

Position Paper
AN EUROPEAN REFERENCE GENOME ATLAS
TO UNDERSTAND, MANAGE AND RESTORE BIODIVERSITY AND ECOSYSTEM SERVICES

Executive Summary

The conservation and restoration of biodiversity is a top European Commission priority highlighted in the European Green Deal. Biodiversity is the key to preserve ecosystem services essential to support human activities, and it is currently under threat worldwide and particularly in Europe. Genomics, the study of the entire genetic material of individuals and communities, provides an information-rich and quantitatively accurate way to measure and monitor the status of biodiversity and the success of its restoration efforts. Specific measures for preserving European ecosystems as a part of a European Commission Biodiversity Strategy should therefore include a comprehensive description of European wildlife genomes, including those of wild relatives of domesticated breeds. The characterization of reference genomes of key European species can help understand past and present demographic trends and predict if, how and to which extent species important to ecosystem services will cope with habitat changes, how their distribution can respond to the ongoing shifts in habitat quality, and what their level of resilience will be in terms of e.g. susceptibility to pathogens and adaptation to a changing environment. Understanding features of the genome related to the ability of organisms to respond to such challenges will help better understand how to preserve ecological community and ecosystem functions. Here we propose that the upcoming Horizon Europe research budget include a large genome initiative, tentatively called European Reference Genome Atlas, with the aim of generating reference genomes representing European biodiversity, ranging from species of importance for agriculture, fisheries, pests, ecosystem function and stability to endangered species, and supporting research with those genomes to advance fundamental questions and needs in science, public health, conservation and biodiversity. The following three problem areas justify a need for this initiative.

- Based on the 2019 UN report on nature decline, one million out of eight million species on the planet are at risk of extinction, many could go extinct within decades. This includes 22.7% of European species.
- The world lost up to €18.5 trillion per year in ecosystem services from 1997 to 2011, and more than €492 billion in annual global crops are at risk.
- The European Green Deal is set to protect the environment and preserve biodiversity, with 40% of the common agricultural overall budget, and 30% of the Maritime Fisheries Fund contributing to ecosystem conservation.

With genomics playing a unifying element of all life sciences, expanding our understanding of and insight in genomes across the full spectrum of biodiversity will substantially enhance scientific excellence and leadership in Europe. All genome studies start from the generation of a reference genome, yet high-quality reference genomes are only available for a small fraction of European species. An European Reference Genome Atlas could provide the necessary basis for this advancement.

Biodiversity and ecosystem services are top European Commission priorities

The European Green Deal promotes biodiversity. In her speech at the European Parliament Plenary Session in November 2019, as President-elect of the European Commission, Ms. Ursula von der Leyen introduced the agenda of the new ‘Geopolitical Commission’ aimed at reinforcing the European Union’s role as an international leader in the transition to a healthy planet (1). President von der Leyen outlined six political guidelines and priorities that will shape the working programme of the European Commission for 2019-2024 (2). The first priority is the European Green Deal, a new growth strategy that aims at mobilizing at least €1 trillion of sustainable investment to transform the EU into the first climate-neutral continent by 2050 (3,4). The European Green Deal envisages a ‘set of deeply transformative policies’ including those aimed at preserving and restoring Europe’s natural environment, biodiversity, and ecosystems (2,3,5). The Commission noted that “*one million of the eight million species on the planet are at risk of being lost*”, with 22.7% of European species so far assessed threatened by extinction (6). One of the transformative policies is a Biodiversity Strategy for increasing the coverage of protected biodiversity-rich land and sea areas, and re- and afforestation of degraded forests (3,7). Additionally, the Farm-to-Fork strategy was devised to attain an environmentally-friendly food system, by enabling European farmers and fishermen to protect the environment and preserve biodiversity; this policy will be funded by at least 40% of the common agricultural overall budget and 30% of the Maritime Fisheries Fund (3,5). From a global perspective, the European Commission aims to foster the role and importance of biodiversity, conservation and ecosystem restoration worldwide at the upcoming conference of the Parties to the United Nations Convention on Biological Diversity (5,8).

