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ENHANCING FOOD SAFETY: ADAPTING TO MICROBIAL RESPONSES UNDER DIVERSE ENVIRONMENTAL STRESSORS

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Background: Microbial adaptation is a fundamental process by which microorganisms dynamically adjust to changes in their environment. Microbial adaptation includes both short-term and long-term mechanisms that enable microorganisms to survive and thrive in changing environmental conditions. Microbial adaptation processes can result in evolutionary changes that provide sustainable advantages. These processes allow microbes to develop traits such as antibiotic resistance and enhanced biofilm formation, ensuring their survival and proliferation in diverse environments. Despite substantial progress, there remains a critical gap in the literature regarding a comprehensive synthesis of microbial adaptation mechanisms and their implications for enhancing food safety and ensuring the sustainable production of industrially valuable biochemicals. **Objectives:** This document seeks to provide a comprehensive overview of recent advancements in understanding resistance mechanisms to various environmental stresses for enhancement of food safety, including oxidative stress, hyperosmotic stress, thermal stress, acid stress, and organic solvent stress. In addition, the study examines the applications of stress-resistant mechanisms in producing diverse biomolecules and valuable chemicals. Finally, the manuscript offers a discuss prospects for identifying stress-resistant mechanisms through systems biology and further engineering these elements using synthetic biology to enhance productivity. **Methods:** The literature review sought to cover the most important aspects of stress-resistant mechanisms in the adaptation processes of microorganisms and their role in food safety and sustainable production of valuable biochemicals. This review was not limited to a specific time period, geographic or language scope, or publication type, although preference was given to peer-reviewed open access sources. **Results:** Researchers have found that adaptive responses of pathogens to factors such as changes in temperature, disinfectants, and storage conditions can pose significant challenges to traditional food safety practices. At the same time, microbial adaptation is an integral part of ecosystem functioning, profoundly influencing processes such as nutrient cycling, decomposition, and soil fertility. The soil microbial community plays a vital role in the safety of cultivated produce, as it acts as a key indicator of soil ecological status and the effectiveness of remediation of contaminated soils. Microorganisms serve as climate change signalling indicators, actively contributing to climate regulation. Higher temperatures, precipitation variations, and higher CO_2 concentrations can increase microbial growth rates, potentially increasing the prevalence of pathogens in both plant and animal foods. Natural and synthetic microbial stressors are effective mechanisms for food quality and safety management. Adaptation to chemical stress provides microbial resistance to polluted environments and industrial processes, with implications for bioremediation, public health, and environmental sustainability. **Conclusion:** Microbial adaptation results from the interplay of environmental stressors, genetic variation, ecological interactions, and anthropogenic impacts that determine the resilience, diversity, and adaptive capacity of microbial communities in a variety of habitats and ecosystems. By manipulating these adaptive pathways through combined or sequential stressors (e.g., low heat and low pH), food technologists can disrupt microbial survival without compromising nutritional value. As the environmental stressor landscape continues to rapidly evolve, driven by anthropogenic activities, climate shifts, and emerging environmental disturbances, monitoring how microorganisms acclimate and evolve in response to these dynamic forces remains important.

Keywords: microbial ecology; food safety; microbial adaptation; genetic adaptations; biotechnology; industrial processes; environmental stressor.

INTRODUCTION

When bacteria exposed to unfavourable environmental conditions, bacteria activate a range of stress response mechanisms to ensure survival. However, the acquisition of stress tolerance or resistance often incurs biological trade-offs, commonly referred to as fitness costs, which may manifest as reduced growth rates, impaired competitiveness, or altered metabolic efficiency under non-stressful conditions. Microbial adaptation constitutes a fundamental process wherein microorganisms dynamically adjust to alterations in their surrounding environment. Figure 1 illustrates a representative mechanism of bacterial adaptation in response to different environmental stressors. These adaptable entities, including bacteria, fungi, viruses, and protists, demonstrate a remarkable ability to acclimate and flourish amidst diverse and often challenging conditions. This adaptive prowess proves indispensable for their survival, proliferation, and enduring presence across a spectrum of ecological niches, encompassing natural habitats, industrial settings, and even within host organisms (Toft & Andersson, 2010). The adaptive arsenal of microbes encompasses an array of mechanisms, spanning genetic mutations, gene regulation, and horizontal gene transfer, thereby affording microorganisms the capability to progressively acclimate to novel environments over extended periods. Adaptation manifests in terms of food safety on varied temporal scales, ranging from swift adjustments through phenotypic plasticity to protracted evolutionary shifts (Goel, 2009).

Microbial adaptation involves both short-term and long-term mechanisms that enable microorganisms to survive and thrive in changing environments (Figure 2). Short-term adaptations are rapid and reversible changes, such as altering gene expression, protein modification, and metabolic flexibility, allowing microbes to quickly respond to environmental fluctuations. For example, as shown in Figure 1 and 2, bacteria can rapidly adjust their metabolic pathways depending on nutrient availability. Long-term adaptations involve genetic changes through mutation, horizontal gene transfer, and genetic recombination, leading to permanent evolutionary changes that provide sustained advantages. These processes allow microbes to develop traits like antibiotic resistance and enhanced biofilm formation, ensuring their survival and proliferation in diverse conditions.

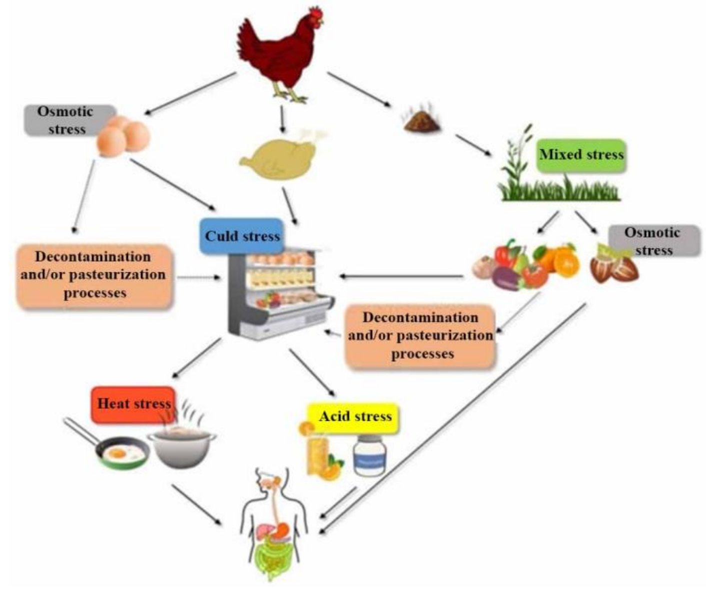

Figure 1. Examples of the different stresses that non-Thyphoidal *Salmonella cells* can face before being ingested with food (Guillén et al., 2021)

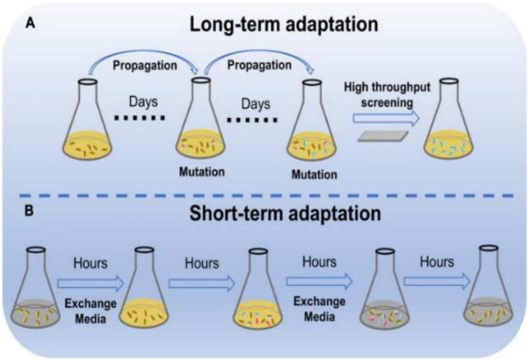

Figure 2. Microbial stress adaptation: a – schematic diagram of long-term adaptation of microorganisms to their environment; b – schematic diagram of short-term adaptation of microorganisms to their environment (Tan et al., 2022, *Creative Commons Attribution License International CC-BY 4.0*)

Recognizing that microbial growth is frequently obstructed by environmental stresses, supporting stress resistance emerges as a strategic imperative for enhancing cell growth and increasing product yields. Extensive efforts have been dedicated to elucidating stress-specific resistance mechanisms in microbial cells (Hosseini et al., 2015). Despite substantial progress, there remains a critical gap in the literature regarding a comprehensive synthesis of microbial adaptation mechanisms and their implications for enhancing food safety and ensuring the sustainable production of industrially valuable biochemicals. This document seeks to provide a comprehensive overview of recent advancements in understanding resistance mechanisms to various environmental stresses for enhancement of food safety, including oxidative stress, hyperosmotic stress, thermal stress, acid stress, and organic solvent stress. In addition, the study examines the applications of stress-resistant mechanisms in producing diverse biomolecules and valuable chemicals. Finally, the manuscript offers a discuss prospects for identifying stress-resistant mechanisms through systems biology and further engineering these elements using synthetic biology to enhance productivity.

SIGNIFICANCE OF UNDERSTANDING MICROBIAL ADAPTATION TO ECOLOGICAL STRESS

Biotechnological applications

Microbial adaptation underpins numerous biotechnological processes, including industrial fermentation, bioremediation, FMCG products (meat, milk, bread), agro-food, and pharmaceuticals, paper, textile and biofuel production. A nuanced comprehension of microbial adaptation mechanisms facilitates the optimization of these processes, engendering heightened efficiency and productivity (de Bruijn et al., 2023).

White biotechnology, commonly referred to as the application of biotechnology in industrial settings, relies heavily on biocatalysts, including enzymes and microorganisms. These biocatalysts play a pivotal role in driving technological advancements within the burgeoning bioeconomy. They are already widely utilized across various sectors such as chemicals, agro-food, and pharmaceuticals, contributing to the production of a diverse array of products ranging from antibiotics to advanced polymers. Heux et al. (2015) presented in their study the knowledge on the discovery and development of enzymes for biomass deconstruction and the potential of systems biology to improve the industrial viability of biocatalysts, with a special focus on their application in the biorefinery sector; discussed and highlighted the synergistic interactions between enzyme biotechnology and microbial biotechnology. The authors highlighted the most important perspectives of enzymes in white biotechnology, namely, it was emphasized that:

– powerful technologies for identifying potentially valuable enzymes for white biotechnology are metagenomic approaches, and the most important approach is soluble protein expression, which requires researchers to develop high-throughput cloning and expression methods;

– biocatalytic processes using microbial communities still need to be better understood, which requires a wider use of structural genomics;

– enzymes are fundamental components of new biological functions and as a consequence, the development of enzyme engineering for synthetic biology technologies is an important direction in science.

Table 1 shows the current achievements of researchers in the field of studying the mechanisms of microorganism adaptation in the context of food safety.

Human health

The continual adaptation of pathogenic microorganisms to environmental stressors precipitates the emergence of antibiotic resistance and heightened virulence, underscoring the imperative of understanding microbial adaptation. Such insights inform the development of strategies to combat infectious diseases and mitigate the proliferation of drug-resistant pathogens, thus safeguarding public health (Zhang et al., 2020).

At the same time, it is known that factors such as changes in temperature, disinfectants and storage conditions can trigger adaptive responses of pathogens, which poses significant challenges to traditional food safety methods. For instance, *Listeria monocytogenes* exhibits cross-protection, where pre-exposure to mild acidic environments enhances its survival under thermal or osmotic stress, complicating food processing protocols. Similarly, *Salmonella enterica* can express cold shock proteins during refrigerated storage, allowing it to persist in cold-chain distributed food products. These insights are essential for developing adaptive and resilient food safety systems in an era of increasing environmental variability. (Losapio et al., 2024).

