

James Cotton

Personal detail

Full name: James Anthony Cotton
Date of Birth: 13 August 1976
Nationality: British

T: +44 1223 494864
james.cotton@sanger.ac.uk
<http://www.sanger.ac.uk/research/projects/parasitegenomics>
<http://www.sanger.ac.uk/people/directory/cotton-james>

Employment

Honorary Senior Lecturer, Royal Veterinary College
July 2016 – Current

Senior Staff Scientist, Wellcome Sanger Institute
July 2010 - Current

RCUK Academic Fellow, Queen Mary, University of London
August 2007- June 2010

Postdoctoral Research Fellow, National University of Ireland Maynooth
February 2006- July 2007

Postdoctoral Research Assistant, The Natural History Museum, London
February 2003-February 2006

Editor, Science Press Internet Services, London
June 2001-September 2002

Education

Open University, UK — BSc (Hons) Mathematical Sciences (first class), 2007

Open University, UK — Diploma in Mathematics, 2005

University of Glasgow, UK — PhD, 2003

University of Oxford, UK —BA (Hons) Biological Sciences (first class), 1997

Research grants awarded

MRC research grant (start 2019). *Exploring the immunological mechanisms contributing to symptomatic and asymptomatic visceral leishmaniasis in Ethiopia: a pilot study.* Co-Investigator: £28,903 to WTSI.

MRC research grant (start June 2018). *Understanding differences in clinical presentations of cutaneous leishmaniasis in an endemic disease focus.* Co-Investigator: £263,151 to WTSI

Carter Center, USA (10/2015-08/2017), *Genomic epidemiology to support Guinea worm eradication.* Joint PI (\$274,126 to WTSI)

BBSRC strategic longer-and-larger grant (01/2015-01/2021), *Building upon the genome: using Haemonchus contortus genomic resources to develop novel interventions to control endemic GI parasites.* Co-investigator (£622,336 to WTSI)

BBSRC research grant (08/2010-08/2013), *Molecular convergence at the sequence level: a genome-wide approach in a novel mammalian model.* Co-investigator: £346,204 to QMUL.

BBSRC Co-Syst grant (06/2008-12/2008), *A novel computational approach to bacterial phylogenomics.* Principal investigator: £5,690 to QMUL.

IRCSET Embark postdoctoral fellowship (10/2006-10/2008). *Prokaryote phylogenomics: lateral transfer, gene duplication and the evolution of bacterial genomes.* €96,300

Irish Center for High-End computing, computer time (2007). €2,395

Teaching experience

Lectures in 3rd year parasitology, Dept of Pathology, University of Cambridge annually 2015-2018; 3rd year 'Health and Disease', Dept. of Anthropology, Univ. of Cambridge, 2017.

Extensive experience in teaching genetics, evolution, statistics and bioinformatics at undergraduate and masters level, Queen Mary, University of London

3rd-year undergraduate course on Bioinformatics Programming, NUI Maynooth, Sep-Dec 2006

1st-year undergraduate course on molecular genetics, NUI Maynooth, Mar-Apr 2006

Intensive course on Molecular Systematics, University of Reading, 2004 and 2005.

Guest lecture, EMBO bioinformatics course, NUI Maynooth, 2003

Level 1 biology demonstrator, University of Glasgow, 1999-2001, 80+ hours over 3 years.

Professional Service

Member of the British Society for Parasitology 2012-. Council member and officer (Programme Secretary), Systematics Association 2009-2012

Associate editor for *PLoS Neglected Tropical Diseases*. Reviewing editor for *Frontiers in Ecology and Evolution*. Reviewed papers for at least 26 different journals.

Grants reviewed for Wellcome, MRC, BBSRC, Italian Ministry of Health, Czech Science Foundation, WHO-TDR, Moore foundation.

PhD supervision (4 students; 100% completed). at *Queen Mary University of London*: Hao-Chih Kuo (Phylogeography and diversification of Taiwanese bats): 2nd Supervisor, awarded 2013; Veronica Comper (Dissecting the effects of ancestral population size on the molecular clock): primary supervisor, awarded 2013; Helen Ward: (female mate choice in greater horseshoe bats): 2nd supervisor, awarded 2014. At *WSI*: : Thomas Crellen (genomics of mass drug administration in *Schistosoma mansoni*): 2nd supervisor, awarded 2017; Duncan Berger (genomic and genetic diversity of schistosomes), 2018-; *De facto* supervisor for Stefano Iantorno (genome plasticity and genetic exchange in *Leishmania tropica*), awarded 2016.

PhD examiner for Diego San Mauro Martin, Universidad Autonoma de Madrid; Radoslaw Suchecki, Dept. of Computer Science, University of East Anglia; Johanna Nader, Norwich Medical School, University of East Anglia. Habilitation examiner for Dr Guillaume Sallé, INRA/U. of Tours.

