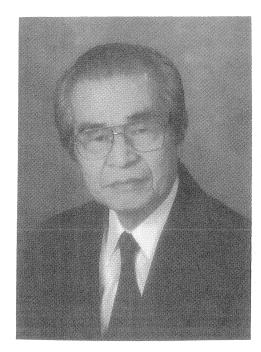# Dr. Masatoshi Nei

Date of Birth: January 2, 1931

Nationality: USA

Position: Evan Pugh Professor of Biology
Pennsylvania State University, University Park

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Pennsylvania State University
328 Mueller Lab
University Park, PA 16802
USA

Education and Career:

1953	B.S. from Miyazaki University, Miyazaki, Japan
1959	Ph.D. from Kyoto University, Japan
1958-1962	Assistant Professor, Kyoto University, Japan
1960-1961	Rockefeller Fellow, University of California and North Carolina State University
1962-1969	Geneticist, National Institute of Radiological Sciences, Chiba, Japan
1969-1972	Associate Professor to Professor of Biology, Brown University, USA
1972-1990	Professor of Population Genetics, University of Texas at Houston, USA
1990-1994	Distinguished Professor of Biology, Pennsylvania State University, University Park
1990-present	Director, Institute of Molecular Evolutionary Genetics, Pennsylvania State University, University Park
1994-present	Evan Pugh Professor of Biology, Pennsylvania State University, University Park

Awards and Distinctions:

1977	Japan Society of Human Genetics Award
1989	Honorary Member, Genetics Society of Japan
1990	Fellow, American Academy of Arts and Sciences
1990	Kihara Prize, Genetics Society of Japan
1993	Fellow, American Association for the Advancement of Science
1996	Honorary Member, Japan Society of Human Genetics
1997	Member, National Academy of Sciences, USA
2000	Honorary Member, Japan Society for Histocompatibility and Immunogenetics

Representative Publications:

Nei, M. 1969. Gene duplication and nucleotide substitution in evolution. *Nature* 221: 40-42.

Nei, M. 1972. Genetic distance between populations. *American Naturalist* 106: 283-292.

Nei, M. 1973. Analysis of gene diversity in subdivided populations. *Proceedings of the National Academy of Sciences USA* 70: 3321-3323.

Nei, M. 1975. *Molecular Population Genetics and Evolution*. North-Holland, Amsterdam and New York.

Nei, M. 1978. Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics 89: 583-590.

Nei, and Li, W. H. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences USA* 76: 5269-5273.

Nei, M. and Roychoudhury, A. K. 1982. Genetic relationship and evolution of human races. *Evolutionary Biology* 14: 1-59.

Saitou, N. and Nei, M. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4: 406-425.

Nei, M. 1987. *Molecular Evolutionary Genetics*. Columbia University Press, New York.

Hughes, A. L. and Nei, M. 1988. Pattern of nucleotide substitution at major histocompatibility complex class I loci reveals overdominant selection. *Nature* 335: 167-170.

Nei, M. Gu., X., and Sitnikova, T. 1997. Evolution by the birth-and-death process in multigene families of the vertebrate immune system. *Proceedings of the National Academy of Sciences USA* 94: 7799-7806.

Nei, M. and Kumar, S. 2000. *Molecular Evolution and Phylogenetics*. Oxford University Press, Oxford.

Academic Achievements:

Dr. Masatoshi Nei is one of the main architects who laid the theoretical foundations of current molecular evolutionary biology. By developing various statistical methods and applying them to molecular data, he pioneered new ways of studying the genetic diversity of populations, evolutionary relationships among organisms, the times of species divergence from common ancestors, the location of gene regions in which natural selection is operating, and related areas. The methods he introduced have made it possible to obtain quantitative estimates of various parameters of evolutionary importance that could not have been measured experimentally. Through these achievements, Dr. Nei has not only made the latest findings at the molecular level available to evolutionary biologists, but has contributed greatly to the birth of molecular evolutionary biology and its establishment as a positive science in which hypotheses can be verified quantitatively, rather than being discussed solely on a conceptual level.

Evolutionary Histories of Populations and Genetic Distance

One of the best-known statistical methods developed by Dr. Nei is concerned with defining the degree of genetic difference between populations and estimating this "genetic distance" from protein and DNA data. Dr. Nei's method, which he proposed in 1972, uses polymorphism data (individual differences in proteins and DNA) to estimate the origins of human and other populations, the times at which they diverged from common ancestral forms, and so on. Under the name "Nei's genetic distance," it has been adopted worldwide by most researchers in related fields and is still frequently used today.

In 1974, Dr. Nei applied his new measure to human populations and showed that the genetic variation among Europeans, Asians, and Africans is only about 10 percent of the average variation within the three major human ethnic groups; he also estimated that Africans diverged from Europeans and Asians about 100,000 years ago, and Europeans and Asians diverged from each other about 50,000 years ago. This was the first evidence pointing to the African origins of modern humans.

Statistical Methods for Studying DNA Evolution

Focusing at an early stage on DNA sequence data, from the late 1970s Dr. Nei initiated mathematical modeling of DNA evolution. In the mid-1980s, he worked on statistical methods for estimating the number of nonsynonymous

substitutions (nucleotide substitutions that result in amino acid replacements) and synonymous substitutions (those that do not result in amino acid replacements), and proposed that the ratio between the two be used to identify gene regions in which natural selection is operating strongly. These methods are now being utilized by a large number of investigators.

Phylogenetic Analysis of DNA and Protein Sequences

During the 1980s, Dr. Nei began to construct a mathematical theory of the phylogenetic relationships of genes, using molecular data such as DNA and protein sequences. He and his collaborators were the first to clarify the theoretical relationships of gene trees and species trees, thus providing a theoretical basis for explaining many experimental observations that had previously defied interpretation. With one of his graduate students, Dr. Nei also developed a technique of inferring molecular phylogenies known as the "neighbor-joining method," which has become the most widely used method of constructing phylogenetic trees.

Evolution of Immune System Genes

In 1988, Dr. Nei turned his attention to the major histocompatibility complex (MHC) genes, which are involved in immune responses such as rejection of organ transplants, and showed that the puzzling variability of these genes in human populations is due to a special pattern of evolutionary change of DNA that occurs when MHC genes protect the host from invaders such as viruses and bacteria. This evolutionary pattern has since been shown to hold true not only for humans but for vertebrates in general.

Dr. Nei also studied "multigene families," in which multiple copies of member genes are present in the genome, as is generally the case for the immune system genes. He discovered that the member genes typically evolve according to a pattern called "birth-and-death evolution," in which, after gene duplication, the member genes evolve more or less independently of one another, with some staying in the genome for a long time and others disappearing.

These achievements laid the foundation on which rests the theoretical framework of current molecular evolutionary biology. Thus, Dr. Nei has made an enormous contribution to the development of his chosen field of inquiry.