Mark Seielstad, PhD
Committee on Nominations
Membership At Large
Biography

I graduated from Pocahontas County High School (Dunmore, West Virginia) in 1988, and entered Stanford University soon thereafter with dual and seemingly disparate interests in both human history and biology. I found the answer to unifying these interests in the study of evolutionary biology. Working initially with the butterfly genus *Colias*, and funded by undergraduate research awards from the Howard Hughes Medical Institute, I split my time between summer field research at the Rocky Mountain Biological Laboratory and laboratory research centered on mitochondrial DNA sequencing in the lab of Professor Ward Watt.

Upon graduation I entered the Biology Ph.D. program at Harvard (funded by a genetics training grant from the National Institutes of Health) to work with Professor Richard (Dick) Lewontin, a well known theoretical and experimental population geneticist. While Dick had worked with human data – and indeed made the surprisingly durable observation in 1972 that some 85% of human variation is found in any one population with <15% unique to particular continents or populations, thus discrediting (or lessening the emphasis on) biological notions of race – his lab at the time was centered on the fruit fly *Drosophila* model. Therefore (and now funded by an NSF Fellowship), I returned to Stanford to work with Luca Cavalli-Sforza, one of the pioneers of human evolutionary genetics and its foremost practitioner at the time. During this time, I performed field research to collect human DNA samples in Sudan, Ethiopia, Mali, Indonesia, Vietnam and Thailand.

My thesis research centered on the paternally inherited chrY and maternally inherited mtDNA. This enabled the study of sex-specific migration rates. Somewhat surprisingly, the data showed at the global and continental levels that the female migration rate was higher than for males. This is almost certainly the result of the typical rules of post-marital residence by which most societies are patrilocal, wherein women typically move from the place of their birth to reside with their husbands in their ancestral home.

After completing my Ph.D., I received a Ruth Kirchstein NRSA from the NIH and was awarded an NIH K22 to fund my postdoctoral studies at the Harvard School of Public Health -- with the intention of studying human health and disease. While there, I rose to begin a tenure-track Assistant Professor position in early 2002. But at the same time, as a result of my frequent research trips to Southeast Asia, I became aware of major investments that the Government of Singapore was making in the area of genomics and biomedical sciences, and went so far as to accept a position at the newly established Genome Institute of Singapore, also in 2002.

While in Singapore, I led a large group of genetic and bioinformatic scientists, postdocs, and students, and ran a high-throughput genomics core facility. During these years I designed and contributed to numerous successful genome-wide disease association studies across a broad swathe of metabolic, autoimmune, infectious and eye diseases.

Now as a tenured Profess at the University of California San Francisco, my research continues into the genetic bases of human health and disease. I have been fortunate to have designed, executed, and led numerous such studies, each of which has led directly to years of productive follow-up research.

From 2010 to 2016 I was principal investigator, and served on the 8 member steering committee, for a large U01 grant from the National Institutes of Health that pioneered the application of whole exome and whole genome sequencing in the search for rare genetic variation underlying the risk of type 2 diabetes. I am currently funded, with my colleagues at the University of the Philippines in Manila by the Commission of Higher Education in the Philippines to perform a large epigenetic and microbiome study of Filipinos living in the Philippines and Filipino migrants to the San Francisco Bay Area. The idea with this nearly $2 million grant is to examine the effects of birthplace, early environment and current environment in a similar genetic population to determine the effects of these factors on the microbiome and epigenetic marks, as well as on the risk of type 2 diabetes and other metabolic diseases.

I have published more than 125 peer-reviewed papers to-date in both high-impact and open access publications, with a strong record of citations by other authors – e.g., a 5-year h-index of 50, and an average of 100 citations per paper (more than 13,000 total citations within the last 5 years alone). In addition, I have given more than 50 invited talks both internationally and domestically since 2000.