



PACCARB

PRESIDENTIAL ADVISORY COUNCIL ON COMBATING ANTIBIOTIC-RESISTANT BACTERIA

Meeting Summary

28th Public Meeting of the Presidential Advisory Council on Combating Antibiotic-Resistant Bacteria

September 9-10, 2026

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Meeting Proceedings

Day 1

Welcome, Overview, and Roll Call

Paul Plummer, D.V.M., Ph.D., DACVIM, DECSRHM, Council Chair; Jason Newland, M.D., M.Ed., Vice Chair; and Sarah McClelland, M.P.H., Designated Federal Official, Public Health Advisor, Office of the Assistant Secretary for Health (OASH), U.S. Department of Health and Human Services (HHS)

Ms. Sarah McClelland welcomed the Council members and public to the 28th Public Meeting of the Presidential Advisory Council on Combating Antibiotic-Resistant Bacteria (PACCARB) at 9:10 a.m. ET. She described the Council's establishment and charter and summarized the rules governing the Council under the Federal Advisory Committee Act and conflict-of-interest guidelines. She acknowledged and thanked the individuals and organizations that submitted written public comment. She then called the roll. (See the appendix for the list of Council members and staff.)

Dr. Paul Plummer welcomed the Council and summarized the agenda, emphasizing that the microbiome represents an important and often overlooked dimension of antimicrobial resistance (AMR), shaping how microbial communities influence resistance, infection prevention, treatment outcomes, and health across people, animals, and the environment. He encouraged the Council to connect emerging microbiome science to the broader AMR landscape and identify practical, actionable opportunities that could improve patient care, public health, and future AMR strategies.

Dr. Jason Newland framed the meeting as an opportunity to view the microbiome not as separate from AMR, but as a key lens for understanding the conditions that allow resistant organisms to emerge and persist across humans, animals, and the environment. He noted that this perspective could help identify innovative prevention strategies and strengthen future One Health approaches to combating AMR. He concluded that the meeting represented an important first step in exploring the connections between microbiome science and AMR and identifying actionable opportunities for microbiome research to inform future strategies and recommendations.

Opening Remarks

Connor Semelsberger, Chief of Staff to the Assistant Secretary for Health

Mr. Connor Semelsberger thanked PACCARB members for their leadership in addressing AMR and emphasized that it remains a major public health priority. Speaking on behalf of the Assistant Secretary for Health, he highlighted the microbiome as a promising area for preventing infections, preserving the effectiveness of antibiotics, and supporting health across people, animals, and the environment. He stressed the importance of continued stewardship, scientific innovation, and cross-sector collaboration to turn microbiome research into practical, evidence-based solutions for combating AMR.

Patient Story: Fecal Microbiota Transplantation in Dog with Protein-Losing Enteropathy

Betty Chow, BVM&S, MRCVS, DACVIM (SAIM), Colorado State University; Alice Hernandez, Rosie's Pet Parent

Ms. Alice Hernandez and Dr. Betty Chow shared the case of Rosie, a dog with chronic gastrointestinal disease, protein-losing enteropathy, and kidney disease whose condition remained difficult to manage despite multiple dietary and medical interventions. Rosie experienced persistent diarrhea, weight loss, low albumin levels, and declining health, prompting Dr. Chow to investigate the role of microbiome dysfunction in her disease progression. Testing revealed significant dysbiosis, leading the care team to pursue fecal microbiota transplantation (FMT) as an adjunctive treatment. Rosie initially received two FMTs followed by regular maintenance treatments. Over time, her gastrointestinal symptoms improved, she gained weight, her albumin levels increased, and measures of microbiome health showed substantial improvement. Although she experienced a temporary setback during an unrelated acute illness that required antimicrobial treatment, she recovered after resuming FMT and continued to show long-term clinical improvement.

Dr. Chow highlighted FMT as a promising tool for managing chronic enteropathy and restoring microbiome health in veterinary patients. She noted that the treatment helped reduce reliance on antimicrobial therapies, allowing clinicians additional time to optimize diet and other medical interventions while maintaining symptom control. Dr. Chow concluded with a discussion of published evidence supporting the use of FMT in dogs with chronic enteropathy and emphasized the potential of microbiome-based approaches to improve outcomes while supporting antimicrobial stewardship.

Microbiome Subcommittee Report-Out

Suchitra Hourigan, M.D., National Institutes of Health

Dr. Suchitra Hourigan presented findings from the PACCARB microbiome subcommittee roundtable, which convened experts from across microbiome research, clinical medicine, regulatory science, and public health to assess the current state of the field and identify future research priorities focused on the human health sector. She noted that microbiome science has evolved from primarily descriptive studies to increasingly mechanistic and translational research, with growing evidence linking the microbiome to metabolic and immune conditions, among others. At the same time, challenges remain in establishing causality, improving reproducibility, and ensuring research reflects diverse populations.

The subcommittee identified ten strategic priorities to advance microbiome science:

1. Expanding controlled interventional studies and effective integration of animal and human research
2. Investing in large-scale data infrastructure
3. Integrating multi-omics approaches
4. Advancing understanding of the virome and other underrepresented microbial communities
5. Strengthening regulatory frameworks for microbiome-based therapies and diagnostics
6. Developing validated microbiome metrics and treating individual-variability as a target for precision medicine
7. Understanding early-life microbiome development and its impacts
8. Investigating the gut-brain axis and implications for neurological disease and prevention
9. Translating cancer microbiome research into other chronic diseases
10. Educating professionals and the public on microbiome and nutrition science

Dr. Hourigan also highlighted evidence-based practices that support microbiome health, including dietary diversity, fiber consumption, fermented foods, antibiotic stewardship, breastfeeding, and healthy lifestyle behaviors. She cautioned that the scientific evidence supporting many direct-to-consumer microbiome tests and commercial probiotic claims remains limited. She concluded that sustained federal investment, coordination, and public education will be critical to translating microbiome research into interventions that improve health outcomes and reduce the burden of chronic and infectious disease.

Discussion

The discussion underscored the need for expanded research on oral, skin, maternal, and infant microbiomes, along with greater understanding of microbiome variation across age, sex, and other biological and behavioral factors; stronger education for healthcare professionals and the public; careful communication about antibiotic benefits and risks; evidence-based regulation of microbiome products; sustained federal investment; and interdisciplinary collaboration that includes dentistry, pharmacy, and other relevant specialties. Council members emphasized the importance of strengthening research methods and representation and translating microbiome science into responsible approaches to antimicrobial stewardship and chronic disease prevention.

Council members emphasized the need to broaden microbiome initiatives beyond the gut and include the clinical disciplines associated with other microbiome body sites. Dr. Jacinda Abdul-Mutakabbir noted that dentistry and pharmacy were not prominently represented at the roundtable, despite the relevance of oral microbiomes and medication-related effects on microbial communities. Dr. Susan Huang similarly called for greater attention to oral and skin microbiome health. Dr. Hourigan shared that the roundtable focused primarily on the gut because it is the most extensively studied, while acknowledging growing evidence linking changes in the oral and dermal microbiomes to conditions such as periodontal disease and atopic dermatitis. She agreed that future efforts would benefit from broader participation by other relevant specialists.

Council members identified a need for microbiome research that better reflects geographic diversity, different stages of life, and populations with distinct health risks. Dr. Abdul-Mutakabbir emphasized examining variation across regions and populations, particularly in communities experiencing high rates of chronic disease. Dr. Huang urged greater attention to maternal and women's health, infants, and aging populations. Dr. Hourigan agreed that these topics are important and were discussed during the subcommittee meeting, but they were not included in her presentation because of time and space limitations. Dr. Padmini Srikantiah asked about microbiome-based strategies to prevent acute infections in preterm infants and the therapeutic potential of microbiome-derived metabolites. Dr. Hourigan described evidence linking maternal microbiome characteristics to preterm birth and noted that microbiome changes may precede infection in infants. She emphasized the value of studying these changes before disease develops, while maintaining research involving people already affected by chronic illness. She also highlighted growing interest in therapies based on microbial products rather than live bacteria, which may offer a simpler regulatory pathway. Dr. Francisco Zgmutt noted the methodological challenges of conducting randomized controlled trials involving infants, and Dr. Hourigan responded that future publications could provide guidance on study design for early-life microbiome research.

Dr. David Jenkins observed that healthcare professional education had received limited emphasis and asked whether clinician education should be further explored. Dr. Hourigan identified

education as a major priority, noting the need to integrate microbiome science into medical education and clinical training because many healthcare providers receive limited exposure to the field. Dr. Robin Patel extended this concern to communication about antibiotic use, stressing that microbiome-informed recommendations to limit antibiotic exposure must be carefully balanced against the essential role of antibiotics in treating serious infections. Dr. Hourigan agreed that antibiotics remain lifesaving when appropriately prescribed and reinforced the need for clear stewardship messaging and education for both healthcare professionals and the public. Dr. Lucas Pantaleon raised concern about the expanding commercial market for probiotics and other microbiome products, questioning whether the evidence supporting these products is sufficient and whether stronger oversight is needed. Dr. Hourigan explained that many commercial products are marketed under dietary supplement frameworks that do not require the same level of evidence as disease-specific therapies. She cautioned that marketing may outpace scientific evidence and emphasized the need for rigorous evidence, public education, and appropriate regulatory oversight.

Dr. Lynn Marks asked about the funding environment and whether future federal support for microbiome research was likely. Dr. Hourigan acknowledged current funding challenges but expressed optimism that federal agencies, including HHS, recognize the importance of microbiome science and may continue supporting the field.

Panel 1: Understanding the Microbiome and Therapeutic Non-Responsiveness

Microbiome Science and Antimicrobial Resistance

Vincent B. Young, M.D., Ph.D., FIDSA, FAAM, University of Michigan

Dr. Vincent Young provided an overview of the relationship between microbiome science and AMR, emphasizing that microbes, antibiotics, and resistance mechanisms have coexisted long before modern medicine. He explained that AMR should be viewed through a One Health lens that recognizes the interconnected roles of humans, animals, and the environment. He distinguished between the microbiota, the community of microorganisms, and the microbiome, which includes both the microorganisms and the environments in which they exist. This broader perspective is important for understanding how microbial communities influence health, disease, and resistance across different ecosystems. Dr. Young described several ways the microbiome can contribute to AMR. Microbial communities serve as reservoirs for antibiotic resistance genes that can be transferred among organisms across human, animal, and environmental settings. He also noted that antibiotics can function not only as antimicrobial agents but also as signaling molecules, influencing microbial behavior and potentially increasing virulence, fitness, or resistance when present at low concentrations in the environment.

