or industrial activities aboard vessels and offshore platforms. These systems, especially older or poorly maintained, lack mechanisms to remove or neutralize heavy metals. Consequently, mercury may accumulate in septic tank sludge, where processes may promote methylmercury production. Regulatory shortcomings and inadequate treatment protocols exacerbate these risks, particularly in international waters or regions with limited enforcement.

Dental Treatment Wastewater

Despite the declining use of amalgam fillings, the aging population's preference for dental restorations continues to contribute to environmental mercury contamination [21]. In the United States alone, over five tons of mercury are annually discharged from the release of inert mercury particles during amalgam removal. These particles enter municipal and septic wastewater via the dental office vacuum systems. The United Nations Environment Program reports dental amalgam placement and removal accounts for significant global mercury use and discharge adding to a substantial environmental burden.

To help reduce environmental expression, dental offices are employing amalgam separators (e.g., Hg5 by Solmetex), which

capture amalgam particles drawn by evacuation systems for recycling. However, separators do not capture soluble mercury species formed by bacterial activity within the oral cavity or evacuation system pipes [22,23]. These systems collect saliva, water, and debris during procedures and harbor diverse microbial communities of oral bacteria such as *Streptococcus mutans*, *Actinomyces* spp., and *Porphyromonas*. Within the evacuation system they exist alongside anaerobic sulfate-reducing bacteria (SRB) of genera like *Desulfovibrio* and *Desulfobacter*. Furthermore, biofilm-forming species such as *Pseudomonas*, *Bacillus*, and fungi like *Candida* colonize the moist interiors of evacuation lines and separator canisters. These microbes' methylate inorganic mercury due to the low-oxygen conditions prevailing in these biofilms and sludge deposits [24-26]. Proteinaceous debris provide organic substrates supporting microbial growth and create microenvironments conducive to mercury methylation. To mitigate dental mercury pollution, regulations have mandated amalgam separators, and international agreements such as the Minamata Convention which aims to limit mercury emissions and promote safer practices globally [27].

Mer Operon and Microbial Mercury Detoxification

Demethylation is a natural enzymatic process involving the cleavage of methyl groups from organic molecules and some microbial species utilize this process to degrade methylmercury for self-preservation [28-31]. Cells respond defensively to inorganic mercury compounds (e.g., mercuric chloride), which disrupt cellular function by binding thiol (-SH) groups in proteins and enzymes. This bacterial mercury resistance is encoded by the mer operon, enabling survival in mercury-contaminated habitats [32]. Central to this operon is the merA gene encoding mercuric reductase, which reduces inorganic Hg^{2+} to volatile elemental Hg^0 . Elemental mercury is inert and diffuses out of the cell, lowering intracellular toxicity.

Organic mercury compounds, such as methylmercury, pose even greater toxicity and persistence than inorganic. This requires coordinated action of merA and merB genes to provide complete detoxification. The merB gene encodes organomercurial lyase, which cleaves carbon-mercury bonds in organic mercury compounds, releasing Hg^{2+} for MerA to reduce to Hg^0 . This two-enzyme system is essential, for without MerA, released inorganic mercury would remain toxic. Furthermore, with both enzymes acting intracellularly the process requires import of mercury ions via membrane proteins (MerT, MerP, MerC) [33]. Regulatory genes such as merR along with plasmid-borne transporters facilitate horizontal gene transfer, enabling rapid spread of mercury resistance across microbial communities. This system provides robust microbial defense, the detoxifying of intracellular mercury and the reduction of extracellular toxic mercury species.

Protease Denaturing by Mercury

Proteins may dominate the fluids found in wastewater systems contributing to organic loads and biofilms. Proteinaceous debris from dental procedures or industrial waste management applications add to the fouling progression by creating surface borne deposits and adding to biofilms. These gelatinous structures capture and retain inorganic and metallic filings. Unprocessed proteins increase biological oxygen demand (BOD), promote eutrophication and under anaerobic conditions, generate ammonia, hydrogen sulfide, and volatile fatty acids. Under normal operating conditions, protease enzymes, in liquid or powder form, are added to the effluent to degrade the proteins into peptides and amino acids, for easier treatment or removal. Effective protein degradation by protease enzymes is critical to reduce these fouling masses

to improve function, control odors and optimize any cleaning treatment [34,35].

