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Evolution: Applications in Human Health and Populations

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The American Institute of Biological Sciences and the National Evolutionary Synthesis Center convened their fourth annual evolution symposium at the 2007 National Association of Biology Teachers conference in Atlanta, Georgia.

Gordon Uno, a botany professor at the University of Oklahoma and education committee chair for the American Institute of Biological Sciences (AIBS), welcomed educators to the fourth annual evolution symposium at the National Association of Biology Teachers (NABT) annual conference. The December 2007 event, hosted by AIBS in conjunction with the National Evolutionary Synthesis Center (NESCent), focused on the human health applications of evolutionary biology. Brian Wiegmann, NESCent's associate director of education and outreach, introduced the six speakers who explored the role evolution plays in disease, medicine, human health, and the social questions surrounding these issues.

Sign, sign, everywhere a sign: Interpreting evidence for recent natural selection on the human genome

Carlos Bustamante, of Cornell University, illustrated statistical methods for inference in population and comparative genomics. Large-scale projects are more cost effective today than in the past, and many are under way to document sequence and haplotype variation in species such as humans and other primates, as well as in domesticated species such as cows, Asian rice, and dogs. What can be done with all these data? These are some of the possibilities: genomewide scans for natural and artificial selection; genomewide views of population structure and admixture; genomewide association mapping of genes underlying complex human diseases; and quantitative trait loci mapping for agronomic traits, such as milk yield in cattle.

Bustamante described three projects with which he is involved. The first, recently completed, aimed to identify human genes potentially involved in recent human adaptive molecular evolution. It analyzed about 20,000 genes from humans and chimpanzees. The second, CanMap, still under way, involves association and selective sweep mapping of genes with large phenotypic effect in domestic dogs. So far, genetic mapping has shown that dogs can be clearly grouped into breeds with well-defined boundaries and loosely clustered into higher-order groups. What CanMap endeavors to do is identify regions of the dog genome associated with certain characteristics, such as skeletal conformation, hair pigmentation and texture, and behavioral trait differences, while taking into account the high genetic relatedness within a breed. The last project, using large single-nucleotide polymorphism chips to study human history and the history of domesticated plant and animal species, has just begun.

Carlos Bustamante is assistant professor in biological statistics and computational biology at Cornell University. Photograph: Oksana Hlodan.

Marc Lipsitch is a professor of epidemiology in the departments of epidemiology and immunology and infectious diseases, Harvard University. Photograph: Richard Chase.

Sex, drugs, and natural selection: Evolutionary perspectives on antibiotic resistance

Marc Lipsitch, of Harvard University, took teachers on a tour of history to show that pathogens have tried just about everything to fight antibiotics, from overexpressing to altering whatever the drug targets. Evolutionary principles are key to this resistance. In most cases, drug-resistant strains are less fit, and bacteria are often resistant to more than one antibiotic. Resistance is passed horizontally on transmissible plasmids, which means that bacteria benefit from "prepackaged" sets of genes that have already proven effective at resistance. Plasmids are also "a source of baroque information, full of curious natural history," Lipsitch pointed out. One study showed that a series of outbreaks of gram-negative bacteria was due to an epidemic of a plasmid, not to any one bacterium.

It's much easier to create the problem of antibiotic resistance than to get rid of it. Even when the use of one drug decreases, the level of resistance to it does not. One reason for this is selective pressure resulting from antibiotic use. Another is ecological contamination. Consider antibiotic susceptibility as a shared resource; by analogy with the "tragedy of the commons," if we all have access to this common resource, we all have the incentive to overuse it.

We have partial solutions for some pathogens, but others present continuing challenges and are without solutions at the moment. A variety of approaches has been tried, from community intervention to controlled dosing. The policy of the World Health Organization (WHO) is to go into the field and monitor people to ensure that they take their medications in proper doses and at the right time. But the bottom line is that even proper use of antibiotics leads to resistance. Vaccines may be preferable for reducing drug-resistant types.

The race between bacterial adaptation and protection of the host

Sandra Romero-Steiner works with disease vaccines at the Centers for Disease Control and Prevention, where she has studied the immune response to vaccines for bacterial meningitis and other bacterial diseases. The two players in the race, bacteria and humans, would seem to be unequally matched: bacteria are unicellular, have approximately 3000 genes, and replicate rapidly; humans have about 100 trillion cells and about 300,000 genes and take around 20 years to produce a new generation. Yet humans win the race only rarely, as we did when we developed successful smallpox and polio vaccines. Why can't we win more often with other vaccines? The answer lies in our poor immune memory—until we can improve it, we won't win.

