

Olivier Fedrigo

Comparative genomics, evolution, sequencing technologies, bioinformatics and conservation



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Education

2003	Ph.D.	Genetics	Iowa State University	Ames, IA
1997	M.S.	Applied Computer Science	Université Denis Diderot	Paris, France
1996	M.S.	Systematics	Université P&M Curie and MNHN	Paris, France
1994	B.S.	Biology and Natural Sciences	Université Denis Diderot	Paris, France

Employment

2025-present	Sr. Principal Scientist, Genomics Research Colossal Biosciences, Dallas, TX I coordinate genomic efforts and lead a team of avian genomicists to support the Dodo and Moa project.
2023-2025	Director of Genomic Resources Colossal Biosciences, Dallas, TX I coordinate genomic efforts and lead a team of avian genomicists to support the Dodo project.
2016-2023	Director of the Vertebrate Genome Laboratory The Rockefeller University, New York, NY I manage a laboratory dedicated to de novo genome assembly research (VGP, EBP, HPRC) but that also serves as a resource center for Rockefeller University. I supervise a team of 10. My role includes experiment design, genome assembly, data analysis, technical development, project management, strategic planning, data management, research paper and grant proposal writing.
2014-2016	Director of the Genome Sequencing Shared Resource Duke Center for Genomic and Computational Biology and Duke Cancer Institute Duke University, Durham, NC I directed a sequencing core facility. I managed a team of 6: Next-generation sequencing, data analysis, data management, business development, strategic planning, project management, outreach, workshops, grant proposal writing and training. Let and involved in research projects leading to publications.
2010-2014	Associate Director of the Genome Sequencing & Analysis Core Facility Institute for Genome Sciences & Policy Duke University, Durham, NC I managed a team of 5 at a sequencing core facility: Next-generation sequencing, data analysis, data management, business development, strategic planning, project management, outreach, workshops, grant proposal writing and training. Involved and led research projects leading to publications.
2004-2010	Postdoctoral Researcher Biology Department and Institute for Genome Sciences & Policy, Wray laboratory Duke University, Durham, NC Comparative genomics. Scans for signatures of positive selection. Primate brain evolution, Mormyrids brain evolution. Gene expression. RNA-seq.

Publications

* co-first author, ◆ corresponding author

h-index= 44, i10-index= 80

1. Thomas, W.R., Lama, T.M., Baldoni, C. et al. (2026) Genomic comparisons shed light on the adaptive basis of brain size plasticity and chromosomal instability in the Eurasian common shrew. *Mol Biol Evol.* 2026 Jan 9:msag006. <https://doi.org/10.1093/molbev/msag006>
2. Lee, S-H., Fedrigo, O., Soler-Clavel, L. et al. Insights into the Evolution of Ancient Shark and Ray Sex Chromosomes. *bioRxiv* <https://doi.org/10.1101/2025.02.26.637739>
3. Gedman, G., Morill Pirovich, K., Openheimer, J. et al. (2025) On the ancestry and evolution of the extinct dire wolf. *bioRxiv* <https://www.biorxiv.org/content/10.1101/2025.04.09.647074v1>
4. Nicholson, M.W., Moreira, L., Boyle, E.A. et al. Long-Term Rock Dove (*Columba livia*) Primordial Germ Cell Culture: A Tool for Avian Conservation. *bioRxiv* <https://www.biorxiv.org/content/10.1101/2025.09.17.676777v2>
5. Nicholson, M.W., Moreira, L., Boyle, E.A. et al. Long-Term Rock Dove (*Columba livia*) Primordial Germ Cell Culture: A Tool for Avian Conservation. *bioRxiv* <https://www.biorxiv.org/content/10.1101/2025.09.17.676777v2>
6. Granger-Neto, H.P., Borges, I.R.F., Cavalcanti, D.B. et al. Chromosome-level genome assembly of the Brazilian merganser (*Mergus octosetaceus*), a rare and elusive waterfowl species. *bioRxiv* <https://www.biorxiv.org/content/10.1101/2025.09.16.676261v1>
7. Biegler, M.T., Belay, B., Wei Wang, W., Szi, C. et al. (2025) Pronounced early differentiation underlies zebra finch gonadal germ cell development. *Dev. Bio.*, January 2025, 527:3-90 <https://doi.org/10.1016/j.ydbio.2024.08.006>
8. Zhou, Y, Jin, J., Xuemei Li, Gedman, G., Pelan, S., et al. (2025) Chromosome-level echidna genome illuminates evolution of multiple sex chromosome system in monotremes, *GigaScience*, Volume 14, 2025, giae112, <https://doi.org/10.1093/gigascience/giae112>
9. Lesturgie, P., Denton, J., Yang, L., Corrigan, S. et al. Short-term evolutionary implications of an introgressed size-determining supergene in a vulnerable population. *Nat. Commun.* 16, 1096 (2025). <https://doi.org/10.1038/s41467-025-56126-z>
10. Velotta, J. P., Iqbal, A., Glenn, E. S., Franckowiak, R. P. et al. (2025) A complete assembly and annotation of the American shad genome yields insights into the origins of diadromy. *GBE*, Volume 17, Issue 1, January 2025, evae276, <https://doi.org/10.1093/gbe/evae276>
11. Al-Ajli, F.O., Formenti, G., Fedrigo, O. et al. (2025) Chromosome-level reference genome assembly of the gyrfalcon (*Falco rusticolus*) and population genomics offer insights into the falcon population in Mongolia. *Sci Rep* 15, 4154 . <https://doi.org/10.1038/s41598-025-88216-9>
12. Kosch, T. A., Berger, L., Skerratt, L.F et al. (2025) A chromosome-level reference genome for the critically endangered Southern Corroboree frog (*Pseudophryne corroboree*). *Wellcome Open Res*, 10:228 <https://wellcomeopenresearch.org/articles/10-228/v1>
13. Alexandre, N., Balacco, J., Tilley, T. et al (2025) A Chromosome-level genome of the Nicobar pigeon, *Caloenas nicobarica*. *J. Hered.* esaf031, <https://doi.org/10.1093/jhered/esaf031>
14. Morin, P. A., Bein, B., Bortoluzzi, C. et al. (2025) Genomic infrastructure for cetacean research and conservation: Reference genomes for eight families spanning the cetacean tree of life. *Front. Mar. Sci.* Sec. Marine Megafauna Volume 12 <https://doi.org/10.3389/fmars.2025.1562045>
15. Laso-Jadart, R., Corrigan, S., Yang, L., Lee, A. et al. (2025) A genomic test of sex-biased dispersal in white sharks. *PNAS* 122 (32). <https://www.pnas.org/doi/abs/10.1073/pnas.2507931122>
16. Fontseré, C., Samuel A. Speak, S. A., Caven, A. J., et al. (2025) Persistent genomic erosion in whooping cranes despite demographic recovery. *Mol. Ecol.* <https://onlinelibrary.wiley.com/doi/10.1111/mec.70088>
17. Baker, N., Abueg, L., Escalona, M., Farquharson, K.A. et al. (2023) A chromosome-level genome assembly for the dugong (*Dugong dugon*). *J. Hered.* <https://doi.org/10.1093/jhered/esae003>
18. Larivière, D., Abueg, L., Brajuka, N., Gallardo-Alba, C., Grüning, B., Ko, B.J., Ostrovsky, A. et al. (2024) Scalable, accessible, and reproducible reference genome assembly and evaluation in Galaxy. *Nat Biotechnol.* <https://doi.org/10.1038/s41587-023-02100-3>
19. Bukhman, Y., Meyer, S., Chu, L-F., Abueg, L., Antosiewicz-Bourget, J. et al. (2024) Chromosome-level genome assembly of the Etruscan shrew, *Suncus etruscus*. *Sci Data*. 11(1):176. <https://doi.org/10.1038/s41597-024-03011-x>

20. Bukhman, Y., Morin, P. A., Meyer, S., Li-Fang Chu, L-F et al. (2024) A high-quality blue whale genome, segmental duplications, and historical demography, *Mol. Biol. Evol.*, Volume 41, Issue 3, March 2024, msae036, <https://doi.org/10.1093/molbev/msae036>
21. Mirahab, S., Rivas-Gonzalez, I., Feng, S., Stiller, J. et al. (2024) A region of suppressed recombination misleads neoavian phylogenomics. *PNAS*. 121 (15) e2319506121. <https://doi.org/10.1073/pnas.2319506121>
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23. Merondun, J., Marques, C.I., Andrade, P., Meshcheryagin, S. et al. (2024) Genetic architecture and evolutionary maintenance of sex-limited polymorphism in cuckoos. *Sci. Adv.* In press *Sci. Adv.* 10 ead15255. <https://doi.org/10.1126/sciadv.adl5255>
24. Sebastianelli, M., Lukhele, S.M., Secomandi, S. et al. (2024) A genomic basis of vocal rhythm in birds. *Nat Commun.* 15, 3095. <https://doi.org/10.1038/s41467-024-47305-5>
25. Cadena, D., Pabon, L., DoNascimento, C. et al. (2024) A reference genome for the Andean cavefish *Trichomycterus rosablanca* (Siluriformes, Trichomycteridae): building genomic resources to study evolution in cave environments. *Journal of Heredity*. esae019, <https://doi.org/10.1093/jhered/esae019>
26. Canesin, L.E.C., Vilaça, S.T., Oliveira, R.R.M. et al. (2024) A reference genome for the Harpy Eagle reveals steady demographic decline and chromosomal rearrangements in the origin of Accipitriformes. *Sci Rep* 14, 19925 <https://doi.org/10.1038/s41598-024-70305-w>
27. Ishigohoka, J., Bascón-Cardozo, K., Bours, et al. (2024) Distinct patterns of genetic variation at low-recombining genomic regions represent haplotype structure. *Evolution*; qpae117 <https://doi.org/10.1093/evolut/qpae117>
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30. Vollger, M.R., Dishuck, P.C., Harvey, W.T., DeWitt, W.S. et al. (2023) Increased mutation and gene conversion within human segmental duplications. *Nature*. 617(7960):325-334. <https://doi.org/10.1038/s41586-023-05895-y>
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38. Theissinger, K., Fernandes, C., Formenti, G., Bista, I. et al. (2023) How genomics can help conservation. *Trend in Genetics* S0168-9525(23)00020-3. <https://doi.org/10.1016/j.tig.2023.01.005>
39. Meyer, B., Moiron, M., Caswara, C., Chow, W. et al. (2023) Sex-specific changes in autosomal methylation rate in ageing common terns. *Frontiers Ecology And Evolution*. Volume 11 - 2023. <https://doi.org/10.3389/fevo.2023.982443>
40. Timoshevskaya, N, Eşkut, K. I, Timoshevskiy, V.A. et al. (2023) An improved sea lamprey (*Petromyzon marinus*) germline genome assembly illuminates the evolution of germline-specific chromosomes. *Cell Reports*. 42(3):112263. <https://doi.org/10.1016/j.celrep.2023.112263>
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42. Lee, H., Greer, S.U., Oavlichin, D.S., Zhou, B., Urban, A.E., Weissman, T. and the Human Pangenome Reference Consortium. (2023) Pan-conserved segment tags identify ultra-conserved sequences across assemblies in the human pangenome, **Cell Reports Methods**, Volume 3, Issue 8, 2023, 100543, ISSN 2667-2375, <https://doi.org/10.1016/j.crmeth.2023.100543>
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46. Lee, YH, Abueg L, Kim, JK, Kim, YW, Fedrigo, O. et al. (2023) Chromosome-level genome assembly of chub mackerel (*Scomber japonicus*) from the Indo-Pacific Ocean. **Sci Data** Dec 8;10(1):880. <https://doi.org/10.1038/s41597-023-02782-z>
47. Toh, H., Yang C., Formenti G., Raja K., Yan L., Tracey A., Chow W., Howe, K., Bergeron, L.A., Zhang, G., Haase, B., Mountcastle, J., **Fedrigo, O.**, Fogg, J., Kirilenko, B., Munegowda, C., Hiller, M., Jain, A., DKihara, D., Rhie, A., Phillippy, A.M., Swanson, S., P. Jiang, Clegg, D.O., Jarvis, E.D., Thomson, J.A., Stewart, R., Chaisson, M.J.P., Bukhman, Y.V. 2022. (2022) A haplotype-resolved genome assembly of the Nile rat facilitates exploration of the genetic basis of diabetes. **BMC Biology** 20, 245. <https://doi.org/10.1186/s12915-022-01427-8>
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Mapping provides clinically valuable insights into genes implicated in critical immune, viral infection, and viral replication pathways in patients with severe COVID-19. *iScience* 18; 25(2): 103760.

