

## Community Health & Epidemiology Seminar Series

### Molecular Evolutionary Genetics and the Health of the Human Community: Leaving Racism Behind?

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CH&E Classroom, Room 409, Centre for Clinical Research, 5790 University Avenue

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**Abstract:** Ancestry tracing by molecular techniques ("23&Me," "Ancestry.ca," etc.) has become popular. Ads show people happily learning about their multi-ethnic or mixed-racial pasts and greeting newly found relatives. The contrast with recent history and extant situations is striking, where the revealing of one's ancestry might cause invalidation of civil and properties rights, and create life-threatening insecurity. Ancestry, whether implied by phenotypical characteristics, geographic origin, or directly determined by molecular techniques, may serve to admit some to groups with social power and privilege, or may act to cause rejection or expulsion by others. Ancestry determination and genomic history are parallel expressions of patterns of human heredity and history. Some groups self-proclaim their heritable "superiority," at times by directly referring to aspects of Darwinian "selection," or "survival of the fittest." Here, I question the attribution of "fitness" to ancestral group or population data, and point to a more general, neutral, and less triumphalist view of overall human evolutionary genomics. As *Homo sapiens*, we are all very closely related: so-called ethnic and racial "differences" are of relatively minor import and are generally irrelevant with reference to capacities allowing biological "survival" or "fitness." Some evolutionary biologists and their acolytes have interpreted human genetic data as proof of some groups having had to pass tight selective criteria, with unrealistic ideas concerning evolutionary "advances" in phenotype, parsimony of genome size, and selection within parts of the overall genome vs. selection of entire populations. An understanding of human evolutionary genomics deeply undercuts arguments favoring or privileging ethnic or racial groups. The evolution of the genome is increasingly understood to have come about from molecular accidents: mixing of genes among populations, invention of both new functional capabilities (ex: verbal communication) and heritable disease by mutation, gene duplication, and neutral evolution with random genetic drift, along with the overall genome maintaining fitness on a population basis. Population differences are geographic, cultural, historic, and social. Ancestral background is largely irrelevant at the biological level, and has often served as a social construct used inappropriately to justify inhumanity.

**Biography:** Dr. Joel W. Adelson is Visiting Professor in the Department of Community Health & Epidemiology, and also has strong ties with the Department of Bioethics at Dalhousie. He is Professor Emeritus at the University of California with present and former affiliations at the University of California, San Francisco Institute for Health & Aging as Professor of Social Medicine and Public Health; the Univ. of California, Irvine's Health Policy Research Institute; Brown University at the Hasbro Children's Hospital; and McGill University at the Montreal Children's Hospital. He obtained his PhD at the University of Southern California; MD, residency and fellowship at UCSF; and MPH in Health Policy and Management at Columbia University. He has long-standing interests in clinical practice, teaching, public and community health, clinical ethics, and molecular evolutionary theory.