

Dr Irene Gallego Romero

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Melbourne Integrative Genomics
School of BioSciences,
University of Melbourne,
Australia

Education

- 2006–2010 **PhD, Biological Anthropology**, *University of Cambridge*, Cambridge, UK.
Thesis title: **Searching for Recent Positive Selection in Indian Populations**. Supervised by Dr. Toomas Kivisild.
- 2002–2006 **BA, Biological Sciences with a specialization in genetics (double honors)**, *University of Chicago*, Chicago, USA.
Undergraduate honours thesis title: **A population-based study of the fertility advantage in carriers of alleles for cystic fibrosis**. Supervised by Prof. Carole Ober.

Research Positions Held

- 06.2017–ongoing **Lecturer in Systems Biology**, *Melbourne Integrative Genomics, School of BioSciences, The University of Melbourne*, Parkville, Australia.
- 06.2017–ongoing **Associate member**, *Centre for Stem Cell Systems, School of Medicine, Dentistry and Health Sciences, The University of Melbourne*, Parkville, Australia.
- 11.2015–05.2017 **Nanyang Assistant Professor**, *School of Biological Sciences and Lee Kong Chian School of Medicine, Nanyang Technological University*, Singapore.
- 03.2011–09.2015 **Sir Henry Wellcome Postdoctoral Fellow, Gilad laboratory**, *Department of Human Genetics, University of Chicago*, Chicago, USA.
Project title: Comparative genomics of gene regulation in primates using stem cells.
- 10.2010–02.2011 **Postdoctoral Research Associate, Human Evolution Group (led by Chris Tyler-Smith)**, *Wellcome Trust Sanger Institute*, Hinxton, UK.
- 06.2005–09.2005 **Metcalf Fellow, Molecular Systematics Department**, *Jodrell Laboratory, Royal Botanic Gardens Kew*, Surrey, UK.
- 09.2004–06.2006 **Undergraduate research assistant, Ober Laboratory**, *Department of Human Genetics, University of Chicago*, Chicago, USA.

Funding and Awards

- 2018–2021 Assistant Investigator, Marsden Fund grant, Royal Society of New Zealand. In collaboration with Prof Murray Cox, Massey University, New Zealand.
- 2015–2017 Nanyang Assistant Professorship, Nanyang Technological University.
- 2011–2015 Sir Henry Wellcome Postdoctoral Fellowship, Wellcome Trust.
- 2006–2009 The Isaac Newton Trust / Cambridge European Trust, University of Cambridge.
2005 Jeff Metcalf Fellowship, University of Chicago

Teaching Experience

- ongoing PhD students supervised: 1 as primary supervisor, 1 as secondary supervisor.
- ongoing **Course coordinator** for BIOL30003: Case Studies in Computational Biology, University of Melbourne. This is the capstone course in the University's new Computational Biology major.
- ongoing **Lecturer** for GENE30004: Genetic Analysis, University of Melbourne.
- 09.2016 **Lecturer**, Molecular Cell Biology for Biomedical Engineers, Nanyang Technological University.

- 09.2012– **Undergraduate student supervisor**, Department of Human Genetics, University of Chicago.
 06.2015 Daily supervision and mentoring of undergraduate students carrying out undergraduate thesis research in the Gilad laboratory.
- 02.2010– **Undergraduate laboratory practical assistant**, Department of Genetics, University of Cambridge.
 04.2010 Supervised first year undergraduate students carrying out basic genetics experiments in a laboratory environment.
- 10.2008– **Undergraduate student supervisor**, Department of Biological Anthropology, University of Cambridge.
 06.2010 Led small-group discussions with second and third year students on material covered by both core and elective courses (principally covering human genetics) as well as assigning and correcting classwork. Additionally assisted undergraduate students in their final year with independent research projects entailing both wet and dry laboratory work.

Service and Committees

- ongoing Ad hoc reviewer, Nature Genetics, Molecular Biology and Evolution, BMC Genomics, BMC Evolutionary Biology, European Journal of Human Genetics, PLOSone, PLOS Genetics.
- ongoing Ad hoc grant reviewer for the Leakey Foundation
- ongoing Member, Australasian Genomics Technologies Association (AGTA); Society for Molecular Biology and Evolution (SMBE)
- 2015 SMBE 2015 symposium organiser (with Nicholas E. Banovich): "Novel Functional Approaches to Evolutionary Genomics"
- 2014-2015 Founding member, University of Chicago Postdoctoral Association, University of Chicago
- 2012-2015 Founding member and president, Human Genetics Postdoc Society, University of Chicago.
- 2012-2014 Co-president and chair of Equality in Science Committee and Policy Committee, Biological Sciences Division Postdoctoral Association, University of Chicago.

