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Education:

1978 *Laurea Summa cum Laude* in biology, Universita' "La Sapienza", Rome, Italy.
1986 PhD, Biology. Yale University, USA.

Positions and Employment

2013-present Senior Res. Scientist, School of Epid. & Public Health, Yale University
2004-present Lecturer, School of Epidemiology and Public Health, Yale University
2001-present Senior Res. Scientist, School of Forestry, Yale University
2001-present Director DNA Analysis facility on Science Hill, Yale University
2000-present Senior Res. Scientist, Dept. Ecol. and Evolutionary Biology, Yale University
1999-present Curatorial Affiliate, Peabody Museum of Natural History
1998-present Lecturer, Yale University
1998-present Director, Molecular Systematics and Conservation Center, Yale University
1986-2000 Postdoctoral Associate to Research Scientists, Yale University
1984-1987 Research Scientist, Università di Roma II
1982-1986 Graduate Student, Yale University
1978-1981 Research Associate, Università di Roma I

Synergistic Activities: ***Associate Editor****:* Molecular Evolution and Phylogenetics (2001-2005), Conservation Genetic (2003-present), BMC Evolutionary Biology (2008-present), PLOS Neglected Tropical Diseases (2010-present). ***Service in professional societies*****:** Scientific Fellow Wildlife Conservation Society (1998-present)**,** American Genetic Association (council member 2004-2007), Society for the Study of Evolution (council member 2006-2008), Systematic Biology Society (council member 2008-2012), Italian Evolutionary Biology Society (Vice President: 2006-2007). ***Public lectures and outreach****:* Several Public lectures on the use of DNA analyses and evolutionary tools in applied biology (Universities, secondary schools, and private societies). ***Workshop Organization*****:** Conservation genetics workshop in Galapagos for Ecuadorian undergraduates and University teachers, workshops on genomics for phylogeographic studies organized at Yale University for Yale and non-Yale students and scientists.

Research Interests and Expertise. I am a Senior Research Scientist at Yale University (USA) and also the director of an inter-disciplinary research and training center (Molecular Systematic and Conservation Genetics Center, MSCG) within the Yale Institute for Biospheric Studies (YIBS) and the DNA Analysis Facility on Science Hill, a core facility for Yale and non Yale users. The mission of the center is to train student and foster research using DNA-based techniques in environmentally related projects. I have trained more than 193 students from USA and abroad, post-doctoral research associates, and faculty. My research interest covers two main areas: conservation genetics and evolutionary genetics of vectors of diseases. I use DNA techniques and integrate them with morphological, ecological and environmental data to understand the

biology or a variety of organisms with special attention to two highly applied fields: conservation genetics and vectors and parasites evolutionary genetics.

Conservation genetics: My main efforts in this field in the past 15 years have been on the unique mega-fauna of the Galapagos islands, specifically Giant Galapagos tortoises and marine iguanas. We used DNA based markers to understand the evolutionary history, population demographics, and biogeography of these species, as well as understand the evolutionary and ecological forces that have impacted their morphology and current distributions. We are currently developing a genomic tool box of novel markers (SNPs) for this non-model organism, the Giant Galapagos tortoise, to move from single gene approaches to genomic ones and use them to help (1) understand their evolutionary history and (2) provide empirical data to support their management and conservation. Research funds for these projects have been provided by: National Geographic Society, Eppley Foundation, Paul and Bay Foundation, Turtle Conservation Society, and the Galapagos Conservancy. As one of my priorities is to train new generations of conservation biologist to take advantage of the most modern DNA technology to help address issue related to conservation and biodiversity, field trips to Galapagos include Yale and non Yale University students, as well as students from Ecuador and other countries, Galapagos National Park personnel, and young scientists.

Vector and parasite population genetics and genomics: For the past 15 years or so I have been using population genetic approaches to help elucidate the evolutionary and ecological forces that have *and* are shaping vectors and parasite distributions over a variety of spatial and temporal scales. The underlying goal is to help to control and monitor vector transmitted diseases by understanding the vector and parasites evolutionary history and demographics and their co-evolution. From an interest in the main vector of malaria in Africa, the mosquitoes of the *Anopheles gambiae* group, where I looked at patterns of genetic diversity of neutral and non-neutral markers (genes associated with insecticide resistance, for instance) at both continental and local scales, in recent years my focus as shifted to a different disease, *sleeping sickness*. This neglected disease widespread in sub-Saharan Africa is caused by *Trypanosoma brucei* parasites vectored only by tsetse flies (multiple *Glossina* species).