Table 1. Microbial adaptation mechanisms in food safety contexts

No.	Microorganism	Adaptation mechanism	Application in food safety	Environmental stressor	Reference
1	*Listeria monocytogenes*	Cross-protection (acid → heat/osmotic resistance)	Development of multi-hurdle preservation strategies to prevent pathogen survival	Acid, Heat, Osmotic Pressure	Severino et al., 2007
2	*Escherichia coli O157:H7*	Efflux pump upregulation & biofilm formation	Redesign of produce wash systems using alternating disinfectants and biofilm disruptors	Sub-lethal Disinfectants (e.g., Chlorine)	Yan et al., 2025
3	*Salmonella enterica*	Cold shock protein expression (e.g., cspA, cspB)	Development of antimicrobial packaging targeting cold-shock protein pathways	Refrigeration (Cold Stress)	Marmion et al., 2022

Emerging research highlights the complexity of microbial evolution under selective pressure, including phenomena like horizontal gene transfer (HGT), which accelerates the dissemination of resistance genes across species and ecosystems. For instance, plasmid-mediated resistance mechanisms in Klebsiella pneumoniae and *Acinetobacter baumannii* have been shown to spread rapidly in healthcare settings, often rendering last-resort antibiotics like carbapenems ineffective. Beyond clinical environments, the interface between agriculture, food systems, and human health – often referred to as the One Health framework – further illustrates how microbial adaptations in livestock or food-processing environments can directly impact community health. Novel surveillance technologies such as whole-genome sequencing (WGS) and metagenomics are now being deployed to track resistance patterns in real-time, enabling faster response and containment strategies. Additionally, advancements in phage therapy, antimicrobial peptides, and CRISPR-based gene editing hold promise for targeted interventions that can disarm pathogens without contributing to resistance development (Donohoue et al., 2018).

Environmental sustainability

The participation of microorganisms in the biogeochemical cycle of terrestrial and aquatic ecosystems is a necessary condition for maintaining ecosystem functions, which is confirmed by recent studies of the relationship between the deterioration of ecosystem functions and the diversity of microbial taxa. Microbial adaptation constitutes an essential of ecosystem functioning, exerting profound influences on processes such as nutrient cycling, decomposition, and soil fertility. Investigating microbial adaptation furnishes predictive insights into the response of microbial communities to environmental perturbations, thereby facilitating informed ecosystem management and conservation endeavours (Lu & Jiang, 2023).

For the safety of production of cultivated products, the soil microbial community plays a vital role, since it acts as the main indicator of the ecological state of soils and the effectiveness of the restoration of contaminated soils. Microorganisms, through their enzymatic activity, are able to change the ecological indicators of soils, such as physicochemical properties, such as soil organic matter (SOM) and acidity, as well as the potential rate of soil respiration, as well as contamination with heavy metals.

Nowadays, the whole world is trying to solve the problem of soil pollution with heavy metals, which has arisen due to progressive urbanization, growing needs for mining and production of products, energy and heat. Heavy metals can be absorbed by roots and fruits of agricultural products and negatively affect human health due to biological processes occurring in the soil in the long term. Under the influence of elevated concentrations of heavy metals, disturbances in the normal activity of soil microbial communities are observed (Naz et al., 2022). For example, the studies conducted clearly indicate structural changes in the bacterial community with an increase in the concentration of cadmium (Cd) or lead (Pb) accumulation. Destruction of the DNA structure of microorganisms and damage to cell membranes, negative effects on the structure of the microbial community and the activity of soil enzymes were found in studies of the effects of Pb and Cd on bacteria, fungi and actinomycetes. On the other hand, Arbuscular mycorrhizal fungi (AM) have shown to be good protectors of plant roots and tubers from Cd and Pb accumulation, as high levels of heavy metals were significantly reduced in plants due to the presence of AM fungi in the soil, which contributes to the production of healthy food (Naz et al., 2022; Shah et al., 2022).

Microbial adaptation to environmental stresses can last for years to decades, with changes in genetic capabilities to improve their functions. Key factors supporting diversification as a driver of microbial community composition following disturbance include gene exchange and loss, as well as mutations, short generation times, and high rates of homologous recombination (Philippot et al., 2021). Physiological responses to stress are accompanied by changes in ecosystem carbon levels, energy, and nutrient flow. For example, heavy metal pollution often affects the output of microbial activity in soils, which is a well-designed useful biological tool (Raiesi & Sadeghi, 2019).

Forestry is also an integral part of ecosystems with deep ecological significance for the conservation of biodiversity, carbon cycling, climate regulation, maintenance of hydrological balance, soil protection, erosion prevention, resource provision, ecotourism development and cultural enrichment. These values not only shape the ecosystems themselves but also intricately intertwine with human society's development and well-being. However, the escalating global temperatures are revealing the increasingly apparent impacts of climate change on forests, posing formidable challenges (Mulder et al., 2011). Consequently, there has been a surge in global research attention toward understanding the multifaceted effects of climate change on forest ecosystems. Pollution stress has been found to have a significant impact on microbiome biodiversity and stability. A growing number of experiments and empirical studies have inconsistently demonstrated that biodiversity loss leads to decreased ecosystem stability (Yang et al., 2023). Interestingly, microbial community stability was found to increase with decreasing diversity in resource-rich paddy soil. And carbon source availability may be the most important environmental factor determining community stability (Yang et al., 2023). Soil microorganisms are known to significantly contribute to climate change through soil carbon (C) cycle feedbacks. Some studies have reported that microbial community composition likely influences the soil respiration thermal response, which drives ecosystem-scale soil-climate feedbacks (Li et al., 2021).

Climate change

Given their sensitivity to environmental fluctuations, microorganisms serve as sentinel indicators of climate change while actively contributing to climate regulation. A comprehensive understanding of microbial adaptation dynamics affords valuable insights into ecosystem resilience and the ramifications of climate change on biodiversity and ecosystem services, thereby informing adaptive strategies (Tiedje et al., 2022). The tough challenge of climate change stands as humanity's most pressing concern. Microbes play a dual role in this global issue, both producing and consuming three significant greenhouse gases: carbon dioxide, methane, and nitrous oxide. Moreover, certain microbial species contribute to human, animal, and plant diseases, which may be exacerbated by the changing climate (Toft & Andersson, 2010). Therefore, concerted microbial research efforts are imperative to mitigate the escalating warming trends and the subsequent cascading impacts, including heatwaves, droughts, and intensified storms.

Given the dynamic nature of climate change, microorganisms exhibit remarkable adaptability to environmental shifts, playing a critical role in both ecosystem stability and global climate regulation. Microbes, due to their sheer numbers and wide distribution, act as both sentinels and drivers of climate change. For instance, Bacillus subtilis and other soil microbes contribute significantly to soil carbon cycling and methane production, directly influencing the atmospheric levels of greenhouse gases. This dual role underscores the necessity of understanding microbial behaviour under changing environmental conditions.

As climate change accelerates, the effects on microbial communities become more pronounced, particularly in agricultural and food systems. Warmer temperatures, fluctuating precipitation, and higher CO_2 concentrations can enhance microbial growth rates, potentially leading to increased pathogen prevalence in both plant and animal-based food products. For example, *Salmonella enterica* and *Escherichia coli* O157:H7 have been shown to thrive under warmer conditions, heightening the risk of foodborne diseases, particularly in regions with poorly regulated food safety practices.

FACTORS DRIVING MICROBIAL ADAPTATION

Microbial adaptation is intricately shaped by a myriad of factors, encompassing environmental stressors, genetic variation, ecological interactions, and evolutionary dynamics. Understanding these drivers provides valuable insights into the mechanisms underpinning microbial resilience and adaptive responses across diverse habitats and conditions (An et al., 2020; Tan et al., 2022).

Natural and synthetic microbial stressors

Temperature variations

Temperature exerts a profound influence on microbial physiology and metabolism, serving as a critical determinant of microbial distribution and activity across ecosystems. Microbes exhibit remarkable adaptations to temperature gradients, enabling survival in extreme thermal environments such as hydrothermal vents, permafrost, and thermal springs. Temperature-driven adaptations encompass alterations in membrane fluidity, enzyme kinetics, and heat shock protein expression, facilitating thermal tolerance and metabolic flexibility. In food safety contexts, these adaptations are crucial for both the resilience and virulence of pathogens that threaten human health, especially as temperature fluctuations increase with climate change.

For example, *Listeria monocytogenes*, a foodborne pathogen found in a variety of refrigerated foods, can grow at temperatures as low as 0 °C, making it a persistent threat in ready-to-eat foods like deli meats and cheeses. This cold tolerance is facilitated by the bacterium's ability to alter the composition of its cell membrane, enhancing fluidity at lower temperatures. Additionally, *Listeria* expresses cold-shock proteins that help the bacteria survive cold storage, posing a unique challenge to food safety protocols that rely on refrigeration to prevent microbial growth. In response, innovative food safety strategies are incorporating modified atmosphere packaging (MAP) and active packaging technologies to reduce pathogen survival during cold storage.

Similarly, heat-resistant microbes such as *Bacillus cereus* and *Clostridium botulinum* can thrive at higher temperatures, particularly in improperly stored food. *Bacillus cereus*, for instance, produces heat-stable spores that allow it to survive cooking processes, only to germinate and proliferate when food is stored at inadequate temperatures. In thermal processing of food, understanding how these spores adapt to temperature extremes has led to the development of double-hurdle methods, combining high temperatures with other preservation techniques such as acidity or low oxygen environments to prevent bacterial growth after processing (Hosseini et al., 2015).

Osmotic stress

Osmotic stress arises from disparities in solute concentrations, imposing challenges to microbial cell integrity and water balance. Microbes exhibit remarkable adaptability to osmotic fluctuations encountered in diverse habitats, such as hypersaline environments, desiccated soils, and marine ecosystems. The ability to cope with osmotic stress is particularly crucial for foodborne pathogens and beneficial microorganisms in various food preservation processes. Osmoadaptation mechanisms include the synthesis of compatible solutes, osmoprotectants, and osmoregulatory systems, which help microbial cells maintain osmotic balance and mitigate the harmful effects of dehydration or excessive water uptake. For example, glycerol, trehalose, and proline are common osmoprotectants that microbes use to stabilize proteins and enzymes under conditions of osmotic stress (Csonka, 1989). These solutes help microbial cells manage water flux, contributing to their survival and function under harsh environmental conditions.

One prominent example in food safety is the adaptation of halophilic bacteria such as *Halobacterium salinarum* and *Vibrio cholerae*, which thrive in highly saline environments such as brined foods or fermented products. In these environments, microbes need to balance the influx of water due to osmotic pressure by synthesizing compatible solutes like K^+ ions and glycine betaine. In fermented foods like pickles or salted fish, understanding how these organisms manage osmotic stress can help optimize fermentation processes and food preservation techniques, ensuring that beneficial bacteria can outcompete spoilage microorganisms and pathogens.

In contrast, desiccation and drying processes in food production also introduce osmotic stress. For instance, dehydrated foods or freeze-dried products are often subject to osmotic imbalance due to the rapid removal of water, which can challenge the integrity of any surviving microorganisms. Pathogens such as *Salmonella* or *Escherichia coli* may use osmoprotectants to survive drying and low-water-activity environments, only to become a risk when rehydrated. An understanding of osmoadaptation mechanisms is critical in preventing pathogen survival during food storage, ensuring safety through proper moisture control and packaging.