Outreach activities

- 2016 *Nature versus Nurture?* Invited speaker, TEDxNTU; Singapore. Full talk available online at https://www.youtube.com/watch?v=uXIW_m01o0U.

Fieldwork Experience

- 2008 **Maharashtra/Madhya Pradesh states**, India.

Publications

Total number of publications: 24, 7 as first author. H-index on Google Scholar: 20

2017

N.E. Banovich*, Y.I. Li*, A. Raj*, M.C. Ward, P. Greenside, D. Calderon, P.Y. Tung, J.E. Burnett, M. Myrthil, S.M. Thomas, C.K. Burrows, **Irene Gallego Romero**, B.J. Pavlovic, A. Kundaje, J.K. Pritchard and Y. Gilad. **Impact of regulatory variation across human iPSCs and differentiated cells**. In press, *Genome Research*. Also available at bioRxiv, doi: 10.1101/091660.
 * denotes equal contribution.

2016

S. Mallick, H. Li*, M. Lipson*, I. Mathieson*, M. Gymrek, F. Racimo, J.P. Spence, M. Zhao, N. Chennagiri, S. Nordenfelt, A. Tandon, P. Skoglund, I. Lazaridis, S. Sankararaman, Q. Fu, N. Rohland, G. Renaud, Y. Erlich, T. Willems, C. Gallo, G. Poletti, F. Balloux, G. van Driem, P. de Knijff, **I. Gallego Romero**, A.R. Jha, D.M. Behar, C.M. Bravi, C. Capelli, T. Hervig, A. Moreno-Estrada, O.L. Posukh, E. Balanovska, O. Balanovsky, S. Karachanak-Yankova, H. Sahakyan, D. Toncheva, L. Yepiskoposyan, C. Tyler-Smith, Y. Xue, M.S. Abdullah, A. Ruiz-Linares, C.M. Beall, A. Di Rienzo, C. Jeong, E.B. Starikovskaya, E. Metspalu, J. Parik, R. Villems, B.M. Henn, U. Hodoglugil, R. Mahley, A. Sajantila, G. Stamatoyannopoulos, J.T. S. Wee, R. Khusainova, E. Khusnutdinova, S. Litvinov, G. Ayodo, D. Comas, M. Hammer, T. Kivisild, W. Klitz, C. Winkler, D. Labuda, M. Bamshad, L.B. Jorde, S.A. Tishkoff, W.S. Watkins, M. Metspalu, S. Dryomov, R. Sukernik, L. Singh, K. Thangaraj, Y.S. Song, S. Pääbo, J. Kelso, N. Patterson, and D. Reich. **The landscape of human genome diversity.** *Nature*, doi:10.1038/nature18964. * denotes equal contribution.

C.K. Burrows*, N.E. Banovich*, B.J. Pavlovic, K. Patterson, **I. Gallego Romero**, J.K. Pritchard and Y. Gilad. **Genetic Variation, Not Cell Type of Origin, Underlies Regulatory Differences in iPSCs.** *PLoS Genetics*, doi: 10.1371/journal.pgen.1005793. Also available at bioRxiv, doi: 10.1101/013888. * denotes equal contribution.

2015

I. Gallego Romero*, B.J. Pavlovic*, I. Hernando-Herraez, X. Zhou, M.C. Ward, N.E. Banovich, C.L. Kagan, J.E. Burnett, C.H. Huang, A. Mitrano, C.I. Chavarria, I.F. Ben-Nun, Y. Li, K. Sabatini, T.R. Leonardo, M. Parast, T. Marques-Bonet, L.C. Laurent, J.F. Loring, and Y. Gilad. **Generation of a Panel of Induced Pluripotent Stem Cells From Chimpanzees: a Resource for Comparative Functional Genomics.** *eLife*, doi: 10.7554/eLife.07103. Also available at bioRxiv, doi: 10.1101/008862. * denotes equal contribution.