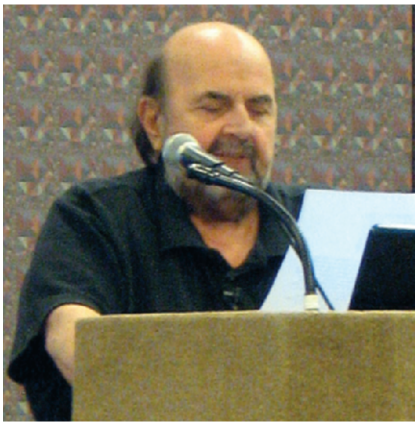
To conduct vaccine evaluations, new methods are needed to measure vaccine-induced protection. Vaccine efficacy trials are commonly performed in large populations, but it becomes more difficult to conduct trials in target populations. An alternative is to use laboratory correlates of protection; that is, measuring quantity and quality of antibodies produced in response to a vaccine. Some conjugate polysaccharide vaccines and protein vaccines have been developed this way and are effective. Romero-Steiner has urged countries to work together to produce a conjugate vaccine for meningitis, a disease affecting 1.2 million people worldwide. Meningitis is prevalent in some of the poorest areas of the world, such as in the parts of northern Africa dubbed the Meningitis Belt, where the disease, which is caused by a single bacterial species, emerges in cycles every 10 to 12 years.

Sandra Romero-Steiner is a senior investigator with the Division of Bacterial and Mycotic Diseases at the Centers for Disease Control and Prevention's National Center for Immunization and Respiratory Diseases. Photograph: Oksana Hlodan.

The road to the viral superhighway: Emerging disease in the time of globalization

George Armelagos, of Emory University, is a proponent of bioarchaeology, the study of the interaction of biological and cultural systems within an evolutionary context. Armelagos reports that an epidemiological transition—the third since the Neolithic age—is now under way; diseases that had been thought to be under control are reemerging, and antibiotic resistance is escalating, as microorganisms develop resistance to multiple antibiotics. Not only may there be many more resistant strains cropping up, but global warming may expand the range of diseases.

The concept of epidemiological transitions was formulated in the early 1970s by A. R. Omran, who used it to describe the control of infectious disease and the rise of chronic and degenerative diseases. The first epidemiological transition began with primary food production; it brought with it sedentary settlements, animal domestication, and an increase in population size. The second saw a decline in infectious disease and the rise of



George Armelagos is the Goodrich C. White Professor of Anthropology and department chair at Emory University. Photograph: Oksana Hlodan.

chronic disease because society developed effective public health measures, such as the polio vaccine. The current, third transition, Armelagos said, is giving us new and reemerging diseases for several reasons:

- Ecological disruption has been the pattern since the Neolithic.
- Antibiotic-resistant pathogens are very likely the result of cultural practices.
- Globalization of disease is unprecedented.
- Travel leads to a virtual viral superhighway.
- Dislocation of humans is extensive—there are 30 million refugees.

The Neolithic "revolution" marks the beginning of social stratification, the prime determinant of health differentials both within and between societies. The inequity gap in health and wealth accelerates with later cultural evolution, and it is now greater than in any other time in human history. The WHO reported in 1995 that "the world's biggest killer and the greatest cause of ill health and suffering across the globe is listed almost at the end of the International Classification of Disease. It is given the code Z59.5—extreme poverty."

The ethical implications of representing evolution and interpreting difference

Sandra Soo-Jin Lee, of Stanford University, is an anthropologist who studies the social and scientific meanings of race in research on human genetic variation and their implications for understanding human differences. Through her work, Lee tries to bring attention to questions such as these: What is the historical legacy of interpretations of evolution and race? How have notions of hierarchy, direction, and progress underpinning evolutionary concepts affected ideas and applications to race? How can the dangers of misinterpretation of the relationship between evolution and race be addressed?