Publications

Preprints not yet published

*Durrant, C., (22 additional authors), **Cotton, J.A.** 2019. Population genomic evidence that human and animal infections in Africa come from the same populations of *Dracunculus medinensis*. *bioRxiv* 808923. (now in press, PLoS NTD).

Van den Broeck, F. (15 additional authors), **Cotton, J.A.** and Dujardin, J.-C. 2019. Ecological divergence and hybridization of Neotropical *Leishmania* parasites. *bioRxiv* 824912. (now in press, PNAS).

*Doyle, S.R., (26 additional authors), **Cotton J.A.** 2020. Extensive genomic and transcriptomic variation defines the chromosome-scale assembly of *Haemonchus contortus*, a model gastrointestinal worm. *bioRxiv* 945246.

Imamura, H. (**Cotton** 8th out of 10 authors), Domagalska, M.A. 2020. Evaluation of whole genome amplification and bioinformatic methods for the characterization of *Leishmania* genomes at a single cell level. *bioRxiv* 957621.

Sloan, M.A., Sadlova, J., Lestinova, T., Sanders, M.J., **Cotton, J.A.**, Volf, P. and Ligoxygakis, P. 2020. The *Phlebotomus papatasi* transcriptomic response to trypanosomatid-contaminate blood is robust but non-specific. *bioRxiv* 867382.

Articles in Journals (77 peer reviewed papers, 92 total, H-index 40 by Google scholar). *indicates JAC as first or corresponding author.

***Cotton, J.A.** and Franssen, S.U. 2020. A way straight-forward for *Leishmania* genetics. *Trends in Parasitology* 36(9):719-721.

Tracey, A., Foster, J.M., Paulini, M., Grote, A., Mattick, J., Tsai, Y.-C., Chung M., **Cotton, J.A.**, Clark T.A., Geber, A., Holroyd, N., Korlach, J. Li, Y., Libro, S., Lustigman, S., Michalski, M.L., Rogers, M.B., Twaddle, A., Dunning Hotopp, J.C., Berriman, M., Ghedin, E. 2020. Nearly complete genome sequence of *Brugia malayi* strain FR3. *Microbiol. Resource Announcements* 9(24).

Foster, J.M., Grote, A., Mattick, J., Tracey, A., Tsai, Y.-C., Chung M., **Cotton, J.A.**, Clark T.A., Geber, A., Holroyd, N., Korlach, J. Li, Y., Libro, S., Lustigman, S., Michalski, M.L., Paulini, M., Rogers, M.B., Teigen, L., Twaddle, A., Welch, L., Berriman, M., Dunning Hotopp, J.C., Ghedin, E. 2020. Sex chromosome evolution in parasitic nematodes of humans. *Nat Comms* 11(1):1-12.

O'Keeffe, A., Hale, C., **Cotton, J.A.**, Yardley, V., Gupta, K., Ananthanarayanan, A., Murdan, S., Croft, S.L. 2020. Novel 2D and 3D assays to determine the activity of anti-Leishmanial drugs. *Microorganisms* 8(6):831.

***Cotton, J.A.**, Durrant, C., Franssen, S., Gelanew, T., Hailu, A., Mateus, D. Sanders, M., Berriman, M., Volf, P. Miles, M. and Yeo, M. 2020. Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of *Leishmania donovani*. *PLoS Negl Trop Dis* 14(4):e0007143 (also *bioRxiv* 516211).