P.H. Sudmant, S. Mallick, B.J. Nelson, F. Hormozdiani, N. Krumm, J. Huddleston, B.P. Coe, C. Baker¹, S. Nordenfelt, M. Bamshad, L.B. Jorde, O.L. Posukh, H. Sahakyan, W.S. Watkins, L. Yepiskoposyan, M.S. Abdullah, C.M. Bravi, C. Capelli, T. Hervig, J.T.S. Wee, C. Tyler-Smith, G. van Driem, **I. Gallego Romero**, A.R. Jha, S. Karachanak-Yankova, D. Toncheva, D. Comas, B. Henn, T. Kivisild, A. Ruiz-Linares, A. Sajantila, E. Metspalu, J. Parik, R. Villems, E.B. Starikovskaya, G. Ayodo, C. Beall, A. Di Rienzo, M. Hammer, R. Khusainova, E. Khusnutdinova, W. Klitz, C. Winkler, D. Labuda, M. Metspalu, S.A. Tishkoff, S. Dryomov, R. Sukernik, N. Patterson, D. Reich, and E.E. Eichler. **Global diversity, population stratification, and selection of human copy number variation.** *Science*, doi: 10.1126/science.aab3761.

I. Garitaonandia*, H. Amir*, F.S. Boscolo*, G.K. Wambua, H.L. Schultheisz, K. Sabatini, R. Morey, S. Waltz, Y-C. Wang, H. Tran, T.R. Leonardo, K. Nazor, I. Slavin, C. Lynch, Y. Li, R. Coleman, **I. Gallego Romero**, G. Altun, D. Reynolds, S. Dalton, M. Parast, J.F. Loring** and L.C. Laurent**. **Increased Risk of Genetic and Epigenetic Instability in Human Embryonic Stem Cells Associated with Specific Culture Conditions** *PLoSone*, doi: 10.1371/journal.pone.0118307. * and ** denote equal contributions.

2014

I. Gallego Romero, A. A. Pai, J. Tung and Y. Gilad. **RNA-seq: Impact of RNA degradation on transcript quantification.** *BMC Biology*, 12:42 doi:10.1186/1741-7007-12-42.

A. Cardona, L. Pagani, T. Antão, D.J. Lawson, C.A. Eichstaedt, B. Yngvadottir, M. Than Than Shwe, J. Wee, **I. Gallego Romero**, S. Raj, M. Metspalu, R. Villems, E. Willerslev, C. Tyler-Smith, B.A. Malyarchuk, M.V. Derenko and T. Kivisild. **Genome-wide analysis of cold adaption in indigenous Siberian populations** *PLoSone*, doi: 10.1371/journal.pone.0098076.

I. Lazaridis, N. Patterson, A. Mitnik, G. Renaud, S. Mallick, P.H. Sudmant, J. Schraiber, S. Castellano, K. Kiranow, C. Economou, R. Bollongino, K.I. Bos, S. Nordenfelt, C. de Filippo, K. Pruefer, A. Tandon, S. Sawyer, C. Posth, G. Ayodo, H.M.A. Babiker, E. Balanovska, O. Balanovsky, C. Beall, H. Ben-Ami, J. Bene, F. Berrada, F. Brighelli, G. Busby, F. Cali, C. Capelli, M. Churnosov, D.E.C. Cole, L. Damba, G. van Driem, S. Dryomov, S. Fedorova, M. Francken, **I. Gallego Romero**, X. Gebremedhin, M. Gubina, M. Hammer, B. Henn, U. Hodoglugil, A. Jha, R. Kittles, E. Khusnutdinova, T. Kivisild, V. Kučinskis, R. Kusainova, L. Kushniarevich, L. Laredj, S. Litvinov, T. Loukidis, R. Mahley, B. Melegh, E. Metspalu, T. Moen, J. Mountain, T. Nyambo, L. Ossipova, J. Parik, F. Platanov, O. Posukh, A. Di Rienzo, V. Romano, I. Rudan, R. Ruizbakiev, H. Sahakyan, A. Salas, M. Shriver, A. Tarekegn, D. Toncheva, S. Turdikulova, I. Uktveryte, O. Utevska, M. Voevoda, J. Wahl, P. Zalloua, L. Yeppiskoposyan, T. Zemunik, M. Thomas, S. Tishkoff, R. Villems, D. Comas, L. Singh, K. Thangaraj, R. Sukernik, M. Metspalu, M. Meyer, E.E. Eichler, J. Burger, M. Slatkin, S. Pääbo, J. Kelso, D. Reich, and J. Krause. **Ancient human genomes suggest three ancestral populations for present-day Europeans.** *Nature*, doi: 10.1038/nature13673. Also available at bioRxiv, doi: 10.1101/001552.