Human history reveals that our ideas of race are coupled with our ideas of social values. For example, in 1758 Linnaeus used this racial classification: American red (reddish, obstinate, and regulated by custom), European white (white, gentle, and governed by law), Asian yellow (sallow, severe, and ruled by opinion), and African black (black, crafty, and governed by caprice). Polygenism, which stresses definite geographic boundaries and different lineages for populations, has a strong influence on how we think of human origins and development of races. Books such as *Types of Mankind,* first published in the 1800s, helped spread polygenism, and slave owners found justification for their racial attitude in this "new" science. The legacy of eugenics in the 20th century, based on the notion of self-direction of human evolution, affected US policy, which limited immigration from certain countries. Today we can still find evolutionary charts in science textbooks that are reminiscent of earlier ideas about the hierarchy of species.

Sandra Soo-Jin Lee is a senior research scholar at the Stanford Center for Biomedical Ethics, Stanford University. Photograph: Oksana Hlodan.

Emerging genomic information, sequencing the human genome, and other technologies for studying variation have stirred the pot. Francis Collins said in 2000 that race is not genetic: "Historians will consider this [completion of the human genome sequence] a turning point.... I am happy that today the only race we are talking about is the human race." Some would argue that we did not need the Human Genome Project to tell us that. Why is it we are still asking whether race exists? The November 2003 issue of *Scientific American* asked that very question, but the cover of that issue showed six women whose main difference was color of skin and hair. More recently, in October 2007, James D. Watson, codiscoverer of the DNA helix, told the *Sunday Times* of London that

For more information, visit these sites:

Speaker bios, video clips, class activities, and curriculum supplements for "Evolution: Applications in Human Health and Populations" are at *www.nescent.org/media/nabt2007/index.html.*

The video of the complete presentations by all six speakers can be found at *www.nescent.org/media/NABT.php#nabt2007.*

The AIBS Web page *www.aibs.org/special-symposia/2007_evolution-in-human-health-populations.html* provides the symposium's program details and slides from the speaker presentations.

he was "inherently gloomy about the prospect of Africa" because "all our social policies are based on the fact that their intelligence is the same as ours—whereas all the testing says not really."

Language matters, Lee said. She suggested that educators might answer student questions about race this way:

- Race is not defined by a set of characteristics or attributes.
- Continental ancestry is not synonymous with racial identity.
- Race emerges from a complex interaction of biological, environmental, and social conditions.
- There are no genes that are found in one population and absent in others.
- Science has a social historical context.

Evolution for everyone: How Darwin's theory can change the way we think about our lives

It is a familiar fact for David Sloan Wilson, of Binghamton University, that 50 percent of Americans claim to disbelieve the theory of evolution. For Wilson, who is known for his work on multilevel selection theory, it is more depressing that the other 50 percent do not connect evolution to their own lives. He calls it the "second wall of resistance," the first being denial of evolution altogether. This wall has been maintained within academia for most of the 20th century, and it continues to plague higher education. Political scientist Ian Lustic said in 2005: "Social scientists treat the life sciences as enclosed within a kind of impermeable wall. Inside the wall, evolutionary thinking is deemed capable of producing powerful and astonishing truths. Outside the wall, in the realm of human behavior, applications of evolutionary thinking are typically treated as irrelevant at best; usually as pernicious, wrong, and downright dangerous."

This fragmentation of knowledge—Wilson called it the "Ivory Archipelago"—must be addressed. He suggested a straightforward approach:

- Make scientific ideas nonthreatening, explanatory, and useful to people.
- Show that evolutionary theory is accomplished with respect to human affairs, in addition to within the biological sciences.
- Expand evolutionary theory beyond the biological sciences to show that it can unify knowledge about humans in the same way that it has unified knowledge about the rest of life.

David Sloan Wilson is a professor in the departments of biology and anthropology at Binghamton University. Photograph: Oksana Hlodan.

Wilson illustrated how this approach works in the activities he conducts with students. One such activity is a game about good and evil. After students define the terms, they are asked to perform three thought experiments: What will happen if you put a good person and an evil person together on a desert island? What will happen if you put a group of good people on one island and a group of evil people on another island? What will happen if you allow one evil individual to paddle over to "Virtue Island"? The student responses illustrate multilevel selection theory: traits associated with goodness can evolve, at least when appropriate conditions are met. Unselfishness is indeed vulnerable to selfishness within groups, but groups of unselfish individuals are likely to survive and reproduce better in purely biological terms than any other kind of group. The outcome of evolution depends on the balance of opposing forces of within-group and between-group selection. Experimental economics and other social sciences have developed many such games, heavily influenced by evolutionary theory, that serve as microcosms for human social behavior.

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