

COLLOQUIUM REPORT



Microbes and Climate Change - Science, People & Impacts



AMERICAN
SOCIETY FOR
MICROBIOLOGY

AMERICAN
ACADEMY OF
MICROBIOLOGY
RECOGNIZING SCIENTIFIC EXCELLENCE

Microbes and Climate Change – Science, People & Impacts

Report on an American Academy of Microbiology Virtual Colloquium held on November 5, 2021.

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Executive Summary

Climate change: a long-term change in the Earth's, or a specific region's, climate

Climate change is unarguably a critical existential threat to humanity in the 21st century. As the most abundant organisms on Earth, microorganisms make considerable contributions to and are greatly affected by a changing climate. Microbes are major drivers of elemental cycles (such as carbon, nitrogen, and phosphorus), important producers and consumers of greenhouse gases, and pertinent pathogens of humans, animals, and plants. While the threat of climate change looms large, conversations about the relationship between it and microorganisms are still rare outside of the microbial sciences community. To understand fully how our climate may change in the future, it is important to learn how a changing climate will impact

microbes and their relationships with humans and their environment, as well as incorporate microbial processes into climate models.

This report is based on the deliberations of experts who participated in a colloquium on 5 November 2021 organized by the American Academy of Microbiology, the honorific leadership group and think tank within the American Society for Microbiology. These experts came from diverse disciplines and sectors and provided multifaceted perspectives and insights. Over the course of the discussion, the group made several major recommendations for academic, policy, and market partners to promote innovation for microbe-driven climate change solutions that support human well-being.

Societal Recommendations are expansive considerations to improve human well-being that encompass academic, industrial, civil, and policy solutions with an emphasis on social justice and equity



Herd of cows walking along dried up river

Major Recommendations

Research Recommendations

- Emphasize interdisciplinary research focused on understanding how microbial activities and metabolic flux alter as climate, precipitation, and temperatures change globally. This will be important for terrestrial, urban, and aquatic microbes that impact global elemental cycles as well as for pathogens that impact human and animal health.
- Provide guidance for experimental design and data collection for studying microbial communities that allows for data comparison across diverse and global ecosystems.
- Incorporate existing data about microbial diversity and activity on consuming and producing greenhouse gases into Earth climate models to improve the current and predictive performance of models.
- Outline specific scientific criteria to evaluate new innovations that allow the scientific community to assess the scientific and societal impacts of these innovations.

Policy and Regulation Considerations

- Increase research investments to generate knowledge and awareness of the contribution of microbes to the generation and consumption of greenhouse gases; incorporate these findings into evidence-based policy and regulatory strategies to address climate change.

- Deploy increased surveillance and detection of zoonotic and vector-borne diseases in animals and humans, including through next-generation sequencing technologies, and incorporate a One Health approach to addressing climate changes' effects on humans, animals, and the environment.
- Enact policies that facilitate public private partnerships between diverse scientists, entrepreneurs and commercial entities, regulatory bodies, policy makers and other stakeholders to translate research discoveries into scalable microbial innovations.
- Develop policies that incentivize innovation of microbe-facilitated processes to support renewable-energy generation and a robust bioeconomy.

Societal Recommendations

- Engage and clearly communicate with the general public in jargon-free and relatable ways to improve comprehension of how microbes participate in the causes and effects of climate change.
- Highlight and prioritize addressing inequitable microbial risk of vulnerable communities at greater risk of infectious disease exposure, altered microbiota, and food insecurity caused by climate change.

Introduction



Climate change is one of the most significant threats to humanity in the 21st century

In 1975, geochemist Wallace Broecker first introduced the terms **climate change** and **global warming** to highlight the possible impact of increasing **carbon dioxide** (CO₂) levels to raise the global temperature (Broecker 1975). Only 4 years later, the National Academy of Sciences ad hoc committee on CO₂ and climate stated, “If carbon dioxide continues to increase, the study group finds no reason to doubt that climate changes will result and no reason to believe that these changes will be negligible” (National Research Council 1979). Since then, the impacts of CO₂ on global temperature and climate have confirmed scientists’ initial hypothesis—anthropogenic activities releasing CO₂ into the atmosphere have changed the Earth’s climate and thus the way of life for all those living on the planet.

Climate change is one of the most significant threats to humanity in the 21st century. Climate change adversely impacts water quality, food security, and global economies. The World Health Organization (WHO) states that it is the “biggest health threat facing humanity” (WHO 2021). Humans’ actions such as burning of fossil fuels, deforestation, and rapid population growth have clearly contributed to climate change. These actions have increased concentrations of greenhouse gases, which, in turn, have increased the Earth’s temperature and altered the climate globally (IPCC 2021, Full Report). To understand the scientific state of the planet, the Intergovernmental Panel on Climate Change (IPCC) formed in 1988 as an international panel of scientists to col-

lect comprehensive climate change information for governments to use to develop climate policies. The recent report from the IPCC found changes to Earth’s climate in every region of the world, noting the unprecedented scale and speed in warming of the planet’s surface over the last 200 years (IPCC 2021, Summary for Policymakers). Impacts of increased temperature, precipitation, and pollution are felt by all life on Earth, including microbes.

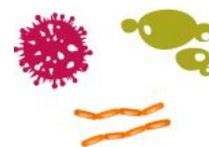
Microorganisms are the most abundant and diverse organisms on Earth (Locey and Lennon 2016). Microbes include viruses, bacteria, archaea, fungi, algae, and protozoa and are found in all areas of the planet, including terrestrial, urban, atmospheric, subsurface, and aquatic ecosystems. While small, microbes’ contributions to the planet’s climate are momentous because of their sheer numbers. Microbes are major drivers of global geochemical cycling, critical symbionts of global crops, and important producers and consumers of greenhouse gases (Table 1). In spite of microbes’ many impacts on and responses to climate change, few outside the microbial science community include microbial activities in their conversations about climate change or in their predictive models.

To improve coordination between climate science and microbiology, in 2011 the American Academy of Microbiology, which is the honorific leadership group and scientific think tank within the American Society for Microbiology, hosted a colloquium entitled “Incorporating Microbial

Processes Into Climate Models” to bridge the gap between two seemingly dissimilar fields. To continue the conversation, the Academy and American Geophysical Union (AGU) jointly published a report specifically about the relationship between microbes and climate change in 2016. Ten years after the initial colloquium, it is evident that while some progress has been accomplished, microbial activities are not fully being incorporated into the understanding and modeling of climate change.

Realization of the continued need to incorporate microbial activities into

climate change assessments and the sense of great urgency outlined in the latest IPCC report prompted the Academy to select climate change as the topic of focus in the Academy’s 5-year scientific portfolio. The portfolio emphasizes promoting the understanding of the relationships between microbes and climate change and building a scientific framework to inform climate change policies and market innovations. To build a foundation for this portfolio, the Academy hosted the colloquium “Microbes & Climate Change—Science, People, & Impacts.” This colloquium builds on



Microorganisms are the most abundant and diverse organisms on Earth



Cyanobacteria, also known as Cyanophyta on water surface. Algal blooms can become a danger to humans and animals.

the foundation from the two previous Academy colloquia and provides updates on the science as well as identifies key knowledge gaps that still exist. Experts from diverse fields, including biogeochemistry, civil engineering, environmental biology, industry, marine biology, policy, public health, systems biology, and microbiology, joined to discuss current understandings and highlight research, policy, and innovation priorities to answer the question, “how to incorporate microbial sciences in climate change initiatives and remediation processes?” Their diverse perspectives, insights, and recommendations have been captured in this report.

As our climate changes, so will the microorganisms that inhabit the planet. Having adapted to the shifts in

Earth’s climate for over 3 billion years, microbes are resilient and will evolve accordingly. Unfortunately, humans are slower to adapt. We must appreciate the links between human, animal, environmental, and microbial health as an important part of confronting this significant threat (Nguyen and Casadevall 2021). As climate change presents unprecedented challenges to humanity, we need novel ideas, unconventional approaches, and progressive innovations. Building on current knowledge, expanding our understanding of microbes, and implementing sustainable and microbe-based innovations are important actions to help contain climate change, combat this urgent crisis, and promote human health and well-being worldwide.



Acropora also known as staghorn coral, turning white by the coral bleaching effects due to global warming and climate change.

How to Use this Report

This report is broken into five sections based on the discussions of experts at the colloquium. Each section highlights the collective views of the participants on current knowledge gaps, outlines future research priorities to support policy and market innovations, and provides specific recommendations for scientists from diverse disciplines. The Conclusions section synthesizes the major discussion topics and presents recommendations for the broader society about resources and policies critical to advance our understanding of the relationship between climate change, microbes, and human well-being and health.

Expanding Our Current Understanding of

Microbial Ecosystems and Climate—A summary of current knowledge about microbial responses to and impacts on climate change in terrestrial, urban, and aquatic environments. Recommendations were made for interdisciplinary studies to understand how microbial metabolism, genetics, and community diversity will change because of climate change through the use of long-term studies of diverse ecosystems. These studies will be important to inform climate models and combat unjust imbalances in microbial risk.

Microbes and Human Health—An outline of how climate change can impact pathogens' geographic, temporal, and temperature ranges as well as their metabolic and virulence capabilities as they adapt to global warming. The importance of a One Health approach to medicine that takes into account environmental and epidemiological surveillance and immunological and socioeconomic factors, especially for vulnerable communities with inequitable microbial exposure, was highlighted.

Microbes and Human Well-Being—A discussion on the ways in which climate change influences food security, water safety, and air quality. The emphasis was placed on the need to study the interconnections among microbial activities, climate, and land use to inform the development of resilient agricultural and wastewater treatment systems.

Microbes in Models and Data Systems—An examination of the gaps in microbial research studies, tools, and data systems and infrastructure that present barriers to inclusion of explicit representation of microbial processes in Earth system climate models. Recommendations were made to prioritize studies on microbial functions, species diversity, and adaptive emergent properties to improve models and coordination of data types to improve comparisons among diverse microbial communities and ecosystems.

Microbial Bioeconomy—A high-level view on the current scientific, policy, and cost hurdles that present barriers for microbial products to move from the bench to the market. A call was made for improved and frequent communications among scientists, policy makers, and entrepreneurs and for the incentivization of sustainable and biobased innovations.

Expanding Our Current Understanding of Microbial Ecosystems And Climate

Elemental flows: flux of elements such as carbon, nitrogen, and phosphorus through the environment

Decades of research have explored the relationship between microbes and their ecosystems. The advent of sequencing and metagenomics uncovered the plethora of microbes present in aquatic, terrestrial, and urban environments. While researchers may understand which microbes are present in the environment, less is known about what the microbes are doing in each environment and how a change in climate will impact

microbial communities and their ecosystem functions. Microbes drive many of the **elemental flows**, such as carbon, nitrogen, and phosphorus, on the planet (Figure 1). They also consume and produce the gases involved in global warming (Table 1). Climate change-induced variations in temperature, humidity, or elemental flux can have large impacts on microbial community structure and metabolic activity (Xue et al. 2016;

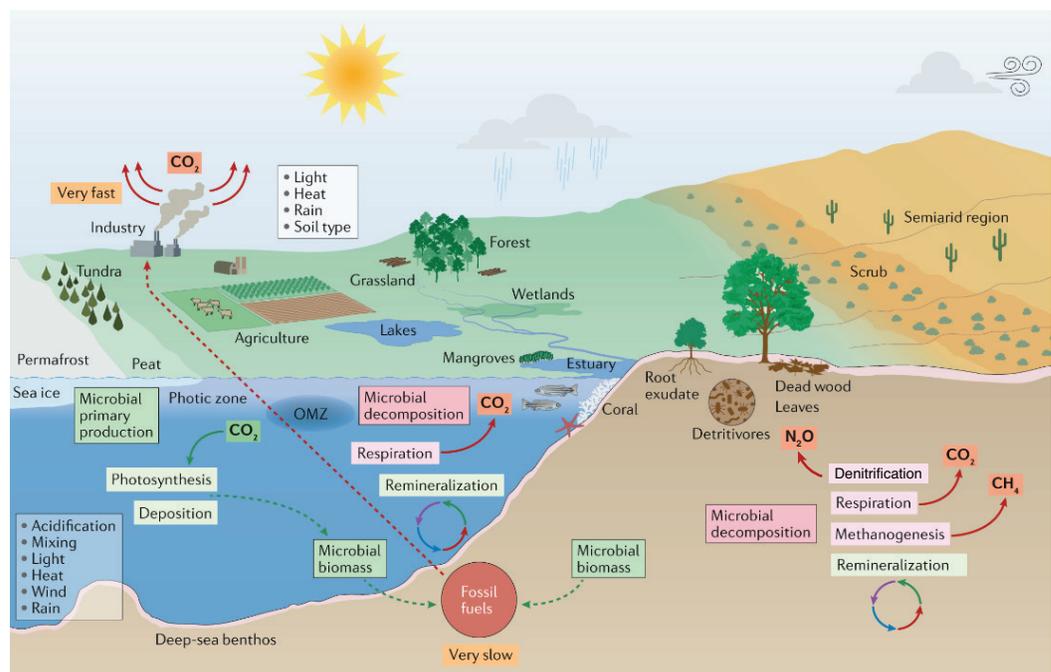


Figure 1. Microorganisms in terrestrial, urban, and aquatic environments consume and generate important greenhouse gases, CO_2 , CH_4 , and N_2O . Terrestrial microbes decompose organic matter, providing nutrients for plants and producing these three gases. Aquatic microbes use photosynthesis to generate and recycle nutrients for marine life while also helping sequester large amounts of carbon in the deep ocean. Human activities such as burning fossil fuels and agriculture release greenhouse gases at a faster pace than microbial consumption, resulting in imbalances in the carbon cycle, which affect microbial responses and impact on climate change. Figure modified from Cavicchioli et al. 2019.

Zhou et al. 2012; Woodcroft et al. 2018). Understanding the impacts of climate change on microbes and their fluxes of **carbon dioxide (CO₂)**, **methane (CH₄)**, and **nitrous oxide (N₂O)** in diverse environments will be key to elucidating how microbes will respond within their local community as well as the broader human community.

Terrestrial

The question of how increased soil temperature will impact soil microbial communities and activities has important implications for food security and global carbon and nitrogen cycling. Studies indicate that climate changes, such as increased temperature, elevated atmospheric CO₂ concentration, increased N deposition, extreme storm events, and flooding or drought conditions, significantly alter microbial community compositions and structure (Figure 2). Indeed, Zhou et al. reported that “warming markedly shifted both the functional and phylogenetic structures of [soil] microbial communities,” which can lead to novel, nonadditive communities and processes emerging (Zhou et al. 2012; Xue et al. 2016).

Changes in diversity can arise as fast-growing bacteria are selected for, altering the dynamics in microbial community structure (Guo et al. 2018). Yet,

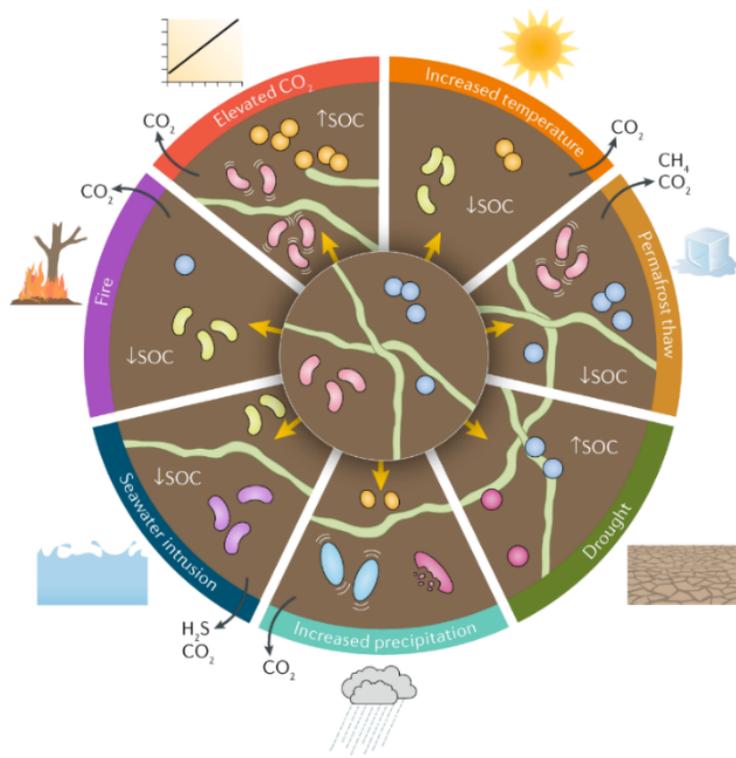


Figure 2. Climate change induces alterations in soil microbial communities. Bacteria (red), archaea (blue), and fungal hyphae (green) in the center are impacted by changes in temperature, precipitation, storms, soil organic carbon (SOC), and greenhouse gases, leading to changes in community structure as indicated by change to orange, green, or purple microbes. Figure from Jansson and Hofmockel 2019.

Table 1. Key Features of Greenhouse Gases Produced and Consumed by Microorganisms^a

Greenhouse Gas	Radiative Forcing ^b (W m ⁻²)	Lifetime (years)	Global Warming Potential ^c
Carbon dioxide (CO ₂)	2.16	Various ^d	1
Methane (CH ₄)	0.54	12	30
Nitrous oxide (N ₂ O)	0.21	109	273

^aBased on IPCC, 2021: Climate Change 2021: The Physical Science Basis. Contribution of Working Group I to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change.

^bEffective **radiative forcing** due to increasing atmospheric concentrations from 1,750 to 2,019. Positive values indicate net gain of energy that contributes to planetary warming.

^cGlobal warming potential relative to CO₂ at 100-year time frame.

^dAtmospheric CO₂ exchanges with multiple terrestrial and land reservoirs; effective lifetimes are centuries to a millennium.

Microbiome:
collection of all
microorganisms in
a location

how climate warming affects microbial alpha-diversity (e.g., species richness), especially of viruses, remains elusive. Long-term field exposure of a grassland ecosystem to elevated CO₂ dramatically altered the composition, structure, and potential interactions of grassland soil microbial communities (He et al. 2010; Zhou et al. 2010; Zhou et al. 2011). Most studies focus on the taxonomic diversity of bacteria and fungi, and there are few data about the soil **virome**. These studies also only examine surface soils in the upper 15 to 20 cm of soil (Ramesh et al. 2019). Less is known about subsurface **microbiomes** and how these communities are impacted by climate changes (Han et al. 2017). Significant increases in storage of microbial biomass carbon in deep soils may be required to reduce atmospheric CO₂ concentrations; thus, research on viromes and subsurface microbial communities is needed to understand which microbes are present and their metabolic and residual impacts in these environments (Brewer et al. 2019; Dynarski et al. 2020).

For the microbes that are known to be present in soil, much remains unknown about the specific role(s) each species plays within the microbial

community, thus limiting our ability to predict how these communities will react to the shifts induced by climate change. Previous studies have lacked an understanding of the alterations in genetic and functional diversity of microbial communities due to warming and the interactions between warming and other environmental factors. To elucidate what these microbes are doing in their ecosystem and how they are interacting with each other, studies exploring the causation–rather than just relying on correlation—are needed to understand the mechanisms driving shifts in microbial communities. This will include taking a “genes-to-ecosystems” approach to shed light on these questions. These research priorities can inform climate models and policies that address climate changes’ impacts (Nash Suding et al. 2003).

Besides temperature, climate change induces additional changes in soil properties like **porosity** and pH and increases chances of fires, droughts, or flooding that physically and chemically disturbs the soil (Figure 2) (Cook et al. 2015; Hart et al. 2005). Though microbes have evolved ways to survive drought stress, shifts in plant life that are more fire or drought resistant

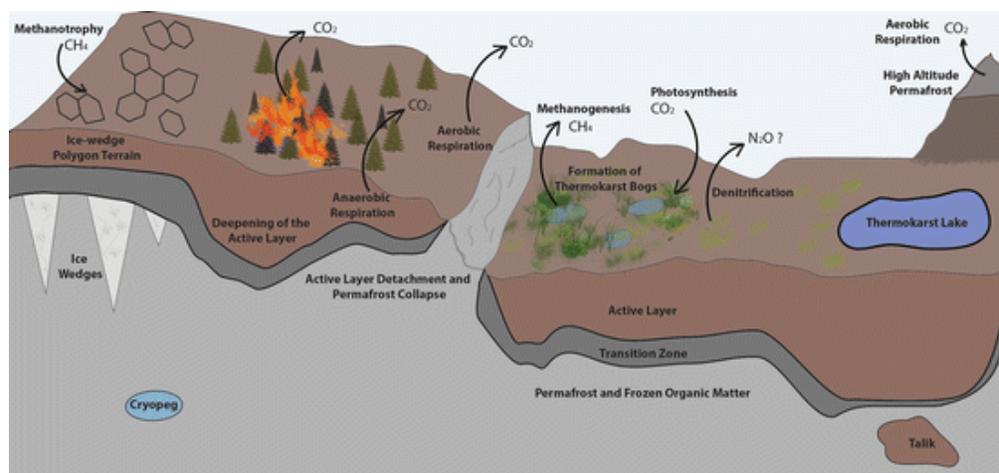


Figure 3. Microbial activity of permafrost consumes (**methanotrophy**, photosynthesis) and produces (respiration, methanogenesis) greenhouse gases. Figure from Altshuler et al. 2017.

will subsequently alter the root-associated microbial community (Barnard et al. 2013; Naylor and Coleman-Derr 2018; de Vries et al. 2018). Drier and hotter soils also lead to decreased microbial diversity and richness that, in turn, can decrease overall productivity (McHugh et al. 2017; Schimel 2018). Excess rain resulting from increases in severe storms can lead to soil erosion, increased nutrient leaching, and even anaerobiosis that can result in CH_4 and N_2O production.

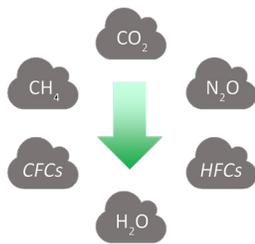
Warming and physical changes to soil can affect nutrient availability and cycling by microbes, which will have unknown cascading effects on the environment (Andrade-Linares et al. 2021). Microorganisms consume and produce the key greenhouse gases CO_2 , CH_4 , and N_2O , which contribute to global warming (Table 1). Altered microbial respiration or denitrification rates of soil microbes because of climate change can affect **microbial metabolism** and nutrient feedback loops, leading to unreliable quantification of these major greenhouse gases that can hinder mitigation strategies (Tian et al. 2020). For example, warming of **permafrost** offers a glimpse of how changes in the soil can dramatically alter carbon pools (see permafrost warming case study) (Figure 3). As permafrost thaws, it releases stored carbon that microbes can use for respiration or the production of CH_4 through **methanogenesis**. These actions can create a positive-feedback loop that increases carbon levels in the atmosphere. More research is needed to understand how changes in microbial metabolism alter the elemental flows of the planet. Higher temperatures are associated with increased metabolic rates (Brown et al. 2004), but the impacts of shifting metabolic kinetics on microbial communities remain poorly studied. Studying how changes in nutrient and carbon availability impact the bacterial, fungal, protistan, and viral commu-

Case Study: Permafrost warming releases stored carbon

Permafrost, which is perennially frozen soil over periods of at least 2 years, covers about 25% of the Earth's land and is home to a plethora of cold-adapted microorganisms (Graham et al. 2011; Jansson and Taş 2014). These frozen soils contain large quantities of organic carbon from remnants of plants, animals, and microbes (Schoor et al. 2008). Currently, the Arctic region stores about double the amount of carbon as is in the atmosphere (Tarnocai et al. 2009). As temperatures increase and the planet warms, permafrost will thaw, rendering large amounts of stored soil organic matter accessible to microbial enzymatic activity that can decompose the organic matter to produce the greenhouse gases CO_2 and CH_4 (Mackelprang et al. 2011; Mackelprang et al. 2016; Schädel et al. 2016; Xue et al. 2016; Biskaborn et al. 2019). Where drainage is impeded, water-saturated thawing permafrost can provide a niche favorable for methanogens, which affects the relative ratio of CO_2 and CH_4 production (Knoblauch et al. 2018; Wei et al. 2018; Heslop et al. 2019). This creates a positive-feedback loop where microbes help deplete permafrost-associated carbon reservoirs and increase CO_2 and CH_4 levels in the atmosphere, which can accelerate climate change (Schoor et al. 2015). This issue is particularly consequential for permafrost peatlands due to their concentrated stockpiles of carbon, which can fuel large CH_4 emissions under thaw-associated habitat change (Varner et al. 2022). Studies of specific permafrost environments—such as the Next-Generation Ecosystem Experiment (NGEE) in Alaska, USA, or the Danish Center for Permafrost (CENPERM) in Scandinavia—help scientists understand these microbial feedback loops and incorporate them into models to predict and plan better for climate change's effects.

nities and how that feeds back into climate change is vital for predicting future climate change impacts for the planet and humans.

Studies focused on monitoring microbiomes over time during periods of warming are needed as well. Unlike most studies that take a “snapshot” of the microbial community, long-term experiments of globally distributed ecosystems will afford information about microbial evolution and ecological dynamics (Vicca et al. 2018). The research community must work with colleagues across disciplines (e.g., botany, ecology, soil science, and geology) to establish consistent protocols and experimental methodologies across different soil depths



Microorganisms consume and produce the key greenhouse gases CO₂, CH₄ and N₂O that contribute to global warming

and time points to provide broad insights from local and regional experiments. This allows ecosystem models to incorporate microbiome information effectively and therefore improve long-term projections of climate change-associated dynamics (Kreft et al. 2017). For example, longer-term (over 10 years) studies of temperate grasslands in Oklahoma, USA, found that warming increased microbial network complexity and stability as well as enhanced microbial succession and temporal scaling of the bacterial and fungal taxonomic and phylogenetic diversity (Guo et al. 2018; Guo et al. 2019; Yuan et al. 2021). These studies can inform biodiversity preservation and land management strategies worldwide.

Urban

Over 50% of the world's population lives in urban areas (<https://www.urbanet.info/world-urban-population/>). Microorganisms' impact on urban environments is also influenced by climate change. Warming accelerates microbial corrosion of civil infrastructure. Microbial adherence and metabolic activity on surfaces lead to **microbiologically influenced corrosion** (Videla and Characklis 1992; Gaylarde et al. 2003; Little et al. 2020). Microbial biofilms directly attach to surfaces, while sulfate-reducing bacteria or methanogens can cause corrosive metal loss (Huttunen-Saarivirta et al. 2012; Li et al. 2016; Jia et al. 2019; Tan et al. 2017). Weak organic and inorganic acids produced by bacteria, fungi, and algae damage concrete and lower the pH of the environment to allow additional microbial colonization (Wei et al. 2014). Microbe-induced damages cost millions to billions of dollars and can even release greenhouse gases that accelerate climate change (Sanchez-Silva and Rosowsky 2008; Conley et al. 2016). Additionally, microbial activity leading to changes in temperature, precipitation, humid-

ity, and soil conditions may directly damage infrastructure. More research about the role of microbes in the corrosion or repair of man-made structures under climate change conditions is needed (Little et al. 2020).

Changes in precipitation and temperature also alter urban areas' groundwater chemistry and levels of dissolved organic carbon (McDonough et al. 2020). This alters nutrient availability and redox conditions, causing shifts in microbial communities that may increase the survival of pathogens (Retter et al. 2021; Danczak et al. 2018). Flooding, which is expected to increase as a result of climate change, raises the risk of exposure of humans to pathogens (Ahern et al. 2005; Taylor et al. 2011). Urban areas are more vulnerable to flooding because of the lack of green-space for rainwater runoff. Stagnant water in flooded areas has been associated with increased transmission of vector-borne diseases, and flooded homes increase exposure to mold (El Sayed et al. 2000; Sáenz et al. 1995; Andersson et al. 1997; CDC 2006). Floods also promote the redistribution and mixing of microorganisms, helping drive **horizontal gene transfer** and assembly of new microbial communities that can result in unknown and unexpected cascading effects (Deng et al. 2019). Research is needed to understand how microbial populations are altered by flooding to inform flood cleanup policies and procedures.