Biodiversity is key to preserve ecosystem services. Biodiversity, the ensemble of life forms living on our planet, is central to maintaining ecosystem functions, and therefore it is widely recognized as a fundamental asset for many sectors of the global economy and for nature-based solutions tackling key societal challenges (9,10). Every single species at a particular level of the food web plays a significant role in preserving the stability of ecological communities. A local change in abundance or the extirpation of even a few species could significantly alter the stability and resilience of an ecosystem. This function is particularly true for keystone species that are crucial to uphold community structure, such as the Iberian lynx or the Mediterranean monk seal, two critically endangered carnivores (11). In addition, the integrity of terrestrial and aquatic ecosystems is pivotal for their capacity to deliver a wide range of services essential to human life (12). The world lost up to an estimated €18.5 trillion per year in ecosystem services from 1997 to 2011 because of land and coastal habitats degradation, and more than €492 billion in annual global crops are at risk from persistent decrease in pollinator communities (13). Biodiversity and habitat quality maintenance are of utmost importance also to constrain opportunities for physical animal-human interactions and zoonotic disease transmission, an increasingly frequent threat to human health as shown by the recent COVID-19 pandemic (14).

Section 2.1.7 of the European Green Deal specifically addresses preservation and restoration of ecosystems and biodiversity, as a crucial priority for the essential services they provide to agriculture, fisheries and aquaculture, food security, water and air filtration, natural disaster risk, pests and diseases mitigation, climate regulation, and discovery of new medicines (3,7). Record amounts of public funds are to be invested to meet these epochal challenges, particularly in advanced research and innovation (5). The

latest figure for Horizon Europe suggests that €80.9 billion will be allocated to research over seven years (2021-2027), with the majority assigned to strategic calls that address the identified priorities (15).

Genome studies and high-quality genome sequences are essential to preserve biodiversity

Biodiversity implies genetic diversity. The importance of genetics and genetic diversity is acknowledged in the current outline of the Biodiversity Strategy, which stresses the preservation of traditional varieties of crops and breeds. Domestic varieties of plants and animals are the result of natural and human-managed selection, sometimes over centuries or millennia. They tend to show a high degree of genotypic and phenotypic adaptation to local conditions with a resulting decline in genetic variation within individual breeds. As stated in the global assessment report on biodiversity and ecosystem services, loss of genetic diversity affects species survival, posing a serious risk to global food security (13). Several domesticated breeds of mammals and birds are already extinct, such as the aurochs (a species of large wild cattle), and many hotspots of agrobiodiversity and wild relatives of many crops are under threat or not formally protected. Wild relatives of domesticated breeds are therefore particularly important as they represent critical reservoirs of genetic and trait diversity that may provide resilience against future climate change, pests and pathogens. They may improve current heavily depleted gene pools of many crops and domestic animals. To protect wild biodiversity, the Biodiversity Strategy aims to build a coherent and resilient trans-European Network of natural areas with ecological corridors that will prevent genetic isolation and allow for animal dispersal. The Biodiversity Strategy simultaneously also plans to address the problem of alien, invasive species that may also threaten biodiversity (7). To achieve this challenge, a broad genomics initiative is warranted.

Genomics is key to preserving biodiversity. Ecosystem restoration and effective intervention to preserve biodiversity need to be grounded in detailed biological knowledge. This knowledge includes the genetics of the species that sustain ecological communities, underpinning their service to humankind. Genetic research in the past focussed on single genes. With the advent of large-scale sequencing technologies, it is now possible to directly study the evolving genome, which is the core entity of life. Genomics, the study of the entire genetic material of individuals, populations and communities, is now a pervasive independent discipline essential to all fields of biology and the life sciences, having accelerated and revolutionized the study of all biological mechanisms. Therefore, understanding the genetic structure of living beings is now a mandatory resource for academic research, industrial research, and policy makers committed to solving local and global issues. Indeed, genomics is already widely applied to address ecological questions that are central to the understanding of the function of ecological communities and that tackle threats, often brought about by human activities (16,17). For instance, in biodiversity restoration, restored ecosystem functions need to be monitored and assessed to confirm success of restoration efforts (17). However, many biotic components of ecosystems are either difficult or impossible to survey using field-based monitoring techniques (for instance because rare species can be elusive or difficult to distinguish). A pan-European genomics initiative could very precisely characterize all the diverse taxonomic groups and monitor trends in their distribution and abundance.