2013

A. Bamberg Migliano, **I. Gallego Romero**, M. Metspalu, M. Leavesley, L. Pagani, T. Antão, D.W. Huang, B.T. Sherman, K. Siddle, C. Scholes, G. Hudjashov, E. Kaitokai, H. Mandui, A. Babalu, M. Belatti, A. Cagan, B. Hopkinshaw, C. Shaw, K. Tabbada, M. Nelis, E. Metspalu, R. Mägi, R.A. Lempicki, R. Villems, M. Mirazón Lahr and T. Kivisild. **Evolution of the pygmy phenotype: evidence of positive selection from genome-wide scans in African, Asian and Melanesian pygmies** *Human Biology*, 85(1-3):251-84.

C. Basu Mallick*, F.M. Iliescu*, M. Möls, S. Hill, R. Tamang, G. Chaubey, R. Goto, S.Y.W Ho, **I. Gallego Romero**, F. Crivellaro, G. Hudjashov, N. Rai, M. Metspalu, C.G.N. Mascie-Taylor, R. Pitchappan, L. Singh, M. Mirazón Lahr, K. Thangaraj, R. Villems and T. Kivisild. **The Light Skin Allele of SLC24A5 in South Asians and Europeans Shares Identity by Descent** *PLoS Genetics*, doi: 10.1371/journal.pgen.1003912. * denotes equal contribution.

S.M. Raj, L. Pagani, **I. Gallego Romero**, T. Kivisild, and W. Amos. **A general linear model-based approach for inferring selection to climate.** *BMC Genetics* doi: 10.1186/1471-2156-14-87.

S.M. Raj, P. Halebeedu, J.S. Kadandale, M. Mirazón Lahr, **I. Gallego Romero**, J.R. Yadhav, M. Iliescu, N. Rai, F. Crivellaro, G. Chaubey, R. Villems, K. Thangaraj, K. Muniyappa, H.S. Chandra, and T. Kivisild. **Variation at Diabetes- and Obesity-Associated Loci May Mirror Neutral Patterns of Human Population Diversity and Diabetes Prevalence in India.** *Annals of Human Genetics*, doi: 10.1111/ahg.12028.

2012

I. Gallego Romero, I Ruvinsky and Y. Gilad. **Comparative studies of gene expression and the evolution of gene regulation** *Nature Reviews Genetics*, doi: 10.1038/nrg3229.

L. Pagani, T. Kivisild, A. Tarekegn, R. Ekong, C. Plaster, **I. Gallego Romero**, Q. Ayub, S.Q. Mehdi, M.G. Thomas, D. Luiselli, E. Bekele, N. Bradman, D.J. Balding and C. Tyler-Smith. **Ethiopian Genetic Diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool** *American Journal of Human Genetics*, doi: 10.1016/j.ajhg.2012.05.015.

D.G. MacArthur, S. Balasubramanian, A. Frankish, N. Huang, J. Morris, K. Walter, L. Jostins, L. Habegger, J.K. Pickrell, S.B. Montgomery, C.A. Albers, Z.D. Zhang, D.F. Conrad, G. Lunter, H. Zheng, Q. Ayub, M.A. DePristo, E. Banks, M. Hu, R.E. Handsaker, J.A. Rosenfeld, M. Fromer, M. Jin, X. Jasmine Mu, E. Khurana, K. Ye, M. Kay, G.I. Saunders, M-M. Suner, T. Hunt, I.H.A. Barnes, C. Amid, D.R. Carvalho-Silva, A.H. Bignell, C. Snow, B. Yngvadottir, S. Bumpstead, D.N. Cooper, Y. Xue, **I. Gallego Romero**, 1000 Genomes Project Consortium, J. Wang, Y. Li, R.A. Gibbs, S.A. McCarroll, E.T. Dermitzakis, J.K. Pritchard, J.C. Barrett, J. Harrow, M.E. Hurles, M.B. Gerstein and C. Tyler-Smith. **A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes** *Science*, doi: 10.1126/science.1215040.

