

I. Genomes and its structure (3 lectures)

Problem of the term “genome”[1]. Smallest [2] and the biggest [3]genomes. Sizes of bacterial genomes: free-living vs symbionts [4–6]. Diversity of genome sizes [7]. Origin of viruses[8]. Viroid genomes [9–13]. Viral genomes[14–18]. Bacterial genome [19–21]. Archeal genome [22–24]. Chimeric origin of eukaryotes [25]. Eukaryotic genomes. Possible role of viruses in appearance of eukaryotic nucleus [26]. Mitochondrial DNA[27]. Chloroplast DNA [28]. Chromosomes and karyotypes [29]. Centromeres [30,31]. Telomeres[32–34]. Karyotype stability[35]. Polyploids [36–38]. Genome rearrangements [39]. Genome assemblies. C-scaffolds [40]. Connection between assembly and karyotype. Fluorescent *in situ* hybridization[41,42]. Difference between damage/error and mutation [43]. Error correction during replication [44]. Mutation classification. Germline cells [45,46]. Polyploid cells in human [47–49]. VDJ recombination[50]. Single cell sequencing and whole genome amplification [51].

II. Gene, genetic code and expression. (1 lecture)

Problem of the term “gene”. Non-coding RNAs. Transport RNAs. Ribosomal RNAs. Long noncodingRNAs. snRNAs. Protein-coding genes. Major difference between prokaryotic and eukaryotic genes. Transcription. Initiation, elongation and termination. Promotor. Exons and introns. Polyadenylation sites [52]. Splicing [53]. G-value paradox [54]. Alternative events[55–57]. case of DSCAM gene: dozens of thousand possible transcripts [58]. Intron retention models [59]. Cases of ID3 [60], IDD14 [61], TGIF2[62] genes: Translation. Genetic code[63]. Selenocystein [64]. Pyrrolysine [65,66]. Ribosomal frameshift [67]. Trans-splicing[68,69]. Origin and evolution of the genetic code [63,70,71].

III. Genome projects (1 lecture)

Assessment of the genome: genome size [72,73], ploidy, hybridization, heterochromatin[29]. Gathering samples. Sample types. Read length and insert size [74]. Sequencing technologies: Sanger[75], Illumina[76], Pacbio, Nanopore. Specific library types: Jumping libraries[77], linked reads [78,79], HiC [80]. Genome assembly. Assessment of genome assembly quality [81–83]. Whole genome alignments. Genome rearrangements. Inversions and translocations. Annotation of the genome. Repeats and mobile elements [84] . Big genome projects: Genome10K [85], Vertebrate genome project[86], Darwin Tree of Life, Earth Biogenome and others.

IV. Conservation genomics (1 lecture)

Conservation biology[87]. Conservation genetics [88,89]. Conservation genomics [90–92]. International Union for Conservation of Nature and Red List[93]. 6th mass extinction [94]. First article on conservation genomics and its features [95]. Genotyping-by-sequencing [96]. RADseq [97]. Genotyping-in-thousands[98]. SNP imputation [99,100]. Runs of homozygosity [101].

Examples of studies in conservation genomics: Tasmanian devil [95], cheetah [102], sea otters [103], sable antelope [104], oryx [105], amazons [106], solenodon [107], wolves [108,109], gorillas [110,111], Iberian lynx [112], woolly mammoth [113] and others [114–120] .