Sewage and wastewater systems are especially susceptible to microbiologically influenced damage and the impacts of climate change (Davis et al. 1998; Okabe et al. 2007). Sewage treatment relies on microbial metabolic activities to degrade waste, producing CO₂, CH₄, and N₂O, which contribute to climate change (Table 1). A recent study shows that temperature and organic input play critical roles in controlling global spatial turnovers of

Microbiologically influenced corrosion: corrosion resulting from the presence and/or activity of microorganisms

bacterial communities in wastewater treatment plants (Wu et al. 2019). Elevated temperatures have also triggered *Legionella pneumophila* (agent of Legionnaires' disease) overgrowth and dramatic changes in treatment system microbial communities, resulting in failure of wastewater treatment and Legionnaires' disease contracted from treatment plants (Kusnetsov et al. 2010; Caicedo et al. 2020; Caicedo et al. 2019). Warming also increases snow melting periods and influent flow rates, which along with increased precipitation and storms can lead to flooding of untreated sewer overflows, exposing people to possible pathogens in wastewater (Schalk et al. 2012; Plósz et al. 2009; Zouboulis and Tolkou 2015). Because climate change is expected to make these events more prevalent in the future, research and innovations are needed to adapt current wastewater treatment plants to be more resilient and sustainable (Verstraete et al. 2022).

Vulnerable, minority, and lower-income communities are especially exposed to climate change-associated impacts because they tend to live in "more polluted, less secure, and high-risk environments" that drive inequitable microbial exposure (Brulle and Pellow 2006; Ishaq et al. 2019). For example, Black and poor communities were disproportionately affected by flooding from Hurricane Katrina in Louisiana, USA, in 2005 (Zoraster 2010). Higher rates of bacterial contamination in drinking water have also been found in immigrant and low-income communities, hurting community health (Calderon et al. 1993; Ciesielski et al. 1991). This "**microbial injustice**" stemming from the unjust and disproportionate microbial exposures and risks of vulnerable communities will worsen as climate change increases the frequency and/or intensity of storms (Ishaq et al. 2019).

Case Study: **Inequitable microbial exposure in urban housing**

Urban populations are growing rapidly, with the United Nations (UN) projecting 68% of the global population living in urban areas by 2050 (<https://population.un.org/wup/Publications/Files/WUP2018-Highlights.pdf>). While living in an urban area reduces overall microbial exposure compared to that in rural environments, exposures to microbes are not equal in urban areas (Mills et al. 2019; Ishaq et al. 2019). Lower-income, minority, and immigrant populations disproportionately live in housing with physical problems that can lead to mold exposure from water damage, dangerous aerosols, and exposure to vectors of disease because of building deterioration (Krieger and Higgins 2002). Living in low-income neighborhoods and crowded conditions are also associated with higher rates of infectious diseases (Wallace 1988; Cohen et al. 2000; Barr et al. 2000). Increased exposure to microbes harms these communities' health inequitably (Ishaq et al. 2019). Global warming and altered precipitation patterns will allow pathogens to expand their geographic and temporal range and expand into novel environments in urban areas (Honeyman et al. 2018). Land management and urban planning strategies along with pathogen surveillance and public health policies must be integrated to preserve the health and well-being of all populations.

Aquatic

Aquatic environments cover more than 70% of Earth's surface. Marine, freshwater, and intertidal ecosystems are home to diverse animal, plant, and microbial species and are vital for humans' well-being and health. Aquatic systems provide us with water for drinking and cleaning as well as a source of food. As in terrestrial environments, climate change causes major impacts to temperature in aquatic ecosystems. Global sea surface temperature has steadily increased (NOAA). Warmer oceans can lead to formation of stronger storms and flooding, decreased ocean life and biodiversity, and altered elemental flux by marine microorganisms. Research is needed to understand and predict what types of cascading effects warming of oceans will have on aquatic and terrestrial life.

Microbial injustice:
inequitable microbial exposure and risk experienced by disadvantaged communities

Marine carbon pump: biologically driven depletion of carbon from air and land to the ocean's interior and seafloor sediments

Climate change alters marine carbon pools. The **marine carbon pump** uses microbial processes to sequester large amounts of carbon in the deep ocean, helping regulate atmospheric CO₂ levels (Figure 4) (Volk and Hofert 1985; Falkowski et al. 1998). But warming may reduce the amount of carbon oceans can sequester (Laufkötter et al. 2016). Actions of the **microbial loop** and **viral shunt** drive carbon cycling in the oceans, though there is a current lack of understanding about microorganisms in deep ocean systems (Azam et al. 1983). Ocean warming impacts microbial communities, which, in turn, affect the overall balance between carbon sequestration and release of CO₂ (Cavan et al. 2019; Wohlers et al. 2009). Studies to uncov-

er how microbial community composition and carbon cycling are impacted by ocean warming under different conditions and in diverse regions will be important to inform Earth climate models and environmental management strategies.

Climate-associated changes to microbial actions impact marine life. For example, corals rely on **symbiotic** microbial communities composed of bacteria, archaea, algae, viruses, and fungi (Taylor et al. 2020; Thurber et al. 2017). Photosynthetic algae provide corals with many of their nutrients as well as their vibrant colors (Taylor et al. 2020). Warming temperatures and increased ocean acidification induce **coral bleaching** and destabilize coral microbiomes (see coral bleaching

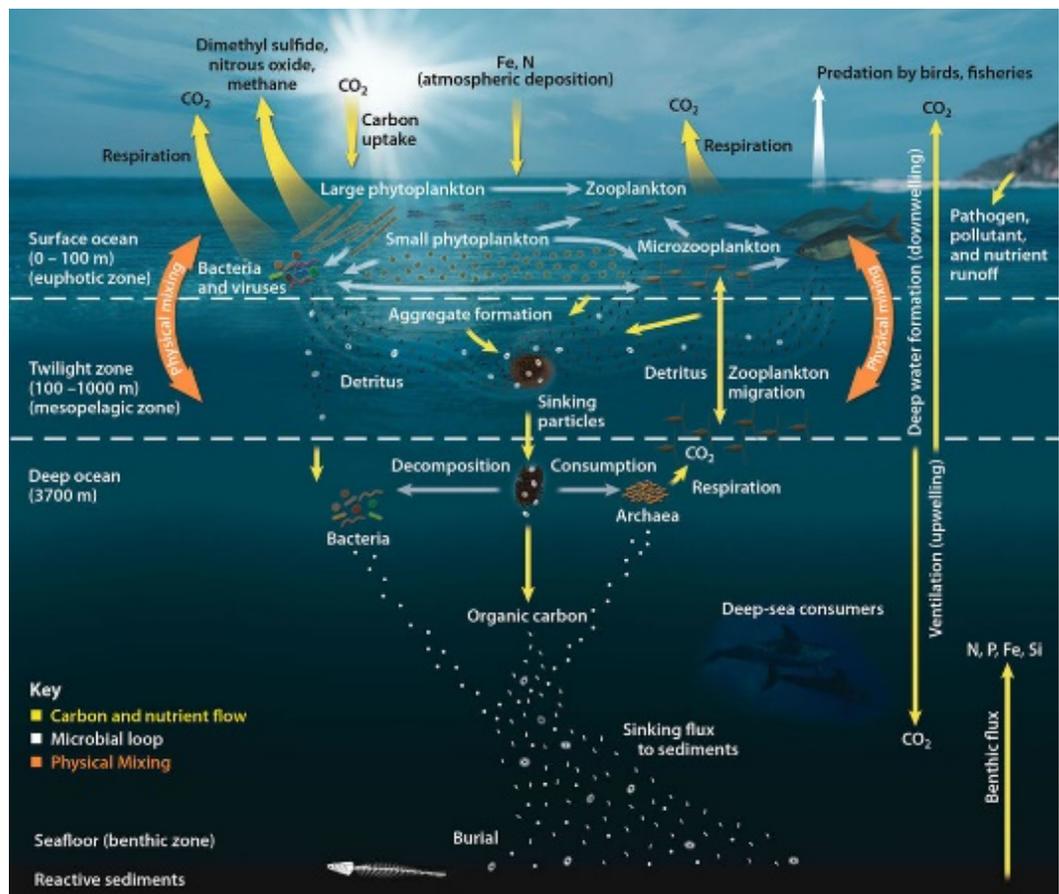


Figure 4. Marine microbes recycle and sequester carbon in the marine carbon pump. Microbial respiration and bacterial lysis provide carbon to marine life, while the viral shunt and photosynthesis lead to carbon sedimentation and storage on the ocean floor. Image is in the public domain.

case study) (Figure 5) (Hoegh-Guldberg et al. 2007; Lesser et al. 2015). Without their symbionts, corals become less resilient and more prone to infections (Carilli et al. 2009; Anthony et al. 2011; Ben-Haim et al. 2003). Because corals are foundational for many benthic ecosystems, the loss of coral systems because of climate change and altered microbiota has devastating cascading impacts on benthic biodiversity (Bell 2008). More research integrating climate, corals, and their associated microbiome into models is necessary to understand the full impact of ocean warming on marine life (Asner et al. 2020; Vega Thurber et al. 2020).

Aquatic pathogens of humans are influenced by warmer temperatures,

especially in coastal zones where humans and nature interface. Increased temperature expands pathogens' temporal and spatial ranges, increasing human exposure to these threats (IPCC 2022, Summary for Policymakers). Infections with *Vibrio* spp., opportunistic marine pathogens, are increasingly reported in higher latitudes and for a longer part of the year (see *Vibrio* case study) (Semenza et al. 2017). In freshwater environments, such as lakes, rivers, and wetlands, **algal blooms** have increased because of changes in nutrient loading, temperature, and precipitation levels (see algal bloom case study) (Paerl et al. 2014). Increased use of fertilizers in agriculture and higher levels of rainfall lead to nutrients, such as nitrogen and

Algal blooms: proliferation and accumulation of algae in aquatic environments beyond normal seasonal growth

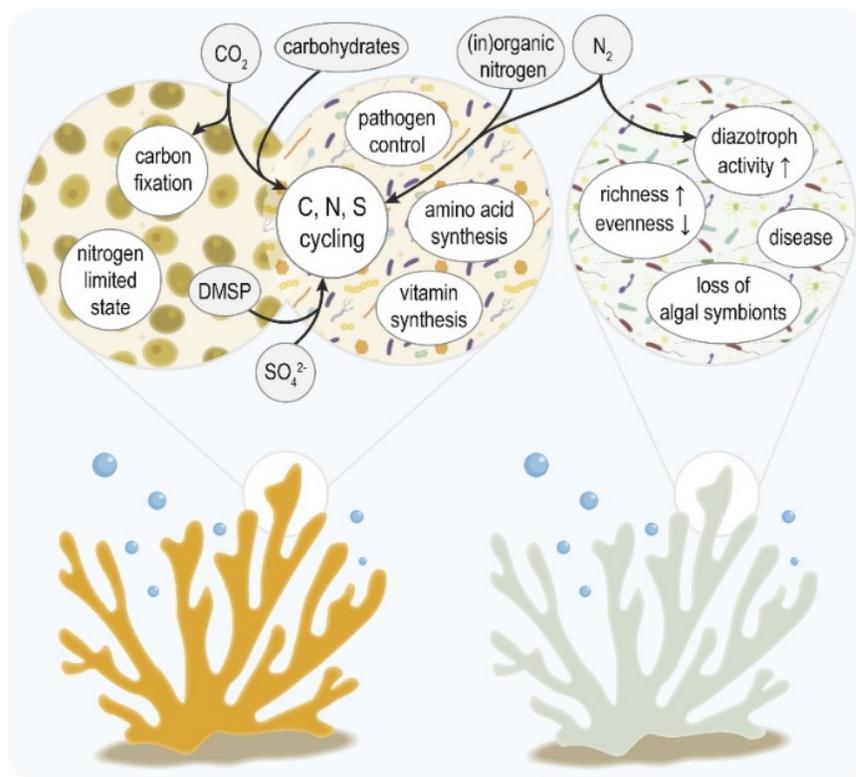


Figure 5. Healthy corals (left) have symbiotic microbial communities to provide them nutrients such as carbohydrates, amino acids, and vitamins as well as defense against pathogens. Warming water and ocean acidification induce coral stress, causing a loss of their algal symbionts and alterations to the coral-associated microbiome, making corals lose their color and thus appear bleached (right). The lack of microbial species richness allows opportunistic pathogens to infect and possibly cause more coral disease. Figure from Vanwonderghem and Webster 2020.

Coral bleaching: stress mechanism of coral where they expel their symbiotic algae (zooxanthellae) that provide their color, thereby appearing faded or 'bleached'

Case study:
Ocean warming induced coral bleaching

Coral reefs are important sources of food, income, and coastal protection for millions of people worldwide and are home to at least 25% of marine species (Woodhead et al. 2019; Vanwonderghem and Webster 2020). Corals are vulnerable to the impacts of anthropogenic activities and climate change, with over 50% of corals dying since the 1950s (Hughes et al. 2017b; Hoegh-Guldberg et al. 2007; Eddy et al. 2021). Coral reefs are composed of tiny animals called polyps living within a calcium carbonate exoskeleton (Rosenberg et al. 2008). Symbiotic microbes provide the polyps with nutrients, with the pigments from photosynthetic algae giving corals their vibrant colors (Taylor et al. 2020). Warming waters and ocean acidification cause coral stress that leads polyps to eject their microbial symbionts, causing corals to lose their color and appear “bleached” because of their white calcium carbonate skeleton (Figure 5) (Baker et al. 2008). As the coral microbiome alters because of bleaching events, corals become less resilient and more prone to infections (Rosenberg et al. 2008; Carilli et al. 2009; Anthony et al. 2011; Ben-Haim et al. 2003). Incidents of coral bleaching have increased as ocean temperatures rise because of climate change (Baker et al. 2008; Hughes et al. 2017; Hughes et al. 2018). For example, recurrent bleaching of the Great Barrier Reef (1998, 2002, and 2016) has caused significant coral loss (Hughes et al. 2017; Dietzel et al. 2020). Using metagenomic analysis, Littman et al. found metabolic and taxonomic differences of the coral microbiome between healthy and thermal bleached Great Barrier Reef corals, with more virulence genes associated with bleached corals (Littman et al. 2011). Since myriad aquatic organisms live in reefs, loss of coral reefs will impact aquatic biodiversity, further impacting human activities such as fishing and tourism (Bell 2008). Models using climate, coral, and microbial data can help inform reef conservation and management strategies that can support human well-being (Asner et al. 2020; Vega Thurber et al. 2020).

into streams and lakes. This escalation of nutrients, known as **eutrophication**, promotes a surge in **cyanobacterial** growth (Dolman et al. 2012; Harke et al. 2016). Excessive algal growth results in decreased oxygen levels, causing fish and aquatic life to die. Additionally, toxins released during algal blooms are a concern for human and environmental health since they can reduce local biodiversity and possibly weaken ecosystem resilience (Wilhelm et al. 2020). Understanding the complex relationship between climate change and aquatic pathogens will inform strategies to enhance public health and environmental management.



Bleached coral, *Acropora* sp.

Current Understanding of Microbial Ecosystems and Climate Summary and Recommendations

Regardless of the environment, climate change will affect microbial communities and their functions. From altering the available pools of carbon to increasing exposure to pathogens, the changes to our climate will impact microbiomes and metabolic activities everywhere. Scientists need to understand how changes in temperature and ecosystems affect microbes, including fungi, viruses, protists, and archaea, and how that feeds back to climate change to inform public health and mitigation policies. To aid our understanding of the cascading effects of climate change on microbes in varied environments, the following research topics are highly recommended to promote *interdisciplinary* studies:

- Examine the relationship between genetic and functional diversity to understand the role different species play in microbial community assembly and interactions and elucidate the mechanisms driving shifts in microbial communities.
- Research the energetics of metabolism and elemental flux by microbes in the terrestrial, urban, and marine environments to factor into terrestrial and aquatic climate models the activities of bacteria, fungi, protists, and viruses.
- Institute long-term experiments of diverse ecosystems, including subsurface soil and deep-sea microbial communities, with consistent protocols to capture the evolution and ecological dynamics for models.
- Explore the role of microbes in microbiologically influenced corrosion of man-made infrastructure and design resilient and sustainable innovations for future urban infrastructure.
- Investigate cascading impacts of flooding, severe storms, droughts, etc., on microbial community structure, functions, and human health.
- Establish efforts to combat climate-mediated microbial injustices, which are changes to the microbial world that inequitably and negatively impact disadvantaged communities, as well as gain understanding of communities most impacted by climate change to shape public health policies, land use management strategies, and carbon-sequestering technologies to buy time as we work to understand microbial processes better.

Microbes and Human Health

One Health:

idea to integrate information about “people, animals, plants, and their shared environment” to inform and promote human health

Zoonotic disease:

infectious disease transmitted from an animal species to humans

Human health is intricately linked to the environment. As climate changes in terrestrial, urban, and aquatic environments, the human, animal, and plant pathogens living in those environments must adapt, presenting opportunities for pathogens to move about and evolve in unknown ways that may increase virulence and host-range. Shifts in temperature, precipitation, humidity, CO₂ concentrations, and nutrient availability can increase water and food-borne infections as well as the risk of zoonotic diseases.

A **One Health** approach that connects pathogen genomic sequencing and surveillance with public health policies is needed to understand the impacts of climate change on the environment, microbes, and human health.

Pathogen Adaptations for a Changing Environment

Earth has experienced past epochs of extreme atmospheric and temperature fluctuations. Over 3.5 billion years ago, cyanobacteria emerged with the ability to **photosynthesize** and produce free O₂ (Baumgartner et al. 2019). Consequently, Earth experienced a sharp rise in oxygen accumulation in the atmosphere, referred to as the “Great Oxidation Event” or “Great Oxygenation Event,” approximately 2 billion years ago (Olejarz et al. 2021). That event is a powerful example of how microbial life can change our planet. While the Great Oxidation Event resulted in a mass extinction of anaerobic life, these conditions also presented an opportunity for aerobic multicellular life to flourish (Schirrmeister et al. 2013). In turn, increased oxygen oxidized atmospheric

methane, decreasing this greenhouse gas and lowering global temperature, resulting in the first Ice Age (Tang and Chen 2013). Since then, the planet has undergone multiple eras of warming and cooling, with microorganisms witnessing and evolving throughout all the swings in temperature and climate. Today’s pathogens arose from these historical changes, and as Earth’s climate continues to change because of anthropogenic activities, understanding how pathogens will adapt and what novel pathogens will emerge in response to these changes will be necessary to protect human health.

Climate change will introduce microbes to novel environments and force humans to adapt to new circumstances. The impact of novel environmental conditions on pathogenesis remains unknown. Alterations in temperature, precipitation, and nutrient availability will undoubtedly affect microbial metabolism and nutrient cycling, which can impact colonization and virulence (Hofreuter et al. 2008; Nuccio and Bäumlner 2014). Research addressing how pathogens’ metabolic activities, enzyme functions, and community dynamics change in response to changing temperature and nutritional status is needed.

Humans are expanding into novel natural environments as well, increasing exposure to pathogens (Figure 6). This, coupled with the environmental changes noted above, raises the possibility of **zoonotic** spillover events and increased interactions with possible animal reservoirs. Fortunately, surveillance studies can help inform the public health responses to zoonotic and new diseases. The National

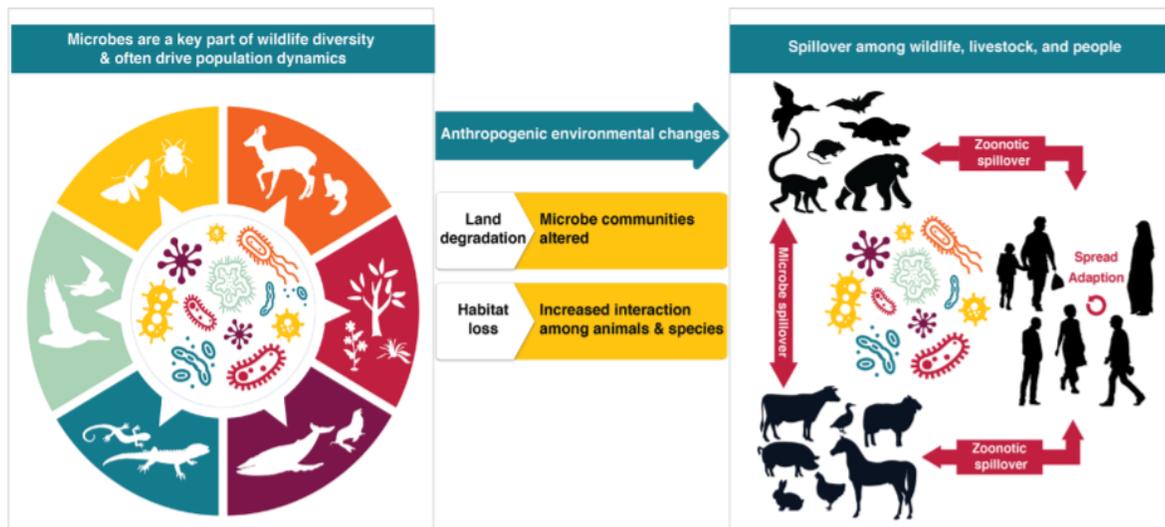


Figure 6. Exposures to zoonotic pathogens increase with greater frequency of human and animal interactions. Microorganisms that naturally evolved with wildlife (left) can spill over to humans because of human expansion into natural habits (center) and increased contact with wildlife or livestock (right). Zoonotic pathogens can cause pandemics when they are transmitted easily among humans and can spread quickly because of urbanization and global travel. Figure from Daszak et al. 2020.

Wastewater Surveillance System implemented by the Centers for Disease Control and Prevention (CDC) during the COVID-19 pandemic helped notify local communities of upcoming rises in COVID-19 cases, affording them more time to prepare (CDC). As humans and animals increasingly interact, surveillance studies also allow for tracking of “spillback” events in which humans reintroduce pathogens back to wildlife. This provides a reservoir for zoonotic pathogens to adapt, acquire new mutations, and establish emerging features that may impact virulence (Fagre et al., 2021; Kuchipudi et al. 2021). Real-time genomic sequencing and surveillance systems of current and emerging pathogens coordinated between those in epidemiology, clinical labs, and public health are critical to protect human health.

Novel environments also include increased spatial and temporal ranges. As temperature increases and climate changes, pathogens and **vector** species are expected to expand their regional distributions (Gorris et al. 2019; Hoegh-Guldberg et al. 2018). The IPCC reports increases in water and food-

borne diseases from “climate-sensitive aquatic pathogens” such as *Vibrio* spp. that are being reported in higher latitudes, and infections are common for extended portions of the year (see *Vibrio* case study) (Semenza et al. 2017; IPCC 2022, Summary for Policymakers). Insect and mammalian vectors will alter their spatial range, permitting unprecedented mixing of animal species and the spread of microorganisms in new ways (Colón-González et al. 2021). Coinfections with pathogens (bacterial, fungal, or viral) in hosts allow for genetic exchange via horizontal gene transfer and the opportunity to share virulence genes or for highly antibiotic-resistant “superbugs” to emerge (Desai et al. 2013; Mentel et al. 2006). Additionally, a warmer environment is more similar to humans’ body temperature. As zoonotic and opportunistic pathogens adapt to a warmer environment, it may inadvertently allow for increased infectivity and pathogenesis (see warm-adapted fungus case study) (Kimes et al. 2011). Investigation into how pathogens or vector hosts are evolving in their environments can inform climate change’s impact on human exposure and public health risk.

Case study: ***Vibrio*'s expanded temporal and spatial range**

Vibrio spp., including *Vibrio parahaemolyticus*, *V. vulnificus*, and *V. cholerae*, are marine bacteria found in warm estuarine and coastal waters and can cause diarrhea, nausea, vomiting, dehydration, and fever when ingested (Pruzzo et al. 2005). As temperatures have increased, infections with these opportunistic pathogens have expanded temporally and spatially. Warming in Europe has led to increased *Vibrio* outbreaks (Vezzulli et al. 2011). The most northerly example occurred in 2014, when Sweden and Finland experienced a heat wave with a concurrent record number of reported *Vibrio* infections (Baker-Austin et al. 2016). To understand this change, the European Centre for Disease Prevention and Control (ECDC) developed the *Vibrio* Map Viewer. Using real-time data on sea surface temperature and salinity, the *Vibrio* Map Viewer helps “predict the occurrence of environmental conditions that favor *Vibrio* proliferation,” acting as an early warning system for the risk of *Vibrio* infections (Semenza et al. 2017). Based on data from the *Vibrio* Map Viewer, infections appear to be reported in higher latitudes and for a longer part of the year (Semenza et al. 2017). As sea surface temperature rises as a result of climate change, *Vibrio* spp. are expected to expand their spatial range north, increasing the risk of infection in regions previously unaffected by these pathogens. Taking a One Health approach by incorporating local ecology and climate impacts into surveillance and monitoring systems allows for an early warning system for *Vibrio* infections that will better help prepare local public health responses and policies (Constantin de Magny et al. 2008). These strategies can serve as examples for future emerging diseases.

Disaster microbiology: proposed field of study focused on the microbial impacts from severe storms and natural disasters

Microorganisms will also need to adapt to more extreme changes spurred by climate change, including storms. Warmer oceans and increased precipitation will result in stronger cyclones, hurricanes, typhoons, and flooding events (Field 2012). These storms can increase pathogen exposures in human populations, especially those of vulnerable communities (Ahern et al. 2005; Taylor et al. 2011; Andersson et al. 2021). Flooding events have been associated with increased incidents of mosquito-borne diseases such as malaria and dengue fever (Coalson et al. 2021). Storms can also impact and disrupt wastewater systems, leading to less effective treatment systems or overflows that expose untreated pathogens to the

local community. The cascading effects of extreme storms remain poorly understood since these storms may drive pathogen mixing and evolution in novel ways. A new field of “**disaster microbiology**” could conceivably emerge to focus on the microbial impacts from ever-increasing severe storms and natural disasters. Paired with increased microbial surveillance systems, these data would be instrumental in informing models and One Health public policies.

In other regions of the world, climate change is expected to increase drought conditions. Dust from droughts may carry pathogens and microbial toxins, expanding their spatial range and endangering human health. To meet this challenge, airborne microbiome surveillance could provide a tool to monitor in real time for increases in airborne infectious agents just as wastewater surveillance systems have been used during the COVID-19 pandemic. This will be especially important as climate change impacts and alters global air currents. Another climate change-induced source of pathogens is permafrost. Global warming is associated with permafrost thawing (see permafrost warming case study), which may unlock novel pathogenic bacteria, fungi, or viruses or antibiotic resistance mechanisms frozen away for millennia. A 2016 outbreak of anthrax disease in Siberia has been associated with the release of *Bacillus anthracis* spores from thawed permafrost (Simonova et al. 2017; Stella et al. 2020). Research examining possible pathogens and their virulence mechanisms from extreme storms or permafrost samples will help inform biomedical studies to tackle novel pathogens uncovered because of climate change.

Pathogen Adaptations Based on Human Physiology

Infectious diseases are a leading

cause of global morbidity (WHO 2020). Though improved sanitation, antibiotics, vaccines, and treatments have greatly reduced deaths from microbial infections, infectious diseases continue to have a substantial global socioeconomic cost (Fonkwo 2008). The Institute of Labor Economics estimated the cost of eight major microbial diseases (HIV/AIDS, malaria, measles, hepatitis, dengue fever, rabies, tuberculosis, and yellow fever) to be about \$8 trillion (U.S.) and more than 156 million life years lost in a single year (Armitage 2021). Climate change will increase the cost and burden of infectious diseases on global populations, making the study of climate change's impact on pathogens vital to preserving human health.