Dr. Young also highlighted the microbiome's potential as a tool for combating AMR. He discussed the concept of colonization resistance, whereby healthy microbial communities help prevent the establishment and growth of pathogenic organisms. He pointed to FMT as an example of a microbiome-based intervention that has proven effective in treating recurrent *Clostridioides difficile* infection and may have broader applications for addressing infections caused by antimicrobial-resistant organisms. Emerging research also suggests that microbiome-based therapies may influence treatment outcomes in areas such as cancer immunotherapy. Dr. Young concluded by emphasizing that addressing AMR requires consideration of biological processes that operate across multiple scales, from microbial interactions within individuals to the movement of resistance genes across healthcare systems, agricultural settings, and the

environment. He stressed that future solutions will require integrated approaches that account for the complex relationships between microbes, hosts, and ecosystems.

Resistance in Agricultural and Environmental Systems

Sydney Everhart, M.S., Ph.D., Michigan State University

Dr. Sydney Everhart discussed how AMR develops and is managed within agricultural and environmental systems, emphasizing that plant disease management is a critical but often overlooked component of the One Health framework. She explained that plant pathogens, particularly fungi, pose significant threats to agricultural production and that disease management relies on a combination of preventive practices, resistant crop varieties, predictive modeling, and targeted chemical interventions.

Dr. Everhart highlighted how fungicide resistance can emerge through genetic mutations and selection pressure, sometimes resulting in rapid declines in treatment effectiveness. She described factors that increase resistance risk, including high genetic diversity, the ability of pathogens to reproduce both sexually and asexually, and long-distance dispersal. She also noted that the development of new fungicides is costly and time intensive, making stewardship of existing products essential.

To reduce the emergence and spread of resistance, Dr. Everhart emphasized the importance of integrated disease management practices, including limiting unnecessary fungicide use, rotating products with different modes of action, applying treatments at appropriate times, and using combination products. She concluded by noting that agricultural systems can serve as reservoirs for AMR and highlighted growing interest in biological controls and other non-chemical approaches to disease management.

Clinical Microbiome and Therapeutic Non-Responsiveness

Cliff McDonald, M.D., Centers for Disease Control and Prevention

Dr. Cliff McDonald introduced the concept of therapeutic non-responsiveness, describing it as poor clinical outcomes that occur despite the use of appropriate standard-of-care treatment. He argued that AMR is only one contributor to treatment failure for infectious disease patients and emphasized the need for a broader, patient-centered framework that considers interactions among the pathogen, antimicrobial therapy, infection context, host factors, the microbiome, and other therapeutic interventions.

Dr. McDonald emphasized the microbiome's critical role in immune function, maintenance of protective barriers, and colonization resistance against pathogens. He explained that disruption of the microbiome, often caused by antibiotic exposure, can increase vulnerability to recurrent infections and other poor outcomes even when pathogens remain susceptible to treatment. Using recurrent *C. difficile* infection as an example, he illustrated how microbiome disruption can contribute to treatment failure independently of AMR.

Dr. McDonald also described the Centers for Disease Control and Prevention's (CDC) emerging strategic focus on pathogen reduction and microbiome restoration, which seeks to eliminate harmful pathogens while preserving or rebuilding healthy microbial communities. He highlighted approaches such as FMT, live biotherapeutics, bacteriophages, and other targeted interventions designed to reduce reliance on traditional antibiotics. He concluded by emphasizing that preserving and restoring the microbiome should be considered an integral component of efforts to combat AMR and improve patient outcomes.

Discussion

During the discussion period, Council members and panelists examined how microbiome disruption, host and pathogen characteristics, environmental conditions, and antimicrobial use interact to shape therapeutic outcomes and the emergence of resistance. The discussion focused on the need for more physiologically relevant research models; standardized measures of therapeutic non-responsiveness and microbiome recovery; integrated surveillance, diagnostics, and data analysis; stronger education and cross-sector coordination; and stewardship approaches that preserve microbial communities in both clinical and agricultural settings.

Dr. Newland asked how host genetics might explain why some people carrying organisms such as *Staphylococcus aureus* develop life-threatening infections while others do not. Dr. McDonald placed genetics within the host domain of the therapeutic non-responsiveness framework and said that genetic and microbiome-related factors likely contribute to susceptibility, although their relationships remain incompletely studied. Dr. Marks similarly emphasized that treatment outcomes reflect multiple interacting factors, not antimicrobial activity alone. Dr. McDonald agreed that this complexity complicates clinical trial design but noted the potential to demonstrate benefit of infectious disease applications of microbiome-based therapies over weeks or months rather than the longer periods required for many chronic diseases.

The discussion highlighted the need for study designs and laboratory systems that better reflect real-world transmission and patient conditions. Dr. Huang asked whether agricultural researchers use randomized field trials to study disease spread and fungicide effectiveness. Dr. Everhart said such trials are routinely conducted in both field and controlled settings, with designs tailored to each pathogen's biology and transmission. Dr. Young added that human movement of plants and agricultural products must also be considered when assessing spread across systems. Turning to clinical testing, Dr. Abdul-Mutakabir noted that antimicrobial susceptibility testing methods are largely optimized for bacterial monocultures and may not reproduce conditions within patients. Dr. McDonald agreed that testing could better account for real-world environments, particularly in biofilm-associated infections, and Dr. Young pointed to organoids, host-microbe interaction models, and continuous culture systems as increasingly sophisticated ways to approximate natural conditions.

Council members considered how therapeutic non-responsiveness and microbiome recovery could be measured more systematically. Dr. Zagmutt asked whether surveillance analogous to AMR monitoring could be developed for therapeutic non-responsiveness. Dr. McDonald said no comparable system currently exists and suggested that mortality, prolonged recovery, readmissions, and recurrent infections might serve as proxies, while acknowledging the difficulty of defining and monitoring the concept. Dr. R. Patel asked what diagnostics could show whether a microbiome has been restored after treatment. Dr. McDonald identified dysbiosis indices, microbial diversity measures, and bile acid metabolism as promising indicators but said standardized measures are still needed. Dr. Srikantiah asked whether artificial intelligence, machine learning, and improved data collection could help understand the many contributors to therapeutic non-responsiveness to help identify the best approaches to prevent and treat nonresponsive infections, especially in low- and middle-income countries. Dr. McDonald agreed that the problem is well suited to advanced analytics, and Dr. Young proposed integrating patient, pathogen, microbiome, and surveillance data to support predictive modeling and discovery.

Council members emphasized that putting systems-based frameworks into practice will require changes in education, policy, and institutional coordination. Dr. Julia Szymczak asked about barriers to implementing therapeutic non-responsiveness and pathogen reduction/microbiome restoration in research, policy, and clinical care. Dr. McDonald said clinicians, researchers, and regulators need greater awareness that AMR is only one contributor to poor outcomes and must also consider patient- and microbiome-related factors. Dr. Young added that medical education has traditionally focused on matching pathogens to drugs rather than understanding disease as an interacting system, suggesting that training approaches should evolve. Mr. Michael Craig asked what PACCARB should prioritize as it continues examining microbiomes and AMR. Dr. Young said scientific, regulatory, and funding structures often separate inherently connected issues and suggested that PACCARB could foster collaboration across disciplines and agencies. Dr. McDonald likewise called for stronger links among basic science, translational research, and implementation across human, animal, agricultural, and environmental settings.

The discussion also connected stewardship to microbiome preservation and resistance management across sectors. Dr. Jenkins asked about regulation and stewardship of agricultural antifungals, alternatives to their use, and the implications of climate change for resistance affecting human pathogens such as *Aspergillus*. Dr. Everhart explained that agricultural practice increasingly uses products with multiple modes of action, while regulatory requirements and economic factors shape availability. She emphasized predictive modeling as a way to optimize applications rather than simply increase use and noted that climate change can stress plants and alter disease patterns. Dr. Pantaleon distinguished colonization from infection and observed that colonized people are sometimes treated despite the absence of infection. He suggested considering measures such as the number needed to treat because unnecessary antimicrobial exposure can disrupt the microbiome.

National Action Plan Update

Casey Sullivan, M.A., Ph.D., U.S. Department of Health and Human Services, Office of the Assistant Secretary for Planning & Evaluation

Dr. Casey Sullivan provided an update on the development of the next iteration of the National Action Plan for Combating Antibiotic-Resistant Bacteria (CARB). She thanked PACCARB members and stakeholders for their participation in the June 2026 public meeting and noted that the feedback provided during that session has been valuable in informing both the action plan and its future implementation. Dr. Sullivan highlighted several themes that emerged from stakeholder discussions and public comments, including the importance of strengthening connections across One Health sectors, improving coordination among government and non-government partners, and accelerating the translation of innovation into practical solutions. She also noted continued emphasis on prevention, complementary research efforts to address different aspects of AMR, and workforce-related challenges. She emphasized that PACCARB's strength lies in its ability to bring together expertise from human, animal, plant, and environmental health sectors to address AMR through an integrated One Health approach. Dr. Sullivan concluded by reporting that work on the next National Action Plan is progressing and that the federal task force is moving toward finalization and publication of the updated plan.

Panel 2: Measuring What Matters: Microbiome Characterization and Diagnostics

Measuring What Matters: Quantitating the Human Microbiome

Scott Jackson, Ph.D., The NEST

Dr. Scott Jackson provided an overview of the rapid growth of microbiome science and its increasing importance for diagnostics and therapeutics. He noted that the human microbiome has emerged as a major target for clinical innovation, attracting substantial investment from both established pharmaceutical companies and biotechnology startups. He highlighted the recent Food and Drug Administration (FDA) approval of two microbiome-based live biotherapeutic products for the treatment of recurrent *C. difficile* infection as evidence that microbiome research is beginning to translate into clinical practice. Dr. Jackson emphasized that FMT and related microbiome-based therapies have demonstrated benefits beyond *C. difficile* treatment, including potential applications for reducing colonization with antimicrobial-resistant organisms. Dr. Jackson concluded by discussing the need for standardized analytical approaches to support development, manufacturing, and regulation of microbiome-based therapeutics. Key measurement challenges he highlighted include identifying which microorganisms are present, determining their abundance and viability, detecting contaminants, assessing product stability, and defining potency and dosage.

National Institute of Standards and Technology Approaches to Microbiome Measurement

Samuel Forry, Ph.D., U.S. Department of Commerce, National Institute of Standards and Technology (NIST)

Dr. Samuel Forry discussed the challenges of accurately measuring microbiomes using metagenomic sequencing and emphasized the importance of measurement quality for research, diagnostics, and therapeutic development. He explained that microbiome analyses involve numerous methodological steps, including sample collection, deoxyribonucleic acid (DNA) extraction, sequencing, bioinformatics, and statistical analysis. Because different researchers may use different methods, results are not always directly comparable, creating challenges for reproducibility and interpretation. To improve measurement reliability, Dr. Forry highlighted NIST's work developing standardized approaches, including the creation of a human fecal reference material. He explained that reference materials help researchers detect measurement drift, compare results across studies, and ensure consistency over time. He also described the use of internal standards, in which known microorganisms are added to samples before processing to help quantify and correct for biases introduced during laboratory analysis.