The bacterial cell's cytoplasm, a densely packed region, holds significant osmotic potential. This characteristic, combined with the semipermeable nature of the cytoplasmic membrane and the semi-elasticity of the cell wall, leads to osmotically induced water influx, creating turgor pressure, which is vital for cellular growth and viability (Bremer & Kramer, 2019). However, this influx can be dangerous when cells are exposed to hyperosmotic conditions, as it may cause plasmolysis, or rupture, if not properly regulated. In the context of food safety, controlling osmotic conditions – such as in sugared or salty foods – can serve as a key method of inhibiting pathogen growth, as many foodborne pathogens cannot survive in environments with low water activity.

pH changes

pH serves as a fundamental environmental parameter influencing microbial growth, metabolism, and community structure. Microbes demonstrate remarkable adaptations to acidic, neutral, and alkaline pH regimes prevalent in terrestrial, aquatic, and extreme environments. pH-adaptive strategies encompass alterations in membrane permeability, proton pumps, and pH homeostasis mechanisms, enabling microbial survival and proliferation in pH-challenging habitats (Liu et al., 2015).

A notable example in food safety is the adaptation of *Lactobacillus* species, which are used extensively in the fermentation of dairy products like yogurt and cheese. These bacteria thrive in acidic environments and are able to maintain internal pH homeostasis despite the low external pH. *Lactobacillus* species utilize proton pumps and acid tolerance mechanisms, such as the synthesis of chaperone proteins, which help stabilize cellular structures under low pH conditions. These adaptive responses are essential in preventing the growth of harmful pathogens like *Salmonella* and *Escherichia coli* during food fermentation, thus enhancing food safety and shelf-life (Arora et al., 2018).

On the other end of the pH spectrum, *Alkaliphilic* bacteria, such as *Bacillus alcalophilus*, are capable of surviving in highly alkaline environments with a pH greater than 9, often encountered in soda lakes or alkaline food processing settings. These bacteria have evolved alkaline-tolerant enzymes and ion-exchange systems, which help them maintain cellular function and integrity in these extreme conditions. In food safety, understanding how these microbes adapt to high pH environments can aid in developing more effective alkaline food preservation methods, such as those used in the preservation of certain pickled or fermented foods, where the alkaline pH is used to control microbial growth.

Toxins and pollutants

For over 70 years, antibiotics have served as indispensable tools in combating bacterial infections, safeguarding countless lives and revolutionizing medicinal practices. Beyond their primary role in disease treatment, these small yet potent bioactive compounds have found application in various other medical contexts. However, despite their monumental contributions to human health, the global proliferation of multidrug-resistant (MDR) bacteria poses a mounting challenge. The escalating prevalence of these resilient pathogens underscores the urgent need for innovative strategies to preserve the efficacy of antibiotics and sustain our ability to combat infectious diseases effectively (Uddin et al., 2021).

In parallel, pesticides play a crucial role in modern agriculture, facilitating enhanced crop yields and ensuring food security. With the continual introduction of novel active ingredients boasting improved efficiencies, pesticide production and consumption have surged worldwide. Yet, alongside their benefits, improper pesticide application and storage practices frequently result in environmental contamination, affecting plant tissues, air, water, and soil. This contamination can induce the development of tolerance, resistance, or persistence in target organisms and even stimulate microbiomes within these environments to evolve mechanisms for pesticide degradation. Consequently, the management of pesticide use and its environmental impact remains a critical concern for agricultural sustainability and ecosystem health (Ramakrishnan et al., 2019).

In the dominion of microbiology, understanding microbial adaptation emerges as definitive, given the numerous environmental stressors that microbes encounter. These stressors, ranging from temperature extremes to fluctuations in osmotic pressure, pH levels, and exposure to toxins (Figure 3), pose significant threats to microbial survival and cellular processes.

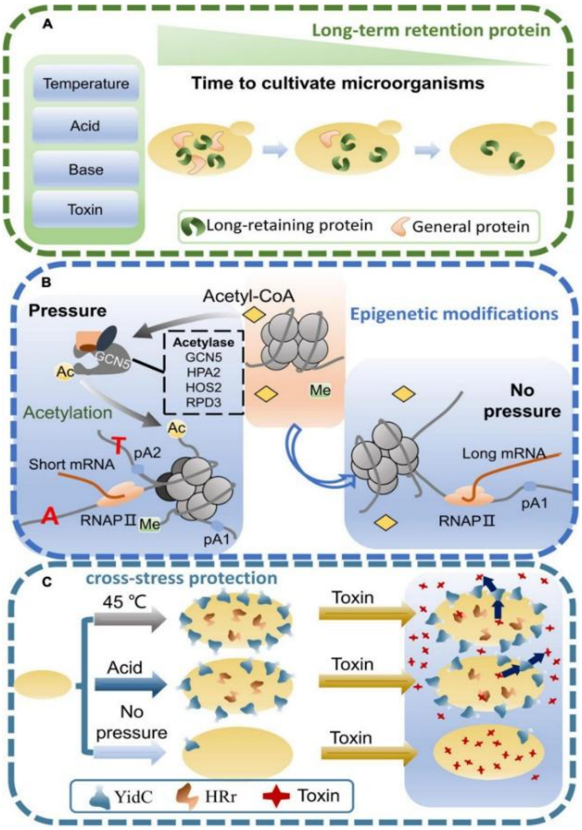

Figure 3. Stress factors and adaptation mechanisms: a – when microorganisms are subjected to environmental stress, the long-retaining proteins are produced to protect the cells for a long time; b – effects of environmental stress on microbial epigenetic modifications; c – microorganisms are adapted to a stressful environment, resulting in cross protection against stress (Tan et al., 2022, *Creative Commons Attribution License International CC-BY 4.0*)

The comprehension of microbial adaptation extends its relevance across a broad spectrum of disciplines, including microbiology, ecology, biotechnology, and medicine. Microbes exhibit remarkable resilience in navigating these challenges, deploying intricate adaptive mechanisms to ensure their functionality and survival in dynamically changing environments (Feckler et al., 2018).

Dependency on nutrient availability

Nutrient availability constitutes a pivotal determinant of microbial growth, diversity, and ecosystem functioning. Microbial populations exhibit dynamic adaptations to fluctuations in carbon, nitrogen, phosphorus, and micronutrient availability encountered in terrestrial, aquatic, and host-associated environments. Adaptive responses encompass metabolic reprogramming, nutrient scavenging, and symbiotic interactions, enabling microbial exploitation of diverse nutritional resources and niche colonization (Li et al., 2017).

Chemical stressors

Microbes encounter a plethora of chemical stressors, including toxic metals, organic pollutants, antimicrobial agents, and xenobiotic compounds, in natural, industrial, and anthropogenic environments. Microbial populations evolve diverse mechanisms to detoxify, sequester, or metabolize toxic substances, encompassing metal resistance genes, xenobiotic degradation pathways, and antibiotic resistance mechanisms. Chemical stress adaptation confers microbial resilience to contaminated habitats and industrial processes, with implications for bioremediation, public health, and environmental sustainability (Abee & Wouters, 1999).

Microbes adapt to fluctuations in nutrient availability by adjusting metabolic pathways, scavenging mechanisms, and nutrient uptake systems. Microbes utilize a diverse range of carbon sources, including sugars, organic acids, and hydrocarbons, and adapt their metabolic machinery accordingly. Similarly, microbes are able to use a variety of strategies to acquire essential nutrients like nitrogen, phosphorus, and sulphur from the environment, especially in nutrient-limited conditions (Garcia-Pausas & Paterson, 2011).

HOST-ASSOCIATED ADAPTATION

Pathogenic microbes adapt to host environments to establish infection and evade host immune responses. Commensal and symbiotic microbes adapt to niches within host organisms, forming mutualistic relationships that benefit both microbe and host. Gut microbiota, for example, adapt to the dynamic conditions of the gastrointestinal tract, influenced by factors such as diet, immune responses, and microbial competition (Olive & Sassetti, 2016).

Genetic variation and evolution

Microbes exhibit high genetic diversity due to rapid mutation rates, horizontal gene transfer, and genetic recombination. Selection pressures in various environments drive the evolution of adaptive traits in microbial populations. Evolutionary processes such as natural selection, genetic drift, and gene flow shape microbial adaptation over time (Boyce, 2022).

Mutation and genetic diversity

Microbial populations harbour extensive genetic diversity, driven by mutation, recombination, and horizontal gene transfer, facilitating adaptive evolution in response to environmental selection pressures. Mutational mechanisms, including point mutations, insertions, deletions, and genome rearrangements, generate genetic variants with altered phenotypic traits, enabling microbial adaptation to changing environments (Martinez & Baquero, 2000).

Horizontal gene transfer (HGT)

Horizontal gene transfer serves as a major driver of microbial adaptation, enabling the acquisition and dissemination of adaptive traits across phylogenetic boundaries. Mechanisms of HGT, including conjugation, transduction, and transformation, mediate the exchange of genetic material encoding antibiotic resistance, metabolic pathways, and virulence factors, shaping microbial community dynamics and adaptive potential (Elena & Lenski, 2003).

Selection pressures and evolutionary dynamics

Microbial populations undergo continual selection pressures in response to environmental fluctuations, driving the evolution of adaptive traits over evolutionary timescales. Natural selection, genetic drift, and gene flow shape microbial adaptation, leading to the emergence of genetic variants with enhanced fitness and ecological success. Evolutionary dynamics underpin microbial diversification, speciation, and niche specialization, influencing ecosystem resilience and stability (Drake, 1991).

ECOLOGICAL INTERACTIONS

Microbial interactions and community dynamics

Microbial adaptation is influenced by interactions within microbial communities, encompassing competition, cooperation, predation, and symbiosis. Competitive interactions drive niche partitioning, resource utilization, and microbial diversity, shaping community structure and ecosystem functioning. Cooperative interactions, such as mutualism and syntrophic, facilitate resource sharing, metabolic cooperation, and niche expansion, enhancing microbial fitness and adaptive capacity (Rodriguez-Verdugo et al., 2019).

Host-microbe interactions

Microbial adaptation is shaped by interactions with host organisms across diverse symbiotic, commensal, and pathogenic associations. Host-associated microbes adapt to host-specific environments, physiological conditions, and immune responses, influencing microbial colonization, virulence, and disease outcomes. Coevolutionary dynamics between hosts and microbes drive the emergence of host-adapted strains, immune evasion strategies, and microbial symbioses, with implications for human health, agriculture, and ecological resilience (Rodriguez-Verdugo et al., 2019).

ANTHROPOGENIC INFLUENCES

Environmental perturbations and anthropogenic stressors

Human activities exert profound impacts on microbial communities and ecosystems, altering environmental conditions, nutrient cycles, and microbial habitats. Anthropogenic stressors, including pollution, habitat destruction, climate change, and antimicrobial use, impose selective pressures on microbial populations, driving adaptive responses and ecological shifts. Microbial adaptation to anthropogenic stressors influences ecosystem services, public health, and environmental sustainability, underscoring the interconnectedness of human and microbial systems (Valliere et al., 2020).

Biotechnological applications and engineered microbes

Microbial adaptation is harnessed in biotechnological applications, spanning industrial processes, bioremediation, agriculture, and medicine. Engineered microbes with enhanced stress tolerance, metabolic capabilities, and bioactive properties are developed for diverse biotechnological purposes, including biofuel production, enzyme synthesis, bioremediation of contaminated sites, and microbial-based therapies. Understanding microbial adaptation informs the design and optimization of biotechnological systems, enhancing efficiency, sustainability, and innovation in bioprocess engineering.