Humans have many defenses against infectious agents, and these include both physical and immunological mechanisms. **Endothermy** is a major physical defense by which the human body temperature creates a thermal barrier for many microorganisms, including fungi (Robert and Casadevall 2009). As stated previously, warmer environments may select for pathogens that can better survive at body and fever temperatures, making them more difficult for the body to clear. Pathogens such as some fungi

may adapt to a rise in temperature, making fungal human diseases more common over an expanded geographic range with global warming (see warm-adapted fungus case study) (Datta et al. 2009; Fernandes et al. 2016; Garcia-Solache and Casadevall 2010). For example, the fungal pathogen *Candida auris* is more heat tolerant than related *Candida* spp., and the emergence of *C. auris* as a human pathogen has been proposed to be associated with warming temperatures (<https://www.cdc.gov/fungal/candida-auris/tracking-c-auris.html>; Casadevall et al. 2019). Other thermal tolerant fungal pathogens are expected to emerge, especially as elevated global temperatures and increased storms allow for expanded fungal temporal and spatial range (Figure 7) (de Crecy et al. 2009; Konopka et al. 2019; Tedersoo et al. 2014; Robert et al. 2015; Nnadi and Carter 2021). Because fungal physiology is more similar to human physiology than that of bacteria, parasites, or viruses, there are limited treatments and no vaccines against fungal infections. Additional and expanded pathogen surveillance, especially for fungal pathogens, in the environment and animal reservoirs can aid in monitoring and preparing for climate-adapted infectious microbes (Casadevall 2020).

Endothermy: ability of an organism to maintain a set temperature

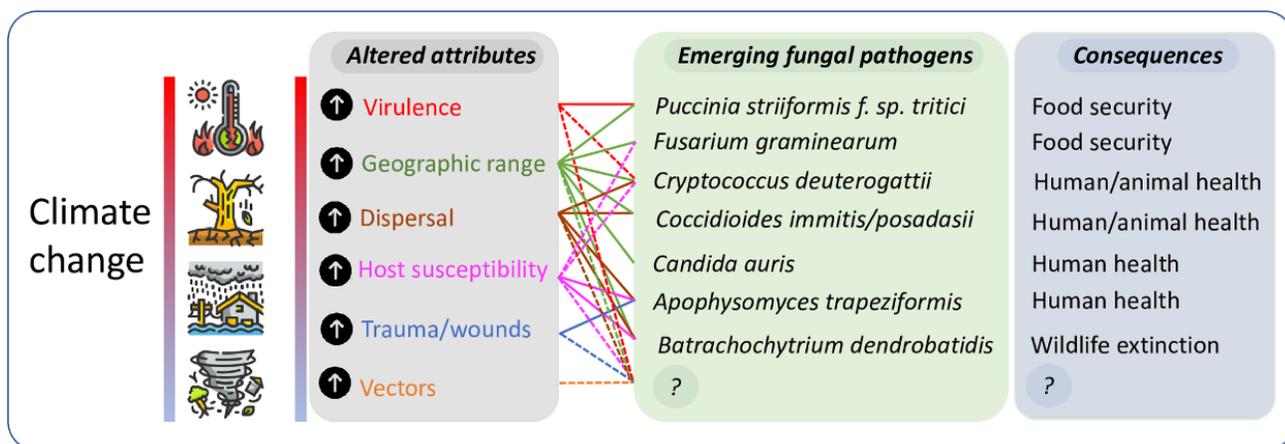


Figure 7. Climate change impacts the environment's temperature, precipitation, and frequency of storms, leading to possible alterations of fungal pathogens' virulence, temporal and spatial range, and host and vector susceptibility. The emergence of novel features by fungi may have far-reaching consequences on human, animal, and environmental health. Figure from Nnadi and Carter 2021.

Case study: Warm-adapted fungal pathogens

Historically, fungi have not caused serious outbreaks in human populations. Most pathogenic fungi cause disease in ectothermic vertebrates, insects, and plants, which are cooler (<30°C) than human body temperature (Casadevall 2019). However, we may see new fungal diseases in humans as global temperatures warm. The first human infection with the opportunistic fungal pathogen *Candida auris* was reported in 2009 (Satoh et al. 2009). Since then, increased *C. auris* infections have been identified throughout the globe (Rhodes and Fisher 2019). Many fungal species are inhibited at human temperatures of 37°C and above, but clinical isolates of *C. auris* are more thermal tolerant than related *Candida* spp. (Robert and Casadevall 2009; Casadevall et al. 2019). Casadevall et al. suggested that *C. auris* originally lived as an environmental fungus that adapted to a warmer environment, overcoming the human thermal barrier to become “the first example of a new pathogenic fungus emerging from human-induced global warming” (Casadevall et al. 2019; Jackson et al. 2019). Consistent with this proposal, *C. auris* was first recovered from the environment in the Andaman Islands, and one of the feral isolates had lower thermal tolerance than clinical strains (Aro-ra et al. 2021; Casadevall et al. 2021). With climate change promoting global temperature rise, increased surveillance for fungal pathogens is needed to monitor and prepare for emerging pathogens (Casadevall 2020).

Dysbiosis:
disruption to
the microbiota
homeostasis

Humans’ innate immunity and adaptive immunity counteract microbial infections as well. But not all microorganisms are detrimental to human health: many human-associated microbes (called the **human microbiome**) have evolved a symbiotic relationship with humans by which microbes provide essential amino acids, nutrients, and vitamins and aid in tissue and immune system development (Belkaid and Hand 2014). Archaea, bacteria, fungi, protists, and viruses all compose the human microbiota, and these vary based on anatomical location (Robinson et al. 2010). Skin microbes help prevent colonization by pathogens and regulate inflammation (Lai et al. 2009; Buffie and Pamer 2013; Belkaid and Segre 2014; Byrd et al. 2018). The gut microbiome helps tune and form the adaptive and innate immune system (Lee and Mazmanian 2010; Naik et al.

2012; Buffie and Pamer 2013). Gut microbe populations release molecules that stimulate antimicrobial peptides (e.g., cryptidins and bacteriocins) or expression of immune responses in the intestines (Kobayashi et al. 2005; Ducluzeau et al. 1976; Cash et al. 2006; Smith et al. 2013). As on the skin, the gastrointestinal microbiome provides resistance to colonization by pathogenic microorganisms (Van der Waaij et al. 1971; Sekirov and Finlay 2009; Buffie and Pamer 2013). Further research about what microbes, especially viruses, are present in different anatomical parts of the body and their role in immunity and defense against pathogens is needed as a foundation for future biomedical research and possible disease treatments.

Shifts to the gastrointestinal microbiome can occur to make the host less resilient to pathogen colonization and disease. Changes in diet resulting from climate change, such as a transition from meat to insect proteins or different mineral contents of food grown in novel regions, may alter the stability, diversity, and community structure of the gut microbiome (Conteville et al. 2019; Catania et al. 2021). These alterations of the microbiome can make humans more susceptible to infections. For example, antibiotic treatment is associated with **dysbiosis** of the microbiome and increased intestinal infections, including *Clostridioides difficile* infections (Reeves et al. 2011; Buffie et al. 2012). Shifts in the ecology and environment because of climate change can indirectly impact gut microbiomes and have unknown cascading impacts on human health and resilience (Greenspan et al. 2020).

We may be seeing firsthand the impacts of altered microbiomes with the rise of allergies and autoimmune diseases (Pascal et al. 2018; Luca and Shoenfeld 2019; Xu et al. 2019; Ray and Ming 2020). Studies have linked the autoimmune diseases Crohn’s

disease and ulcerative colitis to gut microbiome dysbiosis resulting in reduced microbial community stability and diversity (Frank et al. 2007; Gevers et al. 2014). Additionally, climate change may be exacerbating allergies because of increased pollen and air pollution (Ziska et al. 2019; D'Amato et al. 2010). To help overcome microbiota dysbiosis and reduce allergy and autoimmune disease symptoms, some **probiotics** can help facilitate the restoration of the microbial community. Probiotics are defined by the Food and Agri-

culture Organization of the United Nations and the WHO as “live microorganisms which when administered in adequate amounts confer a health benefit on the host” (Hill et al. 2014). Yet much remains unknown about the underlying mechanism and safety of these microbial manipulation strategies (Yang et al. 2014; Liu et al. 2018). More investigation of the mechanism of human-associated microbiota community structure and its relationship with human health is needed to guide future microbe-based treatments and innovations.

Microbes and Human Health Summary and Recommendations

Human health, microorganisms, and the environment form a complex relationship, where the health of one species depends on the others. Changes to the environment will expose microbes with pathogenic potential to novel environments where they can evolve and expand their host, geographic, or temperature range, resulting in a multitude of cascading effects on human health. Meanwhile, climate change-induced alterations to the human-associated microbiome may lead to increased susceptibility to infection and autoimmune diseases. Going forward, the colloquium participants stressed the need to take a One Health approach to studying the role of climate change and microbes in regard to human health and recommended prioritizing the following tools and research foci to inform public health policies:

- Expand air and wastewater genomic sequencing and surveillance systems of pathogenic microbes to provide coordinated computational, environmental, epidemiological, and clinically relevant real-time data for public health modeling and policies.

- Implement a One Health approach to study the relationship between climate change and human health that takes into account the local ecological, microbiological, cultural, and socioeconomic factors.
- Establish a field of disaster microbiology to explore the impacts and evolution of pathogens and vectors after severe natural disasters to inform models and land use strategies.
- Investigate how pathogens will adapt as temperatures rise and the impact of those adaptations on pathogenesis.
- Examine the interactions and relationships between human physiology and the microbiome to understand microbial community structure, dynamics, and the underlying mechanisms to shape future biomedical research and treatments.

Microbes and Human Well-Being

Besides human health, microbes impact multiple facets of life that influence human well-being; however, the relationship between microbes and human quality of life is not as well articulated to the public as much as the connection between microbes and health. Microbes impact agriculture, water safety, air quality, etc., and climate change affects microbial communities, which can have profound cascading effects on quality of life. These effects are especially felt by vulnerable communities that disproportionately bear the brunt of negative consequences resulting from climate change. Some of the effects with strong links to microbes are highlight-

ed below as examples. Scientists must clearly communicate and engage with the public on the role of microbes in people's daily lives to inform them of possible microbial risks and empower them to understand how science can aid in creating a healthier future.

Food Supply, Safety, and Security

Microorganisms greatly impact food production and safety. Similar to their effects on human health, microbes act as both pathogens and promoters of plant and animal health. Plant pathogens decrease crop yield and quality, while beneficial plant microbiomes are associated with promoting plant health and protecting against plant

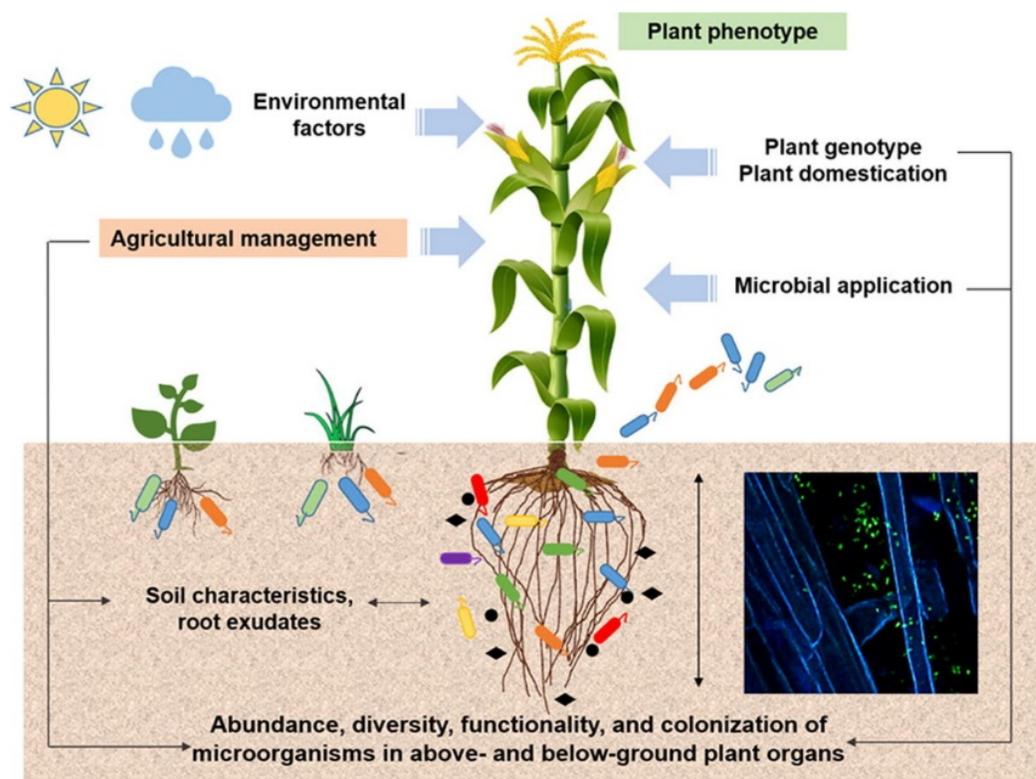


Figure 8. The crop-associated microbiome, which promotes plant health and nutrient availability, is impacted by environmental conditions and agriculture practice. Figure from Compant et al. 2019.

pathogens (Savary et al. 2019; Pollak and Cordero 2020). The plant microbiome consists of microbes found in and on the plant's leaves, flowers, seeds, roots, and soil in the immediate vicinity of the roots (Figure 8) (Turner et al. 2013). Many of the plant microbiome's benefits arise from microbes in the roots and soil microbes associated with the root, called the rhizosphere. Root exudates provide nutrients for bacteria, fungi, algae, and protozoa that comprise the root microbiome, or "rhizobiome" (Vukanti et al. 2020). In return, these microbes supply nutrients to the plant. For example, symbiotic fungi of the Glomeromycota phylum enhance water and nutrient exchange in the roots via their hyphae, and many *Rhizobium* spp. colonize root cells of some plants of the legume family where they fix nitrogen that is used by the plant (Hause and Fester 2004). Because of the nutrient and carbon turnover by the rhizobiome, it presents a vital component of Earth's biogeochemical cycling. Thus, research about plant, soil, and rhizobiome dynamics should be included in Earth climate models for better predictions on climate change and carbon cycling (Philippot et al. 2008).

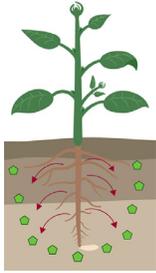
Climate change-induced warming and severe storms help expand the geographical and temporal range of plant pathogens (Anderson et al. 2004). For example, global warming allows persistence of crop pathogens that usually die off during times of frost. Increased diseases of crops are projected to cause food insecurity issues (Fisher et al. 2012). Fortunately, the plant microbiome provides multiple defenses against infections (Hacquard et al. 2017). These microbial communities secrete antibiotics and compete for essential nutrients, thus preventing pathogen colonization (van Elsas et al. 2012; Wei et al. 2015; Gu et al. 2020). Interestingly, rhizobiome communities in "consortia" can exert greater overall disease suppression in plants than a

single microbial species, highlighting the importance of investigating the community diversity and structure of rhizosphere microbiomes (Mendes et al. 2011). Plant microbes also help induce plant hormones (called **phytohormones**) that induce a plant's immunity to pathogens and abiotic factors (Gray 2004). Phytohormones regulate plant growth, development, stress tolerance, and plant-plant and plant-microbe interactions (Miransari et al. 2012; Verma et al. 2016; Gill et al. 2016). Altered plant microbiomes or increased environmental abiotic stress because of climate change can affect the levels of phytohormones, which, in turn, could impact crop yield and pathogen resistance. Thus, the rhizobiome is an important mediator of crop health, but how climate change will impact local rhizobiome structure and diversity is less understood. Studies to elucidate the mechanisms that drive soil and rhizobiome microbial communities in diverse regions are needed to inform models and predict shifts in microbial dynamics that can impact crop production (Li et al. 2018).

Fluctuations in temperature, precipitation, and salinity may change soil's carbon sequestration abilities and physical properties, which may have ramifications for farming and land use practices. Research is needed to understand how climate change and the microbiomes of soil and plants influence soil functions, such as carbon sequestration or water-holding capacity, which can have a drastic impact on soil productivity and greenhouse gas production (National Academies of Sciences, Engineering, and Medicine 2021). For example, application of nitrogen-rich fertilizer followed by heavy rain and elevated temperatures promotes microbial denitrification that generates N_2O gas, and excess fertilizer use leads to nonlinear increases in N_2O emissions from agricultural soils (Saha et al. 2016; Shcherbak et al. 2014). Because environmental,



Microorganisms greatly impact food production and safety



As the global population increases, the world will need sustainable and resilient methods to increase the food supply

microbial, and human activities are all interconnected (Figure 8), integration of data about agroecology, microbiology, climate, and land management is necessary to understand microbial dynamics, which, in turn, will impact soil production and greenhouse gas generation and inform future land use policies (Harkes et al. 2020).

As the global population increases, the world will need sustainable and resilient methods to increase the food supply. Decreased agricultural lands and crop yields result from temperature changes, flooding, or drought induced by climate change (El-Beltagy and Madkour 2012; Egamberdieva et al. 2017). Urbanization has also reduced available farmland. Exploiting plant-microbe interactions can support food security. Since plant-associated microbes play an essential role in plant health, these microbes can

improve crop yield. Microbe-based innovations are one way microbes can help lessen climate change-induced food insecurity issues.

Besides issues with producing food, climate change negatively impacts food safety and security during the transportation from farm to table (Figure 9). Globalization allows food to travel farther around the planet, which also increases opportunities for contamination, rotting, and the transport of agricultural pests and pathogenic microbes. Increased warming can allow for outbreaks of pathogens or toxins in the food supply (Tirado et al. 2010; Liu et al. 2013). For example, fungi produce **mycotoxins** that contaminate human and animal feed stocks postharvest (see mycotoxin case study) (Tefera 2014; Kumar et al. 2017). Warming creates optimum temperatures (~33°C) for mycotoxin

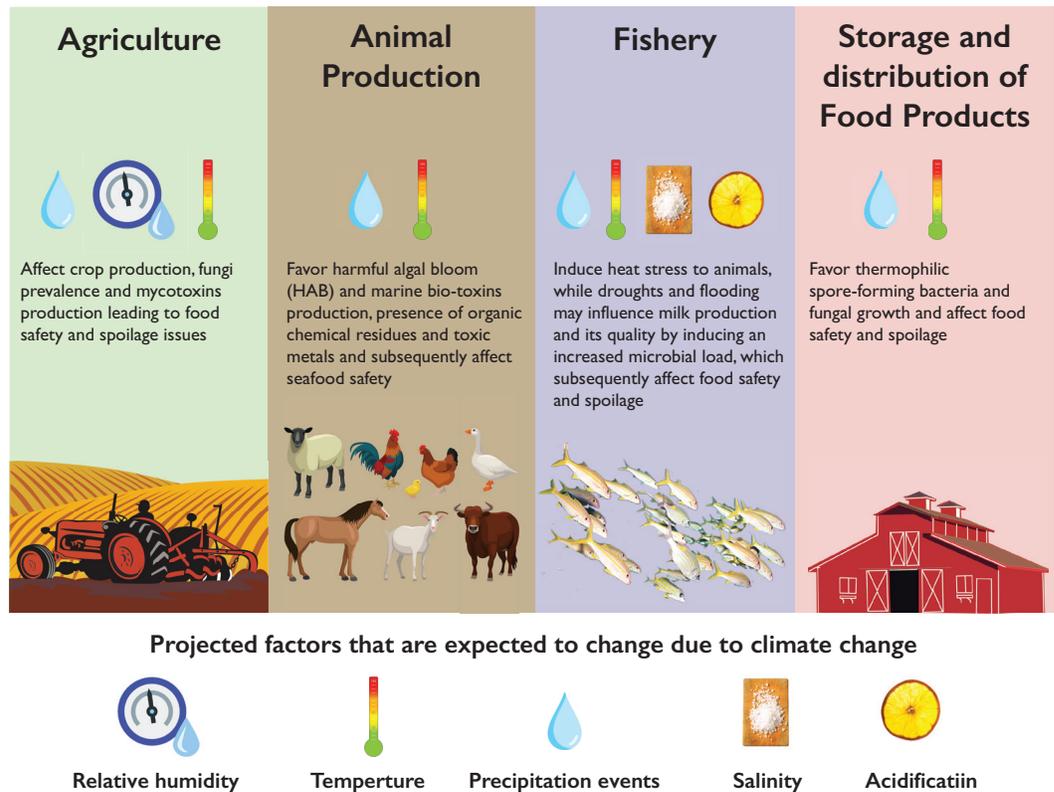


Figure 9. Climate change's projected changes to the environment (bottom) will impact microbes that affect food safety and security. Altered precipitation and humidity create conditions for more crop diseases and algal blooms that decrease agricultural and livestock production. Warmer temperatures enhance outbreaks of pathogens and fungal toxins that can contaminate human and animal feed stocks postharvest.

production in temperate parts of the world (Paterson and Lima 2010). Because fresh foods like fruits and vegetables are prone to contamination and rot, there may be a shift to a diet with more highly processed foods that have a longer shelf life. But highly processed food is known to lead to a less diverse gut microbiome, which is associated with higher rates of obesity, infectious diseases, and mental health issues (Hilmers et al. 2012; Sonnenburg et al. 2016; Aoun et al. 2020; Dietert 2014; Valles-Colomer et al. 2019). Studies have shown that the lower-income communities have a higher exposure to processed food, which makes them more likely to suffer from the above-mentioned adverse health effects (French et al. 2019, Bleiweiss-Sande et al. 2020). Surveillance of stored and in-transit food is needed to track microbial contamination sources and build better food transportation infrastructure. Food storage and transportation strategies that address microbial contamination and microbial innovations, such as a “probiotic spray,” could preserve food for longer times in hotter temperatures. These steps will be critical to provide the global population safe and nutritious food that promotes their well-being and health.

Water and Air Quality

Water is essential for human life. Although water is common in our planet, not all water has equal value. Drinking water must be free of high levels of microbial and chemical contaminants (Prest et al. 2016). Higher temperatures are associated with increased levels of water-borne pathogens and cases of diarrheal disease (see *Vibrio* case study) (Checkley et al. 2000; Tirado et al. 2010). Contaminated drinking water is found more often in minority, immigrant, and low-income communities, which disproportionately negatively impacts their health and water safety (Calderon

Case study:

Mycotoxin contamination of food

Climate change will impact global food security because of increased storms, crop diseases, and food spoilage (Figure 9) (Wheeler and Von Braun 2013). The United Nations predicts that the world population will rise to almost 10 billion people by 2050. To meet the growing nutritional needs of the planet, food preservation after harvest must be considered and optimized, especially in light of climate change’s impacts on temperature and humidity that can increase food spoilage. Maize (corn) is a staple crop across the globe that is prone to contamination with mycotoxins produced by various fungi (Tefera 2014). Since maize is both a human and animal feedstock, human and animal health is at risk with the consumption of contaminated maize (Bennett and Klich 2003; Milićević et al. 2010). Mycotoxin consumption in cattle is associated with abortions and thus economic and food production loss (Still et al. 1971; Kallela and Ettala 1984). As highlighted with cattle, mycotoxin contamination impacts multiple levels of the food chain, further impacting food security. Increased prevalence of mycotoxins is expected as global warming creates optimum temperatures (~33°C) for mycotoxin production in temperate areas of the planet (Paterson and Lima 2010). To preserve global food security, increased surveillance of pathogens and toxins in food will be important for tracking sources of contamination.

1993; Ciesielski et al. 1991). Many pathogens can be transmitted through feces, making sewage and wastewater treatment facilities critical to removing pathogens from drinking water. These treatment plants use microbial and chemical actions to reduce the risk of pathogen exposure and spread of antibiotic resistance genes, but climate change can alter their microbial communities and increase the risk of pathogen growth and spread (Kusnetsov et al. 2010; Caicedo et al. 2020). Wastewater treatment is also susceptible to climate change’s impact on natural disasters and precipitation levels. Sewage systems are prone to microbiologically influenced corrosion and damage from storms (Davis et al. 1998; Okabe et al. 2007). Increased rainfall and flooding create sewer overflows, amplifying possible human exposure to pathogens and contaminated drinking water (Zouboulis and Tolkou 2015; Singh

Case study:
Water safety disrupted by algal blooms

Freshwater environments like lakes, rivers, ponds, and streams are sources for agricultural, domestic, and recreational activities. Drinking water comes from freshwater, which is in limited supply and vulnerable to the effects of climate change (Woodward et al. 2010). Global warming and increased precipitation levels lead to a rise in overgrowth of cyanobacteria in freshwater environments (Paerl et al. 2014). These algal blooms occur when rainwater carries nutrients from farms and urban lands into lakes and rivers, resulting in nutrient increases leading to eutrophication (Dolman et al. 2012; Harke et al. 2016; Glibert 2020). Excess nitrogen and phosphorus levels promote cyanobacterial blooms that cover the water's surface, blocking oxygen-producing photosynthesis of marine plants below and reducing the overall aquatic biodiversity (Figure 10) (Lewis et al. 2011; Chaffin et al. 2013; Wilhelm et al. 2020). Some algal blooms release toxins as well, making the water unsafe for drinking or recreation (Paerl et al. 2014; Janssen 2019). Land use strategies must take into account climate, environmental, and microbial factors to promote human and animal health and water safety.

Water quality is also important for marine life and terrestrial life that are sources of human food (Figure 9). Contaminated irrigation systems, flooding, and runoff from manure and sewage have been associated with vegetables and fruit carrying pathogens, such as *Escherichia coli* O157:H7 and *Salmonella* spp. (Erickson et al. 2010; Beatty et al. 2004; Wendel et al. 2009; Liu et al. 2013). Ocean warming increases the risk for viruses and parasitic diseases in natural marine farming settings, such as for caged salmon. Shellfish is a common source of vibriosis. Warmer waters, salinity changes, and rising sea levels due to climate change are associated with increased *Vibrio* infections (see *Vibrio* case study) (Lipp et al. 2002). Algal blooms can also affect water quality for aquatic life (Figure 10) (see algal bloom case study). Eutrophication resulting from agricultural pollution and urbanization promotes cyanobacterial overgrowth and decreased oxygen levels; affected areas are called "dead zones" (Harke et al. 2016; Glibert 2020). This causes fish death that impacts the food supply and the local aquatic ecosystem. Investigating the relationship between



Water quality is also important for marine and terrestrial life that are sources of human food

and Tiwari 2019). Incentivizing establishment of resilient and sustainable wastewater treatment facilities that take into account local factors (e.g., use of salt water treatment systems in coastal communities) will be important for promoting human health and welfare (Verstraete et al. 2022).



Figure 10. Example of an algal bloom that covers the water's surface, polluting drinking water and preventing recreation activities. Image credit NOAA.

the local environment, microbial communities, and resource management can inform water safety policies.

Cyanobacteria also produce toxins that harm human health, impacting water safety and recreation (Wilhelm et al. 2020). Volatile toxins, as well as microbial cells, can travel by air, enlarging their spatial range (Tesson et al. 2015). Atmospheric dispersion modeling suggests that aerosolized *Legionella* bacteria originating in wastewater treatment plants are associated with cases of Legionnaires' disease in the Netherlands (Kusnetsov et al. 2010; Vermeulen et al. 2021). The

transmission of airborne respiratory pathogens such as influenza virus or SARS-CoV-2 is influenced by humidity levels that can be impacted by climate change (Yang and Marr 2012; Marr et al. 2019). As air currents change and storms become more severe, mobilization of microbes, spores, and their toxins may rise, introducing these microorganisms into new environments and increasing human exposure. Airborne surveillance for pathogens will provide real-time monitoring of air quality, and these data could be integrated into public health and environment management models to inform policies.

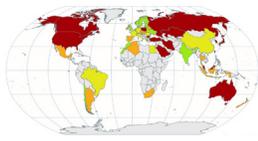
Microbes and Human Well-being Summary and Recommendations

Climate change will affect humanity's quality of life. As the global population surges, food insecurity and water safety will be looming problems exaggerated by a changing climate. Increased environmental stress and natural disasters like flooding, droughts, and severe storms can alter local microbial communities and lead to additional cascading effects on food production and water quality. The colloquium participants urged improved communication strategies to explain how microbes can impact human welfare in terms the general public can relate to and appreciate. They also highlighted interdisciplinary and coordinated research and microbe-based innovation aims that will promote human well-being.

- Study the interconnectedness of human and microbial activities, climate, and land use and integrate these data in a way to inform future environmental management and urban planning strategies.

- Explore the microbial community dynamics and nutrient cycling of the crop-associated microbiome and mechanisms to use plant-microbe interactions to support food security. This research will inform agricultural, public health, and land use models and policies.
- Increase air and wastewater microbial surveillance data systems for air, water, and food supplies to track possible pathogens in real time and provide data to inform public health planning and strategies.
- Develop sustainable agricultural and wastewater innovations and policies that utilize microbial communities to provide resilience to climate change.
- Improve science communication engagement to inform the public about possible risks from microbes in an easy-to-understand way and make them aware of microbes' role in their health and well-being.