Increasing levels of mercury will affect added protease treatments function proportionately (Figure 1). In environments where mercuric species are present, supplied protease may not effectively denature proteins, negating its efficacy as a cleaner and degrader. This occurs due to the inhibition of cysteine proteases through the binding of mercury to the thiol (–SH) groups of active-site cysteine residues. The mercuric binding blocks the nucleophilic function of the thiol to donate an electron pair and attack the peptide bond during protein cleavage which hinders the process. This mechanism contributes to mercury’s broader toxic effects by interfering with critical proteolytic processes [36-40]. Additionally, mercury may induce conformational changes in the enzyme, further disrupting its function. Mercury binding causes enzyme misfolding or denaturation and induces reactive oxygen species (ROS) that oxidize and damage enzymes [41,42]. Even metalloproteases can be inhibited if mercury displaces essential cofactors like zinc, serine, and aspartic proteases, while other more resistant proteases are also vulnerable [43].

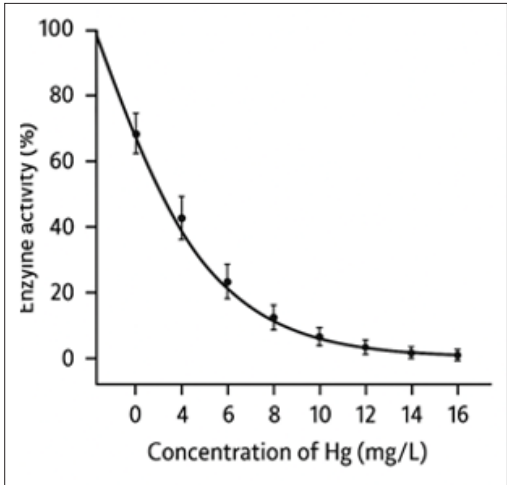


Figure 1: Mercury’s Effect on Enzymatic Activity

Mereduce™ For Toxic Mercury Reduction

The mer operon has been extensively investigated as a biotechnological tool for mercury remediation, supporting efforts to meet EPA and international mandates aimed at reducing mercury emissions. In wastewater systems that receive fecal and urinary inputs, proteolytic and lipolytic microbes play essential roles in maintaining flow and degrading organic matter. However, mercury compounds pose a significant threat to both environmental stability and the functional integrity of microbial communities, particularly protease-producing organisms. Mercury not only inactivates these microbes but also denatures the proteolytic enzymes they secrete. Mercury-resistant and -transformative microbes, commercially marketed as Mereduce™, express the mer operon and have demonstrated the ability to reduce toxic Hg²⁺ to volatile elemental Hg⁰ under laboratory conditions (see Appendix 1).

Report of the bench study of mercury (II) chloride transformation to inert mercury through the exposure to Mereduce microbes

Objective: To investigate the effectiveness of “mereduce” microbes to transform toxic mercuric compounds (mercury (II) chloride) to inert mercury (0).

Materials: 3 bottles (A, B, & Control) of ~350 ml of distilled water spiked with 500-1000 ppb concentrations of mercuric chloride. Two bottles of “mereduce” microbe blends and 2 bottles of organic nutrient broth. One bottle of High-level mercury Hg+2 strips and one bottle of low-level mercury Hg+2 strips capable of registering only Hg+2 ions.

Methods: Study was performed for 5 working days each week for two consecutive weeks, excluding the 2 weekend days. Prior to study, the baseline mercury levels of the distilled water in the 3 bottles (A, B, & Control) were measured in triplicate with SenSafe® Mercury Check strips in accordance with the manufacturer’s direction as follows:

1. Dip one test strip into a 20 mL (=1 oz) water sample for 30 seconds with a constant, gentle back and forth motion.
2. Remove the strip and shake once briskly to remove excess water.
3. Wait 2 minutes.
4. Then match to the color chart on the bottle containing the check strips.

Following the baseline measurement, 1 oz of “mereduce” microbes blends and 0.5 oz of organic nutrient broth were added to “Bottle A” and “Bottle B”. The “Control” bottle did not receive any additives. Then the mercury levels of the water in the 3 bottles were measured again in triplicate with SenSafe® Mercury Check strips as described above. This procedure was administered for each of the 3 bottles at almost the same time on each of the 5 working days of the first week (week 1). No measurement was made on the two weekend days (Saturday & Sunday).