In an example drawn from NIST research, Dr. Forry described an experiment in which fecal samples were analyzed using different laboratory and analytical workflows, including variations in technicians, DNA extraction methods, sequencing approaches, and reference databases. Although the initial results showed substantial variability across methods, the use of internal standards and reference materials significantly reduced measurement differences. To illustrate this point, he described a NIST evaluation of commercial microbiome health assessment services in which identical fecal samples were submitted to eight direct-to-consumer testing providers. Despite receiving the same material, the companies reported markedly different microbiome profiles, diversity measurements, and health-related interpretations. In some cases, providers also offered conflicting recommendations regarding what constituted a desirable abundance of the same microorganism. These findings underscored the extent to which methodological differences

can influence results and highlighted the need for greater standardization and validation before microbiome measurements can be reliably used to guide individual health decisions.

Respiratory Microbiome Strategies for Disease Prevention in Livestock

Chris Belnap, Ph.D., Resilient Biotics

Dr. Chris Belnap discussed the role of the respiratory microbiome in livestock health and the potential for microbiome-targeted therapeutics to prevent infectious disease while reducing reliance on antimicrobials. He explained that respiratory disease remains a major challenge in livestock production and that traditional approaches have often focused on treating disease after infection occurs. Emerging research suggests that maintaining healthy respiratory microbial communities may be an effective preventive strategy that improves animal health and resilience.

Dr. Belnap described how beneficial microbes within the respiratory tract can influence host immunity, pathogen colonization, and overall disease susceptibility. He highlighted efforts to identify microbial populations associated with health and to develop microbiome-based interventions that support protective microbial communities before disease develops. These approaches aim to strengthen natural defenses and reduce the incidence of respiratory infections.

Dr. Belnap emphasized that microbiome-based strategies have the potential to complement existing disease prevention programs, improve animal health outcomes, and support antimicrobial stewardship objectives. He noted that continued research is needed to better understand respiratory microbial ecosystems and to translate these findings into practical interventions that can be implemented at scale in livestock production systems.

Preterm Infant Gut Microbiome Diagnostics to Predict Sepsis and Tailor Antibiotics

Drew Schwartz, M.D., Ph.D., Washington University

Dr. Drew Schwartz discussed emerging efforts to use gut microbiome diagnostics to identify preterm infants at risk for sepsis and support more targeted antibiotic use in neonatal care. He explained that preterm infants are particularly vulnerable to severe infections due to the immaturity of their immune systems and microbiomes. Current approaches often rely on broad-spectrum antibiotics, which can further disrupt the microbiome and potentially increase future health risks. He highlighted research demonstrating that changes in the gut microbiome may occur before the onset of sepsis, creating an opportunity to identify infants at elevated risk before clinical symptoms appear. Dr. Schwartz described efforts to develop microbiome-based diagnostic tools that can detect these changes and provide clinicians with earlier, more precise information about infection risk.

Dr. Schwartz emphasized that microbiome-informed diagnostics could help improve clinical decision-making by allowing providers to better target antibiotic therapy, reduce unnecessary antibiotic exposure, and preserve beneficial microbial communities during a critical period of development. He noted that integrating microbiome data into neonatal care has the potential to improve outcomes while supporting broader antimicrobial stewardship goals.

Discussion

Throughout the discussion, Council members and panelists discussed translating microbiome measurement into diagnostics and the development of preventive interventions and therapies. Topics included measurement standards, neonatal infection risk and stewardship, microbial

transmission and colonization, site-specific interventions, microbiome transplantation, and product oversight.

Dr. Jennie Kwon asked how standards could be established without an agreed definition of a healthy microbiome. Dr. Forry said the field lacks comparable measurement approaches and clinical benchmarks, noting that metagenomic sequencing results cannot reliably be traced to original absolute cell abundances and that rapid technological evolution quickly renders protocols outdated. He stressed that both a clinically meaningful definition of health and a validated, traceable measurement system are essential prerequisites before establishing individual target profiles. Dr. Mark Papich asked whether the United States Pharmacopeia could help establish reference standards or standard testing methods for microbiome products. In response, Dr. Forry described collaboration between NIST and the United States Pharmacopeia but favored fit-for-purpose methods and qualified reference materials over a single sequencing protocol. Dr. Huang asked Dr. Forry to identify the next measurement goals for which NIST is actively pursuing solutions. Dr. Forry identified improved internal standards and reference materials for diverse clinical and environmental samples as priorities, highlighting the trade-off where higher internal-standard volume consumes sequencing reads needed for native organisms, as well as the agency's push to expand reference materials into soil and wastewater.

Dr. Pantaleon asked how resistance genes arise in preterm infants. Dr. Schwartz clarified that preterm infant guts already harbor a substantial repository of resistance genes, and that while organisms and mobile genetic elements are acquired from the environment, early and repeated antibiotic exposure drives their abundance and prevalence. Dr. Abdul-Mutakabbir followed up asking about whether maternal characteristics contributed to AMR genes in preterm infants. Dr. Schwartz said neonatal intensive care unit exposures outweighed the maternal variables examined as drivers of late-onset sepsis (72 hours after birth), although maternal microbiomes remain important for early-onset disease which was excluded from the study presented. He emphasized supporting maternal health through infection prevention while avoiding unnecessary antibiotics. Dr. Srikantiah and Dr. Newland inquired about clinical applications of findings to help inform neonatal intensive care unit discharge or antibiotic selection; Dr. Schwartz explained that longitudinal sequencing could identify likely pathogens, support narrower empiric treatment, reduce unnecessary antibiotics, and inform discharge, dosing, and monitoring.

Dr. Jenkins asked whether microbial transfer among animals and among infants is beneficial or harmful. Addressing the animal sector first, Dr. Belnap said commensal transmission can support healthy colonization in livestock, noting that strains they administered during studies were later detected in untreated animals, although the same environments also supported the spread of pathogens between animals. Shifting to the human health sector, Dr. Schwartz reported similar microbial sharing among infants, observing that across ~2,500 fecal samples, nearly identical strains of *Staphylococcus epidermidis* and *C. difficile* spread across Midwestern neonatal intensive care units, likely representing hospital-adapted or persistent strains. Mr. Craig cautioned that asymptomatic carriage is not necessarily benign, questioning the long-term risk if subsequent antibiotics deplete beneficial microbes. Dr. Schwartz agreed that distinguishing colonization from infection is challenging, noting that infants dominated by single taxa like *E. coli* or *Klebsiella* can remain asymptomatic. However, he emphasized that multidrug-resistant organisms acquired during hospitalization can persist at 12 to 18 months and expand after later antibiotic exposure while organisms like *C. difficile* can cause persistent epithelial changes

without active diarrhea, supporting longitudinal monitoring across childhood to guide One Health and precision-medicine strategies.

Dr. Plummer asked why Dr. Belnap's development strategy focused on the respiratory microbiome rather than the fecal microbiome. Dr. Belnap said interventions target microbial communities where disease occurs and described respiratory disease prevention as an opportunity to reduce illness and antimicrobial use in livestock. Dr. R. Patel asked Dr. Belnap whether the company's work to prevent bovine respiratory disease might translate to human respiratory medicine, noting the substantial use of antibiotics for human respiratory tract infections. Dr. Belnap outlined possible human applications using live commensals or their immunologically active components, while noting safety concerns in the lower respiratory tract. In response to a question from Dr. Pantaleon on beneficial microbe dosing, Dr. Belnap explained that the livestock product was being developed as a single intranasal dose for high-risk periods associated with transport and handling, as repeated handling induces stress and is impractical in production settings.

Dr. Virginia R. Fajt asked panelists to consider what the regulatory environment for microbiome interventions and probiotics should look like and whether access to such products should be controlled by licensed health care professionals. Dr. Schwartz, speaking as a pediatric infectious disease clinician at an institution that bans probiotic use due to unknown formulations, supported stronger oversight to guarantee batch-to-batch consistency in product composition, viable organism concentration, shelf-life stability, and validated medical indications. Dr. Forry added that probiotics are generally characterized less rigorously than approved medical products, creating challenges for demonstrating identity, stability, and fitness for clinical use.

Panel 3: Where Microbiomes Meet: A One Health AMR Perspective

Horizontal Gene Transfer (HGT) and the Spread Of AMR

Ilana Brito, Ph.D., Cornell University

Dr. Ilana Brito discussed the role of horizontal gene transfer (HGT) in the emergence and spread of AMR. She explained that, unlike traditional inheritance in which genes are passed from parent organisms to offspring, HGT allows bacteria to exchange genetic material directly with one another. This process enables AMR genes to move rapidly across bacterial populations, species, and environments, accelerating the spread of resistance.

Dr. Brito highlighted the mechanisms through which resistance genes are transferred, including plasmids, bacteriophages, and other mobile genetic elements. She emphasized that microbial communities in humans, animals, and the environment serve as interconnected reservoirs of resistance genes, reinforcing the importance of a One Health approach to understanding and mitigating AMR. She noted that factors such as antibiotic exposure can influence microbial ecosystems and create conditions that favor the acquisition and spread of resistance genes.

Dr. Brito also described advances in sequencing technologies and computational tools that allow researchers to better characterize gene transfer networks and monitor the movement of resistance determinants across microbiomes. She emphasized that understanding where resistance genes originate, how they move between organisms, and the conditions that promote transfer are essential for developing strategies to limit the spread of AMR and inform future surveillance, prevention, and intervention efforts.

Investigating Swine Worker Microbiomes: On-Farm Considerations

Noelle Noyes, D.V.M., Ph.D., University of Minnesota

Dr. Noelle Noyes discussed research examining the microbiomes of swine workers and the implications of livestock production environments for AMR transmission and microbial exposure. She highlighted how close and repeated contact between workers, animals, and agricultural environments creates opportunities for the exchange of microorganisms and AMR genes, making swine production systems an important setting for One Health research.

By analyzing longitudinal samples from Midwest swine workers, Dr. Noyes' team observed a distinct cyclical pattern where overall bacterial load and diversity on workers' skin and nasal cavities significantly increased during the workday — peaking at lunch and before showering — before biosecurity "shower-out" protocols successfully returned these metrics back to baseline levels. Overlap analysis further revealed that personal air exposures, rather than direct pig contact, served as the primary environmental source for this temporary microbial acquisition.