Microbes in Models And Data Systems



Climate models are important for predicting changes in long-term patterns of temperature, precipitation, and frequency and severity of storm events, both locally and globally

Ten years ago, climate scientists and microbiologists participated in the “Incorporating Microbial Processes Into Climate Models” colloquium to improve coordination between climate science and microbiology. While much work has been accomplished with climate models factoring in microbial activities, the paucity of mention of microbes in the recent IPCC report reveals that more work is needed to connect these two fields. Research studies, tools, and data systems are needed to understand the dynamics of microbial nutrient cycling and community structure in response to climate change. Incorporating microbial activities into Earth climate models can aid in predicting storms, agricultural yields, and infectious diseases that will help public health and policy makers to plan for and outline policies that promote human well-being for all.

Incorporating Microbes into Earth System Climate Models

Climate models are important for predicting changes in long-term patterns of temperature, precipitation, and frequency and severity of storm events, both locally and globally. Earth system climate models take into account the interactions of the atmosphere, land surface, oceans, and sea ice (<https://www.gfdl.noaa.gov/climate-modeling/>). These models are important for predicting changes to the land, oceans, and climate that impact weather and storm conditions in short and long timescales. Though

current models have improved greatly in the last 50 years, incorporating more information about microbial processes and dynamics, such as production and consumption of greenhouse gases, can improve model performance (Wieder et al. 2015; Guo et al. 2020; Gao et al. 2020; Wang et al. 2021). Unfortunately, most current Earth system climate models still have very limited explicit representation of microbial processes that affect carbon and nitrogen cycling in terrestrial and aquatic ecosystems.

Incorporating microbial activities into Earth system climate models is not simple. Microbes transform vast quantities of carbon, nitrogen, and phosphorus each year, and some aspects of microbial populations and their activities appear to be stochastic (Gougoulias et al. 2014; Todd-Brown et al. 2013; Davidson et al. 2014). Scaling microbial actions and outputs from lab or field experiments to a planetary scale for modeling is difficult. Climate change is expected to alter patterns of microbial activity in myriad ways, adding additional layers of complexity and unpredictability. As microbial communities transition and adapt to new temperatures, humidity, etc., understanding changes to microbial community dynamics and nutrient feedback loops and predicting emergent properties of altered communities will be key to improving models. Currently, the lack of reliable time series data about microbial communities and the kinetics of microbial processes to parameterize

models presents a large challenge. Specifically, data about subsurface and deep-ocean microorganisms (like the viral shunt [Figure 4]) are needed, as well as research about how microbial communities adapt to regional and local climate changes. Research investigating how microbial genetic and functional diversity changes over time and how that drives community structure and emerging functions can help inform models (see modeling case study) (Figure 11).

Besides microbes' direct roles (respiration, organic matter production, and nutrient cycling), models should also incorporate compound impacts from feedback loops and microbial interactions with the terrestrial, urban, and aquatic environments. For example, microbes' interactions with plants impact overall production and growth, which, in turn, affect carbon sequestration by plants and the soil

(Philippot et al. 2008; National Academies of Sciences, Engineering, and Medicine 2021). Modeling of carbon, nitrogen, and phosphorus and their interactions is key to predicting the future of climate change, not only because of direct microbial emissions of greenhouse gases like CO₂, CH₄, and N₂O but also because making projections of global carbon and nitrogen cycling with climate change is vital for understanding feedbacks to climate change (Davidson and Janssens 2006; Friedlingstein et al. 2019; Tian et al. 2020). Thus, direct and indirect microbial roles on carbon fluxes in ocean and terrestrial environments may have large influences on the net flux of CO₂ and other greenhouse gases.

While models will not change the future, skillful use of models can aid in preservation of life and economic interests. For example, precise hurricane modeling cannot prevent hurri-

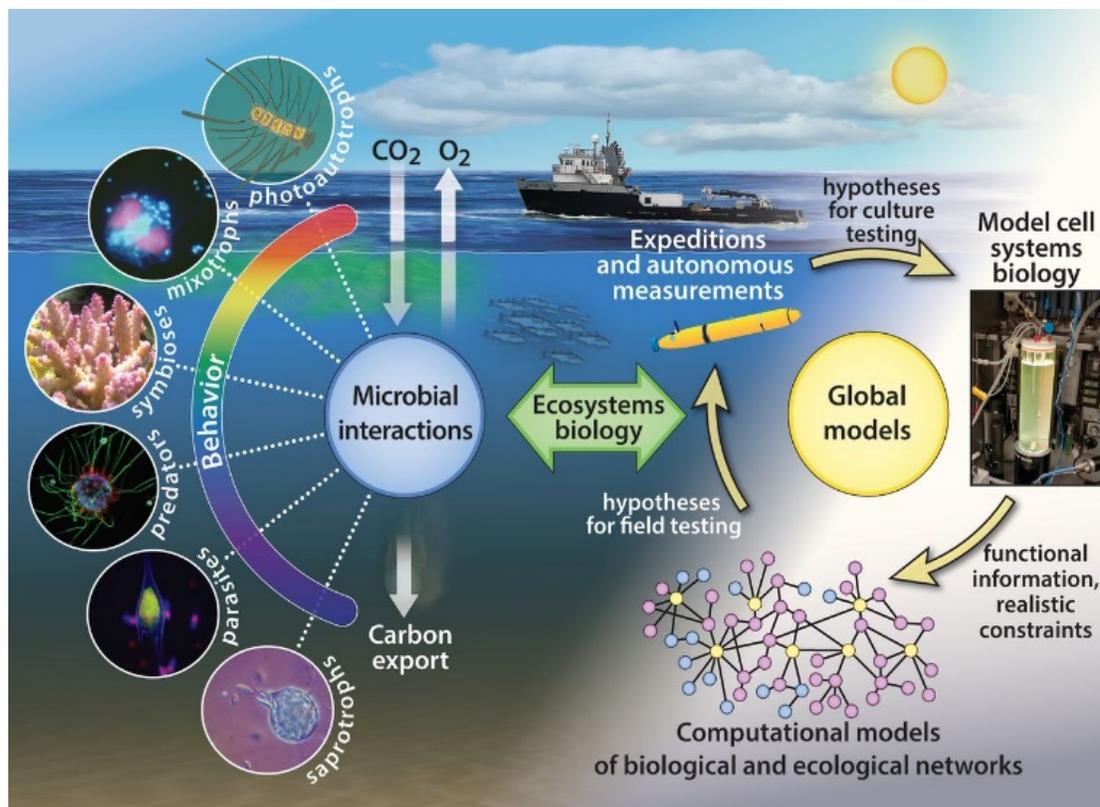


Figure 11. Microbial activities and interactions can be parametrized for computational Earth system models to help understand global carbon cycling. Figure from Worden et al. 2015.

Case study: Modeling microbial emissions

Modeling of carbon emissions helps inform climate change predictions that guide public health and land use policies (Friedlingstein et al. 2019). Humid tropical forests, for example, emit significant amounts of CO₂, CH₄, and N₂O, impacting terrestrial carbon and nitrogen sinks (Bonan 2008; Spahni et al. 2011; Davidson et al. 2012). The topography, temperature, rainfall, and drought along with microbial and plant interactions all impact overall carbon and nutrient fluxes of these environments (O'Connell et al. 2018). Additionally, climate change is predicted to alter precipitation frequencies, which are expected to impact carbon cycling, especially of CH₄ (Neelin et al. 2006; Chadwick et al. 2015; Corlett 2016). Because of these factors, predictions of CH₄ emissions from these tropical forests and wetlands under various environmental conditions are important to factor into the global CH₄ budget (Saunois et al. 2020). Applying the microbial model for methane dynamics-dual Arrhenius and Michaelis-Menten (M3D-DAMM), which includes a microbial methane functional group model, Sihi et al. found that parameters of soil methanogen population growth, death, and efficiencies were ranked the most important for model performance of CH₄ emission from a tropical forest soil (Sihi et al. 2021). Similarly, Song et al. explored the use of various omics data to model microbial communities, gene expression, and enzymatic activity related to biogeochemical cycling of tropical forest soil organic matter (Song et al. 2021). In addition, incorporating microbial functional gene traits data into an ecosystem model significantly reduced parameter uncertainties and improved model prediction of soil microbial respiration in response to climate warming and elevated CO₂ and nitrogen deposition (Guo et al. 2020; Gao et al. 2020b; Wang et al. 2021). These recent examples demonstrate the potential for how integration of microbial dynamics and functions into biogeochemical models could enhance the utility of Earth system models that project feedbacks of the biosphere to climate change.

canes from happening but can allow more time for storm preparation and evacuations that save lives (Bauer et al. 2015). New ways of using models should also be considered. Integrating information about climate modeling with that of the spatial and temporal range of pathogens and vector species can influence health policies and urban planning, which is especially important for vulnerable communities who experience disproportionately high microbial exposure (Semenza et al. 2017; Ishaq et al. 2019). Improved coordination between climate scien-

tists and microbiologists will aid in establishing models that help improve human well-being.

Data Infrastructure and Systems

Improved data systems and infrastructure of microbiology research are needed to improve Earth system climate models. Additional research about microbial communities and their dynamics as climate changes is important for models and will be most useful when represented in a tractable number of parameterizable equations within a coherent numerical model structure (Davidson et al. 2014). Additionally, scaling of microbial processes from controlled experiments to climate models must be considered. Thus, microbiological data must be compatible with climate modeling input and software needs and vice versa (Figure 11).

Enhanced data coordination is also important for integrating microbial processes into models. While individual research groups ("bottom level") and national databases ("top level") each have well-organized data management strategies, improved data coordination between the top level and bottom level is necessary for broad data utilization. Data coordination across fields is needed as well. Systemic coordination among microbiologists, geochemists, ecologists, computational scientists, and modelers will be necessary to build consensus on research and data collection protocols that allow appropriate data interpretation and parameterization of models. While omics technologies are powerful, they must be employed in an effective way in which data can be shared and utilized by other groups. This continuity of research design and data type should also enable data comparison across diverse ecosystems and microbial communities while also taking into account local factors. Agencies must

dedicate funding to building and maintaining these data systems. The Darwin Project represents a model for integrating data about the physiology of marine microorganisms and community structure with environmental data in models to understand marine ecosystem dynamics. These models specifically examine the role of plankton diversity and biogeography in regard to climate change and nitrogen fixation, helping inform predictions about future ocean changes and global nutrient cycling (Anderson et al. 2021).

In addition to Earth climate models, infectious disease models can benefit from improved data coordination to allow for integration of real-time air and water surveillance data. For example, the *Vibrio* Map Viewer utilizes real-time information about sea surface temperature and salinity to predict the risk of *Vibrio* infections (see *Vibrio* case study) (Semenza et al. 2017). Modeling can also help researchers understand microbial dynamics. Modeling of coral reefs and crop rhizobiumes can elucidate mechanisms for disease resistance (Vega Thurber et

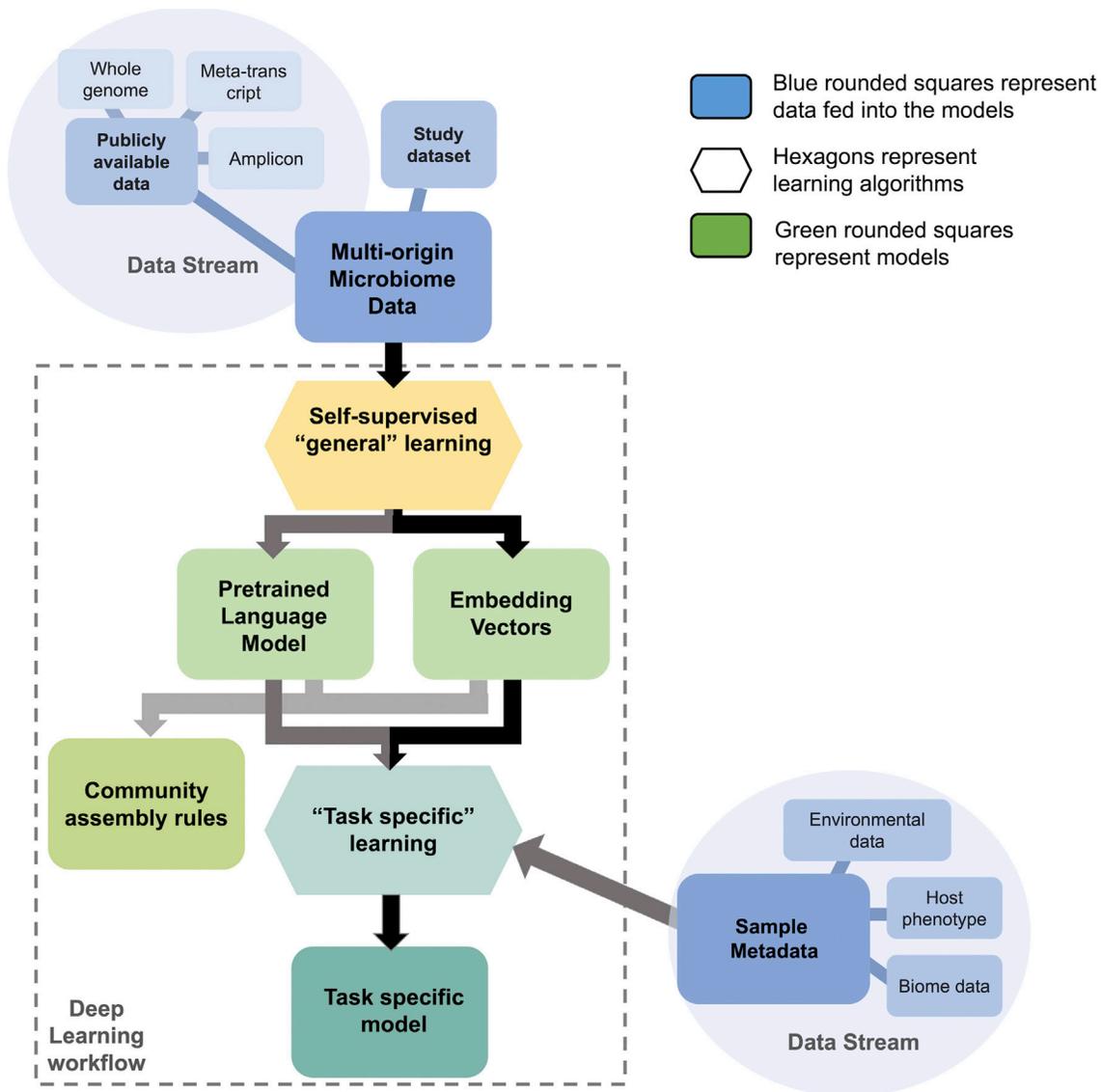


Figure 12. Models (green squares) and machine learning (hexagons) can process complex data sets (blue squares) to help identify microbial dynamics. Figure from David et al. 2022.

al. 2020). Thus, investments in data infrastructure and artificial intelligence deep-learning applications, such as machine learning and statistical learning, to integrate with modeling will assist to inform climate models and advance research promoting human and environmental health (Figure 12) (David et al. 2022). As the link between microbes and health becomes better appreciated by the public, data coordination may help scientists synthesize the data and establish microbi-

al metrics (e.g., bacterial loads in parts per billion in the air or water) that convey health risks and changes induced by climate change. These metrics should act as climate change indicators that help scientists communicate to the public the relationship between microbes and human health as well as the urgency of climate change. Simple, easy-to-understand metrics can improve microbiologists' relationship with the public and empower it to take action on climate change.

Microbes in Models and Data Systems Summary and Recommendations

Models allow scientists to test their understanding of systems through mathematical representations of interacting physical, chemical, and biological processes and then compare model simulations with relevant empirical observations. Once validated with observations, models can also be projected to estimate the possible outcomes of future scenarios, such as climate change. Predicting how the planet's climate will change over the next decades has important implications for the world's food supply, built environment, health, and economy. Including microbial processes and data on distributions of functional microbial communities into Earth climate models may enable better predictions. Unfortunately, knowledge gaps about microbial functions, species diversity, and adaptive emergent properties limit current models. Coordination of data among various research fields about diverse microbial communities will improve modeling and predictions about microbial impacts on climate change and human well-being. Throughout the discussion, the participants made recommendations about research studies, tools, and data systems needed to parameterize climate models with microbial data.

- Coordinate guidance on experimental design, data collection, and research protocols to study microbial communities that allows for data comparison over time and across diverse ecosystems and microbial communities.
- Investigate kinetics, functions, and dynamics of microbial communities, especially of understudied environments like subsurface soil and deep ocean, as they transition and adapt to changing climates.
- Invest in and update data systems across federal science agencies and improve infrastructure to make data sharing and interpretation easier across scientific fields as well as between public and private stakeholders.
- Utilize data about microbes' direct and indirect roles in their local environments on nutrient fluxes (e.g., carbon and nitrogen) for models to inform land management and public health policies and preparation.

Microbes and the Bioeconomy

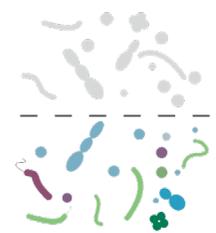
Microbes are important aspects of human health, well-being, and the biogeochemical cycles on Earth. Microbes impact human daily activities in myriad ways each day. And for centuries, humans have exploited microbes and their activities for human gain. Fermented drinks such as beer and wine were first introduced over 13,000 years ago (Liu et al. 2018). Since then, humans have used microbes to clean up chemical pollutants, cure illnesses, produce energy, and much more (FAQ: microbes and oil spills; Ainsworth 2020; Tiedje and Donohue 2008). With the looming threat of climate change, the critical question that was explored at the colloquium was whether microbes can provide effective market solutions to help contain climate change, which is an important step to building a more sustainable and resilient future.

Barriers to Innovation

While microbes provide promising solutions to climate change, there are multiple barriers for taking bench science to the market. Between costs, timing, and regulatory policies, it is a mammoth task to have an idea go from discovery to market and provide sufficient return on investment. As the participants noted, the “current system is not incentivized for innovation.” A common barrier to innovation is the lack of alignment between academic and industrial expectations. Natural-product and synthetic-biology discovery takes time. However, the time frame and return-on-investment expectations by companies may feel unrealistic to scientists who do not understand the complexities involved

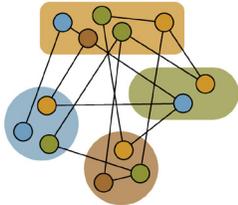
in production and regulation. Opportunity costs or high risk of investments prevent companies from doing basic research and development, such as would be required for novel antibiotic discovery. Thus, basic and foundational research mainly occurs in academia, requiring a transition to the private sector. Academic offices that inform scientists of the product development and technology transfer process as well as market needs can help academic researchers design their studies with well-defined applications early in the research project. However, many technology transfer offices are not fully equipped to support the formation of spin-out companies, seed round fundraising, and associated legal, financial, and organizational challenges. In addition to the market requirements, specific criteria and frameworks for evaluating new innovations for their scientific, financial, and societal impacts need to be established to help researcher-entrepreneurs evaluate their ideas holistically and decide on future directions. Many innovations will not meet all these criteria. Arguably, the emphasis should be placed on the climate solutions that can deliver equitable and sustainable social impacts.

National funding agencies are well placed to identify market needs as well as formulate priorities for research proposals that encourage basic research with unknown eventual impacts and solutions. For example, in the United Kingdom, Innovate U.K. is a government agency that connects researchers and companies to “de-risk, enable and support innovation.” This single organization helps scientists



Microbes are important aspects of human health, well-being, and the biogeochemical cycles on Earth

maneuver the regulatory and industry hurdles and bring innovations to market. Besides funding agencies, university technology transfer offices, scientific societies, state and local agencies, and technology transfer communities can also help bridge the gap between academia and industry as well as advocate for less burdensome regulatory policies. Many times these resources and partners are underutilized and undervalued by the academic community. Thus, it starts with awareness and requires intentional follow-through to build partnerships that deliver impacts beyond the scientific community.



Communication among diverse disciplines and stakeholders is another common hurdle

Communication among diverse disciplines and stakeholders is another common hurdle. Many times scientists lack the training and/or language skills to communicate across fields or industries or with policy makers, product developers, and the general public. Those outside the sciences may not have the biology or engineering foundation to connect how science can be translated into innovations. General education must include both macro- and microbiology concepts to help students, who are the future workforce, to understand the interrelatedness of the two. For scientists, science communication education that incorporates scientific, social, economic, and physiological factors when discussing scientific facts needs to be integrated into graduate training (Kappel and Holmen 2019). Communication involves listening as well as speaking and responding to the other's needs. Thus, scientists should engage in equitable exchanges with the communities that they aim to serve in order to understand the communities' requests and interests that science can help meet and then cocreate research activities and knowledge around the goals of the communities (Harris et al. 2021).

Another hurdle is the lack of diversity in the research community, which

leads to important research topics not being explored (Bernard and Cooperdock 2018). For example, research about the vulnerability of communities of color to climate change and disease may not be instigated or funded because of lack of visibility and inclusion in academia to champion these topics (Robinson et al. 2022). The questions posed by science will become more diverse and more relevant to underserved communities as the scientists themselves become more diverse. Innovations and processes that prioritize equity are necessary. Since climate change is an overarching threat for all of humanity, scientists must make every effort to actively include diverse perspectives and insights when working to address this crisis.

Additional investment in training and encouraging scientists to explore careers in science policy and regulatory agencies should be implemented, allowing scientists who understand the scientific process to be in a position to make judgments about appropriate product regulations. While many scientists think "only facts" should matter, the reality is that policies are shaped by much more. As stated by Dr. Gary Machlis, "science-informed policy stands on three legs: best available science; accurate fidelity to law; and long-term public interest." Projects like Long Term Ecological Research (LTER), funded by the National Science Foundation, could provide a model for building public trust. LTER analyzes ecological data and engages and communicates with the community and policymakers about the science to inform policies and fund innovations. In building a viable **bioeconomy**, earning the public's trust and cooperation must first be considered; otherwise, investments in innovations will be lacking (Rogers 2003).

Regulations present a tremendous hurdle when moving innovations from

Bioeconomy: bio-based economy where products, services, and processes are derived from biological resources

the bench to the market. Products for human consumption, like probiotics and fecal-transplant microbiomes, have strict safety regulations but lack clarity around toxicology requirements. Worries about synthetic biology and genetically altered organisms hinder large-scale experiments that would help inform models or spur innovation. Additionally, different countries have different regulations, which hinder the globalization of innovations. To remove barriers to innovation, regulatory agencies working with scientists and other stakeholders should audit and establish dynamic regulations that stimulate novel innovations while still ensuring the safe deployment of synthetic biology.

Other specific hurdles are based on product types and capabilities of current model organisms (Sherkow 2017). Though microbes are diverse, the number of species used as model organisms is small in comparison. To expand possible microbial innovations, more research is needed to study and engineer new microbes beyond the typical model organisms. Many times consortia of microbes are needed to produce a wanted product, but current U.S. policies do not allow for patents of naturally occurring microbial communities. Instead, these policies encourage the use of pure cultures, which limits understanding of microbial dynamics and discovering novel functions seen only in consortia, as observed in rhizobiome communities for enhanced disease suppression (Mendes et al. 2011). Policies and research guidance on how to work with consortia will be critical to produce more complex products, and regulation of microbial processes and products should be more global in scope to encourage scientists to think about their innovations on a global scale.

Achieving commercial scale with biological systems is a common scientific hurdle to overcome. Because biology

and life constantly change, predicting how living organisms and microbial processes will scale from the bench to a reactor to the field is a challenge. Research, data coordination, and modeling can help overcome this challenge. For example, academic synthetic-biology projects that involve working with, making, or changing an organism in the laboratory often do not scale up to the commercial level. To ensure the potential for scale, early collaboration, communication, and **process engineering** with the producers of the end product must occur. Wastewater treatment facilities may provide insight into how to leverage and scale microbial communities (Daims et al. 2006). Sewage treatment relies on aerobic and anaerobic microbial metabolic activities to degrade waste and provide clean water (Wagner et al. 2002; Ofițeru et al. 2010). Civil and environmental engineers learned how to treat enormous volumes of wastewater each day with only basic information about microbial functions. This model could inform synthetic-biology and natural-product development. Studying these systems can also elucidate gene-to-function relationships in microbial communities and their impact on microbial dynamics and kinetics (Ferreraa and Sánchez 2016).

Microbe-Based Circular Economy

Building a sustainable and resilient bioeconomy involves a mindset change. Products should be “designed for disassembly” in a circular economy (Figure 13). A circular economy involves reducing waste through “restorative or regenerative” design processes that allow for resource recovery and further utilization (Save Our Seas Act 2020). In a circular economy, waste is seen as a feedstock for another product (Scarborough et al. 2018). This mindset very much mimics that of microorganisms, which survive by consuming other organisms’ waste.



Regulations present a tremendous hurdle when moving innovations for the bench to the market

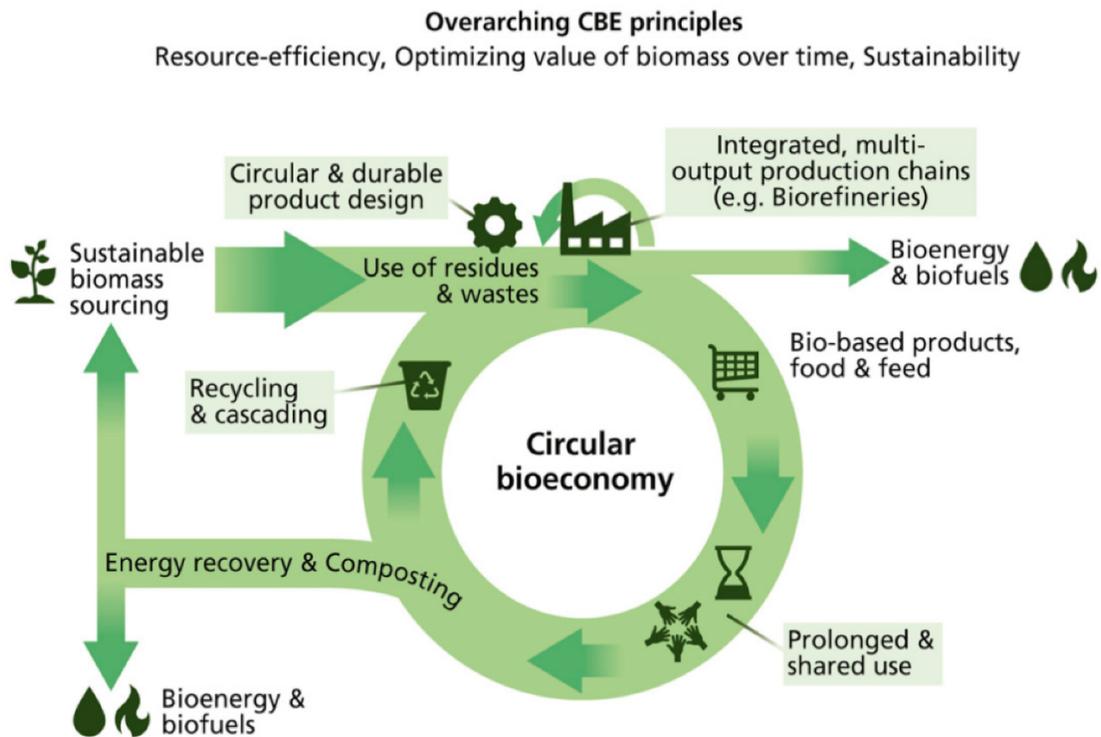


Figure 13. In a circular bioeconomy (CBE), waste products and inputs are recovered, recycled, and re-used to produce goods sustainably from biological sources. Figure modified from Stegmann et al. 2020.

When designing products, the alternative uses of “waste” should be considered as well as the scale of producing that waste.

As mentioned earlier, wastewater treatment facilities offer scientists in concert with engineers and entrepreneurs a current example about how to use microbial communities and their wastes to serve multiple purposes that benefit human, animal, and environmental health (Figure 14). These microbial communities produce vast amounts of greenhouse gases that can be leveraged for renewable energy sources. Large amounts of CH₄ can be recovered as a biogas and used as energy (see wastewater treatment energy capture case study) (Daelman et al. 2012; Crone et al. 2016). Nitrogen from wastewater facilities can also be recovered and recycled into microbial biomass, which can be used as a human, animal, or plant feedstock. Microbe-derived slow-release

nitrogen fertilizers could be used instead of the industrial Haber-Bosch process, which is energetically costly and environmentally damaging (Liu et al. 2017). Thus, these microbe-driven energy sources can provide a greener and more sustainable alternative to fossil fuels. The scale of possible energy production from these treatment systems should also be considered as well as the initial need to provide treated water. In light of these options, research about the dynamics and metabolic activities of wastewater treatment facilities can have important impacts on renewable energy and waste recovery innovations (Ferreraa and Sánchez 2016).

As highlighted by the wastewater treatment example, microorganisms must be considered as *material with a cost*, so that they are taken into account and valued. Addition of new microbes into large reactors becomes costly. Product development around

materials to “hold” microbes and biofilms or to embed them in a synthetic material to improve their retention in reactors will cut microbe-associated costs and make processes more sustainable (Qureshi et al. 2005). Enhanced microbial retention will require interdisciplinary work from microbiologists, engineers, and material scientists. These products also reduce safety worries about microbial contamination of products, which may increase the public’s willingness to embrace these products. Expanding training and increasing the diversity of problem solvers and innovators around microbial processes also will expand the breadth of possible solutions.

**Case study:
Energy capture from wastewater treatment microbes**

Freshwater for human consumption and use is limited; thus, wastewater treatment facilities that remove pollutants and contaminants are vital for replenishing the available water supply. Aerobic and anaerobic microorganisms are critical components of these facilities, removing nitrogen, phosphorus, and organic components (Daims et al. 2006). The process of cleaning wastewater is energy-intensive, and wastewater treatment microbes can produce the greenhouse gases CO₂ and CH₄, which contribute to climate change (Daelman et al. 2012; Verstraete et al. 2022). Efforts to recapture greenhouse gas waste and produce energy from wastewater treatment employ microbial communities in current efforts to build a circular and sustainable bioeconomy (Figure 14) (McCarty et al. 2011; Puyol et al. 2017; Antoniou et al. 2019). CH₄ gas produced by anaerobic digestion of sewage can be used as an alternative source of energy (Puyol et al. 2017; Wainaina et al. 2020). It is estimated that ~1 billion kWh of electricity were generated from sewage and industrial treatment plants in the United States in 2020 alone (<https://www.eia.gov/energyexplained/biomass/landfill-gas-and-biogas.php>). Additional research on the functional capabilities of anaerobic bacteria for CH₄ production and technologies for anaerobic codigestion (digestion of multiple substrates) for energy production are important approaches to building a microbe-based circular economy (Mata-Alvarez et al. 2014).

Biogas production as renewable energy source

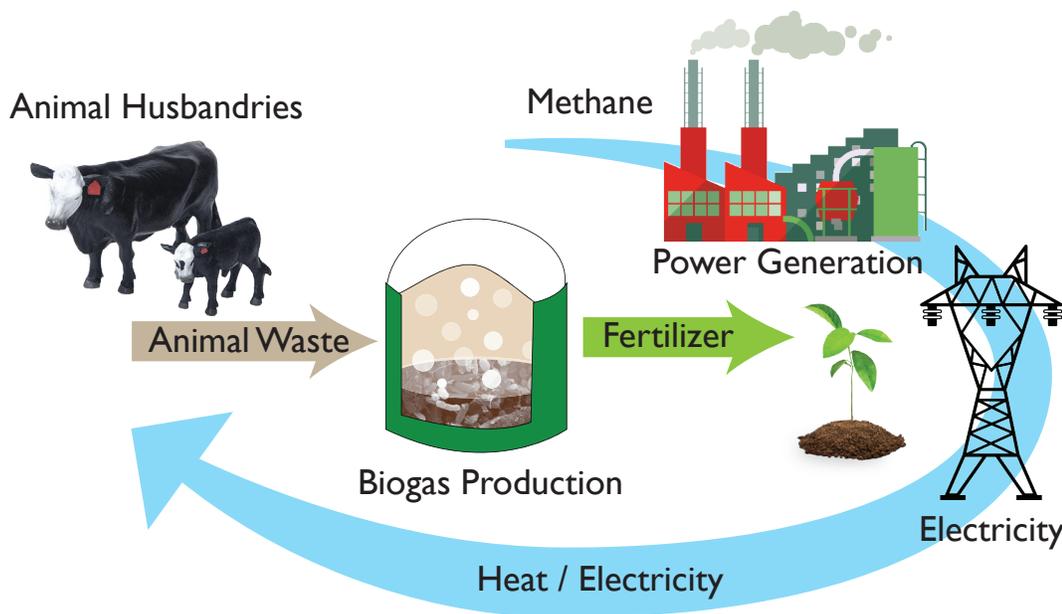


Figure 14. Wastewater treatment microbial communities produce carbon and nitrogen wastes that can be utilized for power generation and agricultural fertilizer to create a circular bioeconomy.

Microbes and the Bioeconomy Summary and Recommendations

In the quest to find solutions for climate change, humans have new opportunities to use microbes to their benefit. Diverse stakeholders from industry, policy, and various fields working together with open communication offer new possibilities to help design a circular and sustainable bioeconomy. Because of current scientific, policy, and cost hurdles that all present barriers for microbial products to move from bench to market, the participants made the following recommendations:

- Incentivize innovation of disassembly to build a circular bioeconomy in which microbial inputs and waste products are valued, recovered, and reutilized.
- Establish specific criteria and frameworks for evaluating new microbe-driven products that allow the scientific community to integrate the scientific and societal impacts of these innovations.
- Create cross-training programs to link microbiology and life sciences to the regulatory, market environment, and industry workforce. These “interdisciplinary” scientists will understand both scientific and business processes to navigate through these challenges more effectively.
- Promote increased diversity among science practitioners and encourage equitable exchanges of ideas and knowledge between scientists and communities seeking solutions to societal problems.
- Request national funding agencies to work together globally to provide clear guidance on market needs and safety regulations for microbial products.
- Leverage scientific societies, trade associations, and federal and state resources to facilitate dialogs and relationships between basic scientists, funding agencies, and industry professionals to build more direct connections between bench science and market needs.



Biogas plant behind maize field

Conclusions

Climate change is an urgent and pressing issue that threatens all life on Earth, from the smallest microbes to human communities. Microorganisms, being the most abundant and diverse organisms on Earth, should thus be considered in models, policies, and innovations to address climate change. To tackle the challenge of determining how to incorporate microbial sciences in current and future climate change initiatives and remediation processes, the American Academy of Microbiology invited participants with diverse expertise and perspectives to outline current barriers, knowledge gaps, and future sectors of research and innovation.

The participants agreed that insufficient research and data are important hindrances to improving predictions about how climate change will impact the planet and people. Besides additional data, the group discussed the possibility that a new way of thinking may be needed to analyze and synthesize the results. Novel ways of approaching science and data may be the essential step in connecting microbes and climate change. Just as calculus was needed to appreciate physics fully, a field of “mathematical biology” may be needed to integrate biological data with new analysis tools, e.g., tools that can resolve problems at different scales of time, space, and complexity. Climate change is a significant threat, and thus, significant changes to scientific thinking and processes (both inside and outside microbiology) will be necessary to confront this threat. One new way of thinking includes finding new ways to incorporate diversity and equity principles

into research aims and experimental design. Microbe-associated injustices resulting from climate change will exacerbate inequities in public health and well-being. Research is needed to outline the microbial, environmental, and societal drivers of these injustices as well as to investigate the impacts of climate change through the lens of equity. Taking a One Health approach that incorporates justice and equity along with microbiology, ecology, and medicine represents an opportunity to further human health and well-being for all (Figure 15).

The participants emphasized that scientists must engage with the general public and vulnerable communities. Collaboration between community leaders and scientists can help amplify the concerns of marginalized groups and incorporate diverse perspectives and insights needed to solve problems. Only by engaging with local communities can scientists align their research goals with the needs and wants of the broader community. The scientific community itself must also become more diverse, so that the questions posed by scientists reflect their diverse cultural backgrounds and concerns. Establishing easy-to-understand metrics about climate change’s impacts on microbes, and, in turn, human health and well-being, can help nonscientists comprehend and conceptualize the impact that climate change has on daily life. Public comprehension can spur action and progress toward reducing greenhouse gas emissions. The group noted that improved science communication by researchers with policymakers and industry will be vital to transition



Climate change is an urgent and pressing issue that threatens all life on Earth, from the smallest microbes to human communities

science from the bench to the market. These innovations should take into account resource recovery, of both microbial inputs and their wastes, as important means to build a sustainable, circular bioeconomy. This coordination of science, policy, and public interest presents opportunities for the general public to engage in science and empowers them to seek out other sustainable climate solutions.

Just as the Academy’s colloquium “Incorporating Microbial Processes Into Climate Models” increased dialogue between microbiologists and climate scientists, hopefully by 2030, the understanding of microbes and climate change will be clearer to the public. This colloquium formed a solid foundation outlining the vast and complex

relationship between climate change and microbes, on which future events and policies can be built. Discussions from the colloquium about the One Health approach to climate change, methane mitigation, microbial diversity, cascading effects, microbe-associated bioenergy, etc., will inspire future Academy colloquia and in-depth discussions (Tiedje et al. 2022). More importantly, the report aims to provide the scientific framework to support actions in policy, education, partnership, communications, etc., to tackle this issue. The report is a strategic step toward the goal of the Academy’s scientific portfolio to integrate microbes in broader scientific discussions and contribute to the global efforts to address climate change.

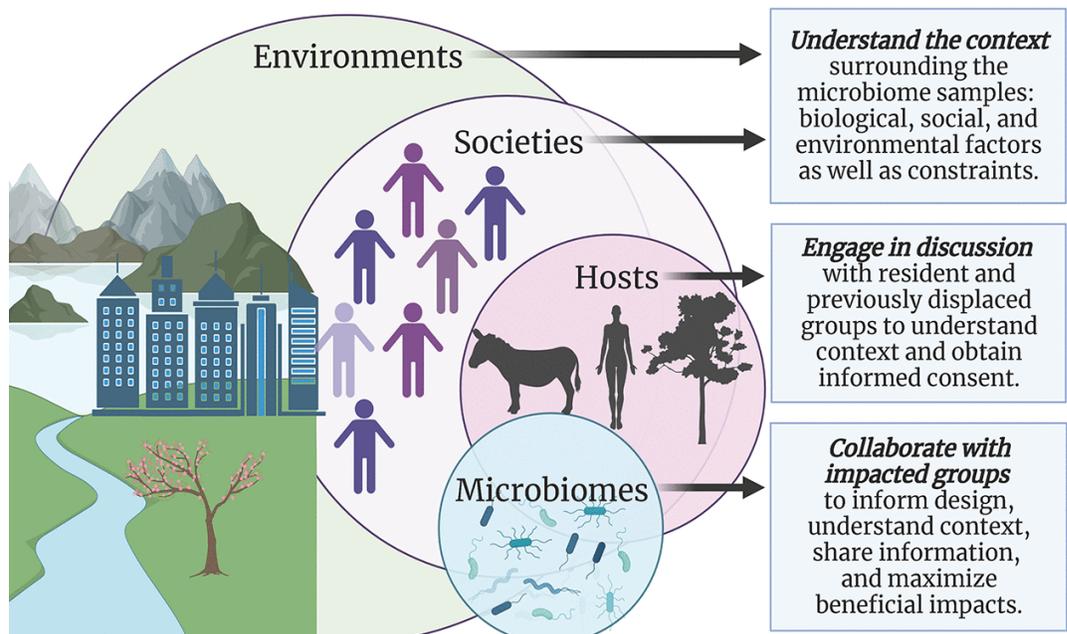


Figure 15. A One Health approach to medicine that integrates animal, environmental, societal, and microbiological data to promote human health equitably. Figure from Robinson et al. 2022.

Major Overall Recommendations for the Future

While microorganisms will undoubtedly be impacted by climate change, their ability to adapt to changing conditions means that they will evolve and become more resilient. Although humans do not have the same capabilities as microbes with regard to physiology, replication rate, and adaptability, we can learn from their example and adapt to our changing environment. More importantly, we also have the consciousness and much of the knowledge and technology needed to avoid the most dangerous scenarios of anthropogenic climate change. Many innovations and novel solutions inside and outside microbiology will be needed to combat climate change. Microbes and their unique capabilities represent an untapped source of innovation and solutions to meet this challenge. All the participants agreed that incorporating microbial sciences into climate change initiatives and remediation processes will help provide a better understanding of and ability to mitigate climate change's future impacts. Over the course of the discussion, the group came to a consensus on several major recommendations for academic, policy, and market partners to drive innovation for microbe-driven climate change solutions that support human and animal well-being.

Research Recommendations

- Emphasize interdisciplinary research aims focused on understanding how microbial activities and metabolic fluxes alter as climate, precipitation, and temperatures change globally. This will be important for terrestrial, urban, and aquatic microbes that impact global elemental cycles as well as for pathogens that impact human and animal health.
- Provide guidance for experimental design and data collection for studying microbial communities that allows for data comparison across diverse and global ecosystems.
- Incorporate existing data about microbial diversity and activity on consuming and producing greenhouse gases into Earth climate models to improve the current and predictive performance of models.
- Outline specific scientific criteria to evaluate new innovations that allow the scientific community to assess the scientific and societal impacts of these innovations.

Policy and Regulation Considerations

- Increase research investments to generate knowledge and awareness of the contribution of microbes to the generation and consumption of greenhouse gases; incorporate these findings into evidence-based policy and regulatory strategies to address climate change.
- Deploy increased surveillance and detection of zoonotic and vector-borne diseases in animals and humans, including through next generation sequencing technologies, and incorporate a One Health approach to addressing climate change's effects on humans, animals, and our environment.
- Enact policies that facilitate public private partnerships between diverse scientists, entrepreneurs and commercial entities, regulatory and policy makers, and other stakeholders to translate research discoveries into scalable microbial innovations.
- Develop policies that incentivize innovation of microbe-facilitated processes to support renewable energy generation and a robust bioeconomy.

Societal Recommendations

- Engage and clearly communicate with the general public in jargon-free and relatable ways to improve comprehension of how microbes participate in the causes and effects of climate change.

- Highlight and prioritize addressing inequities in microbial threats of vulnerable communities at greater risk of infectious disease exposure, altered microbiota, and food insecurity caused by climate change.

Our climate has already changed drastically due to human activity. Fortunately, it is not

too late: human actions can mitigate climate change and its effects. Urgent actions to reduce greenhouse gas emissions and to create innovations that allow us to adapt to climate change's impacts are needed, including by microbiologists (Nguyen and Casadevall 2021). To do so, microorganisms and their activities should be taken into account when developing

Glossary

Algal blooms: proliferation and accumulation of algae in aquatic environments beyond normal seasonal growth

Bioeconomy: biobased economy where products, services, and processes are derived from biological resources

Carbon dioxide (CO₂): greenhouse gas associated with global warming

Cascading effects: unintended or unknown outcomes arising from a change, such as a shift in diversity of a microbial community

Climate change: a long-term change in Earth's, or a specific region's, climate

Coral bleaching: stress mechanism of coral in which they expel their symbiotic algae (zooxanthellae) that provide their color, thereby appearing faded or "bleached"

Cyanobacteria (blue-green algae): photosynthetic bacteria found in aquatic ecosystems

Disaster microbiology: proposed field of study focused on the microbial impacts from severe storms and natural disasters

Dysbiosis: disruption to the microbiota homeostasis

Elemental flows: flux of elements such as carbon, nitrogen, and phosphorus through the environment

Endothermy: ability of an organism to maintain a set temperature

Eutrophication: enrichment of an ecosystem with nutrients

Food insecurity: disruption of food availability or eating habits

Global warming: the increase in Earth's average surface temperature due to rising levels of greenhouse gases

Horizontal gene transfer: passage of genetic material between microorganisms other than by hereditary means

Human microbiome: collection of microorganisms associated with the human body

Marine carbon pump: biologically driven depletion of carbon from air and land to the ocean's interior and seafloor sediments

Methane (CH₄): a greenhouse gas 34 times more potent at absorbing heat in the atmosphere than CO₂ on a 100-year timescale

Methanogenesis: formation of methane by microbes

Methanotrophy: consumption of methane by microbes as a sole carbon and energy source

Microbial injustice: inequitable microbial exposure and risk experienced by disadvantaged communities

research, funding, policies, and innovations to combat climate change. Human health and well-being are intricately linked to the health of the environment, which, in turn, relies on microbial communities to promote the health of terrestrial, urban, and aquatic animals and environments. The colloquium participants all agreed that incorporating microbial sciences

into climate change initiatives and remediation processes will be necessary going forward to confront this significant challenge. By working with microbes, humans can also learn how to adapt to a changing climate and build a healthier, more sustainable, and resilient future.

Microbial loop: process in which dissolved organic carbon is incorporated into microbial biomass to enter higher trophic levels in aquatic ecosystems

Microbial metabolism: all the biochemical reactions that provide microorganisms the energy and nutrients needed to grow and reproduce

Microbiologically influenced corrosion: corrosion resulting from the presence and/or activity of microorganisms

Microbiome: collection of all microorganisms in a location

Mycotoxin: toxin produced by fungi that can negatively impact human and animal health

Nitrous oxide (N₂O): greenhouse gas about 300 times more potent at absorbing heat in the atmosphere than CO₂ on a 100-year timescale

One Health: idea to integrate information about “people, animals, plants, and their shared environment” to inform and promote human health

Permafrost: ground that remains at or below freezing for two consecutive years

Photosynthesis: use of sunlight to synthesize foods from carbon dioxide and water

Phytohormones: chemical regulators of plant growth, development, stress tolerance, and plant-plant and plant-microbe interactions

Porosity: amount of void space

Probiotics: “live microorganisms which when administered in adequate amounts confer a health benefit on the host” as defined by the Food and Agriculture Organization of the United Nations and the WHO

Process engineering: understanding and application of engineering principles and natural laws that ensure transformations of raw material and energy into products at an industrial level

Radiative Forcing: change in energy flux in the atmosphere. Positive values indicate that Earth is receiving more incoming energy from sunlight than it radiates to space, which causes warming.

Symbiotic: mutually beneficial relationship between at least two species

Vector: living organism that transmits an infectious species

Viral shunt: process in which dissolved organic matter in microorganisms is recycled into dissolved organic matter in aquatic ecosystems

Virome: total collection of viruses of a particular ecosystem

Zoonotic disease: infectious disease transmitted from an animal species to humans

References

- Ahern M, Kovats RS, Wilkinson P, Few R, Matthies F. Global health impacts of floods: epidemiologic evidence. *Epidemiol Rev.* 2005 27:36-46. doi: 10.1093/epirev/mxi004.
- Ainsworth C. Therapeutic microbes to tackle disease. *Nature.* 2020 577:S20-S22. doi: 10.1038/d41586-020-00201-6.
- Altshuler I, Goordial J, Whyte LG. Microbial life in permafrost. In: Margesin R (ed), *Psychrophiles: From Biodiversity to Biotechnology.* 2017 Springer, Cham, Switzerland. doi: 10.1007/978-3-319-57057-0_8.
- American Society for Microbiology. FAQ: Microbes & Oil Spills. 2011 American Society for Microbiology, Washington, DC. doi: 10.1128/AAMCol.2-2011.
- American Society for Microbiology. FAQ: Microbes and Climate Change: Report on an American Academy of Microbiology and American Geophysical Union Colloquium Held in Washington, DC, in March 2016. 2017 American Society for Microbiology, Washington, DC. doi: 10.1128/AAMCol.Mar.2016.
- American Society for Microbiology. Incorporating Microbial Processes into Climate Models. 2011 American Society for Microbiology, Washington DC. doi: 10.1128/AAMCol.21Feb.2011.
- American Society for Microbiology. One Health: Fungal Pathogens of Humans, Animals, and Plants: Report on an American Academy of Microbiology Colloquium held in Washington, DC, on October 18, 2017. 2019. American Society for Microbiology, Washington, DC. doi: 10.1128/AAMCol.18Oct.2017.
- Anderson PK, Cunningham AA, Patel NG, Morales FJ, Epstein PR, Daszak P. Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers. *Trends Ecol Evol.* 2004 19(10):535-544. doi: 10.1016/j.tree.2004.07.021.
- Anderson SI, Barton AD, Clayton S, Dutkiewicz S, Rynearson TA. Marine phytoplankton functional types exhibit diverse responses to thermal change. *Nat Commun.* 2021 12(1):6413. doi: 10.1038/s41467-021-26651-8.
- Andersson MA, Nikulin M, Kõljalg U, Andersson MC, Rainey F, Reijula K, Hintikka EL, Salkinoja-Salonen M. Bacteria, molds, and toxins in water-damaged building materials. *Appl Environ Microbiol.* 1997 63(2):387-393. doi: 10.1128/aem.63.2.387-393.1997.
- Andrade-Linares DR, Zistl-Schlingmann M, Foesel B, Dannenmann M, Schulz S, Schloter M. Short term effects of climate change and intensification of management on the abundance of microbes driving nitrogen turnover in montane grassland soils. *Sci Total Environ.* 2021 780:146672. doi: 10.1016/j.scitotenv.2021.146672.
- Anthony KRN, Maynard JA, Diaz-Pulido G, Mumby PJ, Marshall PA, Cao L, Hoegh-Guldberg, O. Ocean acidification and warming will lower coral reef resilience. *Global Change Biol.* 2011 17:1798-1808. doi: 10.1111/j.1365-2486.2010.02364.x.
- Antoniou N, Monlau F, Sambusiti C, Ficara E, Barakat A, Zabaniotou A. Contribution to circular economy options of mixed agricultural wastes management: coupling anaerobic digestion with gasification for enhanced energy and material recovery. *J Clean Prod.* 2019 209:505-514. doi: 10.1016/j.jclepro.2018.10.055.
- Armitage C. The high burden of infectious disease. *Nature.* 2021 598:S9. doi: 10.1038/d41586-021-02909-5.
- Arora P, Singh P, Wang Y, Yadav A, Pawar K, Singh A, Padmavati G, Xu J, Chowdhary A. Environmental isolation of *Candida auris* from the coastal wetlands of Andaman Islands, India. *mBio.* 2021 12(2):e03181-20. doi: 10.1128/mBio.03181-20.
- Asner GP, Vaughn NR, Heckler J, Knapp DE, Balzotti C, Shafron E, Martin RE, Neilson BJ, Gove JM. Large-scale mapping of live corals to guide reef conservation. *Proc Natl Acad Sci U S A.* 2020 117(52):33711-33718. doi: 10.1073/pnas.2017628117.
- Azam F, Fenchel T, Field JG, et al. The ecological role of water-column microbes in the sea. *Mar Ecol Prog Ser.* 1983 10:257-263. doi: 10.3354/meps010257.
- Baker AC, Glynn PW, Riegl B. Climate change and coral reef bleaching: an ecological assessment of long-term impacts, recovery trends and future outlook. *Estuarine Coastal Shelf Sci.* 2008 80(4):435-471. doi: 10.1016/j.ecss.2008.09.003.
- Baker-Austin C, Trinanes JA, Salmenlinna S, Löfdahl M, Siitonen A, Taylor NG, Martinez-Urtaza J. Heat wave-associated vibriosis, Sweden and Finland, 2014. *Emerg Infect Dis.* 2016 22(7):1216-20. doi: 10.3201/eid2207.151996.

- Barnard RL, Osborne CA, Firestone MK. Responses of soil bacterial and fungal communities to extreme desiccation and rewetting. *ISME J*. 2013 7(11):2229-2241. doi: 10.1038/ismej.2013.104.
- Barr RG, Diez-Roux AV, Knirsch CA, Pablos-Méndez A. Neighborhood poverty and the resurgence of tuberculosis in New York City, 1984-1992. *Am J Public Health*. 2001 91(9):1487-1493. doi: 10.2105/ajph.91.9.1487.
- Bauer P, Thorpe A, Brunet G. The quiet revolution of numerical weather prediction. *Nature*. 2015 525(7567):47-55. doi: 10.1038/nature14956.
- Baumgartner RJ, Van Kranendonk MJ, Wacey D, Fiorentini ML, Saunders M, Caruso S, Pages A, Hohmann M, Guagliardo P. Nano-porous pyrite and organic matter in 3.5-billion-year-old stromatolites record primordial life. *Geology*. 2019 47(11):1039-1043. doi: 10.1130/G46365.1.
- Beatty ME, LaPorte TN, Phan Q, Van Duyne SV, Braden C. A multistate outbreak of *Salmonella enterica* serotype Saintpaul infections linked to mango consumption: a recurrent theme. *Clin Infect Dis*. 2004 38(9):1337-1338. doi: 10.1086/383156.
- Belkaid Y, Hand TW. Role of the microbiota in immunity and inflammation. *Cell*. 2014 157(1):121-141. doi: 10.1016/j.cell.2014.03.011.
- Belkaid Y, Segre JA. Dialogue between skin microbiota and immunity. *Science*. 2014 346(6212):95495-9. doi: 10.1126/science.1260144.
- Bell JJ. The functional roles of marine sponges. *Estuarine Coastal Shelf Sci*. 2008 79(3):341-353. doi: 10.1016/j.ecss.2008.05.002.
- Ben-Haim Y, Thompson FL, Thompson CC, Cnockaert MC, Hoste B, Swings J, Rosenberg E. *Vibrio coralliilyticus* sp. nov., a temperature-dependent pathogen of the coral *Pocillopora damicornis*. *Int J Syst Evol Microbiol*. 2003 53(Pt 1):309-315. doi: 10.1099/ijs.0.02402-0.
- Bennett JW, Klich M. Mycotoxins. *Clin Microbiol Rev*. 2003 16(3):497-516. doi: 10.1128/CMR.16.3.497-516.2003.
- Bernard RE, Cooperdock EHG. No progress on diversity in 40 years. *Nat Geosci*. 2018 11:292-295. doi: 10.1038/s41561-018-0116-6.
- Biskaborn BK, Smith SL, Noetzi J, Matthes H, Vieira G, Streletskiy DA, Schoeneich P, Romanovsky VE, Lewkowicz AG, Abramov A, Allard M, Boike J, Cable WL, Christiansen HH, Delaloye R, Diekmann B, Drozdov D, Etzelmüller B, Grosse G, Guglielmin M, Ingeman-Nielsen T, Isaksen K, Ishikawa M, Johansson M, Johansson H, Joo A, Kaverin D, Kholodov A, Konstantinov P, Kröger T, Lambiel C, Lanckman JP, Luo D, Malkova G, Meiklejohn I, Moskalenko N, Oliva M, Phillips M, Ramos M, Sannel ABK, Sergeev D, Seybold C, Skryabin P, Vasiliev A, Wu Q, Yoshikawa K, Zheleznyak M, Lantuit H. Permafrost is warming at a global scale. *Nat Commun*. 2019 10(1):264. doi: 10.1038/s41467-018-08240-4.
- Bleiweiss-Sande R, Scheck JM, Chui K, Goldberg JP, Bailey C, Evans EW. Processed food consumption is associated with diet quality, but not weight status, in a sample of low-income and ethnically diverse elementary school children. *Appetite*. 2020 151:104696. doi: 10.1016/j.appet.2020.104696.
- Bonan GB. Forests and climate change: forcings, feedbacks, and the climate benefits of forests. *Science*. 2008 320(5882):1444-1449. doi: 10.1126/science.1155121.
- Brewer TE, Aronson EL, Arogyaswamy K, Billings SA, Botthoff JK, Campbell AN, Dove NC, Fairbanks D, Gallery RE, Hart SC, Kaye J, King G, Logan G, Lohse KA, Maltz MR, Mayorga E, O'Neill C, Owens SM, Packman A, Pett-Ridge J, Plante AF, Richter DD, Silver WL, Yang WH, Fierer N. Ecological and genomic attributes of novel bacterial taxa that thrive in subsurface soil horizons. *mBio*. 2019 10(5):e01318-19. doi: 10.1128/mBio.01318-19.
- Broecker WS. Climatic change: are we on the brink of a pronounced global warming? *Science*. 1975 189(4201):460-463. doi: 10.1126/science.189.4201.460. PMID: 17781884.
- Brown JH, Gillooly JF, Allen AP, Savage VM, West GB. Toward a metabolic theory of ecology. *Ecology*. 2004. 85:1771-1789. doi: 10.1890/03-9000.
- Brulle RJ, Pellow DN. Environmental justice: human health and environmental inequalities. *Annu Rev Public Health*. 2006 27:103-124. doi: 10.1146/annurev.publhealth.27.021405.102124.
- Buffie CG, Jarchum I, Equinda M, Lipuma L, Gobbourne A, Viale A, Ubeda C, Xavier J, Pamer EG. Profound alterations of intestinal microbiota following a single dose of clindamycin results in sustained susceptibility to *Clostridium difficile*-induced colitis. *Infect Immun*. 2012 80(1):62-73. doi: 10.1128/IAI.05496-11.
- Buffie CG, Pamer EG. Microbiota-mediated colonization resistance against intestinal pathogens. *Nat Rev Immunol*. 2013 13(11):790-801. doi: 10.1038/nri3535.
- Byrd AL, Belkaid Y, Segre JA. The human skin microbiome. *Nat Rev Microbiol*. 2018 16(3):143-155. doi: 10.1038/nrmicro.2017.157.
- Caicedo C, Rosenwinkel KH, Exner M, Verstraete W, Suchenwirth R, Hartemann P, Nogueira R. *Legionella* occurrence in municipal and industrial wastewater treatment plants and risks of reclaimed wastewater reuse: review. *Water Res*. 2019 149:21-34. doi: 10.1016/j.watres.2018.10.080.
- Caicedo C, Verstraete W, Rosenwinkel KH, et al. Growth kinetics of environmental *Legionella pneumophila* isolated from industrial wastewater. *Int J Environ Sci Technol*. 2020 17:625-632. doi: 10.1007/s13762-019-02482-5.

- Calderon RL, Johnson CC, Jr, Craun GF, Dufour AP, Karlin RJ, Sinks T, Valentine JL. Health risks from contaminated water: do class and race matter? *Toxicol Ind Health*. 1993 9(5):879-900. doi: 10.1177/074823379300900510.
- Carilli JE, Norris RD, Black BA, Walsh SM, McField M. Local stressors reduce coral resilience to bleaching. *PLoS One*. 2009 4(7):e6324. doi: 10.1371/journal.pone.0006324.
- Casadevall A. Climate change brings the specter of new infectious diseases. *J Clin Invest*. 2020 130(2):553-555. doi: 10.1172/JCI135003.
- Casadevall A. Global catastrophic threats from the fungal kingdom: fungal catastrophic threats. *Curr Top Microbiol Immunol*. 2019 424:21-32. doi: 10.1007/82_2019_161.
- Casadevall A, Kontoyiannis DP, Robert V. Environmental *Candida auris* and the global warming emergence hypothesis. *mBio*. 2021 12(2):e00360-21. doi: 10.1128/mBio.00360-21.
- Casadevall A, Kontoyiannis DP, Robert V. On the emergence of *Candida auris*: climate change, azoles, swamps, and birds. *mBio*. 2019 10(4):e01397-19. doi: 10.1128/mBio.01397-19.
- Cash HL, Whitham CV, Behrendt CL, Hooper LV. Symbiotic bacteria direct expression of an intestinal bactericidal lectin. *Science*. 2006 313(5790):1126-1130. doi: 10.1126/science.1127119.
- Catania F, Baedke J, Fábregas-Tejeda A, Nieves Delgado A, Vitali V, Long LAN. Global climate change, diet, and the complex relationship between human host and microbiome: towards an integrated picture. *Bioessays*. 2021 43(6):e2100049. doi: 10.1002/bies.202100049.
- Cavan EL, Henson SA, Boyd PW. The sensitivity of subsurface microbes to ocean warming accentuates future declines in particulate carbon export. *Front Ecol Evol*. 2019 6:230. doi: 10.3389/fevo.2018.00230.
- Cavicchioli R, Ripple WJ, Timmis KN, Azam F, Bakken LR, Baylis M, Behrenfeld MJ, Boetius A, Boyd PW, Classen AT, Crowther TW, Danovaro R, Foreman CM, Huisman J, Hutchins DA, Jansson JK, Karl DM, Koskella B, Mark Welch DB, Martiny JBH, Moran MA, Orphan VJ, Reay DS, Remais JV, Rich VI, Singh BK, Stein LY, Stewart FJ, Sullivan MB, van Oppen MJH, Weaver SC, Webb EA, Webster NS. Scientists' warning to humanity: microorganisms and climate change. *Nat Rev Microbiol*. 2019 17(9):569-586. doi: 10.1038/s41579-019-0222-5.
- Centers for Disease Control and Prevention. Health concerns associated with mold in water-damaged homes after Hurricanes Katrina and Rita—New Orleans area, Louisiana, October 2005. *MMWR Morb Mortal Wkly Rep*. 2006 55(2):41-44.
- Centers for Disease Control and Prevention. National Wastewater Surveillance System. 2022 <https://www.cdc.gov/healthywater/surveillance/wastewater-surveillance/wastewater-surveillance.html>.
- Chadwick R, Good P, Martin G, et al. Large rainfall changes consistently projected over substantial areas of tropical land. *Nat Clim Chang*. 2016 6:177-181. doi: 10.1038/nclimate2805.
- Chaffin J, Bridgeman T, Bade D. Nitrogen constrains the growth of late summer cyanobacterial blooms in Lake Erie. *Adv Microbiol*. 2013 3(6A):16-26. doi: 10.4236/aim.2013.36A003.
- Checkley W, Epstein LD, Gilman RH, Figueroa D, Cama RI, Patz JA, Black RE. Effect of El Niño and ambient temperature on hospital admissions for diarrhoeal diseases in Peruvian children. *Lancet*. 2000 355(9202):442-450. doi: 10.1016/s0140-6736(00)82010-3.
- Ciesielski S, Handzel T, Sobsey M. The microbiologic quality of drinking water in North Carolina migrant labor camps. *Am J Public Health*. 1991 81(6):762-764. doi: 10.2105/ajph.81.6.762.
- Coalson JE, Anderson EJ, Santos EM, Madera Garcia V, Romine JK, Dominguez B, Richard DM, Little AC, Hayden MH, Ernst KC. The complex epidemiological relationship between flooding events and human outbreaks of mosquito-borne diseases: a scoping review. *Environ Health Perspect*. 2021 129(9):96002. doi: 10.1289/EHP8887. Erratum in: *Environ Health Perspect*. 2021 129(12):129001.
- Cohen D, Spear S, Scribner R, Kissinger P, Mason K, Wildgen J. "Broken windows" and the risk of gonorrhoea. *Am J Public Health*. 2000 90(2):230-236. doi: 10.2105/ajph.90.2.230.
- Compant S, Samad A, Faist H, Sessitsch A. A review on the plant microbiome: ecology, functions, and emerging trends in microbial application. *J Adv Res*. 2019 19:29-37. doi: 10.1016/j.jare.2019.03.004.
- Conley S, Franco G, Faloona I, Blake DR, Peischl J, Ryerson TB. Methane emissions from the 2015 Aliso Canyon blowout in Los Angeles, CA. *Science*. 2016 351(6279):1317-1320. doi: 10.1126/science.aaf2348.
- Constantin de Magny G, Murtugudde R, Sapiano MR, Nizam A, Brown CW, Busalacchi AJ, Yunus M, Nair GB, Gil AI, Lanata CF, Calkins J, Manna B, Rajendran K, Bhattacharya MK, Huq A, Sack RB, Colwell RR. Environmental signatures associated with cholera epidemics. *Proc Natl Acad Sci U S A*. 2008 105(46):17676-17681. doi: 10.1073/pnas.0809654105.
- Conteville LC, Oliveira-Ferreira J, Vicente ACP. Gut microbiome biomarkers and functional diversity within an Amazonian semi-nomadic hunter-gatherer group. *Front Microbiol*. 2019 10:1743. doi: 10.3389/fmicb.2019.01743.

- Cook BI, Ault TR, Smerdon JE. Unprecedented 21st century drought risk in the American Southwest and Central Plains. *Sci Adv*. 2015 1(1):e1400082. doi: 10.1126/sciadv.1400082.
- Corlett RT. The impacts of droughts in tropical forests. *Trends Plant Sci*. 2016 21(7):584-593. doi: 10.1016/j.tplants.2016.02.003.
- Crone BC, Garland JL, Sorial GA, Vane LM. Significance of dissolved methane in effluents of an aerobically treated low strength wastewater and potential for recovery as an energy product: a review. *Water Res*. 2016 104:520-531. doi: 10.1016/j.watres.2016.08.019. Erratum in: *Water Res*. 2017 111:420.
- Daelman MR, van Voorthuizen EM, van Dongen UG, Volcke EI, van Loosdrecht MC. Methane emission during municipal wastewater treatment. *Water Res*. 2012 46(11):3657-3670. doi: 10.1016/j.watres.2012.04.024.
- Daims H, Taylor MW, Wagner M. Wastewater treatment: a model system for microbial ecology. *Trends Biotechnol*. 2006 24(11):483-489. doi: 10.1016/j.tibtech.2006.09.002.
- D'Amato G, Cecchi L, D'Amato M, Liccardi G. Urban air pollution and climate change as environmental risk factors of respiratory allergy: an update. *J Investig Allergol Clin Immunol*. 2010 20(2):95-102; quiz, 102.
- Danczak RE, Johnston MD, Kenah C, Slattery M, Wilkins MJ. Microbial community cohesion mediates community turnover in unperturbed aquifers. *mSystems*. 2018 3(4):e00066-18. doi: 10.1128/mSystems.00066-18.
- Daszak P, Amuasi J, das Neves CG, Hayman D, Kuiken T, Roche B, Zambrana-Torrel C, Buss P, Dundarova H, Feferholtz Y, Foldvari G, Igbinosa E, Junglen S, Liu Q, Suzan G, Uhart M, Wannous C, Woolaston K, Mosig Reidl P, O'Brien K, Pascual U, Stoett P, Li H, Ngo HT, IPBES secretariat. IPBES (2020) workshop report on biodiversity and pandemics of the intergovernmental platform on biodiversity and ecosystem services, Bonn, Germany. doi: 10.5281/zenodo.4147317.
- Datta K, Bartlett KH, Baer R, Byrnes E, Galanis E, Heitman J, Hoang L, Leslie MJ, MacDougall L, Magill SS, Morshed MG, Marr KA, *Cryptococcus gattii* Working Group of the Pacific Northwest. Spread of *Cryptococcus gattii* into Pacific Northwest region of the United States. *Emerg Infect Dis*. 2009 15(8):1185-91. doi: 10.3201/eid1508.081384.
- David MM, Tataru C, Pope Q, Baker LJ, English MK, Epstein HE, Hammer A, Kent M, Sieler MJ, Jr, Mueller RS, Sharpton TJ, Tomas F, Vega Thurber R, Fern XZ. Revealing general patterns of microbiomes that transcend systems: potential and challenges of deep transfer learning. *mSystems*. 2022 7(1):e0105821. doi: 10.1128/msystems.01058-21.
- Davidson EA, de Araújo AC, Artaxo P, Balch JK, Brown IF, C Bustamante MM, Coe MT, DeFries RS, Keller M, Longo M, Munger JW, Schroeder W, Soares-Filho BS, Souza CM, Jr, Wofsy SC. The Amazon basin in transition. *Nature*. 2012 481(7381):321-328. doi: 10.1038/nature10717. Erratum in: *Nature*. 2012 483(7388):232.
- Davidson EA, Janssens IA. Temperature sensitivity of soil carbon decomposition and feedbacks to climate change. *Nature*. 2006 440(7081):165-173. doi: 10.1038/nature04514.
- Davidson EA, Savage KE, Finzi AC. A big-microsite framework for soil carbon modeling. *Glob Chang Biol*. 2014 20(12):3610-3620. doi: 10.1111/gcb.12718.
- Davis JL, Nica D, Shields K, Roberts DJ. Analysis of concrete from corroded sewer pipe. *Int Biodeterior Biodegradation*. 1998 42(1):75-84. doi: 10.1016/S0964-8305(98)00049-3.
- de Crecy E, Jaronski S, Lyons B, Lyons TJ, Keyhani NO. Directed evolution of a filamentous fungus for thermotolerance. *BMC Biotechnol*. 2009 9:74. doi: 10.1186/1472-6750-9-74.
- De Luca F, Shoenfeld Y. The microbiome in autoimmune diseases. *Clin Exp Immunol*. 2019 195(1):74-85. doi: 10.1111/cei.13158.
- Deng Y, Xu H, Su Y, Liu S, Xu L, Guo Z, Wu J, Cheng C, Feng J. Horizontal gene transfer contributes to virulence and antibiotic resistance of *Vibrio harveyi* 345 based on complete genome sequence analysis. *BMC Genomics*. 2019 20(1):761. doi: 10.1186/s12864-019-6137-8.
- Desai PT, Porwollik S, Long F, Cheng P, Wollam A, Bhonagiri-Palsikar V, Hallsworth-Pepin K, Clifton SW, Weinstock GM, McClelland M. Evolutionary genomics of *Salmonella enterica* subspecies. *mBio*. 2013 4(2):e00579-12. doi: 10.1128/mBio.00579-12. Erratum in: *mBio*. 2013 4(2):e00198-13.
- de Vries FT, Griffiths RI, Bailey M, Craig H, Girlanda M, Gweon HS, Hallin S, Kaisermann A, Keith AM, Kretzschmar M, Lemanceau P, Lumini E, Mason KE, Oliver A, Ostle N, Prosser JI, Thion C, Thomson B, Bardgett RD. Soil bacterial networks are less stable under drought than fungal networks. *Nat Commun*. 2018 9(1):3033. doi: 10.1038/s41467-018-05516-7.
- Dietert RR. The microbiome in early life: self-completion and microbiota protection as health priorities. *Birth Defects Res B Dev Reprod Toxicol*. 2014 101(4):333-340. doi: 10.1002/bdrb.21116.
- Dietzel A, Bode M, Connolly SR, Hughes TP. Long-term shifts in the colony size structure of coral populations along the Great Barrier Reef. *Proc Biol Sci*. 2020 287(1936):20201432. doi: 10.1098/rspb.2020.1432.
- Dolman AM, Rucker J, Pick FR, Fastner J, Rohrlack T, Mischke U, Wiedner C. Cyanobacteria and cyanotoxins: the influence of nitrogen versus phosphorus. *PLoS One*. 2012 7(6):e38757. doi: 10.1371/journal.pone.0038757.

- Ducluzeau R, Dubos F, Raibaud P, Abrams GD. Inhibition of *Clostridium perfringens* by an antibiotic substance produced by *Bacillus licheniformis* in the digestive tract of gnotobiotic mice: effect on other bacteria from the digestive tract. *Antimicrob Agents Chemother.* 1976 9(1):20-25. doi: 10.1128/AAC.9.1.20.
- Dynarski K, Bossio D, Scow K. Dynamic stability of soil carbon: reassessing the “permanence” of soil carbon sequestration. *Frontiers Environ Sci.* 2020 <https://www.frontiersin.org/article/10.3389/fenvs.2020.514701>.
- Eddy TD, Lam VWY, Reygondeau G, Cisneros-Montemayor AM, Greer K, Palomares MLD, Bruno JF, Ota Y, Cheung, WWL. Global decline in capacity of coral reefs to provide ecosystem services. *One Earth.* 2021 4(9):2590-3330. doi: 10.1016/j.oneear.2021.08.016.
- Egamberdieva D, Wirth SJ, Alqarawi AA, Abd Allah EF, Hashem A. Phytohormones and beneficial microbes: essential components for plants to balance stress and fitness. *Front Microbiol.* 2017 8:2104. doi: 10.3389/fmicb.2017.02104.
- El-Beltagy A, Madkour M. Impact of climate change on arid lands agriculture. *Agric Food Secur.* 2012 1:3. doi: 10.1186/2048-7010-1-3.
- El Sayed BB, Arnot DE, Mukhtar MM, Baraka OZ, Dafalla AA, Elnaiem DE, Nugud AH. A study of the urban malaria transmission problem in Khartoum. *Acta Trop.* 2000 75(2):163-171. doi: 10.1016/s0001-706x(99)00098-4.
- Erickson MC, Webb CC, Diaz-Perez JC, Phatak SC, Silvoy JJ, Davey L, Payton AS, Liao J, Ma L, Doyle MP. Surface and internalized *Escherichia coli* O157:H7 on field-grown spinach and lettuce treated with spray-contaminated irrigation water. *J Food Prot.* 2010 73(6):1023-1029. doi: 10.4315/0362-028x-73.6.1023.
- Fagre AC, Cohen L, Eskew EA, Farrell MJ, Glennon E, Joseph MB, et al. Spillover in the Anthropocene: the risk of human-to-wildlife pathogen transmission for conservation and public health. *EcoEvoRxiv.* 2021. [ecoevorxiv.org/sx6p8](https://doi.org/10.1101/2021.06.08.444448).
- Falkowski PG, Barber RT, Smetacek VV. Biogeochemical controls and feedbacks on ocean primary production. *Science.* 1998 281(5374):200-207. doi: 10.1126/science.281.5374.200.
- Fernandes KE, Dwyer C, Campbell LT, Carter DA. Species in the *Cryptococcus gattii* complex differ in capsule and cell size following growth under capsule-inducing conditions. *mSphere.* 2016 1(6):e00350-16. doi: 10.1128/mSphere.00350-16.
- Ferrera I, Sánchez O. Insights into microbial diversity in wastewater treatment systems: how far have we come? *Biotechnol Adv.* 2016 34(5):790-802. doi: 10.1016/j.biotechadv.2016.04.003.
- Field CB, Barros V, Stocker TF, Dahe Q (ed). *Managing the Risks of Extreme Events and Disasters to Advance Climate Change Adaptation: Special Report of the Intergovernmental Panel on Climate Change.* 2012 Cambridge University Press, Cambridge, United Kingdom.
- Fisher MC, Henk DA, Briggs CJ, Brownstein JS, Madoff LC, McCraw SL, Gurr SJ. Emerging fungal threats to animal, plant and ecosystem health. *Nature.* 2012 484(7393):186-194. doi: 10.1038/nature10947.
- Fonkwo PN. Pricing infectious disease. *EMBO Rep.* 2008 9:S13-S17. <https://doi.org/10.1038/embo.2008.110>.
- Frank DN, St Amand AL, Feldman RA, Boedeker EC, Harpaz N, Pace NR. Molecular-phylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. *Proc Natl Acad Sci U S A.* 2007 104(34):13780-13785. doi: 10.1073/pnas.0706625104.
- French SA, Tangney CC, Crane MM, Wang Y, Appelhans BM. Nutrition quality of food purchases varies by household income: the SHoPPER study. *BMC Public Health.* 2019 19(1):231. doi: 10.1186/s12889-019-6546-2.
- Friedlingstein P, Jones MW, O’Sullivan M, Andrew RM, Hauck J, Peters GP, Peters W, Pongratz J, Sitch S, Le Quéré C, Bakker DCE, Canadell JG, Ciais P, Jackson RB, Anthoni P, Barbero L, Bastos A, Bastrikov V, Becker M, Bopp L, Buitenhuis E, Chandra N, Chevallier F, Chini LP, Currie KI, Feely RA, Gehlen M, Gilfillan D, Gkritzalis T, Goll DS, Gruber N, Gutzkunst S, Harris I, Haverd V, Houghton RA, Hurtt G, Ilyina T, Jain AK, Joetzjer E, Kaplan JO, Kato E, Klein Goldewijk K, Korsbakken JI, Landschützer P, Lauvset SK, Lefèvre N, Lenton A, Lienert S, Lombardozzi D, Marland G, McGuire PC, Melton JR, Metzl N, Munro DR, Nabel JEMS, Nakaoka S-I, Neill C, Omar AM, Ono T, Peregón A, Pierrot D, Poulter B, Rehder G, Resplandy L, Robertson E, Rödenbeck C, Séférian R, Schwinger J, Smith N, Tans PP, Tian H, Tilbrook B, Tubiello FN, van der Werf GR, Wiltshire AJ, Zaehle S. Global carbon budget 2019. *Earth Syst Sci Data.* 2019 11:1783-1838. doi: 10.5194/essd-11-1783-2019.
- Gao Q, Wang G, Xue K, Yang Y, Xie J, Yu H, Bai S, Liu F, He Z, Ning D, Hobbie SE, Reich PB, Zhou J. Stimulation of soil respiration by elevated CO₂ is enhanced under nitrogen limitation in a decade-long grassland study. *Proc Natl Acad Sci U S A.* 2020 117(52):33317-33324. doi: 10.1073/pnas.2002780117.
- García-Solache MA, Casadevall A. Global warming will bring new fungal diseases for mammals. *mBio.* 2010 1(1):e00061-10. doi: 10.1128/mBio.00061-10.
- Gaylarde C, Ribas Silva M, Warscheid T. Microbial impact on building materials: an overview. *Mat Struct.* 2003. 36:342-352. doi: 10.1007/BF02480875.

- Gevers D, Kugathasan S, Denson LA, Vázquez-Baeza Y, Van Treuren W, Ren B, Schwager E, Knights D, Song SJ, Yassour M, Morgan XC, Kostic AD, Luo C, González A, McDonald D, Haberman Y, Walters T, Baker S, Rosh J, Stephens M, Heyman M, Markowitz J, Baldassano R, Griffiths A, Sylvester F, Mack D, Kim S, Crandall W, Hyams J, Huttenhower C, Knight R, Xavier RJ. The treatment-naive microbiome in new-onset Crohn's disease. *Cell Host Microbe*. 2014 15(3):382-392. doi: 10.1016/j.chom.2014.02.005.
- Gill SS, Gill R, Trivedi DK, Anjum NA, Sharma KK, Ansari MW, Ansari AA, Johri AK, Prasad R, Pereira E, Varma A, Tuteja N. *Piriformospora indica*: potential and significance in plant stress tolerance. *Front Microbiol*. 2016 7:332. doi: 10.3389/fmicb.2016.00332.
- Glibert PM. From hogs to HABs: impacts of industrial farming in the US on nitrogen and phosphorus and greenhouse gas pollution. *Biogeochemistry*. 2020 150(2):139-180. doi: 10.1007/s10533-020-00691-6.
- Gorris ME, Treseder KK, Zender CS, Randerson JT. Expansion of Coccidioidomycosis endemic regions in the United States in response to climate change. *Geohealth*. 2019 3(10):308-327. doi: 10.1029/2019GH000209.
- Gougoulias C, Clark JM, Shaw LJ. The role of soil microbes in the global carbon cycle: tracking the below-ground microbial processing of plant-derived carbon for manipulating carbon dynamics in agricultural systems. *J Sci Food Agric*. 2014 94(12):2362-2371. doi: 10.1002/jsfa.6577.
- Graham DE, Wallenstein MD, Vishnivetskaya TA, Waldrop MP, Phelps TJ, PfiFFner SM, Onstott TC, Whyte LG, Rivkina EM, Gilichinsky DA, Elias DA, Mackelprang R, VerBerkmoes NC, Hettich RL, Wagner D, Wullschleger SD, Jansson JK. Microbes in thawing permafrost: the unknown variable in the climate change equation. *ISME J*. 2012 6(4):709-712. doi: 10.1038/ismej.2011.163.
- Gray WM. Hormonal regulation of plant growth and development. *PLoS Biol*. 2004 2(9):E311. doi: 10.1371/journal.pbio.0020311.
- Gu S, Wei Z, Shao Z, Friman VP, Cao K, Yang T, Kramer J, Wang X, Li M, Mei X, Xu Y, Shen Q, Kümmerli R, Jousset A. Competition for iron drives phytopathogen control by natural rhizosphere microbiomes. *Nat Microbiol*. 2020 5(8):1002-1010. doi: 10.1038/s41564-020-0719-8.
- Guo X, Feng J, Shi Z, et al. Climate warming leads to divergent succession of grassland microbial communities. *Nat Clim Chang*. 2018 8:813-818. doi: 10.1038/s41558-018-0254-2.
- Guo X, Gao Q, Yuan M, Wang G, Zhou X, Feng J, Shi Z, Hale L, Wu L, Zhou A, Tian R, Liu F, Wu B, Chen L, Jung CG, Niu S, Li D, Xu X, Jiang L, Escalas A, Wu L, He Z, Van Nostrand JD, Ning D, Liu X, Yang Y, Schuur EAG, Konstantinidis KT, Cole JR, Penton CR, Luo Y, Tiedje JM, Zhou J. Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming. *Nat Commun*. 2020 11(1):4897. doi: 10.1038/s41467-020-18706-z.
- Guo X, Zhou X, Hale L, Yuan M, Ning D, Feng J, Shi Z, Li Z, Feng B, Gao Q, Wu L, Shi W, Zhou A, Fu Y, Wu L, He Z, Van Nostrand JD, Qiu G, Liu X, Luo Y, Tiedje JM, Yang Y, Zhou J. Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. *Nat Ecol Evol*. 2019 3(4):612-619. doi: 10.1038/s41559-019-0848-8.
- Hacquard S, Spaepen S, Garrido-Oter R, Schulze-Lefert P. Interplay between innate immunity and the plant microbiota. *Annu Rev Phytopathol*. 2017 55:565-589. doi: 10.1146/annurev-phyto-080516-035623.
- Han C, Wang Z, Si G, Lei T, Yuan Y, Zhang G. Increased precipitation accelerates soil organic matter turnover associated with microbial community composition in topsoil of alpine grassland on the eastern Tibetan Plateau. *Can J Microbiol*. 2017 63(10):811-821. doi: 10.1139/cjm-2017-0157.
- Harke MJ, Steffen MM, Gobler CJ, Otten TG, Wilhelm SW, Wood SA, Paerl HW. A review of the global ecology, genomics, and biogeography of the toxic cyanobacterium, *Microcystis* spp. *Harmful Algae*. 2016 54:4-20. doi: 10.1016/j.hal.2015.12.007.
- Harkes P, van Steenbrugge JJM, van den Elsen SJJ, Suleiman AKA, de Haan JJ, Holterman MHM, Helder J. Shifts in the active rhizobiome paralleling low meloidogyne chitwoodi densities in fields under prolonged organic soil management. *Front Plant Sci*. 2020 10:1697. doi: 10.3389/fpls.2019.01697.
- Harris LA, Garza C, Hatch M, Parrish J, Posselt J, Alvarez Rosario JP, et al. Equitable exchange: a framework for diversity and inclusion in the geosciences. *AGU Adv*. 2021 2:e2020AV000359. doi: 10.1029/2020AV000359.
- Hart SC, DeLuca TH, Newman GS, MacKenzie MD, Boyle SI. Post-fire vegetative dynamics as drivers of microbial community structure and function in forest soils. *Forest Ecol Manag*. 2005 220:166-184. doi: 10.1016/j.foreco.2005.08.012.
- Hause B, Fester T. Molecular and cell biology of arbuscular mycorrhizal symbiosis. *Planta*. 2005 221(2):184-196. doi: 10.1007/s00425-004-1436-x.
- He Z, Xu M, Deng Y, Kang S, Kellogg L, Wu L, Van Nostrand JD, Hobbie SE, Reich PB, Zhou J. Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO₂. *Ecol Lett*. 2010 13(5):564-575. doi: 10.1111/j.1461-0248.2010.01453.x.

- Heslop JK, Winkel M, Walter Anthony KM, Spencer RGM, Podgorski DC, Zito P, et al. Increasing organic carbon biolability with depth in yedoma permafrost: ramifications for future climate change. *J Geophys Res Biogeosci*. 2019 124:2021-2038. doi: 10.1029/2018JG004712.
- Hill C, Guarner F, Reid G, Gibson GR, Merenstein DJ, Pot B, Morelli L, Canani RB, Flint HJ, Salminen S, Calder PC, Sanders ME. Expert consensus document. The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. *Nat Rev Gastroenterol Hepatol*. 2014 11(8):506-514. doi: 10.1038/nrgastro.2014.66.
- Hilmers A, Hilmers DC, Dave J. Neighborhood disparities in access to healthy foods and their effects on environmental justice. *Am J Public Health*. 2012 102(9):1644-1654. doi: 10.2105/AJPH.2012.300865.
- Hoegh-Guldberg O, Jacob D, Taylor M, Bindi M, Brown S, Camilloni I, Diedhiou A, Djalante R, Ebi KL, Engelbrecht F, Guiot J, Hijioka Y, Mehrotra S, Payne A, Seneviratne SI, Thomas A, Warren R, Zhou G. Impacts of 1.5°C global warming on natural and human systems. In: Masson-Delmotte V, Zhai P, Pörtner H-O, Roberts D, Skea J, Shukla PR, Pirani A, Moufouma-Okia W, Péan C, Pidcock R, Connors S, Matthews JBR, Chen Y, Zhou X, Gomis MI, Lonnoy E, Maycock T, Tignor M, Waterfield T (ed), *Global Warming of 1.5°C. An IPCC Special Report on the impacts of global warming of 1.5°C above pre-industrial levels and related global greenhouse gas emission pathways, in the context of strengthening the global response to the threat of climate change, sustainable development, and efforts to eradicate poverty*. 2018 175-311. Cambridge University Press, Cambridge, United Kingdom.
- Hoegh-Guldberg O, Mumby PJ, Hooten AJ, Steneck RS, Greenfield P, Gomez E, Harvell CD, Sale PF, Edwards AJ, Caldeira K, Knowlton N, Eakin CM, Iglesias-Prieto R, Muthiga N, Bradbury RH, Dubi A, Hatziolos ME. Coral reefs under rapid climate change and ocean acidification. *Science*. 2007 318(5857):1737-1742. doi: 10.1126/science.1152509.
- Hofreuter D, Novik V, Galán JE. Metabolic diversity in *Campylobacter jejuni* enhances specific tissue colonization. *Cell Host Microbe*. 2008 4(5):425-33. doi: 10.1016/j.chom.2008.10.002.
- Honeyman AS, Day ML, Spear JR. Regional fresh snowfall microbiology and chemistry are driven by geography in storm-tracked events, Colorado, USA. *PeerJ*. 2018 6:e5961. doi: 10.7717/peerj.5961.
- Hughes TP, Anderson KD, Connolly SR, Heron SF, Kerry JT, Lough JM, Baird AH, Baum JK, Berumen ML, Bridge TC, Claar DC, Eakin CM, Gilmour JP, Graham NAJ, Harrison H, Hobbs JA, Hoey AS, Hoogenboom M, Lowe RJ, McCulloch MT, Pandolfi JM, Pratchett M, Schoepf V, Torda G, Wilson SK. Spatial and temporal patterns of mass bleaching of corals in the Anthropocene. *Science*. 2018 359(6371):80-83. doi: 10.1126/science.aan8048.
- Hughes TP, Barnes ML, Bellwood DR, Cinner JE, Cumming GS, Jackson JBC, Kleypas J, van de Leemput IA, Lough JM, Morrison TH, Palumbi SR, van Nes EH, Scheffer M. Coral reefs in the Anthropocene. *Nature*. 2017 546(7656):82-90. doi: 10.1038/nature22901.
- Hughes TP, Kerry JT, Álvarez-Noriega M, Álvarez-Romero JG, Anderson KD, Baird AH, Babcock RC, Beger M, Bellwood DR, Berkelmans R, Bridge TC, Butler IR, Byrne M, Cantin NE, Comeau S, Connolly SR, Cumming GS, Dalton SJ, Diaz-Pulido G, Eakin CM, Figueira WF, Gilmour JP, Harrison HB, Heron SF, Hoey AS, Hobbs JA, Hoogenboom MO, Kennedy EV, Kuo CY, Lough JM, Lowe RJ, Liu G, McCulloch MT, Malcolm HA, McWilliam MJ, Pandolfi JM, Pears RJ, Pratchett MS, Schoepf V, Simpson T, Skirving WJ, Sommer B, Torda G, Wachenfeld DR, Willis BL, Wilson SK. Global warming and recurrent mass bleaching of corals. *Nature*. 2017 543(7645):373-377. doi: 10.1038/nature21707.
- Huttunen-Saarivirta E, Honkanen M, Lepistö T, Kuokkala V-T, Koivisto L, Berg C-G. Microbiologically influenced corrosion (MIC) in stainless steel heat exchanger. *Appl Surf Sci*. 2012 258(17):6512-6526. doi: 10.1016/j.apsusc.2012.03.068.
- IPCC. *Climate Change 2021: the Physical Science Basis. Contribution of Working Group I to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change*. 2021. Cambridge University Press, Cambridge, United Kingdom.
- IPCC. *Summary for Policymakers. In: Climate Change 2021: the Physical Science Basis. Contribution of Working Group I to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change*. 2021 4-41. Cambridge University Press, Cambridge, United Kingdom.
- IPCC. 2022: *Summary for Policymakers. In: Climate Change 2022: Impacts, Adaptation, and Vulnerability. Contribution of Working Group II to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change*. 2022 1-35. Cambridge University Press, Cambridge, United Kingdom.
- Ishaq SL, Rapp M, Byerly R, McClellan LS, O'Boyle MR, Nykanen A, Fuller PJ, Aas C, Stone JM, Killpatrick S, Uptegrove MM, Vischer A, Wolf H, Smallman F, Eymann H, Narode S, Stapleton E, Cioffi CC, Tavalire HF. Framing the discussion of microorganisms as a facet of social equity in human health. *PLoS Biol*. 2019 17(11):e3000536. doi: 10.1371/journal.pbio.3000536.
- Jackson BR, Chow N, Forsberg K, Litvintseva AP, Lockhart SR, Welsh R, Vallabhaneni S, Chiller T. On the origins of a species: what might explain the rise of *Candida auris*? *J Fungi (Basel)*. 2019 5(3):58. doi: 10.3390/jof5030058.
- Janssen EM. Cyanobacterial peptides beyond microcystins—a review on co-occurrence, toxicity, and challenges for risk assessment. *Water Res*. 2019 151:488-499. doi: 10.1016/j.watres.2018.12.048.

- Jansson JK, Hofmockel KS. Soil microbiomes and climate change. *Nat Rev Microbiol.* 2020. 18:35-46. doi: 10.1038/s41579-019-0265-7.
- Jansson JK, Taş N. The microbial ecology of permafrost. *Nat Rev Microbiol.* 2014 12(6):414-425. doi: 10.1038/nrmicro3262.
- Jia R, Wang D, Jin P, Unsal T, Yang D, Yang J, Xu D, Gu T. Effects of ferrous ion concentration on microbiologically influenced corrosion of carbon steel by sulfate reducing bacterium *Desulfovibrio vulgaris*. *Corrosion Sci.* 2019 153:127-137. doi:10.1016/j.corsci.2019.03.038.
- Kallela K, Ettala E. The oestrogenic *Fusarium* toxin (zearalenone) in hay as a cause of early abortions in the cow. *Nord Vet Med.* 1984 36(9-10):305-309.
- Kappel K, Holmen SJ. Why science communication, and does it work? A taxonomy of science communication aims and a survey of the empirical evidence. *Front Commun.* 2019 4:55. doi: 10.3389/fcomm.2019.00055.
- Khalil M, Berawi M, Heryanto R, Rizalie A. Waste to energy technology: the potential of sustainable biogas production from animal waste in Indonesia. *Renewable Sustainable Energy Rev.* 2019 105:323-331. doi: 10.1016/j.rser.2019.02.011.
- Kimes NE, Grim CJ, Johnson WR, Hasan NA, Tall BD, Kothary MH, Kiss H, Munk AC, Tapia R, Green L, Detter C, Bruce DC, Brettin TS, Colwell RR, Morris PJ. Temperature regulation of virulence factors in the pathogen *Vibrio coralliilyticus*. *ISME J.* 2012 6(4):835-46. doi: 10.1038/ismej.2011.154.
- Knoblauch C, Beer C, Liebner S, et al. Methane production as key to the greenhouse gas budget of thawing permafrost. *Nat Clim Chang.* 2018 8:309-312. doi: 10.1038/s41558-018-0095-z.
- Kobayashi KS, Chamaillard M, Ogura Y, Henegariu O, Inohara N, Nuñez G, Flavell RA. Nod2-dependent regulation of innate and adaptive immunity in the intestinal tract. *Science.* 2005 307(5710):731-734. doi: 10.1126/science.1104911.
- Kreft JU, Plugge CM, Prats C, Leveau JHJ, Zhang W, Hellweger FL. From genes to ecosystems in microbiology: modeling approaches and the importance of individuality. *Front Microbiol.* 2017 8:2299. doi: 10.3389/fmicb.2017.02299.
- Krieger J, Higgins DL. Housing and health: time again for public health action. *Am J Public Health.* 2002 92(5):758-768. doi: 10.2105/ajph.92.5.758.
- Kuchipudi SV, Surendran-Nair M, Ruden RM, Yon M, Nissly RH, Vandegrift KJ, Nelli RK, Li L, Jayarao BM, Maranas CD, Levine N, Willgert K, Conlan AJK, Olsen RJ, Davis JJ, Musser JM, Hudson PJ, Kapur V. Multiple spillovers from humans and onward transmission of SARS-CoV-2 in white-tailed deer. *Proc Natl Acad Sci U S A.* 2022 119(6):e2121644119. doi: 10.1073/pnas.2121644119.
- Kumar P, Mahato DK, Kamle M, Mohanta TK, Kang SG. Aflatoxins: a global concern for food safety, human health and their management. *Front Microbiol.* 2017 7:2170. doi: 10.3389/fmicb.2016.02170.
- Kusnetsov J, Neuvonen LK, Korpio T, Uldum SA, Mentula S, Putus T, Tran Minh NN, Martimo KP. Two Legionnaires' disease cases associated with industrial waste water treatment plants: a case report. *BMC Infect Dis.* 2010 10:343. doi: 10.1186/1471-2334-10-343.
- Lai Y, Di Nardo A, Nakatsuji T, Leichtle A, Yang Y, Cogen AL, Wu ZR, Hooper LV, Schmidt RR, von Aulock S, Radek KA, Huang CM, Ryan AF, Gallo RL. Commensal bacteria regulate Toll-like receptor 3-dependent inflammation after skin injury. *Nat Med.* 2009 15(12):1377-1382. doi: 10.1038/nm.2062.
- Laufkötter C, Vogt M, Gruber N, Aumont O, Bopp L, Doney SC, Dunne JP, Hauck J, John JG, Lima ID, Sefarian R, Völker C. Projected decreases in future marine export production: the role of the carbon flux through the upper ocean ecosystem. *Biogeosciences.* 2016 13:4023-4047. doi: 10.5194/bg-13-4023-2016.
- Lee YK, Mazmanian SK. Has the microbiota played a critical role in the evolution of the adaptive immune system? *Science.* 2010 330(6012):1768-1773. doi: 10.1126/science.1195568.
- Lesser MP, Fiore C, Slattery M, Zaneveld J. Climate change stressors destabilize the microbiome of the Caribbean barrel sponge, *Xestospongia muta*. *J Exp Mar Biol Ecol.* 2016; 475:11-18. doi:10.1016/j.jembe.2015.11.004.
- Lewis WM, Wurtsbaugh WA, Paerl HW. Rationale for control of anthropogenic nitrogen and phosphorus to reduce eutrophication of inland waters. *Environ Sci Technol.* 2011 45(24):10300-10305. doi: 10.1021/es202401p.
- Li H, Zhou E, Ren Y, Zhang D, Xu D, Yang C, Feng H, Jiang Z, Li X, Gu T, Yang K. Investigation of microbiologically influenced corrosion of high nitrogen nickel-free stainless steel by *Pseudomonas aeruginosa*. *Corrosion Sci.* 2016 111:811-821. doi:10.1016/j.corsci.2016.06.017.
- Li M, Wei Z, Wang J, Jousset A, Friman VP, Xu Y, Shen Q, Pommier T. Facilitation promotes invasions in plant-associated microbial communities. *Ecol Lett.* 2019 22(1):149-158. doi: 10.1111/ele.13177.
- Lipp EK, Huq A, Colwell RR. Effects of global climate on infectious disease: the cholera model. *Clin Microbiol Rev.* 2002 15(4):757-770. doi: 10.1128/CMR.15.4.757-770.2002.
- Little BJ, Blackwood DJ, Hinks J, Lauro FM, Marsili E, Okamoto A, Rice SA, Wade SA, Flemming H-C. Microbially influenced corrosion—any progress? *Corrosion Sci.* 2020 170: 108641. doi: 10.1016/j.corsci.2020.108641.

- Littman R, Willis BL, Bourne DG. Metagenomic analysis of the coral holobiont during a natural bleaching event on the Great Barrier Reef. *Environ Microbiol Rep.* 2011 3(6):651-660. doi: 10.1111/j.1758-2229.2010.00234.x.
- Liu C, Hofstra N, Franz E. Impacts of climate change on the microbial safety of pre-harvest leafy green vegetables as indicated by *Escherichia coli* O157 and *Salmonella* spp. *Int J Food Microbiol.* 2013 163(2-3):119-128. doi: 10.1016/j.ijfoodmicro.2013.02.026.
- Liu C, Sakimoto KK, Colón BC, Silver PA, Nocera DG. Ambient nitrogen reduction cycle using a hybrid inorganic-biological system. *Proc Natl Acad Sci U S A.* 2017 114(25):6450-6455. doi: 10.1073/pnas.1706371114.
- Liu L, Wang J, Rosenberg D, Zhao H, Lengyel G, Nadel D. Fermented beverage and food storage in 13,000 y-old stone mortars at Raqefet Cave, Israel: investigating Natufian ritual feasting. *J Archaeol Sci Rep.* 2018 21:783-793. doi: 10.1016/j.jasrep.2018.08.008.
- Liu Y, Alookaran JJ, Rhoads JM. Probiotics in autoimmune and inflammatory disorders. *Nutrients.* 2018 10(10):1537. doi: 10.3390/nu10101537.
- Locey KJ, Lennon JT. Scaling laws predict global microbial diversity. *Proc Natl Acad Sci U S A.* 2016 113(21):5970-5975. doi: 10.1073/pnas.1521291113.
- Mackelprang R, Saleska S, Jacobsen C, Jansson J, Taş N. Permafrost meta-omics and climate change. *Annu Rev Earth Planetary Sci.* 2016 44:439-462. doi: 10.1146/annurev-earth-060614-105126.
- Mackelprang R, Waldrop MP, DeAngelis KM, David MM, Chavarria KL, Blazewicz SJ, Rubin EM, Jansson JK. Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. *Nature.* 2011 480(7377):368-371. doi: 10.1038/nature10576.
- Marr LC, Tang JW, Van Mullekom J, Lakdawala SS. Mechanistic insights into the effect of humidity on airborne influenza virus survival, transmission and incidence. *J R Soc Interface.* 2019 16(150):20180298. doi: 10.1098/rsif.2018.0298.
- Mata-Alvarez J, Dosta J, Romero-Güiza MS, Fonoll X, Peces M, Astals S. A critical review on anaerobic co-digestion achievements between 2010 and 2013. *Renewable Sustainable Energy Rev.* 2014; 36:412-427. doi: 10.1016/j.rser.2014.04.039.
- McCarty PL, Bae J, Kim J. Domestic wastewater treatment as a net energy producer—can this be achieved? *Environ Sci Technol.* 2011 45(17):7100-7106. doi: 10.1021/es2014264.
- McDonough LK, Santos IR, Andersen MS, et al. Changes in global groundwater organic carbon driven by climate change and urbanization. *Nat Commun.* 2020 11:1279. doi: 10.1038/s41467-020-14946-1.
- McHugh TA, Compson Z, van Gestel N, Hayer M, Ballard L, Haverty M, Hines J, Irvine N, Krassner D, Lyons T, Musta EJ, Schiff M, Zint P, Schwartz E. Climate controls prokaryotic community composition in desert soils of the southwestern United States. *FEMS Microbiol Ecol.* 2017 93(10):fix116 doi: 10.1093/femsec/fix116.
- Mendes R, Kruijt M, de Bruijn I, Dekkers E, van der Voort M, Schneider JH, Piceno YM, DeSantis TZ, Andersen GL, Bakker PA, Raaijmakers JM. Deciphering the rhizosphere microbiome for disease-suppressive bacteria. *Science.* 2011 332(6033):1097-1100. doi: 10.1126/science.1203980.
- Mentel M, Spírek M, Jørck-Ramberg D, Piskur J. Transfer of genetic material between pathogenic and food-borne yeasts. *Appl Environ Microbiol.* 2006 72(7):5122-5125. doi: 10.1128/AEM.00293-06.
- Milićević DR, Skrinjar M, Baltić T. Real and perceived risks for mycotoxin contamination in foods and feeds: challenges for food safety control. *Toxins (Basel).* 2010 2(4):572-592. doi: 10.3390/toxins2040572.
- Mills JG, Brookes JD, Gellie NJC, Liddicoat C, Lowe AJ, Sydnor HR, Thomas T, Weinstein P, Weyrich LS, Breed MF. Relating urban biodiversity to human health with the 'holobiont' concept. *Front Microbiol.* 2019 10:550. doi: 10.3389/fmicb.2019.00550.
- Miransari M, Abrishamchi A, Khoshbakht K, Niknam V. Plant hormones as signals in arbuscular mycorrhizal symbiosis. *Crit Rev Biotechnol.* 2014 34(2):123-133. doi: 10.3109/07388551.2012.731684.
- Myhre G, D. Shindell D, Bréon F-M, Collins W, Fuglestedt J, Huang J, Koch D, Lamarque J-F, Lee D, Mendoza B, Nakajima T, Robock A, Stephens G, Takemura T, Zhang H. Anthropogenic and natural radiative forcing. In: Stocker TF, Qin D, Plattner G-K, Tignor M, Allen SK, Boschung J, Nauels A, Xia Y, Bex V, Midgley PM (ed), *Climate Change 2013: the Physical Science Basis. Contribution of Working Group I to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change.* 2013 659-740. Cambridge University Press, Cambridge, United Kingdom.
- Naik S, Bouladoux N, Wilhelm C, Molloy MJ, Salcedo R, Kastenmuller W, Deming C, Quinones M, Koo L, Conlan S, Spencer S, Hall JA, Dzutsev A, Kong H, Campbell DJ, Trinchieri G, Segre JA, Belkaid Y. Compartmentalized control of skin immunity by resident commensals. *Science.* 2012 337(6098):1115-1119. doi: 10.1126/science.1225152.
- Nash Suding K, Goldberg DE, Hartman KM. Relationships among species traits: separating levels of response and identifying linkages to abundance. *Ecology.* 2003 84:1-16. doi: 10.1890/0012-9658(2003)084[0001:RASTSL]2.0.CO;2.

- National Academies of Sciences, Engineering, and Medicine. 2021. Exploring a dynamic soil information system: proceedings of a workshop. The National Academies Press, Washington, DC. doi: 10.17226/26170.
- National Research Council. 1979. Carbon dioxide and climate: a scientific assessment. The National Academies Press, Washington, DC. doi: 10.17226/12181.
- Naylor D, Coleman-Derr D. Drought stress and root-associated bacterial communities. *Front Plant Sci.* 2018 8:2223. doi: 10.3389/fpls.2017.02223.
- Neelin JD, Münnich M, Su H, Meyerson JE, Holloway CE. Tropical drying trends in global warming models and observations. *Proc Natl Acad Sci U S A.* 2006 103(16):6110-6115. doi: 10.1073/pnas.0601798103.
- Nguyen N, Casadevall A. Our health, our action, our planet—a call to action for microbiologists to engage in climate research. *mBio.* 2021 12(5):e0250221. doi: 10.1128/mBio.02502-21.
- Nnadi NE, Carter DA. Climate change and the emergence of fungal pathogens. *PLoS Pathog.* 2021 17(4):e1009503. doi: 10.1371/journal.ppat.1009503.
- NOAA (National Oceanic and Atmospheric Administration). Extended reconstructed sea surface temperature (ERSST.v5). 2021 <https://www.ncei.noaa.gov/products/extended-reconstructed-sst>.
- Nuccio SP, Bäuml AJ. Comparative analysis of Salmonella genomes identifies a metabolic network for escalating growth in the inflamed gut. *mBio.* 2014 5(2):e00929-14. doi: 10.1128/mBio.00929-14.
- O'Connell CS, Ruan L, Silver WL. Drought drives rapid shifts in tropical rainforest soil biogeochemistry and greenhouse gas emissions. *Nat Commun.* 2018 9(1):1348. doi: 10.1038/s41467-018-03352-3.
- Ofiteru ID, Lunn M, Curtis TP, Wells GF, Criddle CS, Francis CA, Sloan WT. Combined niche and neutral effects in a microbial wastewater treatment community. *Proc Natl Acad Sci U S A.* 2010 107(35):15345-15350. doi: 10.1073/pnas.1000604107.
- Okabe S, Odagiri M, Ito T, Satoh H. Succession of sulfur-oxidizing bacteria in the microbial community on corroding concrete in sewer systems. *Appl Environ Microbiol.* 2007 73(3):971-980. doi: 10.1128/AEM.02054-06.
- Olejarz J, Iwasa Y, Knoll AH, Nowak MA. The Great Oxygenation Event as a consequence of ecological dynamics modulated by planetary change. *Nat Commun.* 2021 12(1):3985. doi: 10.1038/s41467-021-23286-7.
- Pachauri RK, Allen MR, Barros VR, Broome J, Cramer W, Christ R, Church JA, Clarke L, Dahe Q, Dasgupta P, Dubash NK, Edenhofer O, Elgizouli I, Field CB, Forster P, Friedlingstein P, Fuglestvedt J, Gomez-Echeverri L, Hallegatte S, Hegerl G, Howden M, Jiang K, Jimenez Cisneros B, Kattsov V, Lee H, Mach KJ, Marotzke J, Mastrandrea MD, Meyer L, Minx J, Mulugetta Y, O'Brien K, Oppenheimer M, Pereira JJ, Pichs-Madruga R, Plattner GK, Pörtner HO, Power SB, Preston B, Ravindranath NH, Reisinger A, Riahi K, Rusticucci M, Scholes R, Seyboth K, Sokona Y, Stavins R, Stocker TF, Tschakert P, van Vuuren D, van Ypersele JP. *Climate Change 2014: Synthesis Report. Contribution of Working Groups I, II and III to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change.* 2014 IPCC, Geneva, Switzerland.
- Paerl HW, Gardner WS, McCarthy MJ, Peierls BL, Wilhelm SW. Algal blooms: noteworthy nitrogen. *Science.* 2014 346(6206):175. doi: 10.1126/science.346.6206.175-a.
- Pascal M, Perez-Gordo M, Caballero T, Escribese MM, Lopez Longo MN, Luengo O, Manso L, Matheu V, Seoane E, Zamorano M, Labrador M, Mayorga C. Microbiome and allergic diseases. *Front Immunol.* 2018 9:1584. doi: 10.3389/fimmu.2018.01584.
- Paterson RRM, Lima N. How will climate change affect mycotoxins in food? *Food Res Int.* 2010 43(7):1902-1914. doi: 10.1016/j.foodres.2009.07.010.
- Philippot L, Hallin S, Börjesson G, et al. Biochemical cycling in the rhizosphere having an impact on global change. *Plant Soil.* 2009 321:61-81. doi: 10.1007/s11104-008-9796-9.
- Plósz BG, Liltved H, Ratnaweera H. Climate change impacts on activated sludge wastewater treatment: a case study from Norway. *Water Sci Technol.* 2009 60(2):533-541. doi: 10.2166/wst.2009.386.
- Pollak S, Cordero OX. Rhizobiome shields plants from infection. *Nat Microbiol.* 2020 5(8):978-979. doi: 10.1038/s41564-020-0766-1.
- Prest EI, Hammes F, van Loosdrecht MC, Vrouwenvelder JS. Biological stability of drinking water: controlling factors, methods, and challenges. *Front Microbiol.* 2016 7:45. doi: 10.3389/fmicb.2016.00045.
- Pruzzo C, Huq A, Colwell RR, Donelli G. Pathogenic Vibrio species in the marine and estuarine environment. In: Belkin S, Colwell RR (ed), *Oceans and Health: Pathogens in the Marine Environment.* 2005. Springer, Boston, MA. doi: 10.1007/0-387-23709-7_9.
- Puyol D, Batstone DJ, Hülsen T, Astals S, Peces M, Krömer JO. Resource recovery from wastewater by biological technologies: opportunities, challenges, and prospects. *Front Microbiol.* 2017 7:2106. doi: 10.3389/fmicb.2016.02106.

- Qureshi N, Annous BA, Ezeji TC, Karcher P, Maddox IS. Biofilm reactors for industrial bioconversion processes: employing potential of enhanced reaction rates. *Microb Cell Fact*. 2005 4:24. doi: 10.1186/1475-2859-4-24.
- Ramesh T, Bolan N, Kirkham M, Wijesekara H, Kanchikerimath M, Srinivasa Rao C, Sandeep S, Rinklebe J, Sik Ok Y, Choudhury B, Wang H, Tang C, Wang X, Song Z, Freeman, O. Soil organic carbon dynamics: impact of land use changes and management practices: a review. *Adv Agron*. 2019; 156:1-107. doi: 10.1016/bs.agron.2019.02.001.
- Ray C, Ming X. Climate change and human health: a review of allergies, autoimmunity and the microbiome. *Int J Environ Res Public Health*. 2020 17(13):4814. doi: 10.3390/ijerph17134814.
- Reeves AE, Theriot CM, Bergin IL, Huffnagle GB, Schloss PD, Young VB. The interplay between microbiome dynamics and pathogen dynamics in a murine model of *Clostridium difficile* Infection. *Gut Microbes*. 2011 2(3):145-158. doi: 10.4161/gmic.2.3.16333.
- Retter A, Karwautz C, Griebler C. Groundwater microbial communities in times of climate change. *Curr Issues Mol Biol*. 2021 41:509-538. doi: 10.21775/cimb.041.509.
- Rhodes J, Fisher MC. Global epidemiology of emerging *Candida auris*. *Curr Opin Microbiol*. 2019 52:84-89. doi: 10.1016/j.mib.2019.05.008.
- Robert V, Cardinali G, Casadevall A. Distribution and impact of yeast thermal tolerance permissive for mammalian infection. *BMC Biol*. 2015 13:18. doi: 10.1186/s12915-015-0127-3.
- Robert VA, Casadevall A. Vertebrate endothermy restricts most fungi as potential pathogens. *J Infect Dis*. 2009 200(10):1623-1626. doi: 10.1086/644642.
- Robinson CJ, Bohannon BJ, Young VB. From structure to function: the ecology of host-associated microbial communities. *Microbiol Mol Biol Rev*. 2010 74(3):453-476. doi: 10.1128/MMBR.00014-10.
- Robinson JM, Redvers N, Camargo A, Bosch CA, Breed MF, Brenner LA, Carney MA, Chauhan A, Dasari M, Dietz LG, Friedman M, Grieneisen L, Hoisington AJ, Horve PF, Hunter A, Jech S, Jorgensen A, Lowry CA, Man I, Mhuireach G, Navarro-Pérez E, Ritchie EG, Stewart JD, Watkins H, Weinstein P, Ishaq SL. Twenty important research questions in microbial exposure and social equity. *mSystems*. 2022 7(1):e01240-21. doi: 10.1128/msystems.01240-21.
- Rogers EM. *Diffusion of Innovations*, 5th ed. 2003 Free Press, New York, NY.
- Rosenberg E, Kushmaro A, Kramarsky-Winter E, Banin E, Yossi L. The role of microorganisms in coral bleaching. *ISME J*. 2009 3(2):139-146. doi: 10.1038/ismej.2008.104.
- Sáenz R, Bissell RA, Paniagua F. Post-disaster malaria in Costa Rica. *Prehosp Disaster Med*. 1995 10(3):154-160. doi: 10.1017/s1049023x00041935.
- Saha D, Rau BM, Kaye JP, Montes F, Adler PR, Kemanian AR. Landscape control of nitrous oxide emissions during the transition from conservation reserve program to perennial grasses for bioenergy. *GCB Bioenergy*. 2017 9:783-795. doi: 10.1111/gcbb.12395.
- Sanchez-Silva M, Rosowsky D. Biodeterioration of construction materials: state of the art and future challenges. *J Mater Civil Eng*. 2008 20(5):352-365. doi: 10.1061/(ASCE)0899-1561(2008)20:5(352).
- Satoh K, Makimura K, Hasumi Y, Nishiyama Y, Uchida K, Yamaguchi H. *Candida auris* sp. nov., a novel ascomycetous yeast isolated from the external ear canal of an inpatient in a Japanese hospital. *Microbiol Immunol*. 2009 53(1):41-4. doi: 10.1111/j.1348-0421.2008.00083.x. Erratum in: *Microbiol Immunol*. 2018 62(3):205.
- Saunio M, Stavert AR, Poulter B, Bousquet P, Canadell JG, Jackson RB, Raymond PA, Dlugokencky EJ, Houweling S, Patra PK, Ciais P, Arora VK, Bastviken D, Bergamaschi P, Blake DR, Brailsford G, Bruhwiler L, Carlson KM, Carrol M, Castaldi S, Chandra N, Crevoisier C, Crill PM, Covey K, Curry CL, Etiope G, Frankenberg C, Gedney N, Hegglin MI, Höglund-Isaksson L, Hugelius G, Ishizawa M, Ito A, Janssens-Maenhout G, Jensen KM, Joos F, Kleinen T, Krummel PB, Langenfelds RL, Laruelle GG, Liu L, Machida T, Maksyutov S, McDonald KC, McNorton J, Miller PA, Melton JR, Morino I, Müller J, Murguía-Flores F, Naik V, Niwa Y, Noce S, O'Doherty S, Parker RJ, Peng C, Peng S, Peters GP, Prigent C, Prinn R, Ramonet M, Regnier P, Riley WJ, Rosentretter JA, Segers A, Simpson IJ, Shi H, Smith SJ, Steele LP, Thornton BF, Tian H, Tohjima Y, Tubiello FN, Tsuruta A, Viovy N, Voulgarakis A, Weber TS, van Weele M, van der Werf GR, Weiss RF, Worthy D, Wunch D, Yin Y, Yoshida Y, Zhang W, Zhang Z, Zhao Y, Zheng B, Zhu Q, Zhu Q, Zhuang Q. The global methane budget 2000-2017. *Earth Syst Sci Data*. 2020 12:1561-1623. doi: 10.5194/essd-12-1561-2020.
- Savary S, Willocquet L, Pethybridge SJ, Esker P, McRoberts N, Nelson A. The global burden of pathogens and pests on major food crops. *Nat Ecol Evol*. 2019 3(3):430-439. doi: 10.1038/s41559-018-0793-y.
- Save Our Seas Act, 2 U.S.C. 2020. <https://www.congress.gov/116/plaws/publ224/PLAW-116publ224.pdf>.
- Scarborough MJ, Lynch G, Dickson M, McGee M, Donohue TJ, Noguera DR. Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. *Biotechnol Biofuels*. 2018 11:200. doi: 10.1186/s13068-018-1193-x.
- Schädel C, Bader MF, Schuur E, et al. Potential carbon emissions dominated by carbon dioxide from thawed permafrost soils. *Nat Clim Chang*. 2016 6:950-953. doi: 10.1038/nclimate3054.