Literature

1. Goldman, A.D.; Landweber, L.F. What Is a Genome? *PLOS Genetics* **2016**, *12*, e1006181, doi:10.1371/journal.pgen.1006181.
2. Flores, R.; Gago-Zachert, S.; Serra, P.; Sanjuán, R.; Elena, S.F. Viroids: Survivors from the RNA World? *Annual Review of Microbiology* **2014**, *68*, 395–414, doi:10.1146/annurev-micro-091313-103416.
3. Pellicer, J.; Fay, M.F.; Leitch, I.J. The Largest Eukaryotic Genome of Them All?: THE LARGEST EUKARYOTIC GENOME? *Botanical Journal of the Linnean Society* **2010**, *164*, 10–15, doi:10.1111/j.1095-8339.2010.01072.x.
4. McCutcheon, J.P.; Moran, N.A. Extreme Genome Reduction in Symbiotic Bacteria. *Nat Rev Microbiol* **2012**, *10*, 13–26, doi:10.1038/nrmicro2670.
5. Nakabachi, A.; Yamashita, A.; Toh, H.; Ishikawa, H.; Dunbar, H.E.; Moran, N.A.; Hattori, M. The 160-Kilobase Genome of the Bacterial Endosymbiont Carsonella. *Science* **2006**, *314*, 267–267, doi:10.1126/science.1134196.
6. Bennett, G.M.; Moran, N.A. Small, Smaller, Smallest: The Origins and Evolution of Ancient Dual Symbioses in a Phloem-Feeding Insect. *Genome Biology and Evolution* **2013**, *5*, 1675–1688, doi:10.1093/gbe/evt118.
7. Dufresne, F.; Jeffery, N. A Guided Tour of Large Genome Size in Animals: What We Know and Where We Are Heading. *Chromosome Res* **2011**, *19*, 925–938, doi:10.1007/s10577-011-9248-x.
8. Krupovic, M.; Dolja, V.V.; Koonin, E.V. Origin of Viruses: Primordial Replicators Recruiting Capsids from Hosts. *Nat Rev Microbiol* **2019**, *17*, 449–458, doi:10.1038/s41579-019-0205-6.
9. Di Serio, F.; Flores, R.; Verhoeven, J.Th.J.; Li, S.-F.; Pallás, V.; Randles, J.W.; Sano, T.; Vidalakis, G.; Owens, R.A. Current Status of Viroid Taxonomy. *Arch Virol* **2014**, *159*, 3467–3478, doi:10.1007/s00705-014-2200-6.
10. Flores, R.; Navarro, B.; Serra, P.; Di Serio, F. A Scenario for the Emergence of Protoviroids in the RNA World and for Their Further Evolution into Viroids and Viroid-like RNAs by Modular Recombinations and Mutations. *Virus Evolution* **2022**, *8*, veab107, doi:10.1093/ve/veab107.
11. Tsagris, E.M.; Martínez de Alba, Á.E.; Gozmanova, M.; Kalantidis, K. Viroids. *Cellular Microbiology* **2008**, *10*, 2168–2179, doi:10.1111/j.1462-5822.2008.01231.x.
12. Legendre, M.; Arslan, D.; Abergel, C.; Claverie, J.-M. Genomics of Megavirus and the Elusive Fourth Domain of Life. *Commun Integr Biol* **2012**, *5*, 102–106.
13. Lee, B.D.; Koonin, E.V. Viroids and Viroid-like Circular RNAs: Do They Descend from Primordial Replicators? *Life* **2022**, *12*, 103, doi:10.3390/life12010103.
14. Roguljic, H.; Sarcevic, S.; Smolic, R.; Lucic, N.R.; Vcev, A.; Smolic, M.; Roguljic, H.; Sarcevic, S.; Smolic, R.; Lucic, N.R.; et al. *Current Management and Novel Therapeutic Strategies to Combat Chronic Delta Hepatitis*; IntechOpen, 2015; ISBN 978-953-51-2128-2.
15. Huang, C.-R.; Lo, S.J. Evolution and Diversity of the Human Hepatitis D Virus Genome. *Advances in Bioinformatics* **2010**, *2010*, 1–9, doi:10.1155/2010/323654.
16. Mahmoudabadi, G.; Phillips, R. A Comprehensive and Quantitative Exploration of Thousands of Viral Genomes. *eLife* **2018**, *7*, e31955, doi:10.7554/eLife.31955.
17. Varsani, A.; Lefeuvre, P.; Roumagnac, P.; Martin, D. Notes on Recombination and Reassortment in Multipartite/Segmented Viruses. *Current Opinion in Virology* **2018**, *33*, 156–166, doi:10.1016/j.coviro.2018.08.013.