On Monday the following week (week 2), the above procedures were repeated for each of the 5 working days of the week. However, in this second week, the mercury level was measured in triplicate with SenSafe® Boris’s Mercury Check strips in accordance with the manufacturer’s direction as follows:

1. Dip one test strip into a 200 mL (=7 oz) water sample for 60 seconds with a constant, gentle back and forth motion.
2. Remove the strip and shake once briskly to remove excess water.
3. Wait 30 seconds.
4. Then match to the color chart on the bottle containing the check strips.

Results: The results of the study are shown in Table 1 below.

Table 1: Results

Table 1. Results as read with the SenSafe® Mercury Check strips									
Week 1 High level	SOLUTION A			SOLUTION B			CONTROL		
	Test 1	Test 2	Test 3	Test 1	Test 2	Test 3	Test 1	Test 2	Test 3
Baseline	1000	1000	1000	1000	1000	1000	1000	1000	1000
Day 1	200	200	200	200	200	200	1000	1000	1000
Day 2	100	100	100	100	100	100	1000	1000	1000
Day 3	50	50	50	100	100	100	1000	1000	1000
Day 4	0	0	0	50	50	50	1000	1000	1000
Day 5	0	0	0	0	0	0	1000	1000	1000
Week 2 Low level	Test 1	Test 2	Test 3	Test 1	Test 2	Test 3	Test 1	Test 2	Test 3
	0.002	0.002	0.002	0.002	0.002	0.002	0.0	0.0	0.0
Day 1	0.002	0.002	0.002	0.002	0.002	0.002	0.0	0.0	0.0
Day 2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Day 3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Day 4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Day 5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

To avoid the addition of externally added proteases, and to prevent the denaturation of proteolytic enzymes essential for protein degradation, effective remediation requires the introduction of specialized microbes that can replicate and remain functional in a mercuric environment. These microbes must sustain enzymatic activity, expressing functional proteases, while exhibiting mercury tolerance, resistance and providing the capacity to transform mercuric species. Technologies that preserve and support the function of both proteolytic enzymes and mer operon-encoded proteins are particularly valuable in mercury-impacted environments [44]. Dental evacuation systems serve as a microcosm of broader infrastructures where mercury releases and biofilm fouling intersect [45].

Anaerobic microenvironments beneath biofilms and surface-bound protein debris can support mercury-methylating microbes such as sulfate-reducing bacteria and Streptococcus mutans [46]. The accumulation of amalgam particles in separator canisters further exacerbates the formation of methylmercury hotspots. To address these challenges, Solmetex developed Power Scrub with Mereduce™, a formulation that employs enzymatic agents derived from mercury-transformative microbes. These specialized, mercury-resistant microbes express multiple enzymatic pathways that degrade organic fouling while simultaneously reducing toxic Hg²⁺ to elemental Hg⁰ via intracellular mechanisms, all while preserving protease activity and supporting broader microbial consortia [47]. This dual-action approach enhances system performance, reduces fouling, and limits the formation and

environmental release of methylmercury. Maintaining biofilm-free surfaces also preserves the efficiency of amalgam separators by keeping sequestered mercury accessible for microbial detoxification during routine maintenance.

To promote microbial viability and establish a sustained demethylation environment, the microbes are supplied in a delivery media that is engineered with oxygenation bubbles and adhesion-promoting surfactants targeting biofilm slime layers. Kick-start enzymes are provided to initiate the breakdown of organic material to a food source for the digestive microbes. Surfactants enhance microbial adherence under flow conditions, allowing membrane transporter proteins to facilitate mercury uptake for intracellular enzymatic reduction. As the surface biofoul and protein masses are digested, embedded amalgam particles are released into separator systems for capture. The repetitive use of this technology provides repeated microbial interaction with mercury species. This cycle helps prevent mercury accumulation, while improving fluid dynamics, and reducing toxic mercury discharge.

The approach is adaptable for use in septic systems, coal refineries and municipal wastewater treatment facilities, where it can function as an adjunct to native microbial populations by enhancing mercury detoxification in fecal and urinary waste streams. Aeration promotes aerobic microbial growth and supports the *mer operon* expression. Furthermore, the use of agricultural probiotic mercury-transforming bacteria may mitigate mercury contamination in coal ash landfills by stabilizing waste matrices and reducing the toxicity of leachate.

Targeted Presentation

Microbial demethylation of mercury is effective across diverse environments, supporting bioremediation strategies involving inoculation of contaminated fluids, microbial concentration within enclosures, biofilm formation, agar gel embedded, or nutrient matrix incorporation [48-50].

Microbes can be adhered to piping surfaces, structural elements, or biological filters to optimize mercury transformation. Surfactants improve microbial colonization in target zones. For optimal demethylation, microbial inoculants are introduced into mercury-containing environments with aerobic conditions promoted by oxygen aeration to induce *mer operon* expression [51].

Immobilization of microbes in alginate beads provides a stable, protective environment with high mercury transformation activity. For example, *Bacillus megaterium* MB1 immobilized in alginate gel successfully removed 80% of mercury from a 10 mg/L solution within 24 hours and retained its effectiveness over repeated use [52]. The elemental mercury produced was sequestered within the gel matrix, efficiently extracting soluble mercury from the surrounding fluid. Similar studies have shown that immobilized mercury-transformative bacteria consistently outperform free-living cultures in detoxifying industrial effluents, highlighting their potential for scalable mercury remediation technologies [53].

Bioabsorbantion Through an Inactive Biomass

Within wastewater systems, applied microbes will die due to adverse environmental conditions or nutrient depletion. Dead mercury-transforming bacteria cannot reduce inorganic mercury, as this enzymatic process requires metabolic activity and cofactors such as NADPH [54]. NADPH is a critical coenzyme in cellular redox reactions, serving as an electron donor in mercury detoxification pathways; its absence in non-viable cells renders

enzymatic reduction impossible [55]. While dead microbial biomass cannot actively transform mercury, it can still passively adsorb Hg^{2+} through functional groups like thiols and carboxylates on the cell wall [56]. This process, known as biosorption, is a metabolically independent, physicochemical mechanism by which both living and dead biological materials remove metals from solutions. The capacity of dead biomass to bind toxic metals makes it suitable for passive remediation applications, such as within amalgam separator canisters, where stable, continuous metal capture is possible under flow conditions.

Near dead transformative bacteria can still contribute to mercury capture through biosorption and bioaccumulation of mercury species just prior to death [57]. Even when dead, their cell walls and surface structures (e.g., peptidoglycan, teichoic acids, lipopolysaccharides, and surface proteins) retain functional groups capable of binding heavy metals [58,59]. Some of the functional groups involved include carboxyl (-COOH), hydroxyl (-OH), amine (-NH₂) and most importantly sulfhydryl (-SH) [60]. These groups can chelate or adsorb mercury species (both inorganic and organic) through processes such as ion exchange, electrostatic attraction and complexation, a chemical process where molecules or ions (called ligands) bind to a central metal ion to form a stable complex [61].

These processes enable dead microbial biomass to function as a passive biofilter or heavy metal “sponge,” effectively trapping mercury without the need for metabolic activity. In contrast, live mercury-transformative microbes actively express genes responsible for converting Hg^{2+} to elemental mercury (Hg^0), which may become trapped within the cytoplasm upon volatilization. Following cell death, this intracellular mercury remains sequestered, thereby reducing its mobility and bioavailability, and effectively removing it from the environment. The continuous introduction of live mercury-transformative microbes into a containment canister serves to replenish and reactivate the biomass, sustaining intracellular mercury transformation and enhancing overall remediation performance [62].

Discussion

Mercury contamination remains a critical environmental and public health issue due to its persistence, toxicity, and bioaccumulative nature. Anthropogenic activities such as coal combustion, dental practices, and wastewater discharge contribute significantly to global mercury emissions, introducing various mercury species into the environment. Of particular concern is methylmercury, a neurotoxic compound that bioaccumulates in aquatic food webs and poses significant risks to human and ecological health.

Microbial transformation, particularly through the expression of the *mer operon*, provides a sustainable and effective strategy for mercury detoxification. This gene cluster encodes enzymes like mercuric reductase (MerA) and organomercurial lyase (MerB), which collectively convert toxic mercury species into less harmful forms, including volatile elemental mercury. These microbial processes are vital in mitigating methylmercury formation and reducing mercury bioavailability.

The deployment of mercury-transformative microbial consortia, such as those in Mereduce™, offers a promising biotechnological approach for managing mercury contamination in high-risk environments including dental evacuation systems, septic tanks, municipal wastewater plants, and coal ash landfills. By combining microbial inoculants with engineered delivery vehicles such as oxygenation bubbles and adhesion surfactants will enhance

microbial survival, enzymatic function, and mercury uptake even under biofouling and anaerobic conditions. Microbial immobilization techniques, such as encapsulation in alginate beads or biomass, enhance the stability and containment of elemental mercury, enabling scalable applications in both industrial and environmental settings. These immobilized systems have shown high efficacy and extended operational lifespans in mercury removal, making them well-suited for integration into larger remediation infrastructures.

Conclusion

Harnessing the natural mercury-transformative capabilities of specialized microbes presents a robust and adaptable solution to global mercury pollution. By preserving enzymatic integrity, preventing methylmercury formation, and reducing toxic discharge, these microbial strategies support safer, more sustainable waste management and environmental protection. Continued development and implementation of such technologies are essential for meeting international mercury reduction goals and safeguarding both human and ecological health.

The use of microbial consortia such as Mereduce™ offers a practical, sustainable approach to mitigating mercury pollution from amalgam residues, wastewater streams and coal ash. By integrating detoxifying bacteria, proteolytic enzymes, and surfactants, Mereduce™ enhances treatment system performance and maintains biofilm-free surfaces. Immobilization techniques, such as alginate bead embedding and biomass, further improve microbial stability, reusability, and mercury contact time, key for deployment in industrial, medical, and rural settings.

This biotechnological strategy complements regulatory tools and supports broader wastewater management goals. For practitioners and policymakers, it presents a scalable solution aligned with global efforts like the Minamata Convention. Continued research into microbial detoxification and delivery systems will be essential to maximize long-term efficacy and environmental resilience.

The underlying technology has been awarded a patent for its composition and delivery methods:

Patent: RA079/214345-U — Composition of Matter, System, and Method for Reducing Toxic Mercury in Wastewater Effluent
Trademark: Mereduce™, U.S. Registration Application Serial No. 90/479,611.

Author's Note

As mentioned within the paper, the release of mercury from both natural and human sources has an insidious, generational impact. While researching and authoring this paper it was vital that the younger generation have both input and review. I relied upon their passion and concerns to understand the urgency presented by mercury contamination. For information regarding Mereduce™ mercury transformation protocols, please reach out to the author.

About the Authors

Michael Radicone is president and chief science officer of I2 Air Fluid Innovation and Specialty Product Lead for HTRI. I2 Air Fluid Innovation has developed and patented technologies that address heat exchange fouling, toxic mercury presence in fluids and flue gas scrubber enhancement. As specialty Product Lead for HTRI, he oversees development and integration of the Vapor Nano Bubble Infusion technology. The recipient of seven governmental grants, he is published and peer reviewed and has presented the technology worldwide.

Grace Witt is a Senior Biomedical Engineering student at Clemson University with a concentration in Biomaterials. She works on an undergraduate research team through the Creative Inquiry program at Clemson University. In this project she works under Dr. Larsen researching how when polymersomes are modified with salts the protein interactions change in serum. This summer she is interning with Celularity's research and development team.

Ryan Radicone is a student researcher who is investigating the application of a technology that delivers a therapeutic drug utilizing a human hair derived keratin 3D scaffold model. The research is intended to determine the scaffold's biocompatibility and bioreactivity of its surface area for both the loading and timed release of therapeutic drugs.

Bennett T. Amaechi is a professor at the University of Texas Health San Antonio (UTHSA). His research, which focused on dental caries and oral care product development and evaluation, has been funded by industrial partners and federal agencies. His teaching and research methods have proven successful, earning him the 2022 Regent's Outstanding Teacher Award by the University of Texas System Boards of Regents, 2019 Presidential Award for Sustained Excellence in Teaching, 2015 Teaching Excellence Award by UTHSA dental school Faculty Assembly, and 2014 Faculty Leadership Award by the UTHSA Faculty Senate.

Bruce Birdwell is a graduate of SUNY At Stony Brook with a BS in Biology & Professional Engineering credits from University of Texas and Louisiana Technology. Career positions have been with Veeco Instruments, Metrology NDE, District Sales Manager, IBA (Ion Beam Application), Particle Accelerators, North America Sales Manager, 3M EMD, Product Launch of SIPP for Potable Water Rehabilitation, Sales Manager, Framatome, SIPP and Coatings for Nuclear Applications, Product Manager & Business Development.