Genomics starts from a reference genome. Genomics typically samples thousands of molecular markers distributed across the genome of a species, providing high resolution of genetic and functional diversity (18). Historically, the genetic study of any living species starts from the generation of a **reference**

genome, which is a high-quality sequence for a chosen individual of that species. While what constitutes a reference genome has evolved since the first genomes were sequenced in the late 1970s, it has remained consistent that such references informed any subsequent genetic study, both in the planning phase and in the analysis and interpretation of results. The most renowned example of this approach is the Human Genome Project that 20 years ago began disclosing the secrets of human genetics, opening a completely new, and still largely unexplored, era for humankind. Over the years, similar projects were devoted to key species employed in human health and disease studies, such as house mice, zebrafish, or domestic chickens. These projects have had profound impacts on the way we conceive and practice biology, having informed an innumerable number of subsequent studies and discoveries. Many of these discoveries were allowed by the higher quality of available sequence data, and particularly by the quality of the reference genomes employed in the analyses. The improvements in our understanding of biological phenomena so far allowed by genomic studies are only beginning, and high-quality reference genomes are still unavailable for most animal and plant lineages of scientific and economic importance.

Genomic resources help define units of conservation. Over the last 10 years, the amount of scientific literature on reference genomes and wildlife genomic diversity has increased considerably, reflecting an expanding community of academic institutions, private foundations, and government agencies all advocating the importance of non-model species genomics for species conservation, biodiversity protection and ecosystem management. Genomics is progressively being proven essential to planning conservation actions (for example www.reviverestore.org). Genomics helps delineate the units of conservation. The detection of species or genetically distinct varieties can support law enforcement, inform resource allocation, and help in decision making regarding restoring habitat corridors or translocations (14,19). In degraded ecosystems native populations are often fragmented and subject to genetic erosion due to increased inbreeding. Ecological restoration often requires reintroduction and/or demographic augmentation, which in turn entails mixing different populations or lineages from within the native distribution of a species to restore genetic diversity and therefore fitness components. Reference genomes of different species can help assess differentiation between lineages, populations and species to better predict the outcome of admixture and make use of such predictions in conservation (16, 20, 21). One notable example is the conservation of European wolves, where admixture events between wolves and feral or even domestic dogs are frequent and hard to detect (22). Similarly, studying high-quality genomes of several salmonid (trout like fish) species led researchers to discover adaptive variants that determine migratory tendencies within highly connected populations, a key aspect for salmonid conservation (23). Reference genomes are also highly important to quantify species richness in pollination (24), replacing time-consuming traditional approaches with metagenomics assays. Pollination is a key and increasingly imperiled function necessary for the reproduction of most plants, with approximately 80% of flowering plant species (including one-third of food crops) relying on vertebrate and invertebrate pollinators (25,26). Reference genomes are necessary to reliably predict the demographics of populations and species' responses to changing environmental conditions. Combining genomically empowered community-level assessments from many sites, predictions will be key to identify which ecosystems are mostly endangered and help to prioritise and organise conservation measures.

Genomics is key to understanding the evolution of biodiversity through time. A reference genome allows reconstructing a species evolutionary histories over hundreds, thousands, or even millions of years before

the present. Such an evolutionary framework is seminal to unveil genomic diversity that has been lost during a species' decline, domestication, hybridization or pandemics (27). It can also be used to understand past and present demographic trends for European species and predict, as in a weather forecast, if and to which extent species important to ecosystem services will cope with habitat changes, how their distribution will respond to the ongoing shifts in habitat quality, and what level of resilience they will need to deal with pathogens and changing environments. This can improve decision making to identify and delineate lineages best suited for restoration and demographic reinforcement (28). Genome data can also provide insights into the mechanisms of adaptation and species survival in extreme environments or environments fluctuating over a short time frame. For instance, recent comparative genomic analyses among mountain sheeps in contrasting environments detected a novel set of candidate genes that are putatively associated with hypoxia responses at high altitudes and water reabsorption in arid environments (29). This study is an excellent example of how genome sequencing can offer novel insights into rapid genomic adaptations to extreme environments in animals, providing a valuable resource for future efforts on livestock breeding in response to climate change.

These examples and considerations clearly show how today, genome research and the characterization of reference genomes are pivotal in applied biodiversity conservation.

A European Reference Genome Atlas: reference genomes for the biodiversity of Europe

This position paper is presented by representatives of some of the major, most impactful and established European Union organizations in the field of genomics, as well as by several of their international collaborators. They include those that have applied genomics to biodiversity and ecosystems conservation. We come together from different backgrounds and perspectives, inspired by the principles of collegiality in the decision-making process and benefits sharing. We are also strong supporters of open science, both in terms of reproducibility and open data policies.