18. Taubenberger, J.K.; Kash, J.C.; Morens, D.M. The 1918 Influenza Pandemic: 100 Years of Questions Answered and Unanswered. *Sci. Transl. Med.* **2019**, *11*, eaau5485, doi:10.1126/scitranslmed.aau5485.
19. Harrison, P.W.; Lower, R.P.J.; Kim, N.K.D.; Young, J.P.W. Introducing the Bacterial ‘Chromid’: Not a Chromosome, Not a Plasmid. *Trends in Microbiology* **2010**, *18*, 141–148, doi:10.1016/j.tim.2009.12.010.
20. Ramírez-Bahena, M.H.; Vial, L.; Lassalle, F.; Diel, B.; Chapulliot, D.; Daubin, V.; Nesme, X.; Muller, D. Single Acquisition of Protelomerase Gave Rise to Speciation of a Large and Diverse Clade within the Agrobacterium/Rhizobium Supercluster Characterized by the Presence of a Linear Chromid. *Molecular Phylogenetics and Evolution* **2014**, *73*, 202–207, doi:10.1016/j.ympev.2014.01.005.
21. Claessen, D.; Rozen, D.E.; Kuipers, O.P.; Søgaard-Andersen, L.; van Wezel, G.P. Bacterial Solutions to Multicellularity: A Tale of Biofilms, Filaments and Fruiting Bodies. *Nat Rev Microbiol* **2014**, *12*, 115–124, doi:10.1038/nrmicro3178.
22. Wang, H.; Peng, N.; Shah, S.A.; Huang, L.; She, Q. Archaeal Extrachromosomal Genetic Elements. *Microbiology and Molecular Biology Reviews* **2015**, *79*, 117–152, doi:10.1128/MMBR.00042-14.
23. Koonin, E.V.; Wolf, Y.I. Genomics of Bacteria and Archaea: The Emerging Dynamic View of the Prokaryotic World. *Nucleic Acids Res* **2008**, *36*, 6688–6719, doi:10.1093/nar/gkn668.
24. Ausiannikava, D.; Mitchell, L.; Marriott, H.; Smith, V.; Hawkins, M.; Makarova, K.S.; Koonin, E.V.; Nieduszynski, C.A.; Allers, T. Evolution of Genome Architecture in Archaea: Spontaneous Generation of a New Chromosome in *Haloferax Volcanii*. *Mol Biol Evol* **2018**, *35*, 1855–1868, doi:10.1093/molbev/msy075.
25. Eme, L.; Spang, A.; Lombard, J.; Stairs, C.W.; Ettema, T.J.G. Archaea and the Origin of Eukaryotes. *Nat Rev Microbiol* **2017**, *15*, 711–723, doi:10.1038/nrmicro.2017.133.
26. Takemura, M. Medusavirus Ancestor in a Proto-Eukaryotic Cell: Updating the Hypothesis for the Viral Origin of the Nucleus. *Frontiers in Microbiology* **2020**, *11*.
27. Karnkowska, A.; Vacek, V.; Zubáčová, Z.; Treitli, S.C.; Petrželková, R.; Eme, L.; Novák, L.; Žárský, V.; Barlow, L.D.; Herman, E.K.; et al. A Eukaryote without a Mitochondrial Organelle. *Current Biology* **2016**, *26*, 1274–1284, doi:10.1016/j.cub.2016.03.053.
28. Molina, J.; Hazzouri, K.M.; Nickrent, D.; Geisler, M.; Meyer, R.S.; Pentony, M.M.; Flowers, J.M.; Pelser, P.; Barcelona, J.; Inovejas, S.A.; et al. Possible Loss of the Chloroplast Genome in the Parasitic Flowering Plant *Rafflesia Lagascae* (Rafflesiaceae). *Molecular Biology and Evolution* **2014**, *31*, 793–803, doi:10.1093/molbev/msu051.
29. Graphodatsky, A.; Perelman, P.; O’Brien, S.J. *Atlas of Mammalian Chromosomes*; John Wiley & Sons, Incorporated, 2020;
30. Barra, V.; Fachinetti, D. The Dark Side of Centromeres: Types, Causes and Consequences of Structural Abnormalities Implicating Centromeric DNA. *Nat Commun* **2018**, *9*, 4340, doi:10.1038/s41467-018-06545-y.
31. Plačková, K.; Bureš, P.; Zedek, F. Centromere Size Scales with Genome Size across Eukaryotes. *Sci Rep* **2021**, *11*, 19811, doi:10.1038/s41598-021-99386-7.
32. Mason, J.M.; Frydrychova, R.C.; Biessmann, H. Drosophila Telomeres: An Exception Providing New Insights. *Bioessays* **2008**, *30*, 25–37, doi:10.1002/bies.20688.
33. Cleal, K.; Baird, D.M. Catastrophic Endgames: Emerging Mechanisms of Telomere-Driven Genomic Instability. *Trends in Genetics* **2020**, *36*, 347–359, doi:10.1016/j.tig.2020.02.001.
34. Nag, S. *Syndromes Associated with Telomere Shortening*; IntechOpen, 2019; ISBN 978-1-78984-575-4.
35. Mudd, A.B.; Bredeson, J.V.; Baum, R.; Hockemeyer, D.; Rokhsar, D.S. Analysis of Muntjac Deer Genome and Chromatin Architecture Reveals Rapid Karyotype Evolution. *Commun Biol* **2020**, *3*, 1–10, doi:10.1038/s42003-020-1096-9.