On *Tryapanosoma brucei* our studies have focused on the population genetics and genomics of both the human and animal infectious strains, looking at the evolutionary relationships of these strains and investigating the role of genetic polymorphisms in pathogenicity, virulence and drug resistance. For the tsetse flies we have focused on two species *Glossina fuscipes* and *pallidipes* in Uganda and Kenya. The overall goal of the projects is to use genetic or genomic level markers coupled with ecological and environmental data to understand the amount of genetic differentiation among population, levels of gene flow, population sizes and their temporal stability, and identify potential corridors for dispersal for these species, and eventually develop suitability maps for these vectors that are based on an integration of ecological and genetic data. We are also interested in looking at the coevolution of vector, parasites and symbionts (*Wolbachia, Wigglesworthis, Sodalis*) that may co-exist within the tsetse fly to explore the genotypic associations among these various organisms that might provide insights on infection and transmission. We are also starting a project on the tsetse gut microbiome to look at similar phenomena at the whole gut level. These projects have been carried out thanks to a long-standing collaboration with Drs Aksoy and Galvani (Yale School of Epidemiology and Public Health, EPH) and several colleagues from African institutions devoted to trypanosomiasis research and capacity building in Kenya and Uganda. Grants supporting these lines of research come mostly

from NIH, which is supporting our efforts through basic research (R01 and R21) and capacity building (Fogarty Institute, ICIDR) grants. Through the NIH Fogarty Institute we have been training scientists from Africa in population genetics and genomic analyses.

We are also collaborating with Drs Ko and Childs (Yale-EPH), Dr Richardson (Providence College), and with several colleagues from the Brazilian FioCruz research institute in Salvador (Brazil) to investigate the patterns of genetic differentiation of the Norvegian rats (*Rattus norvegicus)* in the urban slums of Salvador. This rodent is the main vector of *Leptospir*a, the agent of Leptospirosis, a bacterial disease that affects both humans and animals. The goal of this project is to evaluate patterns and levels of genetic differentiation at a microgeographic scale (within and between city valleys separated by a few hundred meters) to aid in the monitor and control of these rodents.

We are collaborating with Dr Cappello (Yale Medical school) on a project on the evolutionary genomics of the hookworms (*Necator americanus*) in Ghana. We are looking at the patterns of genetic diversity in human infected samples, pre- and post-de-worming treatments. We are using WGS approaches to obtain in-depth reads for identification of low frequency mutations to evaluate the genetic diversity of the beta-tubulin gene within sampled of pooled individuals worms. This gene is of interest because two of the principal benzamidazole resistance variants are in the studied DNA fragment and so could presumably be selected for after drug treatment.

Invasive species:

We are collaborating with Dr. Nathan Havill with the U.S. Forest Service to understanding the ecology and evolution of *invasive forest insects* and their native and introduced ranges, and the develop tools used to mitigate their impacts. Some of the projects include: 1) systematics and population genetics of invasive pests, especially hemlock woolly adelgid, balsam woolly adelgid, gypsy moth, and winter moth; 2) systematics and population genetics of predators and parasitoids being evaluated as biological control agents of invasive species, especially of hemlock woolly adelgid and emerald ash borer; and 3) systematics and biogeography of North American tree species.

We are collaborating with Drs Diuk-Wasser (Columbia University) and Drs Ben-Mamoun and Krause (Yale Medical School and EPH) to look at the population genomics of two tick-transmitted pathogens, whose range is currently expanding in the Eastern US: *Borrellia burgendorfi*, the agent of Lyme Disease, and *Babesia microti*, the agent of babesiosis. We are developing whole genome approaches to screen DNA extraction from field tick samples to analyze the genomic diversity of these two pathogens and identify the taxonomic origin of the tick blood meals.