- *Franssen, S.U., (19 additional authors), **Cotton, J.A.** 2020. Global genome diversity of the *Leishmania donovani* complex. *eLife* 9:e51243 (also *bioRxiv* 710145).
- *Domagalska, M.A. et al. (10 additional authors), **Cotton, J.A.**, Dujardin, J.-C. 2019. Genomes of intracellular *Leishmania* parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. *PLoS Negl Trop Dis* 13(12): e0007900.
- Doyle, S.R. et al. (**Cotton** 15th out of 18 authors). 2019. Evaluation of DNA extraction methods on individual helminth egg and larval stages for whole genome sequencing. *Frontiers in Genetics* 10:826. doi:10.3389/fgene.2019.00826
- *Sloan, M.A., Brooks, K., Otto, T.D., Sanders, M.J., **Cotton, J.A.** and Ligoxygakis, P. 2019. Transcriptional and genomic parallels between the monoxenous parasite *Herpetomonas muscarum* and *Leishmania*. *PLoS Genetics* 15(11): e1008452.
- Inbar, E., Shaik, J., Iantorno, S.A., Romano, A., Nzelu, C.O., Owens, K., Sanders, M.J., Dobson, D., **Cotton, J.A.**, Grigg, M.E., Beverley, S.M., Sacks, D. 2019. Whole genome sequencing of experimental hybrids supports meiosis-like sexual recombination in *Leishmania*. *PLOS Genetics* 15(5):e1008042.
- *Sallé, G., Doyle, S.R., Cortet, J., Cabaret, J., Berriman, M., Holroyd, N. and **Cotton, J.A.** 2019. The global diversity of a major parasitic nematode is shaped by human intervention and climatic adaptation. *Nature Communications* 10 (1), 1-14.
- Rezansoff, A.M., Roz Laing, R., Axel Martinelli, A., Stasiuk, S., Redman, E., Bartley, D., Holroyd, N., Devaney, E., Sargison, N.D., Doyle, S.R., **Cotton, J.A.**, Gilleard, J.S. 2019. The confounding effects of high genetic diversity on the determination and interpretation of differential gene expression analysis in the parasitic nematode *Haemonchus contortus*. *International Journal for Parasitology* 49(11):847-858.
- Shaw, C.D., Imamura, H., Downing, T., Blackburn, G., Westrop, G.D., **Cotton, J.A.**, Berriman, M., Sanders, M., Rijal, S., Coombs, G.H., Dujardin, J.-C., Carter, K.C. 2019. Genomic and metabolomic polymorphism among experimentally selected paromomycin-resistant *Leishmania donovani* strains. *Antimicrobial agents and chemotherapy* 64(1).
- Doyle, S.R. and **Cotton, J.A.** 2019. Genome-wide Approaches to Investigate Anthelmintic Resistance. *Trends in Parasitology* 35(4):289-301.
- *Doyle, S.R., Illingworth, C.J.R. Laing, R., Bartley, D.J., Redman, E., Martinelli, A., Holroyd, N., Morrison, A.A., Rezansoff, A., Tracey, A., Devaney, E., Berriman, M., Sargison N., **Cotton, J.A.** and Gilleard, J.S. 2019. Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, *Haemonchus contortus*. *BMC Genomics* 20:218.
- Coghlan, A. et al. (**Cotton** one of very many authors). 2019. Comparative Genomics of the major parasitic worms. *Nature Genetics* 51:163–174.
- Thiele, E. A., Eberhard, M.L., **Cotton, J.A.**, Durrant, C., Berg, J., Hamm, K. and E. Ruiz-Tiben. 2018. Population genetic analysis of Chadian Guinea worms reveals that parasites from human and non-human hosts are the same species. *PLoS Neglected Tropical Diseases* 12(10): e0006747
- ***Cotton, J.A.**, Berriman, M., Dalén, L. and Barnes, I. 2018. Eradication genomics – lessons for parasite control. *Science* 361:130-131.
- Cuyper, B., Berg, M., Imamura, H., Dumetz, F., De Muylder G., Domagalska, M.A., Rijal, S., Bhattarai, N.R., Maes, I., Sanders M., **Cotton, J.A.**, Meysman, P., Laukens, K., Dujardin, J.-C. 2018. Integrated genomic and metabolic profiling of ISC1, an emerging *Leishmania donovani* population in the Indian subcontinent. *Infection, Genetics and Evolution* 62:170-178.
- Coughlan, S., Taylor, A.S., Feane, E., Sanders, M., Schönian, G., **Cotton, J.A.** and Downing, T. *Leishmania naiffi* and *Leishmania guyanensis* reference genomes highlight genome structure and gene evolution in the *Viannia* subgenus. *Royal Society Open Science* 5(4):172212.
- Sallé, G., Laing, R., **Cotton, J.A.**, Maitland, K., Martinelli, A., Holroyd, N., Tracey, A., Berriman, M., Smith, W.D., Newlands, G.F.J., Hanks, E., Devaney, E. and Britton, C. 2018. Transcriptomic profiling of nematode parasites surviving vaccine exposure. *International Journal of Parasitology* 48(5):395-402.
- *Gilchrist, C.A., **Cotton, J.A.**, Burkey, C., Arju, T., Gilmartin, A., Lin, Y., Ahmed, E., Steiner, K., Alam, M., Ahmed, S., Robinson, G., Zaman, S.A., Kabir, M., Sanders, M., Chalmers, R.M., Ahmed, T., Ma, J.Z., Haque, R., Faruque, A.S.G., Berriman, M. and Petri, W.A. 2018. Genetic diversity of *Cryptosporidium hominis* in a Bangladesh community as revealed by whole-genome sequencing. *Journal of Infectious Diseases* 218:259-264.
- Böhme, U., Otto, T.D., **Cotton, J.**, Steinbiss, S., Sanders, M., Oyola S.O., Nicot, A., Gandon, S., Patra K.P., Herd, C., Bushell, E., Modtzynska, K.K., Billker, O., Vinetz, J.M., Rivero, A., Newbold, C.I. and Berriman, M. 2018. Complete avian malaria parasite genomes reveal features associated with lineage specific evolution in birds and mammals. *Genome Research* 28:547-560.
- Zackay, A., **Cotton, J.A.**, Sanders, M., Hailu, A., Nasereddin, A., Warburg, A., Jaffe, C.L. 2018. Genome wide comparison of Ethiopian *Leishmania donovani* strains reveals differences potentially related to parasite survival. *PLoS Genetics* 14(1):e1007133.
- Sargison, N.D., Redman, E., Morrison, A.A., Bartley, D.J., Jackson, F., Naghra-van Gijzel, H., Holroyd, N., Berriman, M., **Cotton, J.A.** and Gilleard, J.S. 2018. A method for single pair mating in an obligate parasitic nematode. *International Journal of Parasitology* 48:159-165.
- *Iantorno, S.A., Durrant, C., Khan, A., Sanders, M.J., Beverley, S.M., Warren, W.C., Berriman, M. Sacks, D.L., **Cotton, J.A.** and Grigg, M.E. 2017. Gene expression in *Leishmania* is regulated primarily by gene dosage. *mBio* 8(5):e01393-17.
- *Doyle, S.R., Laing, R., Bartley, D.J., Britton, C., Chaudhry, U., Gilleard, J.S., Holroyd, N., Mable, B.K., Maitland, K., Morrison, A.A., Tait, A., Tracey, A., Berriman, M., Devaney, E., **Cotton, J.A.** and Sargison, N.D. 2017. A Genome Resequencing-Based Genetic Map Reveals the Recombination Landscape of an Outbred Parasitic Nematode in the Presence of Polyploidy and Polyanidy. *Genome Biology and Evolution* 10(2):396-409.