References

1. Wu YS, Osman AI, Hosny M, Elgarahy AM, Eltaweil AS, et al. (2024) The toxicity of mercury and its chemical compounds: Molecular mechanisms and environmental and human health implications: A comprehensive review. *ACS Omega* 9.
2. Dehkordi MM, Nodeh ZP, Dehkordi KS, Salmanvandi H, Khorjistan RR, et al. (2024) Soil, air, and water pollution from mining and industrial activities: Sources of pollution, environmental impacts, and prevention and control methods. *Results in Engineering* 23: 102729.
3. Tang WL, Liu YR, Guan WY, Zhong H, Qu XM, et al. (2020) Understanding mercury methylation in the changing environment: Recent advances in assessing microbial methylators and mercury bioavailability. *Science of The Total Environment* 714: 136827.
4. Luo H, Cheng Q, He D, Sun J, Li J, et al. (2023) Recent advances in microbial mercury methylation: A review on methylation habitat, methylator, mechanism, and influencing factors. *Process Safety and Environmental Protection* 170: 286-296.
5. Scheuhammer AM, Basu N, Evers DC, Heinz GH, Sandheinrich M, et al. (2012) Toxicology of mercury in fish and wildlife: Recent advances. In M. S. Bank (Ed.), *Mercury in the Environment: Pattern and Process*. University of California Press 223-238.
6. Grandjean P, Weihe P, Jørgensen P, Clarkson T, Cernichiari E, et al. (1992) Impact of maternal seafood diet on fetal exposure to mercury, selenium, and lead. *Archives of Environmental*