2011

M. Hu, Q. Ayub, J.A. Guerra-Assunção, Q. Long, Z. Ning, N. Huang, **I. Gallego Romero**, L. Mamanova, P. Akan, X. Liu, A.J. Coffey, D.J. Turner, H. Swerdlow, J. Burton, M.A. Quail, D.F. Conrad, A.J. Enright, C. Tyler-Smith and Y. Xue. **Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data** *Human Genetics*, doi: 10.1007/s00439-011-1111-9.

M. Metspalu*, **I. Gallego Romero***, B. Yunusbayev*, G. Chaubey, C. Basu Mallick, G. Hudjashov, M. Nelis, R. Mägi, E. Metspalu, M. Remm, R. Pitchappan, L. Singh, K. Thangaraj, R. Villems, and T. Kivisild. **Shared and unique components of human population structure and genome-wide signals of positive selection in South Asia** *American Journal of Human Genetics*, doi: 10.1016/j.ajhg.2011.11.010. * denotes equal contribution.

M. Rasmussen, X. Guo, Y. Wang, K.E. Lohmueller, S. Rasmussen, A. Albrechtsen, L. Skotte, S. Lindgreen, M. Metspalu, T. Jombart, T. Kivisild, W. Zhai, A. Eriksson, A. Manica, L. Orlando, F. De La Vega, S. Tridico, E. Metspalu, K. Nielsen, M.C. Avila-Arcos, J.V. Moreno-Mayar, C. Muller, J. Dortch, M.T. Gilbert, O. Lund, A. Wesolowska, M. Karmin, L.A. Weinert, B. Wang, J. Li, S. Tai, F. Xiao, T. Hanihara, G. van Driem, A.R. Jha, F.X. Ricaut, P. de Knijff, A.B. Migliano, **I. Gallego Romero**, K. Kristiansen, D.M. Lambert, S. Brunak, P. Forster, B. Brinkmann, O. Nehlich, M. Bunce, M. Richards, R. Gupta, C.D. Bustamante, A. Krogh, R. A. Foley, M.M. Lahr, F. Balloux, T. Sicheritz-Pontén, R. Villems, R. Nielsen, W. Jun and E. Willerslev. **An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia**. *Science*, doi: 10.1126/science.1211177.

I. Gallego Romero, C. Basu Mallick, A Liebert, F Crivellaro, G Chaubey, A Liebert, Y Ital, R. Pitchappan, M. Metspalu, M. Eaaswarkanth, R. Villems, L. Singh, K. Thangaraj, M. G. Thomas, D. Swallow, M Mirazón Lahr, and T. Kivisild. **Herders of Indian and European cattle share their predominant allele for milk tolerance**. *Molecular Biology and Evolution*, doi: 10.1093/molbev/msr190.

2010-2008

G. Chaubey, M. Metspalu, Y. Choi, R. Maagi, **I. Gallego Romero**, P. Soares, M. van Oven, D. M. Behar, S. Rootsi, G. Hudjashov, C. Basu Mallick, M. Karmin, M. Nelis, J. Parik, A. G. Reddy, E. Metspalu, G. van Driem, Y. Xue, C. Tyler-Smith, K. Thangaraj, L. Singh, M. Remm, M. B. Richards, M. Mirazón Lahr, M. Kayser, R. Villems, and T. Kivisild. **Population genetic structure in Indian Austroasiatic speakers: The role of landscape barriers and sex-specific admixture**. *Molecular Biology and Evolution*, doi: 10.1093/molbev/msq288, 2010.

M. Eaaswarkanth, I. Haque, Z. Ravesh, **I. Gallego Romero**, P. R. Meganathan, B. Dubey, F. A. Khan, G. Chaubey, T. Kivisild, C. Tyler-Smith, L. Singh, and K. Thangaraj. **Traces of sub-Saharan and Middle Eastern lineages in Indian Muslim populations**. *European Journal of Human Genetics*, 18(3):354-63, 2010.

I. Gallego Romero, A. Manica, J. Goudet, L. J. Lawson-Handley, and F. Balloux. **How accurate is the current picture of human genetic variation?** *Heredity*, 102(2):120-6, 2009.

I. Gallego Romero and C. Ober. **CFTR mutations and reproductive outcomes in a population isolate**. *Human Genetics*, 122(6):583-8, 2008.

Presentations

Invited

2018 Germany

2018 Lorne Genome meeting, Lorne, Australia.

2017 *Beyond sequence comparisons: iPSCs as models in human functional and evolutionary genomics*, NeuroAnatomy seminar, University of Melbourne, Melbourne, Australia.

- 2015 *Using primate stem cells to model - and understand - human evolution*; Division of Biological Anthropology, Department of Archaeology and Anthropology, University of Cambridge, Cambridge, UK
- 2015 *Induced Pluripotent Stem Cells as Model Systems for Human Evolutionary Biology*; Wellcome Trust Sanger Institute, Hinxton, UK
- 2015 *Induced Pluripotent Stem Cells in Human Evolutionary Biology*; Department of Organismal Biology and Anatomy, University of Chicago, USA
- 2015 *Induced Pluripotent Stem Cells in Human Evolutionary Biology*; School of Biological Sciences, Nanyang Technological University, Singapore
- 2015 *Developing Induced Pluripotent Stem Cells as Models for Evolutionary Biology*; Department of Molecular Cell Biology, University of California Berkeley, USA
- 2014 *Developing Induced Pluripotent Stem Cells as Models for Evolutionary Biology*; Department of Integrative Biology, University of California Berkeley, USA
- 2014 *Divergence of RNA-Seq and Proteomic Signatures Across Evolution*; Next Generation Sequencing European Summit; MipTec, Basel, Switzerland
- 2014 *Combining cellular and genomic approaches to study human evolution*; Center for the Advanced Study of Human Paleobiology; George Washington University, USA

Contributed

- 2017 *Comparative Dynamics of Chromatin Accessibility and Transcription Factor Binding in Humans and Chimpanzees*, Australasian Genomics Technologies Society (AGTA), Hobart, Australia.
- 2016 *Beyond sequence comparisons: functional genomics approaches to studying human evolution*; Centre for Systems Genomics, University of Melbourne, Melbourne, Australia.
- 2015 *Changes in chromatin accessibility and DNA methylation in human and chimpanzee iPSCs*; Cell Symposia: Stem Cell Epigenetics, Sitges, Spain
- 2015 *Changes in Gene Regulation Between Human and Chimpanzee iPSCs*; Sir Henry Wellcome Postdoctoral Fellows Meeting, London, UK
- 2010 *Targets of recent positive selection in Indian populations*; School of Biological Sciences' Bioinformatics day; University of Cambridge, UK
- 2010 *Milking the Indian Cow: Lactase persistence in the Indian subcontinent*; LECHE Symposium, UCL, London, UK
- 2009 *Lactase persistence in the Indian subcontinent*; Current Approaches to Metabolic and Nutritional Disorders: From Genes to Prevention, Norwegian Institute of Public Health, Oslo, Norway
- 2008 *Milking the Indian Cow*; Gonville and Caius College CGAS talks, University of Cambridge, UK

Posters

- 2016 *Patterns of chromatin accessibility and transcription factor binding in human and chimpanzee pluripotent stem cells*; American Society of Human Genetics, Vancouver, Canada
- 2016 *Patterns of chromatin accessibility and transcription factor binding in human and chimpanzee pluripotent stem cells*; Society for Molecular Biology and Evolution, Gold Coast, Australia
- 2015 *A Panel of Induced Pluripotent Stem Cells From Chimpanzees: a Resource for Comparative Genomics*; The Biology of Genomes Conference, Cold Spring Harbor Laboratory, NY, USA
- 2014 *Comparative Developmental Genomics In Primates Using iPSCs*; International Society for Stem Cell Research, Vancouver, Canada
- 2014 *Comparative Developmental Genomics In Primates Using iPSCs*; Society for Molecular Biology and Evolution, Puerto Rico, USA
- 2013 *Comparative developmental genomics of the heart in humans and chimpanzees*; Society for Molecular Biology and Evolution, Chicago, USA

- 2012 *Comparative developmental genomics of the liver in humans and chimpanzees*; International Society for Stem Cell Research, Yokohama, Japan
- 2008 *Tracing the peopling of India through the lactase persistence phenotype*; UKIERI Major Award kickoff conference, Cambridge, UK
- 2008 *Ascertainment bias in genome-wide studies of human polymorphism*; Society for Molecular Biology and Evolution, Barcelona, Spain

Professional References

Available on request.