Microbial adaptation arises from the interplay of environmental stressors, genetic variation, ecological interactions, and anthropogenic influences, driving the resilience, diversity, and adaptive potential of microbial communities across diverse habitats and ecosystems. A holistic understanding of these factors is essential for elucidating microbial responses to environmental change, guiding ecosystem management, and harnessing microbial diversity for biotechnological innovation and sustainability (Schimel et al., 2007).

Mechanisms of microbial adaptation

Microbial adaptation is driven by an array of sophisticated mechanisms that enable microorganisms to dynamically respond to environmental changes. These mechanisms encompass intricate processes at the genetic, molecular, and cellular levels, orchestrating adaptive responses that promote survival and proliferation in challenging conditions (Mitchell et al., 2009).

Some microorganisms inhabit environments characterized by erratic fluctuations, while others occupy more predictable habitats, allowing them to prepare for impending environmental changes. Analogous to classical Pavlovian conditioning, microorganisms may have evolved the ability to anticipate environmental stimuli by adapting to their temporal sequence. In this study, we provide evidence supporting the phenomenon of environmental change anticipation in two model microorganisms, *Escherichia coli* and *Saccharomyces cerevisiae*. Our findings demonstrate that anticipation represents an adaptive trait, as pre-exposure to a stimulus occurring early in the ecological sequence enhances the organism's fitness when subsequently faced with a second stimulus (Bohnert et al., 1995). Furthermore, our laboratory evolution experiment reveals a loss of the conditioned response in *E. coli* strains repeatedly exposed solely to the initial stimulus.

IMPLICATIONS FOR BIOTECHNOLOGY AND ENVIRONMENTAL MANAGEMENT

Microbial adaptation is not merely a concept but a dynamic force driving the forefront of biotechnological advancements and reshaping the paradigms of environmental stewardship. By tapping into the intricate mechanisms of microbial adaptation, we unlock a myriad of potential solutions to complex environmental issues while revolutionizing industrial processes. This approach not only offers practical solutions to mitigate environmental challenges but also holds the key to unlocking unprecedented levels of efficiency, sustainability, and innovation across diverse industrial sectors.

Bioremediation strategies

Bioremediation harnesses the metabolic versatility and adaptive resilience of microorganisms to mitigate environmental pollution and restore contaminated ecosystems. Microbes play pivotal roles in degrading diverse pollutants, including hydrocarbons, heavy metals, pesticides, and industrial chemicals. Understanding microbial adaptation mechanisms – such as enzymatic plasticity, efflux systems, redox flexibility, and biofilm formation – is instrumental in designing tailored bioremediation strategies for specific contaminants and environmental contexts (Joshi et al., 2024).

For example, *Pseudomonas putida*, a model organism for environmental biotechnology, adapts to hydrocarbon-contaminated soils through the expression of catabolic plasmids that encode enzymes for aromatic compound degradation. This ability is further enhanced by the bacterium's resistance to oxidative stress and its capacity to modulate membrane permeability under toxic conditions. Similarly, *Geobacter sulfurreducens* adapts to heavy metal-contaminated environments by reducing uranium and iron through extracellular electron transfer mechanisms, facilitating in situ remediation of groundwater.

In terms of product safety, microbial bioremediation is increasingly being applied to decontaminate food-processing wastewater, which often contains high levels of organic matter, detergents, and residues from preservatives or packaging materials. For instance, *Bacillus subtilis* strains are used in treating effluents from dairy and meat industries, where they adapt to osmotic and chemical stress by producing extracellular enzymes and biosurfactants that degrade complex waste compounds, thereby reducing environmental discharge toxicity and ensuring compliance with food safety regulations.

Adaptive microbial syndicates

Formulating microbial consortia comprising diverse microbial species with complementary metabolic capabilities enhances bioremediation efficacy. Communities of microbial life exert significant influence on system regulation and stability across a spectrum of ecological scales, from the minutest niche to the global arena (de Bruijn et al., 2023). Yet, our understanding of interaction patterns and external factors governing the dynamics of natural microbial communities remains limited due to the constraints of laboratory studies focused on single or few species assemblies. However, the integration of microfluidic technologies with advancements in the fabrication of functional and stimuli-responsive materials has opened pathways to creating artificial microbial environments (Joshi et al., 2024). These environments serve as habitats for both natural and multispecies synthetic consortia, offering opportunities for detailed investigations and the exploration of microbial community dynamics. Moreover, they facilitate the training and directed evolution of microbial communities, allowing researchers to study states of equilibrium and disturbance, as well as the effects of modulated stimuli and spontaneous response triggers. These consortia exhibit synergistic interactions and adaptive responses, enabling efficient degradation of complex pollutant mixtures (Wondraczek et al., 2019).

Engineered biodegradation pathways

Genetic engineering techniques enable the modification of microbial metabolic pathways to enhance pollutant degradation efficiency and broaden substrate specificity. Rational design of microbial strains equipped with specialized enzymes facilitates targeted degradation of recalcitrant contaminants. Facing formidable environmental challenges, environmental biotechnology emerges as a pivotal tool to mitigate or eradicate pollution. Recent years have witnessed a surge in attention towards environmental pollution in China, prompting a comprehensive review of biodegradation research within the nation (Yong & Zhong, 2010). This review encompasses advancements such as the isolation of extremophilic microorganisms capable of degrading pollutants under extreme conditions, as well as investigations into genes and enzymes integral to biodegradation pathways. Moreover, biodegradation engineering stands out as a promising and robust platform, integrating genetic engineering, process engineering, and signal transduction engineering. Furthermore, the integration of pollutant remediation with the generation of renewable bioenergy sources by microorganisms presents an enticing prospect (Pan et al., 2023).

In situ bioremediation technologies

Application of in situ bioremediation approaches, such as bioaugmentation and bio-stimulation, relies on microbial adaptation to optimize pollutant degradation under field conditions. Manipulating environmental parameters, such as nutrient availability and oxygen levels, fosters microbial adaptation and enhances remediation performance (Maitra, 2018).

In situ bioremediation, the treatment of contaminated soil directly at its location, offers several advantages over ex-situ methods. This approach eliminates the need for excavation equipment, making it more cost-effective and reducing the dispersal of dust and contaminants into the surrounding environment. However, there are drawbacks to consider. In situ bioremediation may require more time to achieve complete decontamination, as it relies on natural processes. Additionally, its effectiveness is limited in compacted soil and may be less controllable compared to ex-situ techniques (NRC, 1993).

INDUSTRIAL APPLICATIONS OF STRESS-RESISTANT MICROORGANISMS

Stress-resistant microorganisms exhibit enhanced tolerance to adverse environmental conditions prevalent in industrial settings, offering immense potential for optimizing biotechnological processes and industrial production systems. The microbial biosynthesis of nanoparticles has emerged as a cost-effective and environmentally friendly alternative. This green approach offers numerous advantages, including high stability, water solubility, biocompatibility, rapid production rates, and low cost. Various microorganisms, such as *Candida glabrata*, *Schizosaccharomyces pombe*, *Fusarium oxysporum*, *Saccharomyces cerevisiae*, and *Escherichia coli*, have been harnessed for biosynthesizing cadmium-based quantum dots (QDs). Many reported procedures for QD biosynthesis rely on biological molecules with antioxidant properties, particularly metal-binding molecules rich in thiols. For example, in one notable instance, phytochelatins derived from *S. pombe* have been utilized to synthesize CdS QDs within *E. coli* (Gallardo et al., 2014).

Industrial fermentation

Stress-resistant microbes are employed in industrial fermentation processes for the production of biofuels, pharmaceuticals, enzymes, and fine chemicals. Enhanced stress tolerance enables microbes to thrive in harsh fermentation conditions, such as high temperature, acidity, and substrate inhibition. To standardize cocoa fermentation and minimize losses caused by cocoa bean variability, utilizing a microbial preparation containing pectinolytic strains as a starter culture proves beneficial. This study examines carbon metabolism, fermentative capacity, and the impact of environmental conditions on pectinase synthesis within four yeast strains known for their high pectinolytic activity and stress resilience. The strains exhibit a limited carbon metabolism profile, fermenting glucose and fructose exclusively, and demonstrate optimal growth when these carbon sources are present at 5% (Samagaci et al., 2015).

Bioprocessing technologies

Stress-resistant microorganisms serve as robust biocatalysts in various bioprocessing technologies, including wastewater treatment, biogas production, and bioleaching. Their resilience to fluctuating environmental conditions enhances process reliability and efficiency, minimizing operational disruptions and resource wastage. Anaerobic co-digestion (AcoD) offers an opportunity to leverage excess digestion capacity in existing wastewater treatment plants (WWTPs) for the production of surplus biogas, surpassing the plant's internal energy needs. Industry reports and peer-reviewed literature demonstrate numerous instances where WWTPs have transitioned into net energy producers through AcoD, prompting the exploration of alternative high-value uses for surplus biogas. An emerging global trend involves upgrading biogas to biomethane, a versatile energy source suitable for applications such as town gas or transportation fuel (Nguyen et al., 2021).

Biopolymer production

Microbial production of biopolymers, such as polyhydroxyalkanoates (PHAs) and exopolysaccharides (EPS), relies on stress-resistant microbial strains capable of withstanding adverse growth conditions prevalent in industrial bioreactors. These biopolymers find diverse applications in bioplastics, food additives, and pharmaceutical formulations. Diverse pathways drive the synthesis of biopolymers sourced from nature. These polymers can either be chemically synthesized from biological constituents or harvested from living organisms. Microorganisms, in particular, stand out as prominent producers of biopolymers, offering scalability benefits over plant-derived alternatives. To optimize the production of microbial biopolymers, advancements in genetic engineering techniques are leveraged to engineer growth conditions at the medium level, thus facilitating enhanced production yields (Verma et al., 2020).

POTENTIAL FOR DRUG DEVELOPMENT

Advancements in drug development for food preservation and safety

Microbial adaptation mechanisms play a pivotal role in shaping modern strategies for food preservation and safety. Understanding how microorganisms respond to environmental stressors – such as temperature shifts, osmotic pressure, pH variations, and oxidative conditions – has opened new avenues for developing preservation methods that suppress spoilage organisms and pathogenic microbes, while maintaining food quality. These adaptive traits, once seen primarily as survival tools for microbes, are now being harnessed to design intelligent intervention systems that pre-empt microbial threats across the food production chain (Rahman, 2020).

For example, insights into microbial stress responses – such as the regulation of heat shock proteins, acid tolerance genes, and osmoregulatory systems – inform the optimization of thermal processing, fermentation, and packaging conditions. Spoilage microbes and foodborne pathogens like *Salmonella*, *Listeria monocytogenes*, and *Clostridium botulinum* have shown remarkable flexibility in adjusting their metabolism and membrane integrity to survive adverse conditions. By targeting these adaptive pathways through combined or sequential stressors (e.g., mild heat and low pH), food technologists can disrupt microbial survival without compromising nutritional value.

Moreover, advancements in predictive microbiology and systems biology are enabling the development of smart preservation systems. These systems integrate real-time microbial monitoring, predictive modelling, and adaptive control measures, effectively anticipating microbial behaviour and optimizing shelf life while ensuring microbial safety. Coupled with high-throughput omics technologies and machine learning, this knowledge facilitates the formulation of novel antimicrobials, natural preservatives, and packaging materials that inhibit stress-adapted pathogens.

