Science Café: The Science of Microbes

PNAS: I’m Sandeep Ravindran, and welcome to Science Sessions. Advances in genomic sequencing have transformed our ability to identify and understand the microbes that inhabit different parts of the human body. This week we’re featuring a podcast recording from “The Science of Microbes,” an interactive discussion with microbiologists Julie Segre and Liliana Losada held in Washington, DC on February 27, 2013. The event was part of the celebration of the 150th anniversary of the National Academy of Sciences, and focused on current microbiology research and how it was influenced by a classic 1977 PNAS paper on 16S ribosomal RNA sequencing by Carl Woese and George Fox. Liliana Losada, an assistant professor of infectious disease at the Craig Venter Institute, introduces us to her work on the human microbiome, and starts by describing the impact of Woese’s paper.

Losada: Woese and Fox gave us a molecular technique that really increased the throughput and our capacity to study microorganisms. We can now probe into many different kinds of environments and we can look at the diversity of microorganisms without having to culture them and characterize every single one of the cultures. What I focus on right now is studying the microflora that exists in our nasopharynx, and specifically in children and infants from the day they’re born actually, through their first year of life, to really study what are the dynamics that are occurring in the nasopharynx, and also we’re looking then at the impact of vaccination programs and if the vaccines are affecting, not only the streptococcus, but also other potential microorganisms that are there in their nasopharynx.

PNAS: Julie Segre, a senior investigator at the National Human Genome Research Institute at the National Institutes of Health, describes how she applied whole-genome sequencing to track and limit the spread of drug-resistant bacteria at the NIH in 2011.

Segre: A year-and-a-half ago, we had a patient come in to the NIH clinical center who had a drug-resistant form of Klebsiella pneumoniae, and so she stayed at the NIH for five weeks, and received treatment, and about three weeks after she left, tests which had been negative until that point came up positive for a patient who had an infection. In the end, there were 18 patients who were found to be colonized and infected with this Klebsiella pneumoniae. What we didn’t know at that point was, whether when we had patients 1, and 2, 3, 4, were they related to each other. This is really the point at which we got involved in terms of DNA sequencing. So by looking at the DNA sequence what we saw was that patient 1 had in fact transmitted to patient 4, and had transmitted to patients 2 and 3 independently from 4. And we set up this whole contact-isolation ward, we changed all of the hospital practices. Ultimately we stemmed this cluster of infection.

PNAS: During the remainder of the podcast, Losada and Segre answer questions from the audience.

Audience member: Could you just give a general overview of what are the kinds of microbes that are in the gut or on the skin or in the nose, and what is their function?
**Segre:** The bacteria in the gut is kind of easier, you know, we talk about how it aids in digestion. But for a lot of the other surfaces, I think that they’re educating the immune system, they’re breaking down other products. The ecology of the human dictates what kind of microbial diversity is there. So in the oily regions, the bacteria that live here are *Propionibacterium*, and what they do is they help to break down the oily products that the human cells produce into a natural moisturizing factor. The other types of bacteria in the skin are some *Corynebacterium*, some *Staphylococcus*. You know, a lot of times even what the *Staphylococcus epidermidis* is doing is making sure that other more pathogenic bacteria don’t attach to your skin.

**Losada:** In the lung, or in the upper respiratory tract, what we see is also a very small number of organisms that dominate. *Staphylococcus, Streptococcus*, in some cases *Moraxella*.

**Audience member:** Do both of you want to talk about how the technologies have sort of changed?

**Segre:** There were some technology developments that came along during the genome project, but they really didn’t change that much for about 15 years, and then suddenly, it exploded.

**Losada:** So there are not only innovations from the biological side but also computational and engineering side that are really allowing us to increase the amount of data we produce, and I think right now we’re limited by our human brains and how much we can process.

**Audience member:** Is it time that rather than just hoping that gut bacteria recover, we can introduce things that we have found in the general population to be normal? Fecal transplants for example?

**Segre:** Yes, actually fecal transplant is now FDA approved, and what we’re wrestling with in this country right now is, should a probiotic be regulated as a natural product, a food additive, or a drug. I think we do need to understand how we could use beneficial microbes as part of preventing us from getting in an out-of-whack state. So I think we need to start thinking of all of those sorts of things, because bacterial community is probably really important in terms of promoting health.

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