Dr. Noyes shared various practical and methodological considerations involved in studying microbiomes in agricultural settings. Dr. Noyes described the challenges of collecting and interpreting microbiome data from workers who are continuously exposed to animals, feed, dust, and other environmental factors that can influence microbial composition. She emphasized the need to consider workplace exposures, sampling methods, and environmental context when evaluating microbiome data and assessing potential pathways for AMR dissemination noting that high-resolution genomic sequencing is critical since shared bacterial species (such as *Staphylococcus hominis*) and antimicrobial resistance profiles often diverge at the strain level between pigs and humans.

Dr. Noyes also discussed the value of integrating human, animal, and environmental microbiome data to better understand how microbial communities interact within livestock production systems. She noted that improving knowledge of these interactions may help identify factors that influence the movement of resistance genes and inform future strategies to reduce AMR risks while protecting both worker and animal health.

Drought Drives Antibiotic Resistance Across Soils

Xiaoyu Shan, Ph.D., California Institute of Technology

Dr. Xiaoyu Shan presented research examining how drought conditions influence the abundance and spread of antibiotic resistance in soil ecosystems. He highlighted that environmental stressors, particularly drought, can alter soil microbial communities and create conditions that favor the persistence and proliferation of AMR genes. These findings underscore the importance of considering environmental change as a factor influencing AMR beyond clinical and agricultural settings. The research demonstrated that drought can significantly affect microbial community composition, increasing opportunities for resistant organisms and resistance genes to persist within soil environments. Dr. Shan discussed how changes in moisture levels may alter microbial interactions, nutrient availability, and ecosystem function, potentially affecting the movement and maintenance of resistance determinants across environmental microbial populations.

Dr. Shan emphasized that climate-driven environmental changes should be incorporated into One Health approaches to AMR. Understanding how drought and other environmental stressors

influence resistance dynamics may improve surveillance efforts and help identify emerging risks associated with the spread of AMR across natural ecosystems.

Antimicrobial Resistance in the Agricultural Environment

Michelle Soupir, Ph.D., Iowa State University

Dr. Michelle Soupir discussed the role of agricultural environments in the persistence and movement of AMR. She explained that resistance genes, antimicrobial residues, and resistant microorganisms can be introduced into soil and water systems through agricultural activities, creating environmental pathways that contribute to the broader ecology of AMR. Dr. Soupir described how manure management, runoff, drainage systems, and water movement can influence the transport of AMR genes and organisms across agricultural landscapes.

Her team's field-scale rainfall simulations demonstrated that implementing "nature-based" prairie strips at the edge of agricultural fields significantly reduces the transport of AMR genes and mobile genetic elements in both runoff water and suspended sediment. Furthermore, soil column testing revealed that most of these resistance indicators are successfully retained and filtered within the soil profile. However, she cautioned that higher hydraulic flow rates can expose design limitations, highlighting that conservation strip effectiveness is heavily dependent on volume management.

She highlighted the importance of monitoring environmental pathways and developing management strategies such as anaerobic digestion or liming in manure pits that reduce the spread of resistance while maintaining productive agricultural systems. She noted that improved understanding of how resistance persists and moves through agricultural environments can help inform risk mitigation efforts, support evidence-based policy decisions, and strengthen broader antimicrobial stewardship initiatives.

Discussion

Over the discussion period, Council members and panelists discussed how workplace exposures, environmental stress, HGT, and agricultural waste management shape the movement and health significance of AMR across human, animal, and environmental microbiomes. The discussion also identified methodological gaps in distinguishing transient microbial exposure from colonization and in translating environmental detection of resistance genes into estimates of human or animal health risk.

Dr. Payal K. Patel asked about hand hygiene among swine workers, and Dr. Noyes described established biosecurity training, routine handwashing, task-dependent glove use, and detailed tracking of these practices. Dr. Paige Waterman inquired whether the exact same workers were sampled repeatedly over time and whether their microbiomes successfully returned to baseline by the following day. Dr. Noyes responded that repeated sampling of the same participants across all 28 time points showed that workers' microbiomes generally returned to pre-work profiles after showering, although the clinical significance of the observed changes and some nasal findings remained uncertain. Dr. Zgmutt asked how these patterns compare with other workplaces; Dr. Noyes noted related research in manufacturing, hospitals, and animal facilities. Mr. Craig asked whether workers had concurrent antibiotic exposure during the study and suggested that such exposure might enable the engraftment of an entirely different microbiome. Dr. Noyes responded that individuals using antibiotics were excluded from the study to isolate

workplace effects, while acknowledging that antimicrobial exposure raises important follow-up questions regarding how it could affect microbial engraftment.

Dr. Kwon asked why drought increases soil resistance and whether multi-omics could clarify the mechanisms. Dr. Shan said drought may concentrate naturally occurring antibiotics in reduced water volumes, increasing selective pressure, and induce physiological stress responses, such as membrane remodeling to withstand low water, that coincidentally reduce antibiotic susceptibility by limiting cellular uptake. Responding to Dr. Marks query about whether other environmental stresses have been evaluated, as well as Dr. Abdul-Mutakabbir, who asked whether longer drought periods produce progressively larger increases in AMR, Dr. Shan noted that long-term warming has also increased soil resistance and pointed to a California cropland dataset where a two-month drought produced a substantially larger spike in antibiotic-resistance genes than a one-month drought. Dr. Shan also emphasized the need to determine how resistance selected in soil reaches people and animals.

Dr. Thomas Wittum asked about the relative importance of conjugation, transformation, and transduction. Dr. Brito said the dominant mechanism varies by organism, but conjugation through broad-host-range plasmids appears to be the principal pathway for resistance-gene movement, transformation is especially important in permissive organisms such as *Acinetobacter baumannii* which readily take up environmental DNA, and transduction is probably less prominent. Dr. Abdul-Mutakabbir inquired about whether HGT occurs more frequently in gram-negative versus gram-positive bacteria and whether patterns differ between fermenting and non-fermenting microbes. Dr. Brito identified gamma-proteobacteria as particularly active in acquiring and distributing multidrug-resistance plasmids under strong selective pressure, indicating a specific taxon pattern rather than a broad gram-status split. Dr. Stephanie Black asked about transmission in healthcare settings; Dr. Brito described work in hospitalized patients with leukemia whose antibiotic exposure, dysbiosis, and enrichment with gamma-proteobacteria created conditions conducive to mobile-gene exchange.

Dr. Plummer asked Dr. Soupir whether manure and prairie-strip samples used in her studies had been evaluated for HGT. Dr. Soupir said the study measured selected resistance genes and mobile genetic elements but did not directly assess transfer. Dr. Jenkins asked whether anaerobic digestion makes manure safe enough for land application or if more effective mitigation strategies exist. Dr. Soupir said anaerobic digestion, liming, two-stage storage, and aeration can reduce resistance but not eliminate it, making pretreatment before land application the most effective control point to mitigate downstream runoff from unpredictable precipitation events. She also noted that the feasibility of advanced setups like biogas anaerobic digestion depends heavily on farm size, manure volume, and economics. Dr. Pantaleon questioned whether detected soil resistance genes have been linked directly to infections in people or animals, pointing out that some detected genes confer resistance to antibiotics not recently used on those farms. Dr. Soupir agreed that gene detection alone does not establish pathogenicity or health effects and called for stronger risk-assessment methods that integrate exposure pathways and multiple agricultural, wastewater, community, and healthcare sources across watersheds.

Council Roundtable

Dr. Plummer invited Council members to offer their perspectives on the information presented at this meeting, particularly new or relevant connections between the microbiome and AMR. The feedback is summarized below according to broad categories of interest.

Outcomes, Measurement, and Clinical Translation

- Reframe AMR beyond a “bug–drug” mismatch to include practical measures of therapeutic non-response for clinical and population use.
- Develop standardized, validated, affordable microbiome measurement methods and clinically meaningful benchmarks; longitudinal repositories could help define healthy baselines and change over time.
- Use microbiome data with clinical findings to predict AMR risk, guide treatment, and support prevention in vulnerable populations, including neonates, transplant recipients, oncology patients, and people in intensive care.
- Advance translation of microbiome insights through longitudinal and mechanistic research, product development, implementation planning, and incentives for preventive therapies without displacing antibiotics or traditional resistance surveillance.

Antibiotic Stewardship and Microbiome Effects

- Avoid unnecessary antibiotic exposure as an immediate microbiome intervention to preserve treatment benefits while reducing dysbiosis.
- Investigate the ecological effects of antibiotic use across human, animal, and agricultural settings that remain incompletely understood and require drug-specific evidence.
- Define “microbial withdrawal times” in food-animal research showing how long microbiome disruption and resistance risks persist after treatment, rather than relying only on chemical-residue withdrawal periods.

One Health Integration and Environmental Drivers

- Recognize the interconnected nature of human, animal, plant, soil, and water microbiomes when addressing the movement of organisms and resistance pressures across sectors.
- Expand cross-sector collaboration to include plant and aquatic expertise and examine whether practices such as farm biosecurity can inform healthcare infection prevention.
- Design research and interventions to reflect geographic and community variation, including low- and middle-income countries, underserved U.S. communities, rural hospitals, and pediatric populations.
- Partner with affected sectors and communities to help design solutions, and communication about climate-related AMR risks should remain evidence-based.

Implementation, Incentives, and Access

- Prioritize practical incentives, scalable design, and implementation planning when developing clinical and environmental interventions.
- Sustain investment in standards, longitudinal studies, diagnostic access, veterinary capacity, repositories, education, translation, and preventive-product development.
- Develop tools and resources that support equitable One Health implementation and remain usable in routine human and veterinary care, not only specialized settings.

Education, Communication, and Strategic Direction

- Train clinicians, veterinarians, laboratorians, students, and prescribers to interpret microbiome information within an ecological framework rather than a “one bug, one drug” model.
- Promote evidence-based communications about AMR and microbiome science to avoid increased exposure to ineffective tests, products, and exaggerated claims.

- Consideration of the microbiota in the context of AMR prompts an obvious shift toward preserving microbial health, preventing poor outcomes, and strengthening resilience while retaining antibiotics and resistance surveillance as foundations.

Closing Remarks

Paul Plummer, D.V.M., Ph.D., DACVIM, DECSRHM, Council Chair

Dr. Plummer thanked the presenters and Council members for a productive day of discussion. He noted the need to better measure therapeutic non-responsiveness, define a healthy microbiome, and understand microbiome interactions across One Health settings. Dr. Plummer added that continued progress will require funding, incentives, and improved communication with prescribers. The meeting recessed with plans to continue the discussion the following day with a more clinical examination of microbiome disruption, targeted therapies, and strategies to restore resilience. The meeting recessed at 4:15 p.m.

Day 2

Welcome and Roll Call

Paul Plummer, D.V.M., Ph.D., DACVIM, DECSRHM, Council Chair; Jason Newland, M.D., M.Ed., Vice Chair; and Sarah McClelland, M.P.H., Designated Federal Official, Public Health Advisor, OASH, HHS

Dr. Plummer opened the second day by welcoming attendees and reflecting on the previous day's discussions at 9:05 a.m. ET. He noted that Day 1 established a foundation for understanding the role of microbiome science in AMR, emerging tools for studying microbial communities, and the interconnected dimensions of human, animal, and environmental microbiomes. He emphasized the potential for microbiome science to inform future approaches to preventing, monitoring, and responding to AMR and introduced the day's focus on clinical and applied research.

Dr. Newland highlighted the transition from foundational microbiome science to practical applications. He explained that the day's sessions would examine how microbiome disruption may contribute to AMR, emerging interventions to address these disruptions, and strategies to restore microbiome resilience. He noted that the panels would help identify actionable opportunities to prevent and address AMR in clinical settings.

Ms. McClelland welcomed Council members and thanked the presenters, attendees, and stakeholders for their engagement. She reiterated that PACCARB advises the Secretary of Health and Human Services on programs and policies to address AMR and improve health outcomes. She emphasized the Council's One Health framework, integrating human, animal, and environmental perspectives across its discussions and activities. She then called the roll. (See the appendix for the list of Council members and staff.)

Panel 4: AMR and the Consequences of Microbiome Disruption in Clinical Care

A Moving Target...How Mobile Elements Drive Pathogen Adaptation

Ami Bhatt, M.D., Ph.D., Stanford University

Dr. Ami Bhatt described how cancer therapies and the intensive use of antibiotics can profoundly disrupt the gut microbiome, creating conditions that allow antimicrobial-resistant organisms to thrive. Drawing on studies of hematopoietic stem cell transplant patients, she explained that the gut serves as a major reservoir for pathogens that can later enter the bloodstream and cause serious infections. Her team found that a substantial proportion of bloodstream infections could be traced back to organisms that had previously colonized the gut, including both common gut bacteria and organisms not traditionally associated with the intestinal microbiome.

Dr. Bhatt emphasized that antibiotic-resistant pathogens should not be viewed as static organisms. Through genomic studies, her group demonstrated that bacteria can rapidly adapt within patients during hospitalization. In particular, mobile genetic elements known as insertion sequences, or "jumping genes," can move throughout bacterial genomes and alter gene expression in ways that improve bacterial survival under the selective pressures created by chemotherapy, antibiotics, and a disrupted microbiome. She highlighted study findings of *Enterococcus faecium*, a common hospital-associated pathogen, showing how genetic changes

can enhance the organism's ability to persist and dominate in the gut when beneficial microbes have been depleted.

Dr. Bhatt concluded that microbiome disruption caused by cancer treatment creates opportunities for resistant pathogens to evolve and expand, increasing the risk of infection. She suggested that future therapeutic strategies may need to focus not only on eliminating pathogens but also on preventing bacterial adaptation and preserving microbiome resilience to reduce the burden of AMR.

Losing the Anaerobes, Losing the War Against AMR

Tessa Andermann, M.D., M.P.H., University of North Carolina at Chapel Hill

Dr. Tessa Andermann discussed the critical role of anaerobic bacteria in protecting against AMR. She explained that these beneficial gut microbes provide colonization resistance by occupying ecological niches, producing important metabolites, and maintaining the integrity of the gut barrier. In patients undergoing hematopoietic stem cell transplantation, intensive chemotherapy and antibiotic exposure, particularly to antibiotics with anaerobic activity, can rapidly deplete these protective organisms. As anaerobes are lost, resistant pathogens expand in the gut, increasing the risk of bloodstream infections and poor clinical outcomes.

Dr. Andermann presented evidence showing that antibiotics with greater anaerobic activity are associated with increased diversity and abundance of AMR genes in the gut microbiome. These effects persisted long after antibiotic treatment ended, suggesting that disruption of anaerobic communities has lasting consequences. Her research also demonstrated that patients with the greatest loss of microbial diversity acquired more resistance genes over time, indicating that depletion of beneficial anaerobes creates an environment where resistant organisms can flourish.

Dr. Andermann recommended that antimicrobial stewardship efforts should focus not only on antibiotic spectrum and duration, but also on the degree of anaerobic activity. She recommended incorporating anaerobic activity into stewardship metrics, monitoring resistant organism colonization as an important surveillance endpoint, and prioritizing the development of microbiome-sparing antibiotics and preservation strategies. She concluded that AMR often begins in the gut and that protecting anaerobic microbial communities may be one of the most effective ways to prevent the emergence and spread of resistance.

Uninvited Guests in Undisclosed Locations: Respiratory Microbiomes and Chronic Infection

Katrine Whiteson, Ph.D., University of California, Irvine

Dr. Katrine Whiteson discussed how respiratory microbiomes influence chronic infections, focusing on patients with cystic fibrosis (CF). She challenged the long-held assumption that lungs are sterile, explaining that healthy lungs contain low levels of microbes, many of which originate from the oral cavity. In CF, impaired airway clearance allows these microbes to persist, creating conditions that support chronic infection and the gradual establishment of opportunistic pathogens. Dr. Whiteson described the ecological progression of infection in CF airways, where microbial communities evolve over time and opportunistic pathogens such as *Pseudomonas aeruginosa* become increasingly dominant. While antibiotic therapy has dramatically improved survival among people with CF, infections remain a major clinical challenge. She noted that shorter courses of antibiotics were as effective as longer courses for treating pulmonary exacerbations, highlighting opportunities to reduce antibiotic exposure in a population that

frequently requires treatment. From microbiome and metabolomic analyses, her team observed that microbial communities are highly individualized, yet common patterns emerge as disease progresses and resistant pathogens become more prevalent.

She emphasized that resistant pathogens do not act alone but interact with surrounding microbial communities. Oral bacteria can alter the airway environment and generate metabolites that support the growth and virulence of opportunistic pathogens. These findings suggest that infection risk is influenced not only by the presence of resistant organisms but also by ecological interactions within the microbiome. Dr. Whiteson highlighted opportunities to develop microbiome-aware interventions, including strategies that preserve beneficial microbial communities, promote healthy immune function, and reduce pathogen colonization. She concluded that maintaining healthy microbial ecosystems may represent an important approach for preventing chronic infection and limiting AMR.

Discussion

The discussion examined strategies to prevent and measure microbiome disruption in clinical care, with emphasis on microbiome-sparing therapies, stewardship metrics, nutrition, bacterial adaptation and colonization, and One Health implications in other sectors. Council members also highlighted persistent evidence gaps, including how to define an unhealthy microbiome, compare antibiotic effects across patient groups, and translate promising interventions into practice.

Dr. Fajt asked about enzymes and other approaches that neutralize antibiotics in the gut. Dr. Andermann described oral beta-lactamases and activated charcoal as promising early-stage strategies to protect the microbiome before disruption occurs. Dr. Marks asked what options exist beyond new antimicrobial products, and Dr. Bhatt emphasized that antibiotics and non-antibiotic treatments such as chemotherapy can both damage microbial communities. Dr. Bhatt emphasized that preserving microbiome health requires considering the broader ecological context of microbial communities, including maintaining oral nutrition when feasible and advancing antibiotic stewardship efforts to minimize unnecessary antimicrobial exposure. Dr. Kwon and Dr. Abdul-Mutakabbir raised questions about antibiotic selection and development. Dr. Andermann cautioned that studies of anaerobic activity are confounded because the most active agents are often used in the sickest patients, but said newer drugs with less anaerobic activity may preserve the microbiome while maintaining broad coverage; she also called for more data on how new agents reach and affect the gut across patient populations.

Mr. Craig asked how an unhealthy microbiome might be defined. Dr. Bhatt suggested measuring absolute levels of pathogens and beneficial anaerobes rather than relying only on relative abundance, with metabolites such as B vitamins as possible surrogate markers. Dr. Whiteson emphasized standardized controls and identified pH and redox potential as accessible indicators of microbiome function. Dr. Plummer noted that veterinary medicine has long used such measures and microbial transplants to assess and restore rumen health; Dr. Whiteson said similar approaches are increasingly used in human research but require further validation for clinical care.

Council members inquired about how diet could protect or restore the microbiome before, during, and after antibiotic exposure or gastrointestinal illness. Dr. Whiteson explained that fiber nourishes beneficial colonic microbes and helps prevent degradation of the protective mucus layer; higher intake has been associated with healthier anaerobic communities and lower resistance-gene burdens. Dr. Andermann favored fermented foods over commercial probiotics

for most people and noted that transplant care has shifted toward enteral feeding to preserve the microbiome. Dr. Bhatt called for randomized controlled trials to generate stronger evidence for dietary recommendations about what to decrease the risk of AMR infections. Dr. Pantaleon described a similar movement in companion-animal practice away from routine metronidazole and toward dietary management, highlighting opportunities for One Health collaboration.

Dr. R. Patel asked whether the insertion-sequence expansion observed in *Enterococcus faecium* also occurs in *S. epidermidis*. Dr. Bhatt said insertion sequences are present in *S. epidermidis*, but the same dramatic expansion has not been observed and additional genomic data is needed. Dr. Srikantiah and Dr. Abdul-Mutakabbir asked why insertion-sequence density appeared distinctive in *E. faecium*, how geography might influence the finding, and how it relates to established resistance mechanisms. Dr. Bhatt said hospital adaptation and differing environmental reservoirs may contribute; both point mutations and mobile elements drive adaptation, but Insertion Sequence-Like Element 3 (ISL3)-mediated structural changes may occur more rapidly. Dr. Srikantiah also asked about colonization surveillance, and Dr. Andermann described screening transplant patients for resistant organisms to identify emerging patterns and guide infection prevention. Dr. Huang asked whether *S. epidermidis* detected in the gut may have originated from the skin. Dr. Bhatt said the origin of *S. epidermidis* could not be determined without coordinated skin, respiratory, and environmental sampling which was not done in the presented study.

Panel 5: Targeted Interventions: Treating AMR through Microbiome-based Therapies

From Discovery to Delivery: Fecal Microbiota Transplantation for Humans

Michael Woodworth, M.D., Emory University School of Medicine

Dr. Michael Woodworth discussed the development and implementation of FMT and other microbiome-based therapies as strategies to address AMR. He highlighted the challenge of persistent colonization with multidrug-resistant organisms following treatment of acute infections, noting that while antibiotics may clear active infections, patients often remain colonized for months or years, increasing their risk of future resistant infections. He argued that restoring a healthy microbiome may offer a path to reducing this long-term risk. Dr. Woodworth reviewed evidence linking high levels of resistant organisms in the gut microbiome with increased risks of infection and mortality. He described several microbiome-focused interventions, including FMT and products designed to protect the microbiome from antibiotic-related disruption. Studies have shown modest success in decolonization, and they have also suggested meaningful reductions in subsequent infections, indicating that microbiome restoration can improve clinical outcomes despite incomplete eradication of resistant organisms.

Dr. Woodworth explained that validated microbiome biomarkers could help enrich study populations, making trials smaller, more efficient, and more likely to succeed. He also discussed the regulatory and operational challenges associated with conducting microbiome intervention studies, describing his experience launching FDA-regulated FMT trials and emphasizing the need for dedicated translational research infrastructure and sustained federal support. Dr. Woodworth concluded that innovation alone is insufficient if patients cannot access approved therapies. He noted that uptake of FDA-approved microbiota products for recurrent *C. difficile* infection remains low despite their availability. He recommended expanding support for microbiome clinical trials, validating microbiome-based risk biomarkers, and improving

reimbursement and access pathways so that approved microbiome therapies can be used more broadly in clinical care.

Fecal Microbiota Transplantation (FMT) in Companion Animals

Jan Suchodolski, D.V.M., Ph.D., Texas A&M Veterinary Medicine & Biomedical Sciences

Dr. Jan Suchodolski discussed the growing use of FMT in companion animals and its potential role in managing chronic gastrointestinal disease and microbiome disruption. He explained that chronic inflammatory enteropathies are common in dogs and cats and were historically treated with antibiotics. However, veterinary medicine is increasingly shifting toward nutritional approaches and microbiome-based therapies. While FMT can be highly effective in some animals, responses are variable, highlighting the need to better understand which patients are most likely to benefit.

Dr. Suchodolski described the development of microbiome biomarkers, including a dysbiosis index based on quantitative polymerase chain reaction (PCR) measurements of key bacterial groups. Beneficial organisms such as *Faecalibacterium* and *Clostridium hiranonis* typically decline in disease, while organisms such as *Escherichia coli* and *Streptococcus* increase. These changes can be used to measure microbiome disruption and predict disease severity. He emphasized that quantitative measures provide more reliable information than relative abundance data from sequencing alone and can help identify animals that are more or less likely to respond to microbiome interventions. Using studies in dogs and cats, he showed that antibiotic-induced dysbiosis often responds well to FMT, with the microbiome recovering much more rapidly than it does without intervention. In contrast, animals with severe chronic gastrointestinal disease frequently experience only temporary improvement because underlying inflammation and damage to the intestinal lining continue to drive microbiome disruption. These findings suggest that FMT may be most effective when microbiome changes are the primary problem rather than a consequence of more advanced disease.

Dr. Suchodolski concluded that microbiome diagnostics can help guide the use of FMT and other targeted microbial therapies. He highlighted ongoing efforts to develop probiotics based on specific beneficial bacterial strains and argued that future microbiome-based treatments could reduce reliance on antibiotics by restoring key microbial functions and improving gut health in companion animals.

Engineered Phages to Restore Susceptibility

David Pride, M.D., Ph.D., University of California, San Diego

Dr. David Pride discussed the development of bacteriophage therapies as targeted alternatives to traditional antibiotics for combating antimicrobial-resistant infections. He explained that bacteriophages are viruses that specifically infect bacteria and can eliminate pathogens while largely preserving the surrounding microbiome. Because phages target specific bacterial species rather than broad groups of organisms, phage-based therapies have potential to reduce the collateral damage to beneficial microbial communities that often occurs with antibiotic treatment. Dr. Pride described his laboratory's efforts to build extensive collections of bacteriophages, including large "jumbo phages" that possess unique characteristics allowing them to overcome common bacterial defense mechanisms. These phages can be combined into cocktails containing multiple phage types to broaden their activity against resistant pathogens and reduce the likelihood of treatment failure. He emphasized that advances in phage discovery

and engineering have made it increasingly possible to develop therapies capable of targeting a wide range of clinically important bacteria.

Dr. Pride highlighted progress in developing phage therapies against several major hospital-associated pathogens, including *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, and *Escherichia coli*. He noted that his group has used approaches such as co-evolution, where phages are adapted alongside bacteria, to improve their ability to infect resistant strains and expand their host range. These strategies may help restore susceptibility and provide treatment options when conventional antibiotics are ineffective.

Dr. Pride concluded that phage therapy is evolving beyond a highly individualized, case-by-case intervention into a potentially scalable approach for addressing AMR. He argued that advances in phage engineering, selection, and formulation are making it increasingly feasible to develop broad-spectrum phage cocktails that can be used similarly to conventional antimicrobial therapies while preserving the microbiome and reducing reliance on antibiotics.

Intelligent Automation to Counter Emerging Biothreats

Ashley Trama, Ph.D., Locus Biosciences

Dr. Ashley Trama described how Locus Biosciences is using engineered bacteriophages and artificial intelligence-driven automation to address AMR and emerging biological threats. She explained that the company's platform is designed to identify, predict, and respond to resistant pathogens by combining environmental surveillance, large-scale biological data collection, machine learning, and engineered phage therapies. The goal is to create precision antibacterial treatments that selectively eliminate harmful bacteria while preserving the broader microbiome. Dr. Trama outlined the company's integrated platform, which includes environmental monitoring and predictive analytics capabilities that track the emergence and spread of AMR. By collecting bacterial and bacteriophage samples from wastewater and other sources across the United States, the platform builds extensive libraries of organisms and analyzes millions of phage-bacteria interactions. These data are then used to improve predictions of resistance trends and identify potential therapeutic targets.

Dr. Trama explained that the company engineers bacteriophages to deliver antibacterial payloads that enhance their ability to kill target bacteria and reduce the likelihood of resistance emerging against the therapy itself. Computational modeling is used to rapidly identify optimal combinations of phages and evaluate their effectiveness across large collections of clinically relevant bacterial strains. These approaches have demonstrated broad activity against resistant pathogens, including *Escherichia coli*, and have shown encouraging results in ongoing clinical studies of urinary tract infections.

Dr. Trama also highlighted the importance of manufacturing infrastructure for rapidly responding to emerging threats. She described the company's in-house production and quality systems, which are designed to accelerate the transition from product design to clinical testing. The platform supports development of therapies for a variety of diseases, including urinary tract, respiratory, and ophthalmic infections, while also exploring applications beyond infectious disease, such as targeted bacterial therapies for Crohn's disease. She concluded that combining intelligent automation, predictive surveillance, engineered phages, and scalable manufacturing offers a potential pathway for developing precision antimicrobials that can address both current AMR challenges and future biological threats.

Discussion

The discussion examined the development, evaluation, delivery, and accessibility of microbiome and phage therapies. Topics included biofilm penetration, biomarkers and dysbiosis measurement, treatment resistance and laboratory testing, population-level applications, site-specific delivery, regulatory and reimbursement barriers, and the future evolution of targeted microbial interventions.

Dr. Plummer asked whether different diseases require distinct dysbiosis indices. Dr. Suchodolski said a single index measuring absolute shifts in core bacterial populations appears useful across several diseases and animal species and provides more reliable information than relative abundance alone. Dr. Zagmutt asked how microbiome therapies might evolve. Dr. Woodworth described FMT as a transitional approach likely to give way to defined microbial consortia and live biotherapeutic products, while Dr. Suchodolski anticipated increasingly targeted interventions building on veterinary medicine's shift from routine antibiotics toward nutrition and microbiome management. Dr. Woodworth emphasized that progress will depend on validated biomarkers, clinical trial infrastructure, and sustained funding.

Dr. Szymczak and Dr. Abdul-Mutakabbir asked about barriers to approved microbiota therapies. Dr. Woodworth identified racial and social disparities in utilization, insurance denials, differing treatment pathways, and the need for new prescribing practices and provider education. He suggested that payment models may need to reflect the broader public health benefits of preventing recurrent infection rather than relying solely on individual insurance coverage. Dr. Newland raised similar concerns about making phage therapy available beyond specialized centers. Dr. Trama and Dr. Pride said broader use will require approved indications, scalable manufacturing and supply chains, reimbursement pathways, and clinician familiarity.

Dr. Huang asked whether engineered phages can penetrate biofilms. Dr. Trama reported laboratory evidence that phage cocktails can penetrate biofilms and said engineered antibacterial payloads may diffuse farther to reach less accessible bacteria. Dr. Sam Perdue asked how resistance is being addressed. Dr. Trama described combining multiple mechanisms of action and monitoring susceptibility longitudinally in trials, while Dr. Pride said co-evolution methods for development of therapeutic phages appear to raise the threshold for bacterial resistance. Dr. Ribhi Shawar asked about standardized laboratory methods for evaluating phage susceptibility, resistance, and treatment nonresponse. Dr. Trama explained that her team primarily relies on plaque-based methods and additional laboratory assays to assess bacterial susceptibility to phages and monitor resistance during trials. Dr. Pride noted that his laboratory also uses traditional plaque assays and liquid-based testing but cautioned that some standard methods correlate poorly with observed performance and noted that ATP-based assays are being explored.

Dr. Marks asked about patients in a urinary tract infection trial who achieved clinical but not microbiological cure. Dr. Trama said analyses were ongoing, although at least one bacterial strain was not susceptible to treatment. She added that stool, vaginal, and perianal samples are being collected from a subset of patients to assess microbiome effects. Dr. Huang asked whether phages persist after treatment, and Dr. Trama responded that phages generally disappear once susceptible bacterial targets are eliminated.

Dr. Wittum asked about mechanisms for delivery of phage therapeutics to different infection sites. Dr. Trama described direct administration approaches, including intravesical delivery for urinary tract infections, nebulized therapy for respiratory infections, and topical treatment for

ophthalmic infections. Dr. Kwon asked whether phages could support population-level interventions. Dr. Pride identified targeted decolonization as a potential application but noted uncertainty about durability, while Dr. Trama emphasized the potential for development of cocktails suitable for broad patient populations rather than exclusively individualized treatment. Dr. Jenkins asked whether phages could be used as environmental decontamination tools in healthcare settings to reduce transmission of resistant organisms. Dr. Pride and Dr. Trama noted potential utility but cautioned about selection for phage resistance, manufacturing costs, and deployment challenges. Dr. Chelsey Shivley asked about the use of phage therapies in food animals, particularly given concerns about future restrictions on antibiotic use. Both Dr. Trama and Dr. Pride supported further development, while acknowledging cost and regulatory considerations. Additionally, Dr. Trama noted that adaptable cocktails may offer an advantage over conventional antibiotics. Dr. Perdue encouraged researchers to engage federal program officers to ascertain whether the types of complex translational studies discussed during this session could fit within existing funding mechanisms. He noted that federal agencies may have flexible options for supporting innovative microbiome and phage research.

Panel 6: Restoring Resilience: Addressing AMR by Strengthening Microbiomes

Strengthening Children's Microbiomes through Nutrition

Saurabh Mehta, M.B.B.S., M.D., S.M., Sc.D., Cornell University

Dr. Saurabh Mehta presented research on how nutrition-based interventions during the first two years of life may strengthen the gut microbiome and support resistance to AMR pathogens. He shared how early childhood is a critical period for microbiome development, with his study examining whether diet could serve as a non-pharmaceutical strategy to promote healthy microbial communities and improve colonization resistance. The research was conducted as part of a randomized controlled trial in urban communities in Mumbai, India, where children received meals prepared with biofortified crops rich in iron and zinc. The study was motivated by concerns that iron supplementation, while important for child development, may alter the microbiome in ways that favor potentially harmful bacteria. Researchers found that delivering micronutrients through food-based approaches did not produce the adverse microbiome effects observed with some iron supplements. Instead, children receiving the intervention showed microbiome characteristics associated with improved gut health, including reduced abundance of potential pathogens and increased functional capacity linked to antimicrobial and antioxidant activity.

Dr. Mehta emphasized that the findings are exploratory and require further validation. However, the results suggest that food-based nutritional interventions could provide a scalable, culturally appropriate approach to addressing micronutrient deficiencies while supporting healthy microbiome development. The study highlights the potential for nutrition to complement broader efforts to reduce infection risk and strengthen resilience against AMR.

Nutritional Supplements and Microbiome Health in Animals

Marcio Costa, D.V.M., D.V.Sc., Université de Montréal

Dr. Marcio Costa discussed the role of nutritional supplements and microbiome modulation as alternatives to antibiotics in companion and farm animals. While antibiotics remain widely used, particularly in food animal production, concerns about AMR have increased interest in strategies

such as probiotics, prebiotics, micronutrients, postbiotics, and other feed additives. He noted that although probiotics are commonly used, evidence of their effectiveness is inconsistent, and concerns remain about product quality, regulation, and the potential presence of AMR genes.

Dr. Costa highlighted how dietary supplements can alter the animal gut microbiome and influence health outcomes. Research findings showed that certain feed additives, including zinc oxide, phytochemical compounds, and postbiotics, can substantially change microbiome composition and may improve animal health or reduce disease severity. However, some interventions may also create unintended consequences, such as selecting for bacteria that carry AMR genes. Dr. Costa emphasized that while these products can help modulate the microbiome, they generally do not produce effects as strong as those achieved with antimicrobial drugs.

Dr. Costa shared that limitations in current sequencing technologies and the lack of comprehensive sequence databases for animal-associated bacteria make it difficult to determine which microbial communities are most beneficial. He also described emerging research using bacteria isolated from healthy animals that can successfully colonize the gut and potentially serve as platforms for future microbiome-based therapies, including genetically engineered organisms designed to promote health or suppress harmful bacteria. Dr. Costa stated that nutritional supplements can influence the intestinal microbiome and may help reduce reliance on antibiotics when used appropriately. He emphasized the need for further research to better understand microbiome function in companion and agricultural animals, improve the effectiveness of prebiotics and other alternatives, and address regulatory barriers that limit the development and commercialization of innovative microbiome-based interventions.

Strengthening the Rumen Microbiome: What Adaptation Can Teach Us About Resilience *Philip Myer, Ph.D., University of Tennessee*

Dr. Philip Myer explored how the rumen microbiome in cattle can serve as a model for understanding microbiome resilience and adaptation. He explained that a resilient microbiome is not necessarily one that remains unchanged, but rather one that can successfully adapt to changing conditions while continuing to support animal health and productivity. Diet plays a major role in shaping rumen microbial communities, as microbes enable cattle to digest fiber and convert nutrients into forms the animal can use.

Drawing on studies of dietary transitions in cattle, Dr. Myer showed that microbial communities respond rapidly to changes in feed, but achieving a stable and fully adapted microbiome may take several weeks. These findings suggest that resilience should be evaluated over time and that short-term measurements may not accurately reflect the long-term health or function of the microbiome. Dr. Myer also highlighted emerging efforts to strengthen microbiome resilience through supplementation with native rumen microbes. Research demonstrated that introducing selected microbes could increase microbial connectivity and organization within the rumen ecosystem, potentially improving animal performance and overall stability. Dr. Myer concluded that understanding adaptation, stability, and microbial interactions may help identify new approaches to supporting animal health and reducing reliance on antimicrobial interventions.

Discussion

The discussion examined strategies to strengthen and assess the microbiome in humans and animals, with emphasis on dietary interventions, native microbes, antibiotic effects, host genetics, microbial diversity, and the meaning of resilience across biological systems. Council

members also highlighted the importance of context when evaluating nutrition-based approaches, the influence of social conditions such as food insecurity, and persistent evidence gaps involving long-term microbiome changes, nonbacterial organisms, and the translation of microbiome research into measurable health and production outcomes.

Dr. Pantaleon asked whether efforts to strengthen the rumen microbiome are more likely to succeed through dietary strategies than through probiotics or prebiotics and whether these approaches translate into measurable improvements in animal productivity. Dr. Myer responded that his team focuses on microbes that are native to the rumen and well adapted to that environment. Microbiome studies using these organisms have shown improvements in average daily weight gain. Although some supplemented microbes decline over time, they continue to influence the broader microbial network and contribute to improved microbiome function. Dr. Pantaleon also asked how low-dose antibiotics promote growth in food animals and whether understanding these mechanisms could inform alternative interventions. Dr. Costa explained that antibiotics alter the microbiome in ways that improve feed efficiency and weight gain. Antibiotic exposure can select for microbial communities that extract energy more effectively from food while also helping control disease, which together contribute to improved animal growth.

Dr. Newland asked how nutritional interventions fit alongside antibiotic use in settings where antibiotics have demonstrated protective benefits for children. Dr. Mehta responded that the answer depends heavily on context, noting that his study involved relatively healthy children living in the community rather than populations facing severe infectious disease burdens. He stated that the balance between nutrition-based approaches and antibiotic interventions remains an important area for future study. He emphasized the importance of nutrition as a tool within social medicine and for infectious disease prevention. Dr. Abdul-Mutakabbir asked whether food insecurity could affect microbiome health and contribute to disease risk. Dr. Mehta responded that food insecurity is closely linked with many other factors, including healthcare access and broader social conditions, making it difficult to isolate its direct impact. However, he agreed that food insecurity is an important determinant of health and likely contributes to many poor health outcomes.

Dr. Plummer asked the panelists to discuss the relationship between host genetics and the microbiome. Dr. Myer described ongoing work on heritable microbiome traits and explained that combining host genetic data with microbiome data may improve prediction of important outcomes such as feed efficiency. Dr. Costa added that studies transferring rumen contents between animals have shown that microbiomes often return to their original state over time, suggesting that host genetics exert a strong influence on microbial communities. Dr. P. Patel asked whether vegetarian and non-vegetarian diets influence microbiome composition differently. Dr. Myer explained that diet is one of the strongest drivers of microbial composition in the rumen and that major dietary shifts can produce substantial microbial changes even when some core organisms remain present. Dr. Mehta noted that studying dietary patterns in humans is complicated because the frequency and type of animal-source foods vary considerably among individuals. He reported that additional research is underway to better understand these relationships.

Dr. Plummer asked the panel to discuss microbes beyond bacteria, including fungi, protozoa, and archaea. Dr. Myer explained that these organisms play important roles in digestion, nutrient cycling, and methane production, even though bacterial communities receive most of the research attention. Dr. Costa highlighted the importance of archaea as major contributors to

methane production and noted that they remain understudied. Dr. Mehta added that researchers often collect data on these organisms, but analytical approaches are less standardized than those used for bacterial microbiome studies.

Dr. Jenkins questioned whether researchers are using terms such as “strengthening” and “resilience” consistently, particularly because outcomes that are beneficial in livestock production, such as weight gain, may not be desirable in humans. Dr. Myer responded that concepts such as adaptation, stability, and function can be applied across systems, but the desired outcomes differ depending on the species and context. Dr. Costa agreed and noted that goals vary considerably between human health and animal production. He pointed out that practices that reduce microbial diversity may support growth in livestock, whereas greater diversity is often considered beneficial in human health, underscoring the importance of defining resilience according to the biological system being studied.

Public Comment

Eli Briggs, Infectious Diseases Society of America

Eli Briggs emphasized the need for continued federal support for the development of novel antimicrobials, particularly narrow-spectrum products that minimize disruption of the microbiome. They noted that current financing models do not adequately support antimicrobial innovation because stewardship efforts appropriately limit product use, making it difficult for companies to sustain development programs. They advocated for financing mechanisms that delink revenue from sales volume and also highlighted the importance of strengthening the infectious diseases workforce through programs such as loan repayment initiatives. They argued that shortages of researchers, physician-scientists, and microbiologists are limiting progress in AMR research, stewardship, and patient care.

Amelia Gerst, Biotechnology Innovation Organization

Amelia Gerst discussed the promise of microbiome-based therapies and other targeted antimicrobial innovations but stressed that scientific advances alone will not be sufficient without addressing underlying market failures. They explained that many innovative antimicrobial products are intended to be used sparingly, creating a conflict between stewardship goals and commercial viability. They urged policymakers to implement antimicrobial pull incentives and other reimbursement mechanisms that reward the societal value of innovative therapies rather than sales volume. They noted that these reforms are necessary to sustain investment in antimicrobial and microbiome-based technologies.

Amalia Corby, American Society for Microbiology

Amalia Corby highlighted the significant advances made in microbiome science through federal leadership and investment, while emphasizing that many discoveries have not yet translated into clinical practice. They called for strengthened federal coordination using a One Health framework, sustained support for foundational and translational research, and greater investment in data standards and infrastructure. They also stressed the need for education and engagement efforts to improve the understanding of microbiome science among healthcare providers, researchers, and the public. They called for sustained investment to ensure that microbiome research contributes meaningfully to AMR prevention and public health.

Joshua Narrow, Microbiome Therapeutics Innovation Group

Joshua Narrow highlighted recent progress in the microbiome therapeutics field, including regulatory approvals for microbiome-based products aimed at preventing recurrent *C. difficile* infections. They described ongoing challenges related to evidence standards, regulatory pathways, reimbursement, and adoption of approved products. They called for the development of frameworks that support post-approval evidence generation, improved reimbursement models, and legislative solutions that foster continued innovation. They also encouraged further work to qualify microbiome-based measures of colonization resistance for both drug development and surveillance purposes.

Chloe LeBegue-Polley, Nestlé

Chloe LeBegue-Polley encouraged the PACCARB to broaden the concept of antimicrobial stewardship to include “microbiome stewardship.” They explained that preserving and restoring microbiome resilience should be recognized as an important component of AMR prevention. They highlighted the role of the microbiome in preventing pathogen colonization and recovering from antibiotic-induced disruption. They recommended continued investment in microbiome research, development of microbiota-based interventions, and public education efforts that promote appropriate antibiotic use and greater understanding of microbiome health.

Hua Huang, Ohio State University

Hua Huang highlighted the impact of antibiotic administration practices on the gut microbiome and the development of AMR. They argued that orally administered antibiotics can cause extensive disruption to gut microbial communities and contribute significantly to resistance development. They highlighted research suggesting that alternative methods of administration, such as injectable antibiotics, may reduce microbiome disruption and limit the expansion of resistance genes. They also discussed efforts to reduce antibiotic-resistant bacteria in fermented foods and emphasized the need to consider foodborne sources of AMR as part of broader mitigation strategies.

Ava Alkon, Doctors Without Borders (Médecins Sans Frontières)

Ava Alkon urged the PACCARB to consider how microbiome science can support AMR interventions in low-resource settings. Drawing on experiences from humanitarian healthcare programs, they described the burden of AMR in vulnerable populations, particularly children suffering from severe malnutrition. They explained that repeated infections and repeated antibiotic exposure can contribute to resistant organisms and worsen health outcomes. They called for continued U.S. support for AMR programs in low- and middle-income countries and stressed the importance of interventions that improve diagnosis, infection prevention, and appropriate antimicrobial use.

Douglas Call, Washington State University

Douglas Call advocated for additional research examining the ecological conditions that allow resistant bacteria to colonize and persist within human and animal populations. They noted that antimicrobial exposure alone does not fully explain patterns of colonization and suggested that host and environmental factors, including inflammation and changes in the gut ecosystem, may create conditions that favor resistant organisms. They encouraged greater attention to the interactions among microbiome changes, bacterial transmission, and the persistence of resistance genes across human, animal, and environmental systems.

Marilyn Bruno, Aequor Inc.

Marilyn Bruno emphasized the importance of pursuing nontraditional approaches to combating AMR. They focused on biofilms, which she described as an early and common defense mechanism used by resistant bacteria and fungi. They argued that conventional antibiotics are often ineffective when biofilms are present and highlighted the organization's efforts to develop technologies that remove or prevent biofilm formation. They encouraged policymakers to create pathways that support innovative products targeting biofilms as a means of restoring the effectiveness of existing antibiotics and improving patient outcomes.

Council Roundtable

Dr. Plummer invited Council members to offer their perspectives on the information presented at this meeting. The feedback is summarized below according to broad categories of interest.

One Health, Ecology, and Broadening Ecosystems

- Expand focus beyond the gut microbiome to prioritize understudied microbial ecosystems, including the respiratory, oral, skin, vaginal, soil, plant, and water environments to understand their roles in supporting or hindering AMR mitigation.
- Leverage veterinary medicine's unique advantages where diet, environment, and medication exposure can be tightly controlled to accelerate translational research and comparative insights across species and sectors.
- Reframe health and disease through the lens of microbial ecology, emphasizing diversity, balance, and microbial resilience, recognizing that adaptation and recovery, rather than static stability, define a healthy, resilient microbiome.

Standardization, Diagnostics, and Data Integration

- Establish consensus definitions for key concepts such as dysbiosis, "strengthening", and "unhealthy" microbiomes, which may be more practically achievable than defining a universal "healthy" microbiome, to align multi-disciplinary efforts.
- Harmonize terminology, measurements, and research methods across disciplines to enable comparable results, particularly when translating complex microbiome science into clinical and public health applications.
- Develop precise diagnostic tools capable of identifying patient-specific microbiome disruptions, allowing clinicians to match targeted therapeutic interventions with the distinct needs of diverse patient populations.
- Standardize and integrate the massive volume of microbiome data generated across human, animal, and environmental systems, leveraging agency resources to build accessible, cross-species databases.

Clinical Stewardship, Innovation, and Therapeutics

- Prioritize microbiome preservation alongside restoration by actively utilizing narrow-spectrum antibiotics and robust antimicrobial stewardship to prevent collateral damage to microbial communities during infection treatment.
- Integrate diverse, promising modalities including bacteriophages, microbiota transplants, probiotics, prebiotics, postbiotics, and nutrition into the broader AMR therapeutic toolkit rather than searching for a single silver bullet.
- Shift clinical evaluation from surrogate measures to hard, patient-centered outcomes (such as mortality, infection rates, and growth metrics) to build the robust evidence base required to change clinical practice and policy.

- Address systemic failures in the antimicrobial ecosystem by creating sustainable economic incentives, building workforce capacity, and supporting innovative product pipelines at the intersection of AMR and microbiome science.

Implementation, Accessibility, and Practice Change

- Identify and systematically dismantle barriers to implementation to ensure that scientifically proven, existing microbiome therapies achieve widespread, routine clinical and veterinary adoption.
- Educate healthcare providers on the availability, benefits, and limitations of novel therapies, recognizing that professional practice and public understanding must evolve alongside scientific innovation to achieve impact.
- Support equitable distribution of scientific advancements so that vulnerable populations have access to nutritious food, clinical therapies, and microbiome education, reducing disparities in therapeutic outcomes.
- Translate scientific breakthroughs into clear policy and regulatory pathways, particularly for novel products like bacteriophages, to guide federal funding, priority-setting, and practical integration into clinical medicine and agriculture.
- Promote low-cost, highly accessible dietary strategies, such as increased fiber consumption, as practical, global interventions to support microbiome health and combat AMR in both domestic and resource-limited settings.

Closing Remarks

Paul Plummer, D.V.M., Ph.D., DACVIM, DECSRHM, Council Chair

Dr. Plummer thanked the speakers, Council members, and staff for their contributions to the meeting. He emphasized that addressing AMR requires acknowledging the complexity of the problem, identifying research gaps, and developing practical guidance for federal partners. He noted that the microbiome may be both part of the problem and part of the solution and encouraged the Council to continue exploring its role through a One Health perspective. He concluded by formally closing the 28th Public Meeting at 3:40 p.m.

Appendix: Presidential Advisory Council on Combating Antibiotic-Resistant Bacteria (PACCARB) Members

September 9-10, 2026

PACCARB Voting Members Present

Paul Plummer, D.V.M., Ph.D., DACVIM, DECSRHM, Chair
Jason Newland, M.D., M.Ed., Vice Chair
Stephanie Black, M.D., M.Sc.
Claire Burbick, D.V.M., Ph.D., DACVM (*virtual*)
Virginia R. Fajt, D.V.M., Ph.D., DACVCP (*virtual*)
Susan Huang, M.D., M.P.H.
Jennie H. Kwon, D.O., M.S.C.I., FSHEA, FIDSA
Lynn Marks, M.D.
Payal K. Patel, M.D., M.P.H.
Robin Patel, M.D., DABMM, FIDSA, FACP, FAAM
Julia E. Szymczak, Ph.D.
Thomas Wittum, Ph.D.

Organizational Liaisons Present

American Society of Microbiology

Jacinda Abdul-Mutakabbir, PharmD, MPH, AAHIVP

American Veterinary Medical Association

Mark Papich, D.V.M., M.S., ACVCP

AMR Action Fund

Henry Skinner, Ph.D., MJurr, MBE

Bill & Melinda Gates Foundation

Padmini Srikantiah, M.D., M.P.H.

EpiX Analytics

Francisco Zagmutt, D.V.M., M.P.V.M., Ph.D.

International Society of Antimicrobial Chemotherapy

David Jenkins, BSc (Hons), MB BS, AKC, MSc, FRCPath (*virtual*)

National Institute for Animal Agriculture

Lucas Pantaleon, D.V.M., M.S., M.B.A., DACVIM

Regular Government Employees Present

U.S. Department of Health and Human Services

Mark Albrecht, Ph.D., (for Christopher Houchens), Biomedical Advanced Research and Development Authority (BARDA), Office of the Assistant Secretary for Preparedness and Response

Shelly Coyle, RN, (for Shari Ling), Centers for Medicare and Medicaid Services, *(virtual)*
Michael Craig, M.P.P., Antibiotic Resistance Coordination and Strategy Unit, Centers for
Disease Control and Prevention
Melissa Miller, M.D., M.S., FCCM, Agency for Healthcare Research and Quality,
Administration for Strategic Preparedness and Response (ASPR)
Angela Monahan, M.P.H., Office of Global Affairs
Sam Perdue, Ph.D., National Institutes of Health (NIH)
Ribhi Shawar, Ph.D., (for William Flynn, D.V.M.), Center for Veterinary Medicine, Food and
Drug Administration

U.S. Department of Agriculture

Andrea Cote, (for Gamola Fortenberry), Food Safety and Inspection Service
Roxann Motroni, D.V.M., Ph.D., Agricultural Research Service
Chelsey Shivley, D.V.M., Ph.D., DACAW, for Sarah M. Tomlinson, D.V.M., Animal and Plant
Health Inspection Service

U.S. Department of Defense

Paige Waterman, M.D., FACP, FIDSA, COL MC, Uniformed Services University

U.S. Environmental Protection Agency, U.S. Department of the Interior

Jay Garland, Ph.D.,

Designated Federal Officials

Sarah McClelland, M.P.H., Public Health Advisor, Designated Federal Officer, OASH, HHS

Advisory Council Staff

Joe Bono, Deloitte Consulting LLP
Erin Lauer Tarosky, Deloitte Consulting LLP
Corey Meyer, Ph.D., Deloitte Consulting LLP
Jennifer Roberts, M.P.H., Deloitte Consulting LLP
Abigail Simmons, M.S., Deloitte Consulting LLP
Lauren Plaine, M.P.S., RN, CEN, Deloitte Consulting LLP
Brianna Corrie, Deloitte Consulting LLP

Glossary of Abbreviations

AMR	Antimicrobial Resistance
APHIS	Animal and Plant Health Inspection Service
ASPR	Administration for Strategic Preparedness and Response
BARDA	Biomedical Advanced Research and Development Authority
CARB	Combating Antibiotic-Resistant Bacteria
CDC	Centers for Disease Control and Prevention
CF	Cystic Fibrosis
DNA	Deoxyribonucleic Acid
FDA	Food and Drug Administration
FMT	Fecal Microbiota Transplantation
HGT	Horizontal Gene Transfer
HHS	U.S. Department of Health and Human Services
ISL3	Insertion Sequence-Like Element 3
NIH	National Institutes of Health
NIST	National Institute of Standards and Technology
OASH	Office of the Assistant Secretary for Health
PACCARB	Presidential Advisory Council on Combating Antibiotic-Resistant Bacteria
PCR	Polymerase Chain Reaction