

Scientists

Mixed interests

David Reich

Professor, Department of Genetics, Harvard Medical School, Boston, MA



David Reich's insights into gene flow among human populations and between our closest relatives caught our attention. Curious to know more, *BioTechniques* contacted him to find out about the ambition, character, and motivation that led to his success.

How did you begin studying human evolutionary history?

I have always been interested in science and history. It was a bit of a problem in college because I had broad interests and didn't want to give anything up. I started as a history and sociology major, but later switched and earned my degree in physics. I benefited from the American university system, which allows you to take classes in many different areas, and eventually stumbled upon this field that perfectly combines my interests. It is quantitative and mathematical, but also focuses on how people are related to each other in history, how we came to be where we are now, and how we are personally connected to the world around us. For a long time, I considered my work on human evolution to be a hobby while medical genetics was my job. But now I consider them both to be my job.

What do you consider to be your most significant scientific contribution?

I am privileged to collaborate with Svante Paabo at the Max Planck Institute in Leipzig in analyzing the genome sequences of archaic humans, such as Neanderthals and Denisovans, to compare to modern genomes around the world. What we

learned from these data was surprising and changed our view of how we relate to our closest relatives in history.

Over the last 3 or 4 years, we have found that mixing between very different populations has been a much more common event in human history than we thought. For example, we found a gene flow event where genetic material passed from Neanderthals into the ancestors of all present day non-Africans about 40,000-90,000 years ago. This was a big surprise because we previously believed that when modern humans moved out of Africa 50,000-60,000 years ago, they replaced the Neanderthals they encountered without interbreeding. But now we know that there was interbreeding that affected the genomes of non-Africans. That's really exciting and may be biologically significant since the Neanderthals were pre-adapted to the environment and may have contributed some useful genes to modern humans.

We also worked on the genome sequence of the Denisovans, another archaic group from Siberia that is distantly related to the Neanderthals, and found that these people also interbred with a different group of modern humans. People in New Guinea, Australia, and the Philippines have inherited up to 5% of their DNA from the Denisovans.

What are you working on now?

While we continue to work on archaic DNA, we also compare present day human populations where we have found mixtures between highly differentiated groups. In 2009, we published that Indian populations from South Asia are mixed between two populations as different from each other as Europeans and East Asians. And we recently published a paper showing that all Europeans (with the possible exception of some isolated populations) are the result of a major mixture between two highly different ancestral populations. We now believe that population mixture is the rule in history rather than the exception.

I also work in medical genetics, focusing on medically complicated histories and mixture. Having a good model of the history of mixture

enables us to find genes for disease that are most relevant to the populations in question. A major focus of my lab has been in developing methods for finding genetic risk factors in African Americans that might get missed by applying techniques developed with another population. We found a place in the genome that is responsible for increased risk of prostate cancer in African Americans, but is less significant in other populations. This region also has a major affect for breast, colon, and urinary bladder cancers.

What do you see as the most important open question in your discipline?

For medical genetics, an important question is how to translate the discoveries made in genome wide association studies into drug targets and clinical tests. Currently, there is a debate in our community about how these discoveries actually affect drug discovery. For example, we can often predict increased or decreased risk for disease, but how does that changes a physician's opinion on how to treat the disease?

I think the biggest challenge in human evolutionary history is to develop an understanding of how human populations came out of Africa, moved around the world to where they are today, and how they are related to each other. We currently have only the broadest outlines of this history, but the question is now addressable with modern genetics data for the first time. The data we have are so powerful that I think we will know the answer to these questions in five to ten years.

Interviewed by Kristie Nybo, Ph.D. Image courtesy of Kris Snibbe. 

BioTechniques 54:17 (January 2013)
doi 10.2144/000113982

To purchase reprints of this article, contact: biotechniques@fosterprinting.com