

1. Record Nr.	UNINA9910484864903321
Titolo	Evolution of the human genome . II Human evolution viewed from genomes // Naruya Saitou, editor
Pubbl/distr/stampa	Tokyo, Japan : , : Springer, , [2021] ©2021
ISBN	4-431-56904-9
Descrizione fisica	1 online resource (264 pages)
Collana	Evolutionary Studies
Disciplina	611.01816
Soggetti	Human genome Genoma humà Evolució humana Llibres electrònics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Intro -- Preface -- Contents -- Part I: Non-neutral Evolution on Human Genes -- Chapter 1: Anthropogeny -- 1.1 Getting at the Origins of the Human Phenomenon -- 1.2 Our Evolutionary Roots -- 1.2.1 Homo Sapiens: The Paradoxical Ape -- 1.2.2 Measuring Genetic Distance -- 1.2.3 Ancient Genome Data -- 1.2.4 Limits to Detecting Ancient Selection -- 1.2.5 Phenotypes Are More Than Nucleic Acids and Proteins -- 1.3 Phenotypes: From Fossils to Past Behavior, Current Physiology, and Cognition -- 1.3.1 Fossil Data -- 1.3.2 Archeological Data: Fossilized Behavior -- 1.3.3 Stable Isotopes, Paleoclimate, and Paleonutrition -- 1.3.4 Learning from Living Foragers -- 1.3.5 The Holocene Trap -- 1.3.6 Biological Proxies for Past Behavior -- 1.3.7 The Crying Need for Phenotypic Data of Non-human Hominids -- 1.3.8 Niche Construction and Top-Down Effects -- 1.3.9 The Physical Niche -- 1.3.10 The Socio-Cognitive Niche -- 1.4 The Cultural Niche -- 1.5 Language and Theory of Mind -- 1.5.1 The Brain Needs the Body and the Group -- 1.6 Opportunities and Limitations -- 1.7 Open Minds, Closed Umbrellas -- 1.7.1 The Need for Transdisciplinarity -- 1.8 Why Anthropogeny? -- 1.9 Note of Caution -- References -- Chapter 2: Positive Selection in Human Populations: Practical Aspects and Current

Knowledge -- 2.1 Statistical Approaches to Identify Signals of Positive Selection -- 2.1.1 Using Polymorphism Data -- 2.1.1.1 Tests Based on Long Haplotypes -- 2.1.1.2 Tests Based on Site Frequency Spectrum -- 2.1.1.3 Tests Based on Genetic Differentiation -- 2.2 Practical Challenges in Detecting Positive Selection Using Polymorphism Data -- 2.2.1 Distortions Due to Ascertainment Bias -- 2.2.2 The Confounding Factor of Background Selection -- 2.2.3 Demography Can Mimic Positive Selection -- 2.2.3.1 Migration and Structure -- 2.2.3.2 Population Expansion -- 2.2.3.3 Population Bottleneck. 2.2.3.4 Founder Effect -- 2.2.4 Has a Region of Interest Evolved Under Positive Selection? -- 2.2.4.1 Using Simulations Accounting for Demography -- 2.2.4.2 Outlier Approach -- 2.2.4.3 Combination of Different Tests -- 2.2.5 Selection Not Only by Hard Sweep -- 2.2.5.1 Soft Sweep -- 2.2.5.2 Polygenic Adaptation -- 2.2.5.3 Recent Methodological Advances in Detecting Alternative Sweep Scenarios -- 2.2.6 From Putative Advantageous Mutation to Increased Fitness -- 2.3 Current Knowledge on Positive Selection in the Human Genome -- 2.3.1 Candidate Gene Studies of Positive Selection -- 2.3.2 Genome-Wide Scans for Positive Selection -- 2.3.3 Insights from Published Studies of Positive Selection in Humans -- 2.3.3.1 Functional Categories for the Selected Protein-Coding Genes -- 2.3.3.2 Complex Adaptive Traits -- 2.3.3.3 The Importance of Regulatory Elements -- 2.4 Concluding Remarks -- References -- Chapter 3: Population Genomics of High-Altitude Adaptation -- 3.1 Background -- 3.2 High-Altitude Human Populations -- 3.2.1 Tibet -- 3.2.2 Andes -- 3.2.3 Ethiopia -- 3.3 Physiological Clues of High-Altitude Adaptation -- 3.4 Genetic Basis of High-Altitude Adaptation -- 3.4.1 Two Well-Recognized Genes (EPAS1 and EGLN1) and a Core Pathway (HIF) -- 3.4.2 A Broader Perspective from Multi-omics Resources -- 3.4.3 ``Borrowed Fitness`` from Archaic Hominins -- 3.4.4 Convergent Adaptation -- 3.5 Current Limitations and Future Directions -- References -- Part II: Evolution of Modern Human Populations -- Chapter 4: Mitochondrial DNA -- 4.1 Outline of This Chapter -- 4.2 Characters of mtDNA and Its Merits for Studying Human Populations -- 4.3 Emergence of Modern Humans and Establish of Genetic Diversity of Current Human Populations -- 4.3.1 Neanderthals and Modern Humans -- 4.4 Controversy Between Pedigree Based Estimation and Divergence Based Estimation -- 4.5 Haplogroups. 4.5.1 Phylogeny of Haplogroups -- 4.6 Demographic History Estimation Based on mtDNA -- 4.6.1 mtDNA Research Example Using BSP: Peopling to America -- 4.7 Disease -- 4.7.1 Missing Heritability and mtDNA Variation -- References -- Chapter 5: The Y Chromosome -- 5.1 The Odd Chromosome and Its History -- 5.2 Not All Y Chromosomes Are Created Equal: Polymorphisms in the Y Chromosome -- 5.3 Climbing Down the Y Tree -- 5.4 La Donna e Mobile Ma Non Troppo -- 5.5 Male Lines -- 5.6 A Royal Mystery in Three Acts -- 5.7 Hacking the Y Chromosome -- References -- Chapter 6: Africa -- 6.1 The African Landscape -- 6.2 African Genetic Diversity in a Global Scale -- 6.3 Genetic Diversity Within Africa -- 6.4 Local Genetic Diversity Within Africa -- 6.4.1 North Africans, the Misfit Within the Continent -- 6.4.2 Khoisan-Speakers, the Deepest Branch in the Humankind Tree -- 6.4.3 The Pygmies, the Hunter-Gatherers of the African Equatorial Forest -- 6.4.4 East African Groups, Source and Sink of Genetic Diversity -- 6.4.5 Western and Bantu-Speakers, the Major Component in Africa -- 6.4.6 Madagascar, an Island Between Two Distant Continents -- 6.5 Some Adaptive Variants in African Groups -- References -- Chapter 7: Peopling and Population Structure of West and South Asia -- 7.1 Introduction -- 7.2 Inferences from Uniparental