- Schalk JA, Docters van Leeuwen AE, Lodder WJ, de Man H, Euser S, den Boer JW, de Roda Husman AM. Isolation of *Legionella pneumophila* from pluvial floods by amoebal coculture. *Appl Environ Microbiol*. 2012 78(12):4519-4521. doi: 10.1128/AEM.00131-12.
- Schimel, J. Life in dry soils: effects of drought on soil microbial communities and processes. *Annu Rev Ecol Evol Syst*. 2018 49:409-432. doi: 10.1146/annurev-ecolsys-110617-062614.
- Schirrmeister BE, de Vos JM, Antonelli A, Bagheri HC. Evolution of multicellularity coincided with increased diversification of cyanobacteria and the Great Oxidation Event. *Proc Natl Acad Sci U S A*. 2013 110(5):1791-1796. doi: 10.1073/pnas.1209927110.
- Schuur EA, McGuire AD, Schädel C, Grosse G, Harden JW, Hayes DJ, Hugelius G, Koven CD, Kuhry P, Lawrence DM, Natali SM, Olefeldt D, Romanovsky VE, Schaefer K, Turetsky MR, Treat CC, Vonk JE. Climate change and the permafrost carbon feedback. *Nature*. 2015 520(7546):171-179. doi: 10.1038/nature14338.
- Schuur EAG, Bockheim J, Canadell JG, Euskirchen E, Field CB, Goryachkin SV, Hagemann S, Kuhry P, Laflour PM, Mazhitova HLG, Nelson FE, Rinke A, Romanovsky VE, Shiklomanov N, Tarnocai C, Venevsky S, Vogel JG, Zimov SA. Vulnerability of permafrost carbon to climate change: implications for the global carbon cycle. *BioScience*. 2008 58(8):701-714. doi: 10.1641/B580807.
- Sekirov I, Finlay BB. The role of the intestinal microbiota in enteric infection. *J Physiol*. 2009 587(Pt 17):4159-4167. doi: 10.1113/jphysiol.2009.172742.
- Semenza JC, Trinanes J, Lohr W, Sudre B, Löfdahl M, Martinez-Urtaza J, Nichols GL, Rocklöv J. Environmental suitability of *Vibrio* infections in a warming climate: an early warning system. *Environ Health Perspect*. 2017 125(10):107004. doi: 10.1289/EHP2198.
- Shcherbak I, Millar N, Robertson GP. Global metaanalysis of the nonlinear response of soil nitrous oxide (N₂O) emissions to fertilizer nitrogen. *Proc Natl Acad Sci U S A*. 2014 111(25):9199-9204. doi: 10.1073/pnas.1322434111.
- Shears P. Epidemiology and infection in famine and disasters. *Epidemiol Infect*. 1991 107(2):241-251. doi: 10.1017/s0950268800048895.
- Sherkow JS. Patent protection for microbial technologies. *FEMS Microbiol Lett*. 2017 364(20). doi: 10.1093/femsle/fnx205.
- Sihl D, Xu X, Salazar Ortiz M, O'Connell CS, Silver WL, López-Lloreda C, Brenner JM, Quinn RK, Phillips JR, Newman BD, Mayes MA. Representing methane emissions from wet tropical forest soils using microbial functional groups constrained by soil diffusivity. *Biogeosciences*. 2021 18:1769-1786. doi: 10.5194/bg-18-1769-2021.
- Simonova EG, Kartavaya SA, Titkov AV, Loktionova MN, Raichich SR, Tolpin VA, Lupyan EA, Platonov AE. Anthrax in the territory of Yamal: assessment of epizootological and epidemiological risks. *Problems Particularly Dangerous Infect*. 2017. 2017(1):89-93. (In Russian.) doi: 10.21055/0370-1069-2017-1-89-93.
- Singh S, Tiwari S. Climate change, water and wastewater treatment: interrelationship and consequences. In: Singh R, Kolok A, Bartelt-Hunt S (ed), *Water Conservation, Recycling and Reuse: Issues and Challenges*. 2019: 203-214. Springer, Singapore. doi: 10.1007/978-981-13-3179-4_11.
- Smith PM, Howitt MR, Panikov N, Michaud M, Gallini CA, Bohlooly-Y M, Glickman JN, Garrett WS. The microbial metabolites, short-chain fatty acids, regulate colonic Treg cell homeostasis. *Science*. 2013 341(6145):569-573. doi: 10.1126/science.1241165.
- Song Y, Yao Q, Yang X, et al. Metagenomics-informed soil biogeochemical models projected less carbon loss in tropical soils in response to climate warming. *Res Square*. 20 September 2021; preprint (version 1). doi: 10.21203/rs.3.rs-918612/v1.
- Spahni R, Wania R, Neef L, van Weele M, Pison I, Bousquet P, Frankenberg C, Foster PN, Joos F, Prentice IC, van Velthoven P. Constraining global methane emissions and uptake by ecosystems. *Biogeosciences*. 2011 8:1643-1665. doi: 10.5194/bg-8-1643-2011.
- St Clair SB, Lynch JP. The opening of Pandora's Box: climate change impacts on soil fertility and crop nutrition in developing countries. *Plant Soil*. 2010 335:101-115. doi: 10.1007/s11104-010-0328-z.
- Stegmann P, Londo M, Junginger M. The circular bioeconomy: its elements and role in European bioeconomy clusters. *Resour Conserv Recycling: X*. 2020 6:100029. doi: 10.1016/j.rcrx.2019.100029.
- Stella E, Mari L, Gabrieli J, Barbante C, Bertuzzo E. Permafrost dynamics and the risk of anthrax transmission: a modelling study. *Sci Rep*. 2020 10(1):16460. doi: 10.1038/s41598-020-72440-6.
- Still PE, Macklin AW, Ribelin WE, Smalley EB. Relationship of ochratoxin A to foetal death in laboratory and domestic animals. *Nature*. 1971 234(5331):563-564. doi: 10.1038/234563a0.
- Tan JL, Goh PC, Blackwood DJ. Influence of H₂S-producing chemical species in culture medium and energy source starvation on carbon steel corrosion caused by methanogens. *Corrosion Sci*. 2017; 119:102-111. doi: 10.1016/j.corsci.2017.02.014.
- Tang H, Chen Y. Global glaciations and atmospheric change at ca. 2.3 Ga. *Geosci Frontiers*. 2013 4(5):583-596. doi: 10.1016/j.gsf.2013.02.003.
- Tarnocai C, Canadell JG, Schuur EAG, Kuhry P, Mazhitova G, Zimov S. Soil organic carbon pools in the northern circumpolar permafrost region. *Global Biogeochem Cycles*. 2009 23:GB2023. doi: 10.1029/2008GB003327.

- Taylor J, Lai KM, Davies M, Clifton D, Ridley I, Bid-dulph P. Flood management: prediction of micro-bial contamination in large-scale floods in urban environments. *Environ Int*. 2011 37(5):1019-1029. doi: 10.1016/j.envint.2011.03.015.
- Taylor MW, Radax R, Steger D, Wagner M. Sponge-as-sociated microorganisms: evolution, ecology, and biotechnological potential. *Microbiol Mol Biol Rev*. 2007 71(2):295-347. doi: 10.1128/MMBR.00040-06.
- Tedersoo L, Bahram M, Pöhlme S, Kõljalg U, Yorou NS, Wijesundera R, Villarreal Ruiz L, Vasco-Palacios AM, Thu PQ, Suija A, Smith ME, Sharp C, Saluveer E, Saitta A, Rosas M, Riit T, Ratkowsky D, Pritsch K, Põldmaa K, Piepenbring M, Phosri C, Peterson M, Parts K, Pärtel K, Otsing E, Nouhra E, Njouonkou AL, Nilsson RH, Morgado LN, Mayor J, May TW, Ma-juakim L, Lodge DJ, Lee SS, Larsson KH, Kohout P, Hosaka K, Hiiesalu I, Henkel TW, Harend H, Guo LD, Greslebin A, Grelet G, Geml J, Gates G, Dunstan W, Dunk C, Drenkhan R, Dearnaley J, De Kesel A, Dang T, Chen X, Buegger F, Brearley FQ, Bonito G, Anslan S, Abell S, Abarenkov K. Fungal biogeogra-phy. Global diversity and geography of soil fungi. *Science*. 2014 346(6213):1256688. doi: 10.1126/science.1256688.
- Tefera, T. Post-harvest losses in African maize in the face of increasing food shortage. *Food Sec*. 2012 4:267-277. doi: 10.1007/s12571-012-0182-3.
- Tesson SVM, Skjøth CA, Šantl-Temkiv T, Löndahl J. Airborne microalgae: insights, opportunities, and challenges. *Appl Environ Microbiol*. 2016 82(7):1978-1991. doi: 10.1128/AEM.03333-15.
- Thurber RV, Payet JP, Thurber AR, Correa AM. Virus-host interactions and their roles in coral reef health and disease. *Nat Rev Microbiol*. 2017 15(4):205-216. doi: 10.1038/nrmicro.2016.176.
- Tian H, Xu R, Canadell JG, Thompson RL, Winiwarter W, Suntharalingam P, Davidson EA, Ciais P, Jackson RB, Janssens-Maenhout G, Prather MJ, Regnier P, Pan N, Pan S, Peters GP, Shi H, Tubiello FN, Zaehele S, Zhou F, Arneeth A, Battaglia G, Berthet S, Bopp L, Bouwman AF, Buitenhuis ET, Chang J, Chipperfield MP, Dangal SRS, Dlugokencky E, Elkins JW, Eyre BD, Fu B, Hall B, Ito A, Joos F, Krummel PB, Landolfi A, Laruelle GG, Lauerwald R, Li W, Lienert S, Maavara T, MacLeod M, Millet DB, Olin S, Patra PK, Prinn RG, Raymond PA, Ruiz DJ, van der Werf GR, Vuichard N, Wang J, Weiss RF, Wells KC, Wilson C, Yang J, Yao Y. A comprehensive quantification of global nitrous oxide sources and sinks. *Nature*. 2020 586(7828):248-256. doi: 10.1038/s41586-020-2780-0.
- Tiedje JM, Bruns MA, Casadevall A, Criddle C, Eloë-Fadrosch E, Karl DM, Nguyen NK, Zhou J. Mi-crobes and climate change: a research prospec-tus for the future. *mBio*. 2022 13(2). doi: 10.1128/mbio.00800-22.
- Tiedje JM, Donohue T. Microbes in the energy grid. *Science*. 2008 320(5879):985. doi: 10.1126/sci-ence.1159999.
- Tirado MC, Clarke R, Jaykus LA, McQuatters-Gollop A, Frank JM. Climate change and food safety: a review. *Food Res Int*. 2010 43(7):1745-1765. doi: 10.1016/j.foodres.2010.07.003.
- Todd-Brown KEO, Randerson JT, Post WM, Hoffman FM, Tarnocai C, Schuur EAG, Allison SD. Causes of variation in soil carbon simulations from CMIP5 Earth system models and comparison with observations. *Biogeosciences*. 2013 10:1717-1736. doi: 10.5194/bg-10-1717-2013.
- Turner TR, James EK, Poole PS. The plant microbiome. *Genome Biol*. 2013 14(6):209. doi: 10.1186/gb-2013-14-6-209.
- Valles-Colomer M, Falony G, Darzi Y, Tigchelaar EF, Wang J, Tito RY, Schiweck C, Kurilshikov A, Joossens M, Wijmenga C, Claes S, Van Oudenhove L, Zherna-kova A, Vieira-Silva S, Raes J. The neuroactive poten-tial of the human gut microbiota in quality of life and depression. *Nat Microbiol*. 2019 4(4):623-632. doi: 10.1038/s41564-018-0337-x.
- van der Waaij D, Berghuis-de Vries JM, Lekkerkerk-van der Wees JEC. Colonization resistance of the diges-tive tract in conventional and antibiotic-treated mice. *J Hyg (Lond)*. 1971 69(3):405-411. doi: 10.1017/s0022172400021653.
- van Elsas JD, Chiurazzi M, Mallon CA, Elhottova D, Kristufek V, Salles JF. Microbial diversity determines the invasion of soil by a bacterial pathogen. *Proc Natl Acad Sci U S A*. 2012 109(4):1159-1164. doi: 10.1073/pnas.1109326109.
- Vanwonderghem I, Webster NS. Coral reef micro-organisms in a changing climate. *iScience*. 2020 23(4):100972. doi: 10.1016/j.isci.2020.100972.
- Varner RK, Crill PM, Frolking S, McCalley CK, Burke SA, Chanton JP, Holmes ME; Isogenie Project Co-ordinators, Saleska S, Palace MW. Permafrost thaw driven changes in hydrology and vegetation cover increase trace gas emissions and climate forcing in Stordalen Mire from 1970 to 2014. *Philos Trans A Math Phys Eng Sci*. 2022 380(2215):20210022. doi: 10.1098/rsta.2021.0022.
- Vega Thurber R, Mydlarz LD, Brandt M, Harvell D, Weil E, Raymundo L, Willis BL, Langevin S, Tracy AM, Littman R, Kemp KM, Dawkins P, Prager KC, Garren M, Lamb J. Deciphering coral disease dynamics: inte-grating host, microbiome, and the changing environ-ment. *Front Ecol Evol*. 2020 8:575927. doi: 10.3389/fevo.2020.575927.
- Verma V, Ravindran P, Kumar PP. Plant hormone-me-diated regulation of stress responses. *BMC Plant Biol*. 2016 16:86. doi: 10.1186/s12870-016-0771-y.

- Vermeulen LC, Brandsema PS, van de Kasstele J, Bom BCJ, Sterk HAM, Sauter FJ, van den Berg HHJL, de Roda Husman AM. Atmospheric dispersion and transmission of *Legionella* from wastewater treatment plants: a 6-year case-control study. *Int J Hyg Environ Health*. 2021 237:113811. doi: 10.1016/j.ijheh.2021.113811.
- Verstraete W, Yanuka-Golub K, Driesen N, De Vrieze J. Engineering microbial technologies for environmental sustainability: choices to make. *Microb Biotechnol*. 2022 15(1):215-227. doi: 10.1111/1751-7915.13986.
- Vezzulli L, Brettar I, Pezzati E, Reid PC, Colwell RR, Höfle MG, Pruzzo C. Long-term effects of ocean warming on the prokaryotic community: evidence from the vibrios. *ISME J*. 2012 6(1):21-30. doi: 10.1038/ismej.2011.89.
- Vicca S, Stocker B, Reed S, Wieder W, Bahn M, Fay P, Janssens I, Lambers H, Peñuelas J, Piao S, Rebel K, Sardans J, Sigurdsson B, Van Sundert K, Wang Y-P, Zaehle S, Ciais P. Using research networks to create the comprehensive datasets needed to assess nutrient availability as a key determinant of terrestrial carbon cycling. *Environ Res Lett*. 2018 13(12):125006. doi: 10.1088/1748-9326/aaeae7.
- Videla HA, Characklis WG. Biofouling and microbially influenced corrosion. *Int Biodeterior Biodegradation*. 1992 29(3):195-212. doi: 10.1016/0964-8305(92)90044-O.
- Volk T, Hoffert MI. Ocean carbon pumps: analysis of relative strengths and efficiencies in ocean-driven atmospheric CO₂ changes. In: Sundquist E, Broecker W (ed), *The Carbon Cycle and Atmospheric CO₂: Natural Variations Archean to Present*. 1985 American Geophysical Union, Washington D.C. 99-110. doi: 10.1029/GM032p0099.
- Vukanti RVNR. Structure and Function of Rhizobiome. In: Varma A, Tripathi S, Prasad R (ed), *Plant Microbe Symbiosis*. 2020 Springer, Cham, Switzerland. 241-261. doi: 10.1007/978-3-030-36248-5_13.
- Wagner M, Loy A, Nogueira R, Purkhold U, Lee N, Daims H. Microbial community composition and function in wastewater treatment plants. *Antonie Van Leeuwenhoek*. 2002 81(1-4):665-680. doi: 10.1023/a:1020586312170.
- Wainaina S, Awasthi MK, Sarsaiya S, Chen H, Singh E, Kumar A, Ravindran B, Awasthi SK, Liu T, Duan Y, Kumar S, Zhang Z, Taherzadeh MJ. Resource recovery and circular economy from organic solid waste using aerobic and anaerobic digestion technologies. *Bioresour Technol*. 2020 301:122778. doi: 10.1016/j.biortech.2020.122778.
- Wallace R. A synergism of plagues: "planned shrinkage," contagious housing destruction, and AIDS in the Bronx. *Environ Res*. 1988 47(1):1-33. doi: 10.1016/s0013-9351(88)80018-5.
- Wang G, Gao Q, Yang Y, Hobbie SE, Reich PB, Zhou J. Soil enzymes as indicators of soil function: a step toward greater realism in microbial ecological modeling. *Glob Chang Biol*. 2022 28(5):1935-1950. doi: 10.1111/gcb.16036.
- Wei S, Cui H, Zhu Y, Lu Z, Pang S, Zhang S, Dong H, Su X. Shifts of methanogenic communities in response to permafrost thaw results in rising methane emissions and soil property changes. *Extremophiles*. 2018 22(3):447-459. doi: 10.1007/s00792-018-1007-x.
- Wei S, Jiang Z, Liu H, Zhou D, Sanchez-Silva M. Microbiologically induced deterioration of concrete—a review. *Braz J Microbiol*. 2014 44(4):1001-1007. doi: 10.1590/S1517-83822014005000006.
- Wei Z, Yang T, Friman VP, Xu Y, Shen Q, Jousset A. Trophic network architecture of root-associated bacterial communities determines pathogen invasion and plant health. *Nat Commun*. 2015 6:8413. doi: 10.1038/ncomms9413.
- Wendel AM, Johnson DH, Sharapov U, Grant J, Archer JR, Monson T, Koschmann C, Davis JP. Multi-state outbreak of *Escherichia coli* O157:H7 infection associated with consumption of packaged spinach, August-September 2006: the Wisconsin investigation. *Clin Infect Dis*. 2009 48(8):1079-1086. doi: 10.1086/597399.
- Wheeler T, von Braun J. Climate change impacts on global food security. *Science*. 2013 341(6145):508-513. doi: 10.1126/science.1239402.
- Wieder WR, Allison SD, Davidson EA, Georgiou K, Hararuk O, He Y, Hopkins F, Luo Y, Smith MJ, Sulman B, et al. Explicitly representing soil microbial processes in Earth system models. *Global Biogeochem Cycles*. 2015 29:1782-1800. doi: 10.1002/2015GB005188.
- Wilhelm SW, Bullerjahn GS, McKay RML. The complicated and confusing ecology of *Microcystis* blooms. *mBio*. 2020 11(3):e00529-20. doi: 10.1128/mBio.00529-20.
- Wohlers J, Engel A, Zöllner E, Breithaupt P, Jürgens K, Hoppe HG, Sommer U, Riebesell U. Changes in biogenic carbon flow in response to sea surface warming. *Proc Natl Acad Sci U S A*. 2009 106(17):7067-7072. doi: 10.1073/pnas.0812743106.
- Woodcroft BJ, Singleton CM, Boyd JA, Evans PN, Emerson JB, Zayed AAF, Hoelzle RD, Lambertson TO, McCalley CK, Hodgkins SB, Wilson RM, Purvine SO, Nicora CD, Li C, Frolking S, Chanton JP, Crill PM, Saleska SR, Rich VI, Tyson GW. Genome-centric view of carbon processing in thawing permafrost. *Nature*. 2018 560(7716):49-54. doi: 10.1038/s41586-018-0338-1.
- Woodhead AJ, Hicks CC, Norström AV, Williams GJ, Graham NAJ. Coral reef ecosystem services in the Anthropocene. *Funct Ecol*. 2019; 33:1023-1034. doi: 10.1111/1365-2435.13331

- Woodward G, Perkins DM, Brown LE. Climate change and freshwater ecosystems: impacts across multiple levels of organization. *Philos Trans R Soc Lond B Biol Sci.* 2010 365(1549):2093-2106. doi: 10.1098/rstb.2010.0055.
- Worden AZ, Follows MJ, Giovannoni SJ, Wilken S, Zimmerman AE, Keeling PJ. Environmental science. Rethinking the marine carbon cycle: factoring in the multifarious lifestyles of microbes. *Science.* 2015 347(6223):1257594. doi: 10.1126/science.1257594.
- World Health Organization. Climate change and health. October 2021. <https://www.who.int/news-room/fact-sheets/detail/climate-change-and-health>.
- World Health Organization. The top 10 causes of death. December 2020. <https://www.who.int/news-room/fact-sheets/detail/the-top-10-causes-of-death>.
- Wu L, Ning D, Zhang B, Li Y, Zhang P, Shan X, Zhang Q, Brown MR, Li Z, Van Nostrand JD, Ling F, Xiao N, Zhang Y, Vierheilig J, Wells GF, Yang Y, Deng Y, Tu Q, Wang A, Global Water Microbiome Consortium, Zhang T, He Z, Keller J, Nielsen PH, Alvarez PJJ, Cridle CS, Wagner M, Tiedje JM, He Q, Curtis TP, Stahl DA, Alvarez-Cohen L, Rittmann BE, Wen X, Zhou J. Global diversity and biogeography of bacterial communities in wastewater treatment plants. *Nat Microbiol.* 2019 4(7):1183-1195. doi: 10.1038/s41564-019-0426-5. Erratum in: *Nat Microbiol.* 2019 4(12):2579.
- Xu H, Liu M, Cao J, Li X, Fan D, Xia Y, Lu X, Li J, Ju D, Zhao H. The dynamic interplay between the gut microbiota and autoimmune diseases. *J Immunol Res.* 2019 2019:7546047. doi: 10.1155/2019/7546047.
- Xue K, Yuan MM, Shi ZJ, Qin Y, Deng Y, Cheng L, Wu L, He Z, Van Nostrand JD, Bracho R, Natali S, Schuur EAG, Luo C, Konstantinidis KT, Wang Q, Cole JR, Tiedje JM, Luo Y, Zhou J-Z. Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. *Nat Clim Chang.* 2016 6:595-600. doi: 10.1038/nclimate2940.
- Yang G, Liu ZQ, Yang PC. Treatment of allergic rhinitis with probiotics: an alternative approach. *N Am J Med Sci.* 2013 5(8):465-468. doi: 10.4103/1947-2714.117299.
- Yang W, Marr LC. Mechanisms by which ambient humidity may affect viruses in aerosols. *Appl Environ Microbiol.* 2012 78(19):6781-6788. doi: 10.1128/AEM.01658-12.
- Yuan MM, Guo X, Wu L, et al. Climate warming enhances microbial network complexity and stability. *Nat Clim Chang.* 2021 11:343-348. doi: 10.1038/s41558-021-00989-9.
- Zhao L, Zhang F, Ding X, Wu G, Lam YY, Wang X, Fu H, Xue X, Lu C, Ma J, Yu L, Xu C, Ren Z, Xu Y, Xu S, Shen H, Zhu X, Shi Y, Shen Q, Dong W, Liu R, Ling Y, Zeng Y, Wang X, Zhang Q, Wang J, Wang L, Wu Y, Zeng B, Wei H, Zhang M, Peng Y, Zhang C. Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. *Science.* 2018 359(6380):1151-1156. doi: 10.1126/science.aao5774.
- Zhou J, Deng Y, Luo F, He Z, Tu Q, Zhi X. Functional molecular ecological networks. *mBio.* 2010 1(4):e00169-10. doi: 10.1128/mBio.00169-10.
- Zhou J, Deng Y, Luo F, He Z, Yang Y. Phylogenetic molecular ecological network of soil microbial communities in response to elevated CO₂. *mBio.* 2011 2(4):e00122-11. doi: 10.1128/mBio.00122-11.
- Zhou J, Xue K, Xie J, et al. Microbial mediation of carbon-cycle feedbacks to climate warming. *Nat Clim Chang.* 2012 2:106-110. doi: 10.1038/nclimate1331.
- Ziska LH, Makra L, Harry SK, Bruffaerts N, Hendrickx M, Coates F, Saarto A, Thibaudon M, Oliver G, Damielis A, Charalampopoulos A, Vokou D, Heidmarsson S, Gudjohnsen E, Bonini M, Oh JW, Sullivan K, Ford L, Brooks GD, Myszkowska D, Severova E, Gehrig R, Ramón GD, Beggs PJ, Knowlton K, Crimmins AR. Temperature-related changes in airborne allergenic pollen abundance and seasonality across the northern hemisphere: a retrospective data analysis. *Lancet Planet Health.* 2019 3(3):e124-e131. doi: 10.1016/S2542-5196(19)30015-4. Erratum in: *Lancet Planet Health.* 2019 3(11):e446.
- Zoraster RM. Vulnerable populations: Hurricane Katrina as a case study. *Prehosp Disaster Med.* 2010 25(1):74-78. doi: 10.1017/s1049023x00007718.
- Zouboulis A, Tolkou A. Effect of climate change in wastewater treatment plants: reviewing the problems and solutions. In: Shrestha S, Anal A, Salam P, van der Valk M (ed), *Managing Water Resources under Climate Uncertainty.* 2015 Springer, Cham, Switzerland. doi: 10.1007/978-3-319-10467-6_10.
- Zytynska SE, Eicher M, Rothballer M, Weisser WW. Microbial-mediated plant growth promotion and pest suppression varies under climate change. *Front Plant Sci.* 2020 11:573578. doi: 10.3389/fpls.2020.573578.

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