We argue that specific measures for preserving species and ecosystems as part of a European Commission Biodiversity Strategy should consider a comprehensive description of genomes of European species. We therefore suggest that wildlife genomics, and high-quality reference genomes in particular, should have a preeminent role in the framework of the EU Biodiversity Strategy 2030 and the upcoming Horizon Europe programme in the form of publicly available databases and resources. In particular, we propose to initiate a large genome initiative, tentatively called **European Reference Genome Atlas**, with the goal of capturing the biodiversity of Europe by sequencing and generating reference-quality genomes for representatives of the over 200 thousands European species of eukaryotes, not yet done, ranging from species of importance for agriculture, pests, ecosystem function and stability to endangered species.

Contrary to specific countries, the EU currently lacks the type of sustained, systematic financial and institutional leverage required for supranational initiatives of this kind. Yet, we believe that with the appropriate support, cross-country infrastructure and coordination, the fundamental goals of a European Reference Genome Atlas are within reach. While the implementation of projects generating reference genomes for European species are certainly ambitious, today's technological advances make it fundable, and a coordinated effort of pan-European and international research groups makes it feasible. We believe

that support should be granted on a sustained multi-year basis, with competitive grants that promote coordination among scientists of different nationalities and backgrounds.

We think such a call should express minimum quality standards for reference genomes, to have near complete and error free genome assembly data, as well as suggest areas of study with those genomes, including those described above. Reference genomes are the start point of genetic studies, so the quality of the data going into analyses affects the quality of the end product. Even existing high-quality reference genomes have been generated using different approaches because of different intended questions and/or purposes, resulting in extreme variation of genome quality. This often makes it difficult to conduct comparative studies, such as comparing all species from one genus or family, or all strains of one species for a particular gene or phenotype. Only very recently this situation has started to change thanks mainly to: 1) the continual improvement in throughput and accuracy of the sequencing technologies experienced in the last decade that eased and democratized the generation of high-quality reference genomes, and; 2) the coordinated efforts of growing communities of scientists, including the one we represent.

Similar to the influence that the Human Genome Project had in the last two decades, we argue that this approach will set solid, accurate, scalable and comparable foundations for hundreds if not thousands of scientific projects, for conservation assessments, monitoring projects and restoration efforts to come. Having a long-lasting impact within the upcoming Horizon Europe programme, this initiative will firmly establish the EU as the world-leading union in the area of genome research, biodiversity conservation and restoration.

Signatory list

EU Countries (in alphabetical order by country)

Qi Zhou, ERC Group Leader
Department of Neurobiology and Development
University of Vienna, AUSTRIA

Professor Toomas Kivisild, Department of Human Genetics
Professor Filip Volckaert, Director of the Laboratory of Biodiversity and Evolutionary Genomics
Katholieke Universiteit Leuven, BELGIUM

Associate Professor Pavel Hulva
Department of Zoology
Charles University, CZECH REPUBLIC

Professor Tom Gilbert, Director, Center for Evolutionary Hologenomics
Associate Professor Antton Alberdi, Coordinator of the Earth HoloGenome Initiative
Professor Anders J Hansen, Director, GLOBE Institute

Associate Professor Eline Lorenzen, GLOBE Institute
Associate Professor Morten T Limborg, GLOBE Institute
Professor Guojie Zhang, Director, Villum Centre for Biodiversity Genomics and Chair, B10K Genome Project and Global Ant Genomics Alliance
Tenure-track Assistant Professor Rasmus Heller, Section for Bioinformatics, Department of Biology, University of Copenhagen, DENMARK.
Associate Professor Ida Moltke, Dept. of Biology, University of Copenhagen, DENMARK,
Associate Professor Bent Petersen at GLOBE Institute and Deputy Director for Centre of Excellence for Omics-Driven Computational Biodiscovery (COMBio), AIMST University, Malaysia
Tenure-Track Assistant Professor Morten Tange Olsen, GLOBE Institute

Professor Urmas Saarma
Institute of Ecology and Earth Sciences
University of Tartu, ESTONIA

Professor Riho Gross
Chair of Aquaculture
Institute of Veterinary Medicine and Animal Science
Estonian University of Life Sciences
Tartu, ESTONIA

Professor Jouni Aspi
Ecology and Genetics Research Unit
University of Oulu, FINLAND