36. Havelka, M.; Kašpar, V.; Hulák, M.; Flajšhans, M. Sturgeon Genetics and Cytogenetics: A Review Related to Ploidy Levels and Interspecific Hybridization. *Folia Zoologica* **2011**, *60*, 93–103, doi:10.25225/fozo.v60.i2.a3.2011.
37. Vasil'ev, V.P. Mechanisms of Polyploid Evolution in Fish: Polyploidy in Sturgeons. In *Biology, Conservation and Sustainable Development of Sturgeons*; Carmona, R., Domezain, A., García-Gallego, M., Hernando, J.A., Rodríguez, F., Ruiz-Rejón, M., Eds.; Springer Netherlands: Dordrecht, 2009; Vol. 29, pp. 97–117 ISBN 978-1-4020-8436-2.
38. Holland, L.Z.; Ocampo Daza, D. A New Look at an Old Question: When Did the Second Whole Genome Duplication Occur in Vertebrate Evolution? *Genome Biol* **2018**, *19*, 209, doi:10.1186/s13059-018-1592-0.
39. Wijchers, P.J.; de Laat, W. Genome Organization Influences Partner Selection for Chromosomal Rearrangements. *Trends in Genetics* **2011**, *27*, 63–71, doi:10.1016/j.tig.2010.11.001.
40. Lewin, H.A.; Graves, J.A.M.; Ryder, O.A.; Graphodatsky, A.S.; O'Brien, S.J. Precision Nomenclature for the New Genomics. *GigaScience* **2019**, *8*, giz086, doi:10.1093/gigascience/giz086.
41. Yano, C.F.; Bertollo, L.A.C.; Cioffi, M. de B. Fish-FISH: Molecular Cytogenetics in Fish Species. In *Fluorescence In Situ Hybridization (FISH)*; Liehr, T., Ed.; Springer Protocols Handbooks; Springer Berlin Heidelberg: Berlin, Heidelberg, 2017; pp. 429–443 ISBN 978-3-662-52957-7.
42. Beklemisheva, V.R.; Perelman, P.L.; Lemskaya, N.A.; Kulemzina, A.I.; Proskuryakova, A.A.; Burkanov, V.N.; Graphodatsky, A.S. The Ancestral Carnivore Karyotype As Substantiated by Comparative Chromosome Painting of Three Pinnipeds, the Walrus, the Steller Sea Lion and the Baikal Seal (Pinnipedia, Carnivora). *PLoS ONE* **2016**, *11*, e0147647, doi:10.1371/journal.pone.0147647.
43. Siriwardena, S.U.; Chen, K.; Bhagwat, A.S. Functions and Malfunctions of Mammalian DNA-Cytosine Deaminases. *Chem. Rev.* **2016**, *116*, 12688–12710, doi:10.1021/acs.chemrev.6b00296.
44. Ganai, R.A.; Johansson, E. DNA Replication—A Matter of Fidelity. *Molecular Cell* **2016**, *62*, 745–755, doi:10.1016/j.molcel.2016.05.003.
45. Hansen, C.L.; Pelegri, F. Primordial Germ Cell Specification in Vertebrate Embryos: Phylogenetic Distribution and Conserved Molecular Features of Preformation and Induction. *Frontiers in Cell and Developmental Biology* **2021**, *9*.
46. Nicholls, P.K.; Schorle, H.; Naqvi, S.; Hu, Y.-C.; Fan, Y.; Carmell, M.A.; Dobrinski, I.; Watson, A.L.; Carlson, D.F.; Fahrenkrug, S.C.; et al. Mammalian Germ Cells Are Determined after PGC Colonization of the Nascent Gonad. *Proceedings of the National Academy of Sciences* **2019**, *116*, 25677–25687, doi:10.1073/pnas.1910733116.
47. Wang, M.-J.; Chen, F.; Lau, J.T.Y.; Hu, Y.-P. Hepatocyte Polyploidization and Its Association with Pathophysiological Processes. *Cell Death Dis* **2017**, *8*, e2805, doi:10.1038/cddis.2017.167.
48. Zhang, J.; Qiao, Q.; Xu, H.; Zhou, R.; Liu, X. Human Cell Polyploidization: The Good and the Evil. *Seminars in Cancer Biology* **2022**, *81*, 54–63, doi:10.1016/j.semcancer.2021.04.005.
49. Heib, T.; Hermanns, H.M.; Manukjan, G.; Englert, M.; Kusch, C.; Becker, I.C.; Gerber, A.; Wackerbarth, L.M.; Burkard, P.; Dandekar, T.; et al. RhoA/Cdc42 Signaling Drives Cytoplasmic Maturation but Not Endomitosis in Megakaryocytes. *Cell Reports* **2021**, *35*, 109102, doi:10.1016/j.celrep.2021.109102.
50. Papavasiliou, F.N.; Schatz, D.G. Somatic Hypermutation of Immunoglobulin Genes: Merging Mechanisms for Genetic Diversity. *Cell* **2002**, *109*, S35–S44, doi:10.1016/S0092-8674(02)00706-7.
51. Huang, L.; Ma, F.; Chapman, A.; Lu, S.; Xie, X.S. Single-Cell Whole-Genome Amplification and Sequencing: Methodology and Applications. *Annu. Rev. Genom. Hum. Genet.* **2015**, *16*, 79–102, doi:10.1146/annurev-genom-090413-025352.
52. Gruber, A.R.; Martin, G.; Keller, W.; Zavolan, M. Means to an End: Mechanisms of Alternative Polyadenylation of Messenger RNA Precursors: Alternative Polyadenylation of Messenger RNA Precursors. *WIREs RNA* **2014**, *5*, 183–196, doi:10.1002/wrna.1206.

53. Maniatis, T.; Tasic, B. Alternative Pre-mRNA Splicing and Proteome Expansion in Metazoans. *Nature* **2002**, *418*, 236–243, doi:10.1038/418236a.
54. Schad, E.; Tompa, P.; Hegyi, H. The Relationship between Proteome Size, Structural Disorder and Organism Complexity. *Genome Biol* **2011**, *12*, R120, doi:10.1186/gb-2011-12-12-r120.
55. Kim, E.; Goren, A.; Ast, G. Alternative Splicing: Current Perspectives. *BioEssays* **2008**, *30*, 38–47, doi:10.1002/bies.20692.
56. Kim, E.; Magen, A.; Ast, G. Different Levels of Alternative Splicing among Eukaryotes. *Nucleic Acids Research* **2007**, *35*, 125–131, doi:10.1093/nar/gkl924.
57. Keren, H.; Lev-Maor, G.; Ast, G. Alternative Splicing and Evolution: Diversification, Exon Definition and Function. *Nature Reviews Genetics* **2010**, *11*, 345–355.
58. Neves, G.; Zucker, J.; Daly, M.; Chess, A. Stochastic yet Biased Expression of Multiple Dscam Splice Variants by Individual Cells. *Nat Genet* **2004**, *36*, 240–246, doi:10.1038/ng1299.
59. Sakabe, N.J.; de Souza, S.J. Sequence Features Responsible for Intron Retention in Human. *BMC Genomics* **2007**, *8*, 59, doi:10.1186/1471-2164-8-59.
60. Forrest, S.T.; Barringhaus, K.G.; Perlegas, D.; Hammarskjöld, M.-L.; McNamara, C.A. Intron Retention Generates a Novel Id3 Isoform That Inhibits Vascular Lesion Formation. *J. Biol. Chem.* **2004**, *279*, 32897–32903, doi:10.1074/jbc.M404882200.
61. Seo, P.J.; Kim, M.J.; Ryu, J.-Y.; Jeong, E.-Y.; Park, C.-M. Two Splice Variants of the IDD14 Transcription Factor Competitively Form Nonfunctional Heterodimers Which May Regulate Starch Metabolism. *Nat Commun* **2011**, *2*, 303, doi:10.1038/ncomms1303.
62. Melhuish, T.A.; Wotton, D. The Tgif2 Gene Contains a Retained Intron within the Coding Sequence. *BMC Molecular Biol* **2006**, *7*, 2, doi:10.1186/1471-2199-7-2.
63. Moura, G.R.; Paredes, J.A.; Santos, M.A.S. Development of the Genetic Code: Insights from a Fungal Codon Reassignment. *FEBS Letters* **2010**, *584*, 334–341, doi:10.1016/j.febslet.2009.11.066.
64. Schmidt, R.L.; Simonović, M. Synthesis and Decoding of Selenocysteine and Human Health. *Croat Med J* **2012**, *53*, 535–550, doi:10.3325/cmj.2012.53.535.
65. Brugère, J.-F.; Atkins, J.F.; O’Toole, P.W.; Borrel, G. Pyrrolysine in Archaea: A 22nd Amino Acid Encoded through a Genetic Code Expansion. *Emerging Topics in Life Sciences* **2018**, *2*, 607–618, doi:10.1042/ETLS20180094.
66. Krzycki, J.A. The Direct Genetic Encoding of Pyrrolysine. *Current Opinion in Microbiology* **2005**, *8*, 706–712, doi:10.1016/j.mib.2005.10.009.
67. Atkins, J.F.; Loughran, G.; Bhatt, P.R.; Firth, A.E.; Baranov, P.V. Ribosomal Frameshifting and Transcriptional Slippage: From Genetic Steganography and Cryptography to Adventitious Use. *Nucleic Acids Research* **2016**, *44*, 7007–7078, doi:10.1093/nar/gkw530.
68. Horiuchi, T.; Aigaki, T. Alternative Trans-Splicing: A Novel Mode of Pre-mRNA Processing. *Biology of the Cell* **2006**, *98*, 135–140, doi:10.1042/BC20050002.
69. Lei, Q.; Li, C.; Zuo, Z.; Huang, C.; Cheng, H.; Zhou, R. Evolutionary Insights into RNA Trans-Splicing in Vertebrates. *Genome Biology and Evolution* **2016**, *8*, 562–577, doi:10.1093/gbe/evw025.
70. Giulio, M. Genetic Code Origin: Are the Pathways of Type Glu-TRNAGln → Gln-TRNAGln Molecular Fossils or Not? *Journal of Molecular Evolution* **2002**, *55*, 616–622, doi:10.1007/s00239-002-2357-6.
71. Santos, M.A.S.; Gomes, A.C.; Santos, M.C.; Carreto, L.C.; Moura, G.R. The Genetic Code of the Fungal CTG Clade. *Comptes Rendus Biologies* **2011**, *334*, 607–611, doi:10.1016/j.crv.2011.05.008.
72. Sohn, J.; Nam, J.-W. The Present and Future of *de Novo* Whole-Genome Assembly. *Brief Bioinform* **2016**, bbw096, doi:10.1093/bib/bbw096.
73. Ranallo-Benavidez, T.R.; Jaron, K.S.; Schatz, M.C. GenomeScope 2.0 and Smudgeplot for Reference-Free Profiling of Polyploid Genomes. *Nat Commun* **2020**, *11*, 1432, doi:10.1038/s41467-020-14998-3.

