

Report 34: Commensal Organisms (Microbiome) and Health

Convener: Thomas Vogt

Brief History: Ten times more bacterial DNA exists in our bodies than human DNA. In other words, there are ten times more bacterial cells than human cells in every person. The microbiome and humans have evolved together. There is increasing recognition that the microbiome influences human health, the environment influences the microbiome, and conversely the microbiome influences how we respond to the environment. Important discoveries are often made when new technologies and new concepts in biology are introduced. Study of the microbiome is at this stage and the time is ripe for the NIEHS to explore opportunities in how environmental health sciences can contribute to this field.

Discussion Highlights:

- The human body may be viewed as a scaffold for hosting a wide variety of commensal organisms (microbes, viruses, fungi, parasites).
- There are approximately 10 times more genes in the microbiome than the human genome.
- The commensal relationships are reciprocally influential along the continuum of health to disease. Commensal organisms can alter human responses (eg immune and metabolic) to their environment.
- These commensal populations are highly dynamic and therefore can be envisioned to be early and sensitive readouts of environmental exposures, conditions, and potential health effects.
- Four systems were focused on: skin, respiratory, GI, and urogenital.
- The group acknowledged that these populations are differentially influenced at each life-stage—perinatal was a key example.
- A key opportunity is that contemporary technologies are ripe for application to this field (DNA sequencing, metabolomics, proteomics, etc.) and an interdisciplinary approach is critical.
- The group recognized the microbiome poses a problem of significant complexity with respect to determining a reference dataset. Individual microbiomes are altered by nutritional status, diet, administration of antibiotics, etc.
- The microbiome is believed to represent a very appealing “sensor pad” for environmental sampling (diet/nutrition, ambient environmental conditions, toxicants, exposures, etc.)
- Humans are a particularly approachable population for this type of inquiry. Animal modeling can be leveraged for building on human studies or informing human studies.
- The microbiome is being approached by multiple institutes and groups, e.g. the NIH Microbiome Project, the Metabiome Project but not necessarily with an environmental health focus.

- Interdisciplinary skill sets across a wide range of expertise are required to advance this area: microbiology, ecology, biology, epidemiology, bioinformatics, statistics, genetics/genomics, nutrition, toxicology, etc. This opportunity clearly cuts across all divisions of the NIEHS.
- The group highlighted a real gap and the need for training in the microbiome across a variety of disciplines.
- The group felt that the biological opportunity represented a low to moderate risk with a very significant impact within the time period of the 5-year strategic plan.

Recommendations:

- NIEHS should launch a commensal organism/microbiome program.
- NIEHS should look to partner with other agencies and institutes who have existing commensal organism projects.
- An NIEHS program has significant potential in environmental surveillance and in doing so impact knowledge of the human/environment interaction and to inform policy.
- The NIEHS project has significant potential to better our understanding of the microbiome and its importance or application for prevention, intervention, and management of a variety of diseases.

Discussion Participants:

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