Thus, leveraging microbial adaptation mechanisms has transitioned from a purely defensive stance to a proactive and precision-based strategy, marking a significant leap forward in securing the safety and longevity of food in the face of evolving microbial threats.

Antibiotic discovery

Exploration of microbial adaptation mechanisms in antibiotic-producing microorganisms unveils novel biosynthetic pathways and antimicrobial compounds with therapeutic potential. Screening microbial biodiversity for natural product discovery identifies bioactive molecules capable of overcoming antibiotic resistance mechanisms. The amalgamation of antibiotics presents a promising avenue for enhancing treatment efficacy and mitigating resistance evolution. When antibiotics are merged, their impact on cellular function can either be augmented or diminished, resulting in synergistic or antagonistic interactions. Recent research has shed light on the underlying mechanisms of these interactions by elucidating the collective effects of antibiotics on cell physiology (Bollenbach, 2015).

Targeting virulence factors

Disruption of microbial virulence factors essential for pathogenesis represents a promising approach for developing alternative antimicrobial therapies. Understanding microbial adaptation in host-pathogen interactions elucidates vulnerabilities exploitable for therapeutic intervention, such as inhibiting quorum sensing or biofilm formation. The global public health challenge of diminishing antimicrobial efficacy necessitates urgent improvement of our arsenal against infectious diseases. With a noticeable scarcity in new antibacterial drugs, exploring alternative sources for prototype compounds becomes imperative. Plants offer a promising avenue due to their natural production of a diverse array of secondary metabolites, serving as a robust chemical defines against microorganisms in the environment. Therefore, leveraging plant species as a reservoir of potential antimicrobial agents holds considerable promise in addressing this pressing issue (Silva et al., 2016).

Precision antimicrobial therapy

Tailoring antimicrobial therapies based on microbial adaptation profiles and genomic signatures enables precision medicine approaches for treating drug-resistant infections. Personalized treatment regimens account for individual microbial susceptibility patterns and adaptability dynamics, optimizing therapeutic outcomes while minimizing collateral damage to beneficial microbiota. The escalating prevalence of infections attributable to multidrug-resistant pathogens underscores the imperative of adopting a "patient-centred" approach to antimicrobial therapies. Within this context, the implementation of therapeutic drug monitoring (TDM) for emerging antimicrobial agents holds promise as a valuable strategy. However, to maximize their clinical utility, expert interpretation of TDM results is essential (Gatti & Pea, 2023).

FUTURE DIRECTIONS AND CHALLENGES

The path of microbial adaptation investigation is boosted by a twofold imperious: to confront emerging challenges and harness technological advancements for a comprehensive understanding of the intricate mechanisms governing microbial responses to environmental stressors. As the landscape of environmental stressors continues to evolve rapidly, driven by anthropogenic activities, climatic shifts, and emerging ecological perturbations, researchers are tasked with deciphering how microorganisms acclimate and evolve in response to these dynamic forces. This research trajectory encompasses a multidisciplinary approach, integrating insights from genomics, metagenomics, transcriptomics, proteomics, metabolomics, and single-cell analysis to illuminate the molecular underpinnings of microbial adaptation. Furthermore, advancements in computational biology, machine learning, and predictive modelling empower researchers to discern complex patterns in microbial adaptation dynamics and forecast microbial responses to environmental changes with unprecedented precision. Moreover, CRISPR-based genome editing technologies and high-throughput cultivation platforms offer powerful tools for manipulating microbial genomes and characterizing adaptive phenotypes across diverse microbial taxa. As researchers navigate this ever-expanding frontier of microbial adaptation research, they are not only poised to unravel the fundamental principles governing microbial resilience and adaptation but also to pioneer transformative solutions for mitigating environmental challenges, advancing biotechnological innovation, and safeguarding human and environmental health.

Emerging environmental stressors

The landscape of environmental stressors confronting microbial communities is continually evolving, spurred by anthropogenic activities, climatic shifts, and emerging ecological perturbations. Understanding and mitigating the impacts of these novel stressors represent pressing imperatives for microbial adaptation research (Benedetti et al. 2022).

Climate change-induced stressors

Rapid climate change is heralding unprecedented shifts in temperature regimes, precipitation patterns, and habitat availability, imposing novel selective pressures on microbial populations. Investigating how microorganisms acclimate and evolve in response to these climatic upheavals is paramount for predicting ecosystem dynamics and safeguarding biodiversity (Aggarwal et al. 2022).

Pollutant and contaminant dynamics

The proliferation of synthetic chemicals, pharmaceuticals, and industrial pollutants introduces novel stressors into microbial habitats, exerting profound ecological and health ramifications. Charting the adaptive trajectories of microbial communities in response to these contaminants is crucial for devising targeted remediation strategies and mitigating environmental pollution (Subedi et al. 2015).

Urbanization and habitat fragmentation

Urban expansion and habitat fragmentation pose unprecedented challenges to microbial communities, disrupting ecological connectivity, and altering microbial diversity and function. Unravelling the adaptive strategies employed by urban-adapted microbes is essential for managing urban ecosystems and mitigating the ecological consequences of urbanization (Riley et al. 2003).

Unexplored mechanisms of microbial adaptation

While significant strides have been made in elucidating microbial adaptation mechanisms, vast swathes of microbial diversity remain enigmatic, underscoring the need to probe hitherto unexplored facets of microbial adaptation (Seufferheld et al. 2008).

Microbial dark matter

The microbial dark matter, comprising uncultured and genetically uncharacterized microbial taxa, represents a vast reservoir of untapped adaptive potential. Unlocking the genomic and physiological attributes of these elusive microbes holds the key to unveiling novel adaptation mechanisms and expanding our understanding of microbial biodiversity (Solden et al., 2016).

Microbial interactions and community dynamics

Microbial adaptation is intricately intertwined with interspecies interactions and community dynamics, yet our comprehension of these complex networks remains rudimentary. Investigating how microbial communities coalesce, compete, and coevolve in response to environmental stressors promises to yield profound insights into ecosystem resilience and stability (van Vliet et al. 2022).

Non-genetic determinants of adaptation

Beyond genetic variation, microbial adaptation is shaped by a myriad of non-genetic factors, including epigenetic modifications, post-transcriptional regulation, and phenotypic plasticity. Unravelling the contributions of these non-genetic determinants to microbial adaptation represents a frontier of inquiry with far-reaching implications for evolutionary biology and biotechnology (Frankel et al., 2014).

Technological advancements for studying adaptation

Advancements in analytical techniques, computational tools, and high-throughput methodologies are revolutionizing our capacity to probe microbial adaptation dynamics with unprecedented resolution and scope (Postollec et al., 2011). These innovations allow researchers to investigate how microorganisms respond to environmental stressors – such as temperature shifts, pH changes, osmotic fluctuations, and nutrient limitations – with fine-scale precision. In the context of food safety, these technologies are particularly valuable for tracking microbial behaviour in real time, predicting potential risks, and designing more effective intervention strategies.

For example, next-generation sequencing (NGS) and metagenomics have enabled the comprehensive analysis of microbial communities in complex food matrices and environments, allowing scientists to identify previously undetected microbial species and track the emergence of stress-resistant strains. These tools are crucial for monitoring how pathogenic bacteria such as *Listeria monocytogenes* or *Salmonella enterica* adapt to processing environments like refrigeration or vacuum packaging (Wang et al., 2021).

In parallel, transcriptomics and proteomics offer insights into how microbial gene expression and protein profiles change under specific environmental stressors, revealing the molecular pathways involved in survival and adaptation. For instance, transcriptomic studies have shown how *E. coli* alters the expression of stress-response genes in acidic foods, guiding the development of pH-based food preservation techniques.

Omics approaches

Genomics, metagenomics, transcriptomics, proteomics, and metabolomics empower comprehensive profiling of microbial communities and their adaptive responses to environmental perturbations. Integrating multi-omics datasets enables holistic elucidation of adaptation mechanisms and ecological interactions within microbial ecosystems (Sharma et al. 2022).

Single-cell analysis

Single-cell technologies afford unparalleled insights into microbial heterogeneity and phenotypic diversity, enabling the dissection of adaptive responses at the individual cell level. Leveraging single-cell omics approaches illuminates rare and transient adaptation events, shedding light on elusive microbial adaptation strategies (Wu & Tzanakakis, 2013).

Machine learning and predictive modelling

Machine learning algorithms and predictive modelling frameworks harness big data analytics to decipher complex patterns in microbial adaptation dynamics. By discerning predictive features of adaptive phenotypes, these computational tools facilitate the design of targeted interventions and the forecasting of microbial responses to environmental changes. The advent of next-generation sequencing technologies has transformed the study of the human microbiome, propelling it into a rapidly expanding research field. This technological advancement has democratized access to high-throughput sequencing, leading to a wealth of microbiome data that offer unprecedented insights into human health and disease (Wang et al., 2021).

CRISPR-based tools for genetic manipulation

CRISPR-based genome editing technologies enable precise manipulation of microbial genomes, facilitating functional characterization of genes and regulatory elements underlying adaptation. CRISPR-enabled high-throughput screening platforms expedite the discovery of adaptive genetic variants and elucidation of gene function in diverse microbial taxa (Donohoue et al., 2018).

Microfluidics and high-throughput cultivation

Microfluidic devices and high-throughput cultivation platforms streamline the cultivation and characterization of diverse microbial isolates under controlled environmental conditions. These technologies expedite the identification of adaptive phenotypes, niche-specific adaptations, and biotechnologically relevant traits across microbial taxa (Hegab et al., 2013).

By exploring the mechanisms underlying microbial adaptation – such as genetic adaptations (mutation and horizontal gene transfer), phenotypic plasticity, and epigenetic modifications. we have elucidated how microorganisms thrive in challenging conditions (Table 3).

DISCUSSIONS

Recap of key findings

Adaptability of microorganisms

Microorganisms exhibit remarkable adaptability, enabling them to thrive across diverse environmental conditions, from extreme temperatures to varying pH levels and exposure to toxins (Table 1, 2). This adaptability is foundational to their survival and proliferation in a wide range of habitats.

Mechanisms of microbial adaptation

The mechanisms of microbial adaptation are multifaceted, encompassing genetic mutations, phenotypic plasticity, epigenetic modifications, genetic regulation, horizontal gene transfer, and evolutionary dynamics. These mechanisms collectively underscore the resilience and versatility of microbial life.

Implications for biotechnology and environmental management

Understanding microbial adaptation holds significant implications for biotechnological applications, disease management, environmental sustainability, and climate change mitigation. This knowledge can drive advancements in these fields by harnessing microbial capabilities for practical benefits.