Dr. Jérôme Salse, Research Director
Dr. Charles Poncet, Dr. Michaela West
INRAE-UCA UMR GDEC 1095
Genotyping and Sequencing Platform (Gentyane)
Clermont-Ferrand, FRANCE

Professor Michael Hiller, Head, Comparative Genomics Group
Dr. Miklós Bálint, Head, Functional Environmental Genomics
LOEWE-Centre for Translational Biodiversity Genomics
Senckenberg Nature Research Society & Goethe-University
Frankfurt am Main, GERMANY

Dr. Camila Mazzoni, Head of Bioinformatics and Group Leader
Dr. Daniel W. Förster, Research group leader
Leibniz Institute for Zoo and Wildlife Research
Berlin, GERMANY

Dr. Eugene W. Myers, Group Leader
Max Planck Institute of Molecular Cell Biology and Genetics
Dresden, GERMANY

Dr. Philipp Schiffer, Research Group Leader, Wormlab
Junior Professor Ann-Marie Waldvogel, Group Leader, Ecological Genomics
Institute of Zoology
University of Cologne, GERMANY

Professor Bernhard Misof, Director, Head of Center for Molecular Biodiversity Research
Zoological Research Museum (ZFMK)
Bonn, GERMANY

Dr. Joanna Malukiewicz, Marie-Curie Post-Doctoral Fellow
Primate Genetics Laboratory, German Primate Research Center
Leibniz Institute for Primate Research, Göttingen, Germany

Dr. Periklis Makrythanasis, Group Leader
Biomedical Research Foundation of the Academy of Athens
Athens, GREECE

Dr. Grigorios Krey, Director
Dr. Chrysoula Gubili, Associate Researcher
Fisheries Research Institute, Hellenic Agricultural Organisation “DEMETER”
Nea Peramos, Kavala, GREECE

Professor Enikő Magyari
Department of Environmental and Landscape Geography
Eötvös Loránd University
Budapest, HUNGARY

Associate Professor Claudio Ciofi, Associate Head and Group Leader
Dr. Alessio Iannucci
Department of Biology
University of Florence, ITALY

Professor Aureliano Bombarely
Group Leader, Applied and Evolutionary Genobotany Laboratory
Department of Bioscience
University of Milan, ITALY

Professor Graziano Pesole
ELIXIR Italy, Head of Node
Department of Biosciences, Biotechnologies and Biopharmaceutics
University of Bari “A. Moro”, ITALY

Dr. Cristiano Vernesi
PI, Forest Ecology and Biogeochemical Cycle Unit, Chair of G-BiKE (Genomic Biodiversity Knowledge for resilient Ecosystems, COST Action CA 18134)
Research and Innovation Centre
Fondazione Edmund Mach, Trento, ITALY

Professor Giorgio Bertorelle
Department of Life Sciences and Biotechnology
University of Ferrara, ITALY

Professor Alberto Pallavicini
Dr. Marco Gerdol
Laboratory of Applied and Comparative Genomics
Department of Life Sciences
University of Trieste, ITALY

Dr. Laima Baltrunaite, Senior Researcher
Laboratory of Mammalian Ecology, Nature Research Centre
Vilnius, LITHUANIA

Dr. Robert W. Mysłajek, Associate Professor
Department of Ecology, Institute of Functional Biology and Ecology
University of Warsaw, POLAND

Dr. Magdalena Niedzialkowska
Mammal Research Institute, Polish Academy of Sciences
Białowieża, POLAND

Dr Marta Szulkin, Associate Professor
Centre of New Technologies
University of Warsaw, POLAND

Dr. Miguel Carneiro, Group Leader Evolutionary Genetics and Genomics
Dr. Raquel Godinho
CIBIO/InBIO
University of Porto, PORTUGAL

Professor Agostinho Antunes
Head of the Evolutionary Genomics and Bioinformatics Group
CIIMAR, University of Porto, PORTUGAL

Dr. Carlos Fernandes
cE3c - Centre for Ecology, Evolution and Environmental Changes
University of Lisbon, PORTUGAL

Professor Elena Buzan, Vice-Dean
Faculty of Mathematics, Natural Sciences and Information Technologies
University of Primorska, SLOVENIA

Professor Dušan Gömöry
Technická univerzita vo Zvolene, SLOVAKIA

Professor Montserrat Corominas
Group Leader, Developmental Biology and Genomics Laboratory
University of Barcelona, SPAIN

Professor Andone Estonba
Department of Genetics, Physical Anthropology and Animal Physiology
University of the Basque Country, SPAIN