- Dumetz, F. et al. (Cotton 15th out of 18 authors). 2017. Modulation of aneuploidy in *Leishmania donovani* during adaptation to different in vitro and in vivo environments and its impact on gene expression. *mBio* 8(3):e00599-17.
- *Cotton, J.A. 2017. The expanding world of human leishmaniasis. *Trends in Parasitology* 33(5): 341-344.
- Coughlan, S., Mulhair, P., Sanders, M., Schönian, G., Cotton, J.A. and Downing T. 2017. The genome of *Leishmania adleri* from a mammalian host highlights chromosome fission in *Sauroleishmania*. *Scientific Reports* 7:43747.
- Rutledge, G. et al. (Cotton 6th out of 22 authors). 2017. *Plasmodium malariae* and *P. ovale* genomes provide insights into malaria parasite evolution. *Nature* 542:101-104.
- Valdivia, H.O., Almeida, L.V., Roatt, B.M., Reis-Cunha, J. L., Pereira A.A.S., Gontijo, C., Fujiwara, R.T., Reis, A.B., Sanders, M.J., Cotton, J.A. and Bartholomeu, D.C. 2017. Comparative genomics of canine-isolated *Leishmania (Leishmania) amazonensis* from an endemic focus of visceral leishmaniasis in Governador Valadares, southeastern Brasil. *Scientific Reports* 7:40804.
- *Cotton, J.A., Steinbiss, S., Yokoi, R., Tsai, I.J. and Kikuchi, T. 2016. An expressed, endogenous Nodavirus-like element captured by a retrotransposon in the genome of the plant parasitic nematode *Bursaphelenchus xylophilus*. *Scientific Reports* 6:39749.
- Bennuru, S., Cotton, J.A., (13 additional authors). 2016. Stage-specific transcriptome and proteome analyses of the filarial parasite *Onchocerca volvulus* and its *Wolbachia* endosymbiont. *mBio* 7:e02028-16.
- *Cotton, J.A. et al. (25 additional authors). 2016. The genome of *Onchocerca volvulus*, agent of river blindness. *Nature Microbiology* 2:16216.
- Eves-van den Akker, S. et al. (Cotton 9th out of 34 authors). 2016. The genome of the yellow potato cyst nematode, *Globodera rostochiensis*, reveals insights into the basis of parasitism and virulence. *Genome Biology* 17:124.
- Crellen, T., Walker, M., Lamberton, P.H.L., Kabatereine, N.B., Tukahebwa, E.M., Cotton, J.A. and Webster, J.P. 2016. Reduced efficacy of praziquantel against *Schistosoma mansoni* is associated with multiple-rounds of mass drug administration. *Clinical Infectious Diseases: ciw506*.
- Mondelaers, A., Sanchez-Cañete, M. P., Hendrickx, S., Eberhardt, E., Garcia-Hernandez, R., