

CV – Maud FAGNY

Research Experience

- 2021- Laboratoire de Génétique Quantitative et Évolution, Le Moulon, INRAE, Gif-sur-Yvette, France
- 2020-2021 Éco-anthropologie, CNRS UMR 7206, MNHN, Université de Paris, Paris, France
- 2019-2020 Laboratoire de Génétique Quantitative et Évolution, Le Moulon, INRAE, Gif-sur-Yvette, France
- 2018 Epigenetics and Environment Laboratory, Centre National de Recherche en Génétique Humaine, CEA – Institut François Jacob, Evry, France.
Head of lab: Jorg Tost
- 2015-2017 Department of Biostatistics, Harvard T.H. Chan School of Public Health/Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, USA.
Head of lab: John Quackenbush
- 2011-2015 Human Evolutionary Genetics Unit, CNRS URA3012, Institut Pasteur, Paris, France
Supervisor: Lluís Quintana-Murci
- Sep-Dec 2010 Center for Geogenetics, University of Copenhagen, Copenhagen, Denmark
Supervisor: Ludovic Orlando
- Feb-May 2010 LBBE, CNRS UMR 5558, Université Lyon I, Lyon, France.
Supervisor: Sylvain Mousset
- Jun-Jul 2009 LJC, Ecole Normale Supérieure de Lyon, France
Supervisor: Laurence Lemelle

Education

- 2011-2015 PhD in Human Evolutionary Genetics. Institut Pasteur / Université Paris VI, France
- 2009-2011 Master Biosciences. Ecole Normale Supérieure de Lyon, France
- 2008-2009 Licence (Bachelor) Fundamental Biology. Ecole Normale Supérieure de Lyon, France
- 2006-2008 CPGE (Bachelor) Biology, Chemistry, Physics, Geology. Lycée Henri IV, Paris, France.

Fundings

- Marie Skłodowska Curie Individual Fellowship 2019. PATTERN: “Detecting Polygenic Adaptation Targeting Gene Expression Regulation In Humans Using eQTL Networks.”

Awards

- Best Poster Award Genomes and Genetics Department retreat. Institut Pasteur, June 2012
- Finalist of The Walter M. Fitch Award SBE 2015. Vienna, July 2015

Talks at academic seminar

- 2020 Identification of key tissue-specific, biological processes through integration of enhancer information in gene regulatory networks, online semIDEEV.
- 2019 Characterizing regulatory mutations in tissues with eQTL networks. ENS Paris, France.
Characterizing cancer risk SNPs using expression quantitative trait loci bipartite networks. NCMM, Oslo, Norway.
Characterizing cancer risk SNPs using expression quantitative trait loci bipartite networks. Université d’Oslo, Norway.
- 2018 Characterizing regulatory mutations in tissues with eQTL networks. Musée de l’Homme, Paris, France.
- 2017 eQTL networks: Mapping SNPs to functions. Channing Division of Network Medicine, Boston.
- 2015 Humans in an adaptive world: A Genetic and Epigenetic History of the Human Genome. Massachusetts Institute of Technology, Boston. Dana-Farber Cancer Institute, Boston.
- 2014 Genetic and epigenetic determinants of human adaptation to different lifestyles and modes of subsistence. Université Paris VII / National Museum of Natural History

Invited lab visits

2019 Kuijjer lab, NCMM, Oslo, Norway (1week)

Supervising and mentoring activities.

2020 Supervision of 1 Master Student
Project: Pleiotropy and the selection of complex characters: how does the genetic architecture of a complex character constrain its evolution?

2019 Supervision of 1 Research Engineer (IE) from the DyGAP team

2018 Supervision of 2 Research Engineers (IE) from the bioanalyst/biostatistics team of the LEE

2016-2017 Undergrad student, 6 month internship (once a week).
Project: Deciphering genetic basis of autoimmune diseases using eQTL networks.

2015-2018 Mentoring of a PhD student in statistics
Project: Propagating errors in eQTL networks

2017 Supervision of 3 summer students (6 weeks)
Project: Consequences of cardio-vascular diseases on gene expression profile

2016 Supervision of 1 summer student (10 weeks)
Project: Deciphering genetic basis of cancer risk using eQTL networks.

2014 Supervision of a master student (4 months)
Project: Genetic basis of population variation of DNA methylation profiles.

Teaching

2021 AgroParisTech UC 2A “Ce que nous apprennent les génomes”: “Les réseaux biologiques” – 2h

2017 Harvard T.H. Chan School of Public Health - BST 280: Introductory Genomics & Bioinformatics for Health Research (Grad School) – Introduction to R Bioconductor – 2h

2016-2017 Harvard T.H. Chan School of Public Health - BST 280: Introductory Genomics & Bioinformatics for Health Research (Grad School) – Introduction to Human Evolutionary Genomics – 2h

2013-2015 Institut Pasteur - Human population genomics and genetic epidemiology (Master) – 3h

Non-academic teaching as part of the Enseigner association:
Support courses (biology, physics, chemistry and math) to high-school students.

Other institutional and administrative responsibilities

2021- Organizing and advertizing the semIDEEV and lab seminars.

2018 Volunteer staff member at the RECOMB meeting

2017 Organization of monthly postdoc meetings in DFCI.

2013-2015 PhD Student representative at the Genome and Genetics Department council.

2014-2015 Organization of monthly meeting between the Human evolutionary genetics team at Institut Pasteur and the Human genetics of infectious diseases: Complex predisposition team at Institut Imagine.

2010 Student representative at the board of the school ENS de Lyon.

Conference Contributions (Oral presentation)

2021 Identification of key tissue-specific, biological processes through integration of enhancer information in gene regulatory networks, Maize Genome Meeting 2021.

2018 RECOMB Genetics Satellite Meeting. Paris, France. Investigating cancer risk germline mutations using eQTL networks.

2016 Celebration of Young Investigators in Cancer Research. Boston. A network-based approach for eQTL interpretation and SNP functional characterization.

2015 SMBE 2015. Vienna. (**Finalist of The Walter M. Fitch Award**) Human epigenomic variation is driven by historical and recent changes in habitat and lifestyle.

2014 Human Genome Meeting 2014. Geneva. Genetic and epigenetic determinants of human adaptation to different lifestyles and modes of subsistence.
Young Researchers in Life Science 2014. Paris. Genetic and epigenetic determinants of human adaptation to different lifestyles and modes of subsistence.

Conference Contributions (Poster presentation)

- 2019 22nd National Congress on Transposable Elements. Lyon, France.
- 2018 RECOMB 2018. Paris, France. Investigating cancer risk germline mutations using eQTL networks
- 2017 12th Annual Postdoc and Graduate Student Retreat. Dana-Farber Cancer Institute. Boston
- 2016 CSHL Meeting "The Biology of Genomes". Cold Spring Harbor Laboratory.
2016 PQG Conference. Boston.
12th Annual Postdoc and Graduate Student Retreat. Dana-Farber Cancer Institute. Boston
- 2015 CSHL Meeting "The Biology of Genomes". Cold Spring Harbor Laboratory.
EMBO Conference: "Genetic Control of Development and Evolution 2015". Paris.
- 2014 Congrès des Jeunes Chercheurs 2014. Paris.
- 2013 European Society of Human Genetics Conference 2013. Paris.
RECOMB 2013. Lyon.
- 2012 Jacques Monod Conference "Theoretical and empirical advances in evolutionary genomics". Roscoff.
Congrès des Jeunes Chercheurs 2012. Paris.
CSHL Meeting "The Biology of Genomes". Cold Spring Harbor Laboratory.
- 2011 EMBO meeting "Host Control of Infectious Disease". Paris.

Service

- Peer review *eLife; Cancer Research; Annals of Botany; CMSB 2017 (Computational Methods for Systems Biology), Seminars in Cell and Developmental Biology*
- Editor role *Frontiers In Genetics* – Guest Editor - Applications and Methods in Genomic Networks.

Publications

First Author

Fagny M, Patin E, Enard D, Barreiro LB, Quintana-Murci L, Laval G (2014) Exploring the occurrence of classic selective sweeps in humans using whole-genome sequencing data sets. *Molecular Biology and Evolution* **31**(7):1850-68. <https://doi.org/10.1534/genetics.116.195594> (65 citations)

Fagny M, Patin E, MacIsaac JL, Rotival M, Flutre T, Jones MJ, Siddle KJ, Quach H, Harmant C, McEwen LM, Froment A, Heyer E, Gessain A, Betsem E, Mouguiama-Daouda P, Hombert J-M, Perry GH, Barreiro LB, Kobor MS, Quintana-Murci L. (2015) The Epigenomic Landscape of African Rainforest Hunter-Gatherers and Farmers. *Nature Communications* **6**. <https://doi.org/10.1038/ncomms10047> (38 citations)

Fagny M, Paulson JN, Kuijjer ML, Sonawane AR, Chen C.-Y., Lopes-Ramos CM, Glass K, Quackenbush J, Platig J. (2017) Exploring regulation in tissues with eQTL networks. *Proceedings of the National Academy of Sciences of the United States of America* **114**, E7841–E7850. <https://doi.org/10.1073/pnas.1707375114> (29 citations)

Fagny M, Kuijjer ML, Platig J, Lin X, Quackenbush J. (2019) Nongenetic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. *British Journal of Cancer*. <https://doi.org/10.1038/s41416-019-0614-3>

Fagny M, Kuijjer ML, Stam M, Joets J, Turc O, Rozière J, Pateyron S, Venon A, Vitte C. (2021) Identification of key tissue-specific, biological processes by integrating enhancer information in maize gene regulatory networks. *Frontiers in Genetics* **11**:606285. <https://doi.org/10.3389/fgene.2020.606285>

Fagny M, Austerlitz F (2021) Polygenic Adaptation: Integrating Population Genetics and Gene Regulatory Networks. *Trends In Genetics* **37**(7):631-638. <https://doi.org/10.1038/s41416-019-0614-3>

Other contributions

Deschamps M, Laval G, **Fagny M**, Itan Y, Abel L, Casanova J-L, Patin E, Quintana-Murci L. (2016) Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. *The American Journal of Human Genetics* **98**(1):5-21. <https://doi.org/10.1016/j.ajhg.2015.11.014> (140 citations)

Horvath S, Gurven M, Levine ME, Trumble BC, Kaplan H, Allayee H, Ritz BR, Chen B, Lu AT, Rickabaugh TM, Jamieson BD, Sun D, Li S, Chen W, Quintana-Murci L, **Fagny M**, Kobor MS, Tsao PS, Reiner AP, Edlefsen KL, Absher D, Assimes TL. (2016) An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. *Genome Biology* **7**(1):171. <https://doi.org/10.1186/s13059-016-1030-0> (204 citations)

Gopalan S, Carja O, **Fagny M**, Patin E, Myrick JW, McEwen L, Mah SM, Kobor MS, Froment A, Feldman MW, Quintana-Murci L, Henn BM. (2017) Trends in DNA methylation with age replicate across diverse human populations. *Genetics* **206**(3):1659-1674. <https://doi.org/10.1534/genetics.116.195594> (30 citations)

Chaix R, Alvarez-López MJ, **Fagny M**, Lemee L, Regnault B, Davidson RJ, Lutz A, Kaliman P. (2017) Epigenetic clock analysis in long-term meditators. *Psychoneuroendocrinology* **85**, 210–214. <https://doi.org/10.1016/j.psyneuen.2017.08.016> (20 citations)

Paulson JN, Chen C.-Y., Lopes-Ramos CM, Kuijjer ML, Platig J, Sonawane AR, **Fagny M**, Glass K, Quackenbush J. (2017) Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. *BMC Bioinformatics* **18**. <https://doi.org/10.1186/s12859-017-1847-x> (15 citations)

Lopes-Ramos CM, Paulson JN, Chen C.-Y., Kuijjer ML, **Fagny M**, Platig J, Sonawane AR, DeMeo DL, Quackenbush J, Glass K. (2017) Regulatory network changes between cell lines and their tissues of origin. *BMC Genomics* **18**, 723. <https://doi.org/10.1186/s12864-017-4111-x> (9 citations)

Sonawane AR, Platig J, **Fagny M**, Chen C.-Y., Paulson JN, Lopes-Ramos CM, DeMeo DL, Quackenbush J, Glass K, Kuijjer ML. (2017) Understanding Tissue-Specific Gene Regulation. *Cell Reports* **21**, 1077–1088. <https://doi.org/10.1016/j.celrep.2017.10.001> (67 citations)

Barry JD, **Fagny M**, Paulson JN, Aerts H, Platig J, Quackenbush J. (2018) Histopathological Image QTL Discovery of Immune Infiltration Variants. *iScience* **5**, 80–89. <https://doi.org/10.1016/j.isci.2018.07.001> (2 citations)

Weber A, Schwarz SC, Tost J, Trümbach D, Winter P, Busato F, Tacik P, Windhorst AC, **Fagny M**, Arzberger T, Catriona McLean C, van Swieten JC, Schwarz J, Weisenhorn DV, Wurst W, Adhikary T, Dickson DW, Höglinger GU, Müller U. (2018) Epigenome-wide DNA methylation profiling in Progressive Supranuclear Palsy reveals major changes at DLX1. *Nature Communications* **9**. <https://doi.org/10.1038/s41467-018-05325-y> (3 citations)

Husquin LT, Rotival M, **Fagny M**, Quach H, Zidane N, McEwen LM, MacIsaac JL, Kobor MS, Aschard H, Patin E, Quintana-Murci L. Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. (2018) *Genome Biology* **19**, 222 <https://doi.org/10.1186/s13059-018-1601-3> (10 citations)

Fogel O, Bugge Tinggaard A, **Fagny M**, Sigrist N, Roche E, Leclere L, Deleuze J-F, Batteux F, Dougados M, Miceli-Richard C, Tost J. Deregulation of microRNA expression in monocytes and CD4+ T lymphocytes from patients with axial spondyloarthritis. (2019) *Arthritis Res Ther* **21**, 51 <https://doi.org/10.1186/s13075-019-1829-7>

Chaix R, **Fagny M**, Cosin-Tomás M, Alvarez-López M, Lemee L, Regnault B, Davidson RJ, Lutz A, Kaliman P. Differential DNA methylation in experienced meditators after an intensive day of mindfulness-based practice: Implications for immune-related pathways. (2019) *Brain Behavior and Immunity* <https://doi.org/10.1016/j.bbi.2019.11.003>

Chen C.-Y., Lopes-Ramos CM, Kuijjer ML, Paulson JN, Sonawane AR, **Fagny M**, Platig J, Glass K, Quackenbush J, DeMeo DL. (2020) Sex differences in gene expression and regulatory networks across twenty-nine human tissues. *Cell Reports* **31**(12):107795. <https://doi.org/10.1016/j.celrep.2020.107795>

Kuijjer ML, **Fagny M**, Marin A., Quackenbush J, Glass K. (2020) PUMA: PANDA Using MicroRNA Associations. *Bioinformatics* **36**(18):4765-4773 <https://doi.org/10.1093/bioinformatics/btaa571>

Books, Chapters and Monographies

Fagny M (2015) Thèse: L'Homme face à son environnement: une histoire génétique et épigénétique du génome humain. <https://tel.archives-ouvertes.fr/tel-01234659/>

Manuscripts with preprints

Gaynor SM, **Fagny M**, Lin X, Platig J, Quackenbush J. (2019) *bioRxiv* <https://doi.org/10.1101/515551>