Professor Roderic Guigó
Coordinator, Bioinformatics and Genomics Program,
Centre de Regulació Genòmica
Barcelona, SPAIN

Dr. Ivo G. Gut
Director, Centre Nacional d'Anàlisi Genòmica
Barcelona, SPAIN

Professor Tomas Marques, Director
Professor Carles Lalueza-Fox
Institute of Evolutionary Biology (UPF/CSIC)
Universitat Pompeu Fabra, SPAIN

Professor Marc Martí-Renom
Structural Genomics Group Leader
Centre Nacional d'Anàlisi Genòmica - Centre de Regulació Genòmica (CNAG-CRG)
The Barcelona Institute of Science and Technology (BIST)
Barcelona, SPAIN

Professor Marta Riutort
Professor Julio Rozas
Department Genetics, Microbiology and Statistics
Biodiversity Research Institute (IRBio)
Barcelona, SPAIN

Dr. Borja Milá, Group Leader
Professor Rafael Zardoya
National Museum of Natural Sciences
Spanish National Research Council (CSIC)
Madrid, SPAIN

Professor Love Dalén
Research Leader, Centre for Palaeogenetics
Swedish Museum of Natural History
Stockholm, SWEDEN

Dr. Björn Nystedt, Co-director
Dr. Olga Pettersson, Project Coordinator
National Bioinformatics Infrastructure Sweden, SciLifeLab
Uppsala University, SWEDEN

Dr. Katerina Guschanski
Professor Jacob Höglund
Department of Ecology and Genetics/Animal Ecology
Evolutionary Biology Centre
Uppsala University, SWEDEN

Professor Anti Vasemägi
Department of Aquatic Resources
Swedish University of Agricultural Sciences
Drottningholm, SWEDEN

EU Associated Countries (in alphabetical order by country)

Professor Sargis Aghayan
Department of Zoology
Yerevan State University, ARMENIA

Professor Svein-Ole Mikalsen
Faculty of Science and Technology
University of the Faroe Islands, FAROE ISLANDS

Professor Snæbjörn Pálsson
Department of Biology
University of Iceland, ICELAND

Professor Shai Meiri
Dr. Meirav Meiri
Dr. Tali Magory
School of Zoology & Steinhardt Museum of Natural History
Tel Aviv University, ISRAEL

Professor Kjetill Sigurd Jakobsen
Chair, Centre for Ecological and Evolutionary Synthesis
University of Oslo, NORWAY

Associate Professor Phil B. Pope
Associate Professor Dr. Simen Rød Sandve
Faculty of Biosciences
Norwegian University of Life Sciences, NORWAY

Michael D. Martin, Associate professor
Andrew D. Foote, Associate professor
Hans Stenøien, Professor
Department of Natural History
NTNU University Museum
Norwegian University of Science and Technology (NTNU)
Trondheim, NORWAY

Dr. Andreas Hejnol
University of Bergen, NORWAY

Dr. Trond Jørgensen
The Arctic University of Norway, NORWAY

Dr. Marko Raković
Senior Bird Curator
Natural History Museum of Belgrade, SERBIA

Dr. Glauco Camenisch, Department of Evolutionary Biology and Environmental Studies
Dr. Andrea Patrignani, Group Leader Single Molecule Sequencing, Functional Genomics Center
University of Zurich, SWITZERLAND

Professor Ole Seehausen
Institute of Ecology & Evolution (IEE), University of Bern, Bern
& Department Head, Department of Fish Ecology & Evolution
Swiss Federal Institute of Aquatic Science and Technology, Eawag, Kastanienbaum, SWITZERLAND

Dr. Mehmet Somel
Department of Biological Sciences
Middle East Technical University, TURKEY

Other Countries (in alphabetical order by country)

Professor Mark Blaxter, Lead for Tree of Life Programme and Senior Group Leader
Dr. Kerstin Howe, Senior Scientific Manager
Wellcome Sanger Institute
Hinxton, UNITED KINGDOM

Professor Richard Durbin
Dr. Shane McCharty
Department of Genetics
University of Cambridge, UNITED KINGDOM

Dr. Gary Carvalho
Molecular Ecology and Fisheries Genetics Laboratory
Bangor University, UNITED KINGDOM