74. Turner, D.J. Next-Generation DNA Sequencing Technologies. In *Encyclopedia of Analytical Chemistry*; American Cancer Society, 2011 ISBN 978-0-470-02731-8.
75. Sanger, F.; Nicklen, S.; Coulson, A.R. DNA Sequencing with Chain-Terminating Inhibitors. *Proceedings of the National Academy of Sciences* **1977**, *74*, 5463–5467, doi:10.1073/pnas.74.12.5463.
76. Ansorge, W.J. Next-Generation DNA Sequencing Techniques. *New Biotechnology* **2009**, *25*, 195–203, doi:10.1016/j.nbt.2008.12.009.
77. Leggett, R.M.; Clavijo, B.J.; Clissold, L.; Clark, M.D.; Caccamo, M. NextClip: An Analysis and Read Preparation Tool for Nextera Long Mate Pair Libraries. *Bioinformatics* **2014**, *30*, 566–568, doi:10.1093/bioinformatics/btt702.
78. Zheng, G.X.Y.; Lau, B.T.; Schnall-Levin, M.; Jarosz, M.; Bell, J.M.; Hindson, C.M.; Kyriazopoulou-Panagiotopoulou, S.; Masquelier, D.A.; Merrill, L.; Terry, J.M.; et al. Haplotyping Germline and Cancer Genomes with High-Throughput Linked-Read Sequencing. *Nature Biotechnology* **2016**, *34*, 303.
79. Weisenfeld, N.I.; Kumar, V.; Shah, P.; Church, D.M.; Jaffe, D.B. Direct Determination of Diploid Genome Sequences. *Genome Res.* **2017**, *27*, 757–767, doi:10.1101/gr.214874.116.
80. Lieberman-Aiden, E.; van Berkum, N.L.; Williams, L.; Imakaev, M.; Ragoczy, T.; Telling, A.; Amit, I.; Lajoie, B.R.; Sabo, P.J.; Dorschner, M.O.; et al. Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. *Science* **2009**, *326*, 289–293, doi:10.1126/science.1181369.
81. Simão, F.A.; Waterhouse, R.M.; Ioannidis, P.; Kriventseva, E.V.; Zdobnov, E.M. BUSCO: Assessing Genome Assembly and Annotation Completeness with Single-Copy Orthologs. *Bioinformatics* **2015**, *31*, 3210–3212, doi:10.1093/bioinformatics/btv351.
82. Seppey, M.; Manni, M.; Zdobnov, E.M. BUSCO: Assessing Genome Assembly and Annotation Completeness. In *Gene Prediction: Methods and Protocols*; Kollmar, M., Ed.; Methods in Molecular Biology; Springer: New York, NY, 2019; pp. 227–245 ISBN 978-1-4939-9173-0.
83. Manni, M.; Berkeley, M.R.; Seppey, M.; Simão, F.A.; Zdobnov, E.M. BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes. *Molecular Biology and Evolution* **2021**, *38*, 4647–4654, doi:10.1093/molbev/msab199.
84. Richard, G.-F.; Kerrest, A.; Dujon, B. Comparative Genomics and Molecular Dynamics of DNA Repeats in Eukaryotes. *Microbiology and Molecular Biology Reviews* **2008**, *72*, 686–727, doi:10.1128/MMBR.00011-08.
85. Koepfli, K.-P.; Paten, B.; and O'Brien, S.J. The Genome 10K Project: A Way Forward. *Annual Review of Animal Biosciences* **2015**, *3*, 57–111, doi:10.1146/annurev-animal-090414-014900.
86. Rhie, A.; McCarthy, S.A.; Fedrigo, O.; Damas, J.; Formenti, G.; Koren, S.; Uliano-Silva, M.; Chow, W.; Fungtammasan, A.; Kim, J.; et al. Towards Complete and Error-Free Genome Assemblies of All Vertebrate Species. *Nature* **2021**, *592*, 737–746, doi:10.1038/s41586-021-03451-0.
87. Soulé, M.E. What Is Conservation Biology? *BioScience* **1985**, *35*, 727–734, doi:10.2307/1310054.
88. Allendorf, F.W.; Hohenlohe, P.A.; Luikart, G. Genomics and the Future of Conservation Genetics. *Nat Rev Genet* **2010**, *11*, 697–709, doi:10.1038/nrg2844.
89. Frankham, R. Conservation Genetics. *Annual Review of Genetics* **1995**, *29*, 305–327, doi:10.1146/annurev.ge.29.120195.001513.
90. Kliver, S.F. Whole genome approach in conservation biology and its perspectives. *Ecol genet* **2021**, *19*, 281–298, doi:10.17816/ecogen65152.
91. Fuentes Pardo, A.P.; Ruzzante, D.E. Whole-Genome Sequencing Approaches for Conservation Biology: Advantages, Limitations and Practical Recommendations. *Molecular Ecology* **2017**, *26*, 5369–5406, doi:10.1111/mec.14264.
92. Ryder, O.A. Conservation Genomics: Applying Whole Genome Studies to Species Conservation Efforts. *Cytogenet. Genome Res.* **2005**, *108*, 6–15, doi:10.1159/000080796.