Table 3. Stress adaptation presented in table with their stress, organism, and approach with references

No	Stress	Organism	Approach	Reference
1	Oxidative	*Escherichia coli*	Overexpression of Dps, a DNA-binding protein that protects against oxidative stress	Choi et al., 2000
		Saccharomyces cerevisiae	Expression of a glutamate Decarboxylase homolog to enhance stress resistance	Coleman et al., 2001
		Candida utilis	Control of dissolved oxygen levels in the environment to mitigate oxidative stress	Liang, 2008a
		Candida utilis	Addition of H_2O_2, a known oxidative stress inducer, to study stress response mechanisms	Liang et al., 2008b
		Candida infirmominiatum	Addition of glycine betaine, a compatible solute, to enhance stress tolerance	Liu et al., 2011
2	Hyperosmotic	*Escherichia coli*	Overproduction of trehalose, a compatible solute, to counteract osmotic stress	Purvis et al., 2005
		Lactococcus lactis	Expression of DnaK, a chaperone protein, to assist in protein folding under stress	Abdullah-Al-Mahin et al., 2010
		Torulaspora glabrata	Addition of proline, an osmoprotectant, to alleviate hyperosmotic stress	Xu et al., 2010
		Candida glabrata	Accumulation of arginine, an osmoprotectant, to enhance stress resistance	Xu et al., 2011
		Escherichia coli	Expression of IrrE, a radiation resistance protein, to confer osmotic stress tolerance	Ma et al., 2011
3	Thermal	*Kluyveromyces marxianus*	Induction of mutation in response to thermal stress	Ballesteros et al., 1993
		Lactococcus lactis, and Lactococcus paracasei	Overproduction of GroESL, a chaperonin complex, to assist in protein folding under heat stress	Compan & Touati, 1993
		Saccharomyces cerevisiae	Application of evolutionary engineering methods to develop thermotolerant strains	Cakar et al., 2005
		Saccharomyces cerevisiae	Utilization of genome shuffling techniques to enhance thermal stress resistance	Shi et al., 2009
4	Acid	*Propionibacterium acidipropionici*	Execution of adaptive growth strategies to advance acid stress resistance	Zhu et al., 2010
		Propionibacterium acidipropionici	Implementation of adaptive evolution strategies to improve acid stress resistance	Zhu et al., 2010
		Propionibacterium acidipropionici	Utilization of genome shuffling techniques to enhance acid stress resistance	Guan et al., 2012
		Lactobacillus casei	Application of metabolic engineering approaches to develop acid-tolerant strains	Zhang et al., 2020
		Pediococcus jensenii	Implementation of metabolic engineering strategies targeting acid resistance elements	Guan et al., 2016
5	Organic solvent	*Saccharomyces cerevisiae*	Utilization of transcription machinery engineering to enhance solvent tolerance	Alper et al., 2006
		Saccharomyces cerevisiae	Overexpression of TRP1–5 and TAT2 genes to improve solvent tolerance	Hirasawa et al., 2007
		Saccharomyces cerevisiae	Deletion of URA7 and GAL6 genes to enhance solvent tolerance	Yazawa et al., 2007
		Escherichia coli	Overproduction of GroESL, a chaperonin complex, to enhance solvent tolerance	Zingaro & Papoutsakis, 2013
		Corynebacterium glutamicum	Implementation of adaptive evolution strategies to enhance solvent tolerance	Oide et al., 2015

Applications in bioremediation and industry

Microbial adaptation is integral to bioremediation strategies, industrial fermentation processes, and the development of novel antimicrobial agents, vaccines, and therapeutic interventions. By leveraging the adaptive traits of microorganisms, these applications can be optimized to address various environmental and health challenges.

Summary of implications

Biotechnological advancements

Biotechnological advancements rely heavily on microbial adaptation. Insights into adaptive mechanisms drive the development of robust microbial strains for industrial applications, including biofuel production, bioremediation, and pharmaceutical manufacturing. Understanding these mechanisms is crucial for optimizing microbial performance and enhancing the efficiency of these processes.

Human health and disease management

In the realm of human health, understanding microbial adaptation dynamics is critical for combating infectious diseases, particularly in the face of escalating antibiotic resistance and the emergence of novel pathogens. Insights gleaned from studying microbial adaptation inform the design of targeted therapeutic strategies and public health interventions, contributing to improved disease management and prevention.

Environmental sustainability

Environmental sustainability hinges on microbial adaptation, as microbial communities play pivotal roles in nutrient cycling, pollutant degradation, and ecosystem resilience. Harnessing microbial adaptation holds promise for mitigating the impacts of climate change, preserving biodiversity, and restoring degraded ecosystems. This understanding can guide strategies for environmental management and conservation.

Suggestions for further research

Emerging environmental stressors

Investigating the role of microbial adaptation in response to emerging environmental stressors, such as microplastics, nanomaterials, and pharmaceutical contaminants, presents a fertile ground for future research endeavours. Understanding these interactions will be essential for developing effective mitigation strategies.

Host-microbe interactions

Exploring the interplay between microbial adaptation and host-microbe interactions within complex ecosystems, including the human microbiome, soil microbiome, and aquatic environments, offers insights into microbial community dynamics and ecosystem functioning. This research can inform the management of microbial communities for health and environmental benefits.

Molecular mechanisms of adaptation

Advancing our understanding of microbial adaptation mechanisms at the molecular level, including the role of epigenetic modifications, non-coding RNAs, and microbial communication networks, holds promise for uncovering novel targets for biotechnological innovation and therapeutic intervention. Detailed molecular studies can lead to breakthroughs in microbial engineering and treatment strategies.

Integrative approaches

Integrating multi-omics approaches, computational modelling, and ecological niche modelling can provide a comprehensive understanding of microbial adaptation dynamics across spatial and temporal scales. These integrative approaches will aid in predictive modelling and management strategies for diverse ecosystems and microbial communities, enhancing our ability to respond to environmental changes and challenges.

CONCLUSION

In this comprehensive review, we have delved into the pivotal role of microbial adaptation to diverse environmental stressors, highlighting its significance within microbial ecology and its wide-ranging implications across biotechnology, environmental management, and public health. The case studies provided underscore the remarkable resilience of microbes in extreme environments and offer valuable insights into their adaptive strategies.

Microbial adaptation stands as a cornerstone of microbial ecology, influencing the dynamics of ecosystems, industrial processes, and human health. Through this review, several key findings have emerged, shedding light on the intricate mechanisms and implications of microbial adaptation to various environmental stresses. Understanding these mechanisms is crucial for leveraging microbial capabilities in biotechnological applications, including bioremediation and industrial processes, as well as their potential contributions to drug development.

Finally, we discussed the future directions and challenges in understanding microbial adaptation, emphasizing the ongoing necessity for research. Continued investigation is essential to unravel the intricate interplay between microorganisms and their environment, which will further enhance our ability to leverage microbial adaptation for scientific and practical advancements. This knowledge will be instrumental in developing innovative strategies for environmental management, improving industrial processes, and advancing public health initiatives.

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Author's statements

Contributions

Conceptualization: I.M., M.N.B., M.R.A.; Data curation: I.M.; Formal Analysis: I.M., M.R.A.; Investigation: I.M., M.R.A.; Methodology: I.M.; Project administration: I.M., M.R.A.; Resources: I.M., M.N.B.; Software: I.M.; Supervision: M.S.K., M.A.K., M.A.; Validation: M.A.; Visualization: M.A.K.; Writing – original draft: I.M.; Writing – review & editing: M.N.B., I.M.

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REFERENCES

Abdullah-Al-Mahin, S. S., Higashi, C., Matsumoto, S., & Sonomoto, K. (2010). Improvement of multiple-stress tolerance and lactic acid production in lactococcus lactis NZ9000 under conditions of thermal stress by heterologous expression of escherichia coli dnaK. *Applied and Environmental Microbiology*, 76(13), 4277–4285. https://doi.org/10.1128/AEM.02878-09.

Abee, T., & Wouters, J. A. (1999). Microbial stress response in minimal processing. *International Journal of Food Microbiology*, 50(1–2), 65–91. https://doi.org/10.1016/S0168-1605(99)00078-1.

Aggarwal, A., Frey, H., McDowell, G., Drenkhan, F., Nusser, M., Racoviteanu, A., & Hoelzle, M. (2022). Adaptation to climate change induced water stress in major glacierized mountain regions. *Climate and Development*, 14(7), 665–677. https://doi.org/10.1080/17565529.2021.1971059.

Alper, H., Moxley, J., Nevoigt, E., Fink, G. R., & Stephanopoulos, G. (2006). Engineering yeast transcription machinery for improved ethanol tolerance and production. *Science*, 314(5805), 1565–1568. https://doi.org/10.1126/science.1131969.

An, S. Q., Potnis, N., Dow, M., Vorhölter, F. J., He, Y. Q., Becker, A., ... & Tang, J. L. (2020). Mechanistic insights into host adaptation, virulence and epidemiology of the phytopathogen Xanthomonas. *FEMS Microbiology Reviews*, 44(1), 1–32. https://doi.org/10.1093/femsre/fuz024.

Arora, S., Rani, R., & Ghosh, S. (2018). Bioreactors in solid state fermentation technology: Design, applications and engineering aspects. *Journal of Biotechnology*, 269, 16–34. https://doi.org/10.1016/j.jbiotec.2018.01.010.

Ballesteros, I., Oliva, J. M., Ballesteros, M., & Carrasco, J. (1993). Optimization of the simultaneous saccharification and fermentation process using thermotolerant yeasts. *Applied Biochemistry and Biotechnology*, 39, 201–211. https://doi.org/10.1007/BF02918990.

Benedetti, M., Giuliani, M. E., Mezzelani, M., Nardi, A., & Regoli, F. (2022). Emerging environmental stressors and oxidative pathways in marine organisms: Current knowledge on regulation mechanisms and functional effects. *Biocell*, 46(1), 37. https://doi.org/10.32604/biocell.2022.017507.

Bohnert, H. J., Nelson, D. E., & Jensen, R. G. (1995). Adaptations to environmental stresses. *The Plant Cell*, 7(7), 1099–1111. https://doi.org/10.1105/tpc.7.7.1099.

Bollenbach, T. (2015). Antimicrobial interactions: Mechanisms and implications for drug discovery and resistance evolution. *Current Opinion in Microbiology*, 27, 1–9. https://doi.org/10.1016/j.mib.2015.05.008.

Boyce, K. J. (2022). Mutators enhance adaptive micro-evolution in pathogenic microbes. *Microorganisms*, 10(2), 442. https://doi.org/10.3390/microorganisms10020442.

Bremer, E., & Kramer, R. (2019). Responses of microorganisms to osmotic stress. *Annual Review of Microbiology*, 73, 313–334. https://doi.org/10.1146/annurev-micro-020518-115504.

Cakar, Z. P., Seker, U. O., Tamerler, C., Sonderegger, M., & Sauer, U. (2005). Evolutionary engineering of multiple-stress resistant saccharomyces cerevisiae. *FEMS Yeast Research*, 5(6–7), 569–578. https://doi.org/10.1016/j.femsyr.2004.10.010.

Choi, S. H., Baumler, D. J., & Kaspar, C. W. (2000). Contribution of dps to acid stress tolerance and oxidative stress tolerance in escherichia coli O157: H7. *Applied and Environmental Microbiology*, 66(9), 3911–3916. https://doi.org/10.1128/AEM.66.9.3911-3916.2000.

Coleman, S. T., Fang, T. K., Rovinsky, S. A., Turano, F. J., & Moye-Rowley, W. S. (2001). Expression of a glutamate decarboxylase homologue is required for normal oxidative stress tolerance in saccharomyces cerevisiae. *Journal of Biological Chemistry*, 276(1), 244–250. https://doi.org/10.1074/jbc.M007103200.

Compan, I., & Touati, D. (1993). Interaction of six global transcription regulators in expression of manganese superoxide dismutase in escherichia coli K-12. *Journal of Bacteriology*, 175(6), 1687–1696. https://doi.org/10.1128/jb.175.6.1687-1696.1993.

National Research Council (NRC), Division on Engineering, Physical Sciences, Commission on Engineering, Technical Systems, & Committee on In Situ Bioremediation. (1993). In situ bioremediation: When does it work?. National Academies Press.

Csonka, L. N. (1989). Physiological and genetic responses of bacteria to osmotic stress. *Microbiological Reviews*, 53(1), 121–147. https://doi.org/10.1128/mr.53.1.121-147.1989.

Donohoue, P. D., Barrangou, R., & May, A. P. (2018). Advances in industrial biotechnology using CRISPR-cas systems. *Trends in Biotechnology*, 36(2), 134–146. https://doi.org/10.1016/j.tibtech.2017.07.007.

Drake, J. W. (1991). A constant rate of spontaneous mutation in DNA-based microbes. *Proceedings of the National Academy of Science*, 88(16), 7160–7164. https://doi.org/10.1073/pnas.88.16.7160.

Elena, S. F., & Lenski, R. E. (2003). Evolution experiments with microorganisms: the dynamics and genetic bases of adaptation. *Nature Reviews Genetics*, 4(6), 457–469. https://doi.org/10.1038/nrg1088.

Feckler, A., Goedkoop, W., Konschak, M., Bundschuh, R., Kenngott, K. G., Schulz, R., ... & Bundschuh, M. (2018). History matters: Heterotrophic microbial community structure and function adapt to multiple stressors. *Global Change Biology*, 24(2), e402-e415. https://doi.org/10.1111/gcb.13859.

Frankel, N. W., Pontius, W., Dufour, Y. S., Long, J., Hernandez-Nunez, L., & Emonet, T. (2014). Adaptability of non-genetic diversity in bacterial chemotaxis. *Elife*, 3, e03526. https://doi.org/10.7554/eLife.03526.

Gallardo, C., Monras, J. P., Plaza, D. O., Collao, B., Saona, L. A., Duran-Toro, V., & Perez-Donoso, J. M. (2014). Low-temperature biosynthesis of fluorescent semiconductor nanoparticles (CdS) by oxidative stress resistant antarctic bacteria. *Journal of Biotechnology*, 187, 108–115. https://doi.org/10.1016/j.jbiotec.2014.07.017.

Garcia-Pausas, J., & Paterson, E. (2011). Microbial community abundance and structure are determinants of soil organic matter mineralisation in the presence of labile carbon. *Soil Biology and Biochemistry*, 43(8), 1705–1713. https://doi.org/10.1016/j.soilbio.2011.04.016.

Gatti, M., & Pea, F. (2023). The expert clinical pharmacological advice program for tailoring on real-time antimicrobial therapies with emerging TDM candidates in special populations: How the ugly duckling turned into a swan. *Expert Review of Clinical Pharmacology*, 16(11), 1035–1051. https://doi.org/10.1080/17512433.2023.2274984.

Goel, R. (2009). Metagenomics–A Tool for Identification and Characterization of Uncultivable Microbial Diversity. *Dr. HS Tripathi*.

Guan, N., Li, J., Shin, H. D., Du, G., Chen, J., & Liu, L. (2016). Metabolic engineering of acid resistance elements to improve acid resistance and propionic acid production of propionibacterium jensenii. *Biotechnology and Bioengineering*, 3(6), 1294–1304. https://doi.org/10.1002/bit.25902.

Guan, N., Liu, L., Zhuge, X., Xu, Q., Li, J., Du, G., & Chen, J. (2012). Genome shuffling improves acid tolerance of propionibacterium acidipropionici and propionic acid production. *Advances in Chemical Research*, 15, 143–152.

Guillén, S., Nadal, L., Álvarez, I., Mañas, P., & Cebrián, G. (2021). Impact of the Resistance Responses to Stress Conditions Encountered in Food and Food Processing Environments on the Virulence and Growth Fitness of Non-Typhoidal Salmonellae. *Foods*, 10(3), 617. https://doi.org/10.3390/foods10030617.

Hegab, H. M., ElMekawy, A., & Stakenborg, T. (2013). Review of microfluidic microbioreactor technology for high-throughput submerged microbiological cultivation. *Biomicrofluidics*, 7(2), 021502 (2013). https://doi.org/10.1063/1.4799966.

Heux, S., Meynial-Salles, I., O'Donohue, M. J., & Dumon, C. (2015). White biotechnology: State of the art strategies for the development of biocatalysts for biorefining. *Biotechnology Advances*, 33(8), 1653–1670. https://doi.org/10.1016/j.biotechadv.2015.08.004.

Hirasawa, T., Yoshikawa, K., Nakakura, Y., Nagahisa, K., Furusawa, C., Katakura, Y., ... & Shioya, S. (2007). Identification of target genes conferring ethanol stress tolerance to Saccharomyces cerevisiae based on DNA microarray data analysis. *Journal of Biotechnology*, 131(1), 34–44. https://doi.org/10.1016/j.jbiotec.2007.05.010.

Hosseini Nezhad, M., Hussain, A. M., & Britz, L. M. (2015). Stress responses in probiotic Lactobacillus casei. *Critical Reviews in Food Science and Nutrition*, 55(6), 740–749. https://doi.org/10.1080/10408398.2012.675601.

Joshi, S. S., Jadhav, M. P. K., Chourasia, N. K., Jadhav, M. P. J., Pathade, K. N., & Kanimozhi, K. R. (2024). Bioremediation strategies for soil and water pollution harnessing the power of microorganisms. *Migration Letters*, 21(S8), 1–20.

Li, F., Chen, L., Zhang, J., Yin, J., & Huang, S. (2017). Bacterial community structure after long-term organic and inorganic fertilization reveals important associations between soil nutrients and specific taxa involved in nutrient transformations. *Frontiers in Microbiology*, 8, 187. https://doi.org/10.3389/fmicb.2017.00187.

Li, J., Zhu, T., Singh, B. K., Pendall, E., Li, B., Fang, C., & Nie, M. (2021). Key microorganisms mediate soil carbon-climate feedbacks in forest ecosystems. *Science Bulletin*, 66(19), 2036–2044. https://doi.org/10.1016/j.scib.2021.03.008.

Liang, G. B., Du, G. C., & Chen, J. (2008a). A novel strategy of enhanced glutathione production in high cell density cultivation of Candida utilis – cysteine addition combined with dissolved oxygen controlling. *Enzyme and Microbial Technology*, 42(3), 284–289. https://doi.org/10.1016/j.enzmictec.2007.10.008.

Liang, G., Liao, X., Du, G., & Chen, J. (2008b). Elevated glutathione production by adding precursor amino acids coupled with ATP in high cell density cultivation of candida utilis. *Journal of Applied Microbiology*, 105(5), 1432–1440. https://doi.org/10.1111/j.1365-2672.2008.03892.x.

Liu, J., Wisniewski, M., Droby, S., Vero, S., Tian, S., & Hershkovitz, V. (2011). Glycine betaine improves oxidative stress tolerance and biocontrol efficacy of the antagonistic yeast cystofilobasidium infirmominiatum. *International Journal of Food Microbiology*, 146(1), 76–83. https://doi.org/10.1016/j.ijfoodmicro.2011.02.007.

Liu, S., Ren, H., Shen, L., Lou, L., Tian, G., Zheng, P., & Hu, B. (2015). pH levels drive bacterial community structure in sediments of the qiantang river as determined by 454 pyrosequencing. *Frontiers in Microbiology*, 6, 285. https://doi.org/10.3389/fmicb.2015.00285.

Losapio, G., Genes, L., Knight, C. J., McFadden, T. N., & Pavan, L. (2024). Monitoring and modelling the effects of ecosystem engineers on ecosystem functioning. *Functional Ecology*, 38(1), 8–21. https://doi.org/10.1111/1365-2435.14315.

Lu, X., & Jiang, Y. (2023). Advancements in studying the effects of climate change on forest ecosystems. *Advances in Resources Research*, 3(4), 151–177. https://doi.org/10.50908/arr.3.4_151.

Ma, R., Zhang, Y., Hong, H., Lu, W., Lin, M., Chen, M., & Zhang, W. (2011). Improved osmotic tolerance and ethanol production of ethanologenic escherichia coli by IrrE, a global regulator of radiation-resistance of deinococcus radiodurans. *Current Microbiology*, 62, 659–664. https://doi.org/10.1007/s00284-010-9759-2.

Maitra, S. (2018). In situ bioremediation – An overview. *Life Science Informatics Publications.* 4(6), 576–598. https://doi.org/10.26479/2018.0406.45.

Marmion, M., Macori, G., Ferone, M., Whyte, P., & Scannell, A. G. M. (2022). Survive and thrive: Control mechanisms that facilitate bacterial adaptation to survive manufacturing-related stress. *International Journal of Food Microbiology*, 368, 109612. https://doi.org/10.1016/j.ijfoodmicro.2022.109612.

Martinez, J. L., & Baquero, F. (2000). Mutation frequencies and antibiotic resistance. *Antimicrobial Agents and Chemotherapy*, 44(7), 1771–1777. https://doi.org/10.1128/aac.44.7.1771-1777.2000.

Mitchell, A., Romano, G. H., Groisman, B., Yona, A., Dekel, E., Kupiec, M., & Pilpel, Y. (2009). Adaptive prediction of environmental changes by microorganisms. *Nature*, 460(7252), 220–224. https://doi.org/10.1038/nature08112.

Mulder, C., Boit, A., Bonkowski, M., De Ruiter, P. C., Mancinelli, G., der Heijden, M. G., & Rutgers, M. (2011). A belowground perspective on dutch agroecosystems: How soil organisms interact to support ecosystem services. *Advances in Ecological Research*, 44, 277–357. https://doi.org/10.1016/B978-0-12-374794-5.00005-5.

Naz, M., Dai, Z., Hussain, S., Tariq, M., Danish, S., Khan, I. U., ... & Du, D. (2022). The soil pH and heavy metals revealed their impact on soil microbial community. *Journal of Environmental Management*, 321, 115770. https://doi.org/10.1016/j.jenvman.2022.115770.

Nguyen, L. N., Kumar, J., Vu, M. T., Mohammed, J. A., Pathak, N., Commault, A. S., & Nghiem, L. D. (2021). Biomethane production from anaerobic co-digestion at wastewater treatment plants: A critical review on development and innovations in biogas upgrading techniques. *Science of the Total Environment*, 765, 142753. https://doi.org/10.1016/j.scitotenv.2020.142753.

Oide, S., Gunji, W., Moteki, Y., Yamamoto, S., & Inui, M. (2015). Thermal and solvent stress cross-tolerance conferred to corynebacterium glutamicum by adaptive laboratory evolution. *Applied and Environmental Microbiology*, 81(7), 2284–2298. https://doi.org/10.1128/AEM.03973-14.

Olive, A. J., & Sassetti, C. M. (2016). Metabolic crosstalk between host and pathogen: Sensing, adapting and competing. *Nature Reviews Microbiology*, 14(4), 221–234. https://doi.org/10.1038/nrmicro.2016.12.

Pan, J., Wang, G., Nong, J., & Xie, Q. (2023). Biodegradation of benzo (a) pyrene by a genetically engineered bacillus licheniformis: Degradation, metabolic pathway and toxicity analysis. *Chemical Engineering Journal*, 478, 147478. https://doi.org/10.1016/j.cej.2023.147478.

Philippot, L., Griffiths, B. S., & Langenheder, S. (2021). Microbial community resilience across ecosystems and multiple disturbances. *Microbiology and Molecular Biology Reviews*, 85(2). https://doi.org/10.1128/mmbr.00026-20.

Postollec, F., Falentin, H., Pavan, S., Combrisson, J., & Sohier, D. (2011). Recent advances in quantitative PCR (qPCR) applications in food microbiology. *Food Microbiology*, 28(5), 848–861. https://doi.org/10.1016/j.fm.2011.02.008.

Purvis, J. E., Yomano, L. P., & Ingram, L. O. (2005). Enhanced trehalose production improves growth of escherichia coli under osmotic stress. *Applied and Environmental Microbiology*, 71(7), 3761–3769. https://doi.org/10.1128/AEM.71.7.3761-3769.2005.

Rahman, M. S. (2020). Food preservation: an overview. *Handbook of food preservation*, 7–18.

Raiesi, F., & Sadeghi, E. (2019). Interactive effect of salinity and cadmium toxicity on soil microbial properties and enzyme activities. *Ecotoxicology and Environmental Safety*, 168, 221–229. https://doi.org/10.1016/j.ecoenv.2018.10.079.

Ramakrishnan, B., Venkateswarlu, K., Sethunathan, N., & Megharaj, M. (2019). Local applications but global implications: Can pesticides drive microorganisms to develop antimicrobial resistance? *Science of the Total Environment*, 654, 177–189. https://doi.org/10.1016/j.scitotenv.2018.11.041.

Riley, S. P., Sauvajot, R. M., Fuller, T. K., York, E. C., Kamradt, D. A., Bromley, C., & Wayne, R. K. (2003). Effects of urbanization and habitat fragmentation on bobcats and coyotes in southern california. *Conservation Biology*, 17(2), 566–576. https://doi.org/10.1046/j.1523-1739.2003.01458.x.

Rodríguez-Verdugo, A., Vulin, C., & Ackermann, M. (2019). The rate of environmental fluctuations shapes ecological dynamics in a two-species microbial system. *Ecology Letters*, 22(5), 838–846. https://doi.org/10.1111/ele.13241.

Samagaci, L., Ouattara, H. G., Goualie, B. G., & Niamke, S. L. (2015). Polyphasic analysis of pectinolytic and stress-resistant yeast strains isolated from ivorian cocoa fermentation. *Journal of Food Research*, 4(1), 124. https://doi.org/10.5539/jfr.v4n1p124.

Schimel, J., Balser, T. C., & Wallenstein, M. (2007). Microbial stress-response physiology and its implications for ecosystem function. *Ecology*, 88(6), 1386–1394. https://doi.org/10.1890/06-0219.

Seufferheld, M. J., Alvarez, H. M., & Farias, M. E. (2008). Role of polyphosphates in microbial adaptation to extreme environments. *Applied and Environmental Microbiology*, 74(19), 5867–5874. https://doi.org/10.1128/AEM.00501-08.

Severino, P., Dussurget, O., Vêncio, R. Z., Dumas, E., Garrido, P., Padilla, G., ... & Buchrieser, C. (2007). Comparative transcriptome analysis of Listeria monocytogenes strains of the two major lineages reveals differences in virulence, cell wall, and stress response. *Applied and Environmental Microbiology*, 73(19), 6078–6088. https://doi.org/10.1128/AEM.02730-06.

Shah, G. M., Ali, H., Ahmad, I., Kamran, M., Hammad, M., ... & Rashid, M. I. (2022). Nano agrochemical zinc oxide influences microbial activity, carbon, and nitrogen cycling of applied manures in the soil-plant system. *Environmental Pollution*, 293, 118559. https://doi.org/10.1016/j.envpol.2021.118559.

Sharma, P., Singh, S. P., Iqbal, H. M., & Tong, Y. W. (2022). Omics approaches in bioremediation of environmental contaminants: An integrated approach for environmental safety and sustainability. *Environmental Research*, 211, 113102. https://doi.org/10.1016/j.envres.2022.113102.

Shi, D. J., Wang, C. L., & Wang, K. M. (2009). Genome shuffling to improve thermotolerance, ethanol tolerance and ethanol productivity of Saccharomyces cerevisiae. *Journal of Industrial Microbiology and Biotechnology*, 36(1), 139–147. https://doi.org/10.1007/s10295-008-0481-z.

Silva, L. N., Zimmer, K. R., Macedo, A. J., & Trentin, D. S. (2016). Plant natural products targeting bacterial virulence factors. *Chemical Reviews*, 116(16), 9162–9236. https://doi.org/10.1021/acs.chemrev.6b00184.

de Bruijn, F. J., Smidt, H., Cocolin, L. S., Sauer, M., Dowling, D. N., & Thomashow, L. (Eds.). (2022). Good microbes in medicine, food production, biotechnology, bioremediation, and agriculture. John Wiley & Sons.

Solden, L., Lloyd, K., & Wrighton, K. (2016). The bright side of microbial dark matter: lessons learned from the uncultivated majority. *Current Opinion in Microbiology*, 31, 217–226. https://doi.org/10.1016/j.mib.2016.04.020.

Subedi, B., Aguilar, L., Robinson, E. M., Hageman, K. J., Bjorklund, E., Sheesley, R. J., & Usenko, S. (2015). Selective pressurized liquid extraction as a sample-preparation technique for persistent organic pollutants and contaminants of emerging concern. *TrAC Trends in Analytical Chemistry*, 68, 119–132. https://doi.org/10.1016/j.trac.2015.02.011.

Tan, Y. S., Zhang, R. K., Liu, Z. H., Li, B. Z., & Yuan, Y. J. (2022). Microbial adaptation to enhance stress tolerance. *Frontiers in Microbiology*, 13, 888746. https://doi.org/10.3389/fmicb.2022.888746.

Tiedje, J. M., Bruns, M. A., Casadevall, A., Criddle, C. S., Eloe-Fadrosh, E., Karl, D. M., ... & Zhou, J. (2022). Microbes and climate change: a research prospectus for the future. *MBio*, 13(3), e00800-22. https://doi.org/10.1128/mbio.00800-22.

Toft, C., & Andersson, S. G. (2010). Evolutionary microbial genomics: insights into bacterial host adaptation. *Nature Reviews Genetics*, 11(7), 465–475. https://doi.org/10.1038/nrg2798.

Uddin, T. M., Chakraborty, A. J., Khusro, A., Zidan, B. R. M., Mitra, S., Emran, T. B., ... & Koirala, N. (2021). Antibiotic resistance in microbes: History, mechanisms, therapeutic strategies and future prospects. *Journal of Infection and Public Health*, 14(12), 1750–1766. https://doi.org/10.1016/j.jiph.2021.10.020.

Valliere, J. M., Wong, W. S., Nevill, P. G., Zhong, H., & Dixon, K. W. (2020). Preparing for the worst: Utilizing stress?tolerant soil microbial communities to aid ecological restoration in the anthropocene. *Ecological Solutions and Evidence*, 1(2), e12027. https://doi.org/10.1002/2688-8319.12027.

van Vliet, S., Hauert, C., Fridberg, K., & Ackermann, M. (2022). Dal Co A (2022) Global dynamics of microbial communities emerge from local interaction rules. *PLOS Computational Biology*, 18(3), e1009877. https://doi.org/10.1371/journal.pcbi.1009877.

Verma, M. L., Kumar, S., Jeslin, J., & Dubey, N. K. (2020). Microbial production of biopolymers with potential biotechnological applications. Biopolymer-based formulations (pp. 105–137) *Elsevier*. https://doi.org/10.1016/B978-0-12-816897-4.00005-9.

Wang, Y., Bhattacharya, T., Jiang, Y., Qin, X., Wang, Y., Liu, Y., ... & Chen, L. (2021). A novel deep learning method for predictive modeling of microbiome data. *Briefings in Bioinformatics*, 22(3), bbaa073. https://doi.org/10.1093/bib/bbaa073.

Wondraczek, L., Pohnert, G., Schacher, F. H., Kohler, A., Gottschaldt, M., Schubert, U. S., & Brakhage, A. A. (2019). Artificial microbial arenas: Materials for observing and manipulating microbial consortia. *Advanced Materials*, 31(24), 190028. https://doi.org/10.1002/adma.201900284.

Wu, J., & Tzanakakis, E. S. (2013). Deconstructing stem cell population heterogeneity: single-cell analysis and modeling approaches. *Biotechnology Advances*, 31(7), 1047–1062. https://doi.org/10.1016/j.biotechadv.2013.09.001.

Xu, S., Zhou, J., Liu, L., & Chen, J. (2010). Proline enhances Torulopsis glabrata growth during hyperosmotic stress. *Biotechnology and Bioprocess Engineering*, 15, 285–292. https://doi.org/10.1007/s12257-009-0131-y.

Xu, S., Zhou, J., Liu, L., & Chen, J. (2011). Arginine: A novel compatible solute to protect Candida glabrata against hyperosmotic stress. *Process Biochemistry*, 46(6), 1230–1235. https://doi.org/10.1016/j.procbio.2011.01.026.

Yan, X., Tao, R., Zhou, H., Zhang, Y., Chen, D., Ma, L., & Bai, Y. (2025). Sublethal sanitizers exposure differentially affects biofilm formation in three adapted Salmonella strains: A phenotypic-transcriptomic analysis of increased biofilm formed by ATCC 14028. *International Journal of Food Microbiology*, 111189. https://doi.org/10.1016/j.ijfoodmicro.2025.111189.

Yang, X., Cheng, J., Franks, A. E., Huang, X., Yang, Q., Cheng, Z., ... & He, Y. (2023). Loss of microbial diversity weakens specific soil functions, but increases soil ecosystem stability. *Soil Biology and Biochemistry*, 177, 108916. https://doi.org/10.1016/j.soilbio.2022.108916.

Yang, X., Li, Y., Niu, B., Chen, Q., Hu, Y., Yang, Y., ... & Zhang, G. (2021). Temperature and precipitation drive elevational patterns of microbial beta diversity in alpine grasslands. *Microbial Ecology*, 1–13. https://doi.org/10.1007/s00248-021-01901-w.

Yazawa, H., Iwahashi, H., & Uemura, H. (2007). Disruption of URA7 and GAL6 improves the ethanol tolerance and fermentation capacity of Saccharomyces cerevisiae. *Yeast*, 24(7), 551–560. https://doi.org/10.1002/yea.1492.

Yong, Y. C., & Zhong, J. J. (2010). Recent advances in biodegradation in china: New microorganisms and pathways, biodegradation engineering, and bioenergy from pollutant biodegradation. *Process Biochemistry*, 45(12), 1937–1943. https://doi.org/10.1016/j.procbio.2010.04.009.

Zhang, C., Sun, R., & Xia, T. (2020). Adaption/resistance to antimicrobial nanoparticles: Will it be a problem?. *Nano Today*, 34, 100909. https://doi.org/10.1016/j.nantod.2020.100909.

Zhu, Y., Li, J., Tan, M., Liu, L., Jiang, L., Sun, J., & Chen, J. (2010). Optimization and scale-up of propionic acid production by propionic acid-tolerant propionibacterium acidipropionici with glycerol as the carbon source. *Bioresource Technology*, 101(22), 8902–8906. https://doi.org/10.1016/j.biortech.2010.06.070.

Zingaro, K. A., & Papoutsakis, E. T. (2013). GroESL overexpression imparts Escherichia coli tolerance to i-, n-, and 2-butanol, 1, 2, 4-butanetriol and ethanol with complex and unpredictable patterns. *Metabolic Engineering*, 15, 196–205. https://doi.org/10.1016/j.ymben.2012.07.009.