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Funding and awards

2021	Contributed to a HHMI equipment request proposal: “HHMI Equipment Request: Scaling-up and Advancing to Telomere-to-Telomere Genome Assemblies for the Scientific Community”. Awarded to E.D. Jarvis	\$1,326,735.46
2020	Wrote a grant proposal: “Examining tolerance and infection susceptibility of candidate wild reservoirs and domestic intermediate hosts of SARS-CoV-2 through comparative genomics”. Awarded to E.D Jarvis by Rockefeller University	\$120,000.00
2019	Contributed to a NIH proposal: “Center for Human Reference Genome Diversity”. sub-awarded to E.D. Jarvis (5 years)	~\$1,250,000
2018	Contributed to a HHMI Transformative Technology Competition proposal: “A High-Performance Computing Cluster for Producing High Quality Genome Assemblies and Analyses at Scale”. Awarded to E.D. Jarvis	\$906,117.65
2014	Wrote a NC Biotechnology Center (Institutional Development; awarded to G. Wray): “Automated Library Preparation System for Next-Generation Sequencing”	\$165,000.00
2011	Wrote a NIH S10 Grant proposal awarded to G. Wray: “Illumina HiSeq 2000 System”	\$690,000.00
2010	Wenner-Gren Foundation: “Uncovering the genetic bases of the Energy Trade-Off Hypothesis using the elephant- nose fish” to Olivier Fedrigo (PI)	\$18,815.00
2009	SMBE award - Postdoctoral Poster Prize at the 17th SMBE Annual Meeting	n/a

Teaching Experience

2021-2022	Bioinformatics Resource Center workshop: “Genome Assembly” (Rockefeller University)
2015-2016	GCB Academy: Introduction to Next-Generation sequencing lectures; RNA-Seq library preparation workshops (Duke University)
2011	Human Genetics annual workshop: “Duke Bioinformatics Workshop” (Duke University)
2011	An introduction to Next-Generation Sequencing (Duke University)

2007	Phylogenetics tutorial: “Dissecting the phylogenetic signal: The Good, the Bad and the Ugly”. (Duke University)
2003	Teaching Assistant, BIOL 256L Fundamentals of Human Anatomy and Physiology - Laboratory.

Recent Presentations

2024	East and Central AfricaBP Open Institute Workshop: “Advances in Biotechnology and De-Extinction: Assessing Economic Benefits and Challenges”
2022	Resource Center Lecture Series, Rockefeller University: “Fantastic genomes and how to sequence them”
2022	Long Read Sequencing Workshop at JAX: “Towards high-quality reference assemblies for all vertebrate genomes”
2020	AGBT Bionano Rise & Shine Series: “Towards high quality reference assemblies for all Vertebrate genomes”
2019	University of Florida Genetics Institute: “The Vertebrate Genomes Project: Building accurate and complete reference genomes for all vertebrates”
2019	PAG Bionano Genomics workshop: “The Vertebrate Genomes Project: Building accurate and complete reference genomes for all vertebrates”
2018	Upstate New York Genomics Symposium, Cornell Ithaca - The Vertebrate Genomes Project: Building accurate and complete reference genomes for all vertebrates