93. IUCN IUCN 2020. The IUCN Red List of Threatened Species. Version 2020-2: Table 1b 2020.
94. Ceballos, G.; Ehrlich, P.R.; Raven, P.H. Vertebrates on the Brink as Indicators of Biological Annihilation and the Sixth Mass Extinction. *Proc Natl Acad Sci USA* **2020**, *117*, 13596–13602, doi:10.1073/pnas.1922686117.
95. Miller, W.; Hayes, V.M.; Ratan, A.; Petersen, D.C.; Wittekindt, N.E.; Miller, J.; Walenz, B.; Knight, J.; Qi, J.; Zhao, F.; et al. Genetic Diversity and Population Structure of the Endangered Marsupial *Sarcophilus Harrisii* (Tasmanian Devil). *PNAS* **2011**, *108*, 12348–12353, doi:10.1073/pnas.1102838108.
96. Narum, S.R.; Buerkle, C.A.; Davey, J.W.; Miller, M.R.; Hohenlohe, P.A. Genotyping-by-Sequencing in Ecological and Conservation Genomics. *Molecular Ecology* **2013**, *22*, 2841–2847, doi:10.1111/mec.12350.
97. Davey, J.W.; Blaxter, M.L. RADSeq: Next-Generation Population Genetics. *Brief Funct Genomics* **2010**, *9*, 416–423, doi:10.1093/bfgp/elq031.
98. Campbell, N.R.; Harmon, S.A.; Narum, S.R. Genotyping-in-Thousands by Sequencing (GT-Seq): A Cost Effective SNP Genotyping Method Based on Custom Amplicon Sequencing. *Molecular Ecology Resources* **2015**, *15*, 855–867, doi:10.1111/1755-0998.12357.
99. Shi, S.; Yuan, N.; Yang, M.; Du, Z.; Wang, J.; Sheng, X.; Wu, J.; Xiao, J. Comprehensive Assessment of Genotype Imputation Performance. *HHE* **2018**, *83*, 107–116, doi:10.1159/000489758.
100. Wood, A.R.; Perry, J.R.B.; Tanaka, T.; Hernandez, D.G.; Zheng, H.-F.; Melzer, D.; Gibbs, J.R.; Nalls, M.A.; Weedon, M.N.; Spector, T.D.; et al. Imputation of Variants from the 1000 Genomes Project Modestly Improves Known Associations and Can Identify Low-Frequency Variant - Phenotype Associations Undetected by HapMap Based Imputation. *PLoS ONE* **2013**, *8*, e64343, doi:10.1371/journal.pone.0064343.
101. Brüniche-Olsen, A.; Kellner, K.F.; Anderson, C.J.; DeWoody, J.A. Runs of Homozygosity Have Utility in Mammalian Conservation and Evolutionary Studies. *Conserv Genet* **2018**, *19*, 1295–1307, doi:10.1007/s10592-018-1099-y.
102. Dobrynin, P.; Liu, S.; Tamazian, G.; Xiong, Z.; Yurchenko, A.A.; Krashennnikova, K.; Kliver, S.; Schmidt-Küntzel, A.; Koepfli, K.-P.; Johnson, W.; et al. Genomic Legacy of the African Cheetah, *Acinonyx Jubatus*. *Genome Biology* **2015**, *16*, 277, doi:10.1186/s13059-015-0837-4.
103. Beichman, A.C.; Koepfli, K.-P.; Li, G.; Murphy, W.; Dobrynin, P.; Kliver, S.; Tinker, M.T.; Murray, M.J.; Johnson, J.; Lindblad-Toh, K.; et al. Aquatic Adaptation and Depleted Diversity: A Deep Dive into the Genomes of the Sea Otter and Giant Otter. *Molecular Biology and Evolution* **2019**, msz101, doi:10.1093/molbev/msz101.
104. Gooley, R.M.; Tamazian, G.; Castañeda Rico, S.; Murphy, K.R.; Dobrynin, P.; Ferrie, G.M.; Haefele, H.; Maldonado, J.E.; Wildt, D.E.; Pukazhenth, B.S.; et al. Comparison of Genomic Diversity and Structure of Sable Antelope (*Hippotragus Niger*) in Zoos, Conservation Centers, and Private Ranches in North America. *Evolutionary Applications* **2020**, n/a, doi:10.1111/eva.12976.
105. Humble, E.; Dobrynin, P.; Senn, H.; Chuven, J.; Scott, A.F.; Mohr, D.W.; Dudchenko, O.; Omer, A.D.; Colaric, Z.; Lieberman Aiden, E.; et al. Chromosomal level Genome Assembly of the Scimitar horned Oryx: Insights into Diversity and Demography of a Species Extinct in the Wild. *Mol Ecol Resour* **2020**, 1755-0998.13181, doi:10.1111/1755-0998.13181.
106. Kolchanova, S.; Kliver, S.; Komissarov, A.; Dobrynin, P.; Tamazian, G.; Grigorev, K.; Wolfsberger, W.; Majeske, A.; Velez-Valentin, J.; Valentin de la Rosa, R.; et al. Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. *Genes* **2019**, *10*, 54, doi:10.3390/genes10010054.
107. Grigorev, K.; Kliver, S.; Dobrynin, P.; Komissarov, A.; Wolfsberger, W.; Krashennnikova, K.; Afanador-Hernández, Y.M.; Brandt, A.L.; Paulino, L.A.; Carreras, R. Innovative Assembly Strategy Contributes to Understanding the Evolution and Conservation Genetics of the Endangered *Solenodon Paradoxus* from the Island of Hispaniola. *GigaScience* **2018**, *7*, giy025.