Professor Erich D. Jarvis, Head, Laboratory of Neurogenetics of Language and Chair, Vertebrate Genomes Project
Dr. Giulio Formenti, Dr. Olivier Fedrigo, Dr. Sadye Paez, Dr. Konstantina Theofanopoulou
The Rockefeller University, USA

References

1. Von der Leyen U (2019) *Speech in the European Parliament plenary session, Ursula von der Leyen President-elect of the European Commission*. Brussels: European Commission, 27 November 2019.
2. Von der Leyen U (2019) *A Union that strives for more – My agenda for Europe, political guidelines for the next European Commission 2019-2024, by candidate for President of the European Commission Ursula von der Leyen*. Brussels: European Commission, July 2019.
3. European Commission (2019) *Communication on the European Green Deal, COM(2019)640*. Brussels: European Commission, December 2019.
4. European Commission (2020) *Communication on the Sustainable Europe Investment Plan – European Green Deal Investment Plan, COM(2020) 21 final*. Brussels: European Commission, January 2020.

5. European Parliamentary Research Service (2020) *Briefing – The von der Leyen Commission's priorities for 2019-2024*. Brussels: European Parliament.
6. IUCN (2020) *European Red List of Threatened Species*. <https://www.iucn.org/regions/europe/our-work/species/european-red-list-threatened-species>
7. European Commission (2020) *Communication on the EU Biodiversity Strategy for 2030 - Bringing nature back into our lives*. Brussels: European Commission, 20 May 2020.
8. European Parliamentary Research Service (2020) *Preparing the post-2020 biodiversity framework*. Brussels: European Parliament, January 2020.
9. Balmford A, et al. (2002) Economic reasons for conserving wild nature. *Science* **297**:950-953.
10. Barbier EB, Burgess JC, and Dean TJ (2018) How to pay for saving biodiversity. *Science* **360**:486-488.
11. Temple HJ and Cuttelod A (2009) *The Status and Distribution of Mediterranean Mammals*. Gland, Switzerland and Cambridge, UK: IUCN.
12. European Commission (2020) *Restoring Biodiversity and Ecosystem Services*. Brussels: European Commission.
13. Díaz S, et al., eds. (2019) *Summary for Policymakers of the Global Assessment Report on Biodiversity and Ecosystem Services of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services*. Bonn: IPBES secretariat.
14. Johnson CK, et al. (2020) Global shifts in mammalian population trends reveal key predictors of virus spillover risk. *Proceedings of the Royal Society of London B* **287**:20192736.
15. Wallace N (2020) Europe bets R&D spending will bring jobs to battered economy. *Science* **368**:1044.
16. Supple MA and Shapiro B (2018) Conservation of biodiversity in the genomics era. *Genome Biology* **19**:131.
17. Breed MF, et al. (2019) The potential of genomics for restoring ecosystems and biodiversity. *Nature Reviews Genetics* **20**:615-628.
18. Ellegren H (2014) Genome sequencing and population genomics in non- model organisms. *Trends in Ecology & Evolution* **29**:51–63.
19. Funk WC, et al. (2012) Harnessing genomics for delineating conservation units. *Trends in Ecology & Evolution* **27**:489-496.
20. Dasmahapatra KK, et al. (2012) Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* **487**:94.
21. De Manuel M, et al. (2016) Chimpanzee genomic diversity reveals ancient admixture with bonobos. *Science* **354**:477-481.
22. Cahill JA, et al. (2016) Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. *Science Advances* **2**:e1501714.
23. Prince DJ, et al. (2017) The evolutionary basis of premature migration in Pacific salmon highlights the utility of genomics for informing conservation. *Science Advances* **3**:e1603198.

24. Bell KL, et al. (2017) Applying pollen DNA metabarcoding to the study of plant–pollinator interactions. *Applications in Plant Sciences* **5**:1600124.
25. Klein A-M, et al. (2007) Importance of pollinators in changing landscapes for world crops. *Proceedings of the Royal Society of London B* **274**:303-313.
26. Ollerton J, Winfree R, and Tarrant S (2011) How many flowering plants are pollinated by animals? *Oikos* **120**:321–326.
27. Pont C, et al. (2019) Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. *Genome Biology* **20**:29.
28. Rossetto M, et al. (2018) Restore and Renew: a genomics-era framework for species provenance delimitation. *Restoration Ecology* **27**:538-548.
29. Yang J, et al. (2016) Whole-genome sequencing of native sheep provides insights into rapid adaptations to extreme environments. *Molecular Biology and Evolution* **33**:2576-2592.