Markers -- 7.3 Inferences from the Nuclear Genome -- References --  
Chapter 8: Europe -- 8.1 Introduction: Genes and the Neolithic -- 8.2  
The Making of the European Paleolithic Populations -- 8.3 The Genetic  
Legacy of Paleolithic Europe -- 8.4 The Genetic Legacy of Neolithic  
Europe -- 8.5 More Complex Models, More Complex Facts -- 8.6 Post-  
Neolithic Events in the European Gene Pool -- 8.7 Comparing Models  
-- 8.8 Conclusion -- References -- Chapter 9: Southeast Asia -- 9.1  
Introduction -- 9.2 Contact with Archaic Humans in Southeast Asia.  
9.3 Ancient Migrants and Hunter Gatherers -- 9.4 Human Diversity in  
Mainland Southeast Asia -- 9.5 Impact of Human Expansions Driven by  
Agriculture -- 9.6 Concluding Remarks and Perspectives -- References  
-- Chapter 10: Australia and Oceania -- 10.1 Geography and Ecology  
of Australia and Oceania -- 10.2 Australia -- 10.3 Oceania -- 10.3.1  
Near Oceania in the Pleistocene -- 10.3.2 The Austronesian Expansion  
and the Colonisation of Remote Oceania -- 10.3.3 Duality of Oceanian  
Heritage -- 10.3.4 Evidence for Contact Between South America and  
Polynesia -- 10.3.5 The Unique History of Santa Cruz -- 10.4 Archaic  
Admixture in Australia and Oceania -- 10.5 Conclusions -- References  
-- Chapter 11: America -- 11.1 Introduction -- 11.2 Peopling of the  
American Continents During the Prehistoric Age -- 11.2.1 Environment  
-- 11.2.2 First Humans of the American Continents -- 11.3 Genetic  
Analysis of Contemporary Native Americans -- 11.3.1 Genome Analysis  
with mtDNA and the Y Chromosome -- 11.3.2 Genome Analysis with  
Nuclear DNA -- 11.4 Genetic Complexities and Ethical Issues on  
Genome Analysis of Native Americans -- References -- Chapter 12:  
Simulations of Human Dispersal and Genetic Diversity -- 12.1  
Introduction -- 12.2 Modelling and Simulating Human Dispersal --  
12.3 Realistic Simulation with Spatially Explicit Simulations -- 12.4  
SPLATCHE: An Example of Spatially Explicit Simulation Program --  
12.4.1 Spatial Structure -- 12.5 Main Results and Discussion -- 12.5.1  
Genes Surfing the Waves of Expansion -- 12.5.2 Hybridization During  
Expansion -- 12.5.3 Limitations and Future Developments -- 12.6  
Conclusion -- References -- Index.

---