108. Robinson, J.A.; Brown, C.; Kim, B.Y.; Lohmueller, K.E.; Wayne, R.K. Purging of Strongly Deleterious Mutations Explains Long-Term Persistence and Absence of Inbreeding Depression in Island Foxes. *Current Biology* **2018**, *28*, 3487-3494.e4, doi:10.1016/j.cub.2018.08.066.
109. Robinson, J.A.; Räikkönen, J.; Vucetich, L.M.; Vucetich, J.A.; Peterson, R.O.; Lohmueller, K.E.; Wayne, R.K. Genomic Signatures of Extensive Inbreeding in Isle Royale Wolves, a Population on the Threshold of Extinction. *Science Advances* **2019**, *5*, eaau0757, doi:10.1126/sciadv.aau0757.
110. McManus, K.F.; Kelley, J.L.; Song, S.; Veeramah, K.R.; Woerner, A.E.; Stevison, L.S.; Ryder, O.A.; Ape Genome Project, G.; Kidd, J.M.; Wall, J.D.; et al. Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. *Mol Biol Evol* **2015**, *32*, 600–612, doi:10.1093/molbev/msu394.
111. van der Valk, T.; Díez-del-Molino, D.; Marques-Bonet, T.; Guschanski, K.; Dalén, L. Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. *Current Biology* **2019**, *29*, 165-170.e6, doi:10.1016/j.cub.2018.11.055.
112. Abascal, F.; Corvelo, A.; Cruz, F.; Villanueva-Cañas, J.L.; Vlasova, A.; Marcet-Houben, M.; Martínez-Cruz, B.; Cheng, J.Y.; Prieto, P.; Quesada, V.; et al. Extreme Genomic Erosion after Recurrent Demographic Bottlenecks in the Highly Endangered Iberian Lynx. *Genome Biol* **2016**, *17*, 251, doi:10.1186/s13059-016-1090-1.
113. Rogers, R.L.; Slatkin, M. Excess of Genomic Defects in a Woolly Mammoth on Wrangel Island. *PLoS Genet* **2017**, *13*, e1006601, doi:10.1371/journal.pgen.1006601.
114. Nuijten, R.J.M.; Bosse, M.; Crooijmans, R.P.M.A.; Madsen, O.; Schaftenaar, W.; Ryder, O.A.; Groenen, M.A.M.; Megens, H.-J. The Use of Genomics in Conservation Management of the Endangered Visayan Warty Pig (*Sus Cebifrons*). *International Journal of Genomics* **2016**, *2016*, 1–9, doi:10.1155/2016/5613862.
115. Feng, S.; Fang, Q.; Barnett, R.; Li, C.; Han, S.; Kuhlwilm, M.; Zhou, L.; Pan, H.; Deng, Y.; Chen, G.; et al. The Genomic Footprints of the Fall and Recovery of the Crested Ibis. *Current Biology* **2019**, *29*, 340-349.e7, doi:10.1016/j.cub.2018.12.008.
116. Cortes-Rodriguez, N.; Campana, M.; Berry, L.; Faegre, S.; Derrickson, S.; Ha, R.; Dikow, R.; Rutz, C.; Fleischer, R. Population Genomics and Structure of the Critically Endangered Mariana Crow (*Corvus Kubaryi*). *Genes* **2019**, *10*, 187, doi:10.3390/genes10030187.
117. Yang, J.; Wariss, H.M.; Tao, L.; Zhang, R.; Yun, Q.; Hollingsworth, P.; Dao, Z.; Luo, G.; Guo, H.; Ma, Y.; et al. De Novo Genome Assembly of the Endangered Acer Yangbiense, a Plant Species with Extremely Small Populations Endemic to Yunnan Province, China. *Gigascience* **2019**, *8*, doi:10.1093/gigascience/giz085.
118. Sutton, J.T.; Helmkampf, M.; Steiner, C.C.; Bellinger, M.R.; Korlach, J.; Hall, R.; Baybayan, P.; Muehling, J.; Gu, J.; Kingan, S.; et al. A High-Quality, Long-Read De Novo Genome Assembly to Aid Conservation of Hawaii's Last Remaining Crow Species. *Genes* **2018**, *9*, 393, doi:10.3390/genes9080393.
119. Yi, L.; Dalai, M.; Su, R.; Lin, W.; Erdenedalai, M.; Luvsantseren, B.; Chimedtseren, C.; Wang, Z.; Hasi, S. Whole-Genome Sequencing of Wild Siberian Musk Deer (*Moschus Moschiferus*) Provides Insights into Its Genetic Features. *BMC Genomics* **2020**, *21*, 108, doi:10.1186/s12864-020-6495-2.
120. Mays, H.L.; Hung, C.-M.; Shaner, P.-J.; Denvir, J.; Justice, M.; Yang, S.-F.; Roth, T.L.; Oehler, D.A.; Fan, J.; Rekulapally, S.; et al. Genomic Analysis of Demographic History and Ecological Niche Modeling in the Endangered Sumatran Rhinoceros *Dicerorhinus Sumatrensis*. *Current Biology* **2018**, *28*, 70-76.e4, doi:10.1016/j.cub.2017.11.021.