- Health: *An International Journal* 47: 185-195.
7. Yu RQ, Barkay T (2022) Microbial mercury transformations: Molecules, functions, and organisms. In *Advances in Applied Microbiology Academic Press* 118: 31-90.
8. Gao Z, Zheng W, Li Y, Liu Y, Wu M, et al. (2022) Mercury transformation processes in nature: Critical knowledge gaps and perspectives for moving forward. *Journal of Environmental Sciences* 119: 152-165.
9. Priyadarshane M, Chatterjee S, Rath S, Dash HR, Das S (2022) Cellular and genetic mechanism of bacterial mercury resistance and their role in biogeochemistry and bioremediation. *Journal of Hazardous Materials* 423 (Part A).
10. Kumar A, Kumar V, Bakshi P, Parihar RD, Radziemska M, et al. (2024) Mercury in the natural environment: Biogeochemical cycles and associated health risks. *Journal of Geochemical Exploration* 267: 107594.
11. Bourtsalas AC, Themelis NJ (2019) Major sources of mercury emissions to the atmosphere: The U.S. case. *Waste Management* 85: 90-94.
12. Boening DW (2000) Ecological effects, transport, and fate of mercury: A general review. *Chemosphere* 40: 1335-1351.
13. Branfireun BA, Cosio C, Poulain AJ, Riise G, Bravo AG (2020) Mercury cycling in freshwater systems – An updated conceptual model. *Science of The Total Environment* 745: 140906.
14. Gustin MS, Bank MS, Bishop K, Bowman K, Branfireun B, et al. (2020) Mercury biogeochemical cycling: A synthesis of recent scientific advances. *Science of The Total Environment* 737: 139619.
15. Hilgendorf IR, Swanson HK, Lewis CW, Ehrman AD, Power M (2022) Mercury biomagnification in benthic, pelagic, and benthopelagic food webs in an Arctic marine ecosystem. *Science of The Total Environment* 841: 156424.
16. Charvát P, Klimeš L, Pospíšil J, Klemes JJ, Varbanov PS (2020) An overview of mercury emissions in the energy industry – A step to mercury footprint assessment. *Journal of Cleaner Production* 267: 122087.
17. Ishihara N (2000) Excretion of methyl mercury in human feces. *Archives of Environmental Health* 55: 44-47.
18. Sandborgh Englund G, Elinder CG, Johanson G, Lind B, Skare I, et al. (1998) The absorption, blood levels, and excretion of mercury after a single dose of mercury vapor in humans. *Toxicology and Applied Pharmacology* 150: 146-153.
19. Engqvist A, Colmsjö A, Skare I (1998) Speciation of mercury excreted in feces from individuals with amalgam fillings. *Archives of Environmental Health* 53: 205-213.
20. Wang X, Mao Y (2019) Mercury in municipal sewage and sewage sludge. *Bulletin of Environmental Contamination and Toxicology* 102: 643-649.
21. Stone ME, Cohen ME, Liang L, Pang P (2003) Determination of methyl mercury in dental-unit wastewater. *Dental Materials* 19: 675-679.
22. Hylander LD, Lindvall A, Gahnberg L (2006) High mercury emissions from dental clinics despite amalgam separators. *Science of The Total Environment* 362: 74-84.
23. Paryag A, Paryag AS, Rafeek RN, Pilgrim A (2010) Mercury pollution from dental amalgam waste in Trinidad and Tobago. *Journal of Water Resource and Protection* 2: 717-725.
24. Zeng L, Luo G, He T, Guo Y, Qian X (2016) Effects of sulfate-reducing bacteria on methylmercury at the sediment–water interface. *Journal of Environmental Sciences* 46: 214-219.
25. Lin TY, Kampalath RA, Lin CC, Zhang M, Chavarria K, et al. (2013) Investigation of mercury methylation pathways in biofilm versus planktonic cultures of *Desulfovibrio* desulfuricans. *Environmental Science & Technology* 47: 5695-5702.
26. Zhao X, Rockne KJ, Drummond JL, Hurley RK, Shade CW, et al. (2008) Characterization of methyl mercury in dental wastewater and correlation with sulfate-reducing bacterial DNA. *Environmental Science & Technology* 42: 2780-2785.
27. Mackey TK, Contreras JT, Liang BA (2014) The Minamata Convention on Mercury: Attempting to address the global controversy of dental amalgam use and mercury waste disposal. *Science of The Total Environment* 472: 125-129.
28. Barkay T, Miller SM, Summers AO (2003) Bacterial mercury resistance from atoms to ecosystems. *FEMS Microbiology Reviews* 27: 355-384.
29. Chang-ye H, Ma B, Hu S, Wu C (2024) Tailored bacteria tackling environmental mercury: Inspired by natural mercuric detoxification operons. *Environnemental Pollution* 341 : 123016.
30. Schiering N, Kabsch W, Moore MJ, Distefano MD, Walsh CT, et al. (1991) Structure of the detoxifying enzyme mercuric ion reductase from *Bacillus* sp. strain RC607. *Nature* 352 : 168-172.
31. Figueiredo N, Serralheiro ML, Canário J, Duarte A, Hintelmann H, et al. (2018) Evidence of mercury methylation and demethylation by the estuarine microbial communities obtained in stable Hg isotope studies. *International Journal of Environmental Research and Public Health* 15: 2141.
32. Dash HR, Das S (2012) Bioremediation of mercury and the importance of bacterial mer genes. *International Biodeterioration & Biodegradation* 75: 207-213.
33. Naguib MM, El-Gendy AO, Khairalla AS (2018) Microbial diversity of mer operon genes and their potential roles in mercury bioremediation and resistance. *The Open Biotechnology Journal* 12: 56-77.
34. Wang S, Zhao Y, Breslawec AP, Tingting Liang, Zhifen Deng, et al. (2023) Strategy to combat biofilms: a focus on biofilm dispersal enzymes. *npj Biofilms Microbiomes* 9.
35. Molobela IP, Cloete TE, Beukes M (2010) Protease and amylase enzymes for biofilm removal and degradation of extracellular polymeric substances (EPS) produced by *Pseudomonas fluorescens* bacteria. *African Journal of Microbiology Research* 4: 1515-1524.
36. Ynalvez R, Gutierrez J, Gonzalez Cantu H (2016) Mini-review: Toxicity of mercury as a consequence of enzyme alteration. *BioMetals* 29: 781-788.
37. Müller A, Saenger W (1993) Studies on the inhibitory action of mercury upon proteinase K. *Journal of Biological Chemistry* 268: 26150-26154.
38. Clarkson TW, Magos L (2006) The toxicology of mercury and its chemical compounds. *Critical Reviews in Toxicology* 36: 609-662.
39. Tamás MJ, Sharma SK, Ibstedt S, Jacobson T, Christen P (2014) Heavy metals and metalloids as a cause for protein misfolding and aggregation. *Biomolecules* 4: 252-267.
40. Klaassen CD (Ed.). (2013). *Casarett and Doull's Toxicology: The Basic Science of Poisons* (8th ed.). McGraw-Hill Education.
41. Liu Z, Lee C, Wakeham SG (2006) Effects of mercuric chloride and protease inhibitors on degradation of particulate organic matter from the diatom *Thalassiosira pseudonana*. *Organic Geochemistry* 37: 1003-1018.
42. Chen J, Ye Y, Ran M, Li Q, Ruan Z, et al. (2020) Inhibition of tyrosinase by mercury chloride: Spectroscopic and docking studies. *Frontiers in Pharmacology* 11: 81.
43. Jacob-Ferreira AL, Passos CJ, Jordão AA, Fillion M, Mergler

- D, et al. (2009) Mercury exposure increases circulating net matrix metalloproteinase (MMP)-2 and MMP-9 activities. *Basic & Clinical Pharmacology & Toxicology* 105: 281-288.
44. Nascimento AM, Chartone-Souza E (2003) Operon mer: Bacterial resistance to mercury and potential for bioremediation of contaminated environments. *Genetics and Molecular Research* 2: 092-101.
45. Suprono MS, Won J, Savignano R, Zhong Z, Ahmed A, et al. (2021) A clinical investigation of dental evacuation systems in reducing aerosols. *Journal of the American Dental Association* 152: 455-462.
46. Zhao A, Sun J, Liu Y (2023) Understanding bacterial biofilms: From definition to treatment strategies. *Front Cell Infect Microbiol* 13: 1137947.
47. Schiering N, Kuo CF, Howard AJ, Walsh CT (1991) X-ray crystal structure of the detoxifying enzyme mercuric ion reductase from *Bacillus* sp. strain RC607. *Biochemistry* 30: 8946-8954.
48. Zeroual Y, Moutaouakkil A, Dzairi FZ, Talbi M, Chung PU, et al. (2003) Biosorption of mercury from aqueous solution by *Ulva lactuca* biomass. *Bioresource Technology* 90: 349-351.
49. Jhariya U, Chien M F, Umetsu M, Kamitakahara M (2025) New insights into immobilized bacterial systems for removal of heavy metals from wastewater. *International Journal of Environmental Science and Technology* 22: 8319-8334.
50. Jafari SA, Cheraghi S (2014) Mercury removal from aqueous solution by dried biomass of indigenous *Vibrio parahaemolyticus* PG02: Kinetic, equilibrium, and thermodynamic studies. *International Biodeterioration & Biodegradation* 92: 12-19.
51. Zhao W, Gan R, Xian B, Wu T, Wu G, et al. (2024) Overview of methylation and demethylation mechanisms and influencing factors of mercury in water. *Toxics* 12: 715.
52. Chien M, Nakahata R, Ono T, Miyauchi K, Endo G (2012) Mercury removal and recovery by immobilized *Bacillus megaterium* MB1. *Frontiers of Chemical Science and Engineering* 6: 192-197.
53. Wang L, Hou D, Cao Y, Ok YS, Tack FMG, et al. (2020) Remediation of mercury contaminated soil, water, and air: A review of emerging materials and innovative technologies. *Environment International* 134: 105281.
54. Schiering N, Kabsch W, Moore MJ, Distefano MD, Walsh CT, et al. (1991) Structure of the detoxification catalyst mercuric ion reductase from *Bacillus* sp. strain RC607. *Nature* 352: 168-172.
55. Summers AO (1986) Organization, expression, and evolution of genes for mercury resistance. *Annual Review of Microbiology* 40: 607-634.
56. Hansda A, Kumar V (2016) A comparative review towards the potential of microbial cells for heavy metal removal with emphasis on biosorption and bioaccumulation. *World Journal of Microbiology and Biotechnology* 32.
57. Wang J, Chen C (2009) Biosorbents for heavy metals removal and their future. *Biotechnology Advances* 27: 195-226.
58. Volesky B, Holan ZR (1995) Biosorption of heavy metals. *Biotechnology Progress* 11: 235-250.
59. Das N (2010) Recovery of precious metals through biosorption—A review. *Hydrometallurgy* 103: 180-189.
60. Wang J, Chen C (2009) Biosorbents for heavy metals removal and their future. *Biotechnology Advances* 27: 195-226.
61. Wolesky B (2007) Biosorption and me. *Water Research* 41: 4017-4029.
62. Das S, Dash HR (2014) Microbial bioremediation: A potential tool for restoration of contaminated areas. In S. Das (Ed.), *Microbial biodegradation and bioremediation* 01-21.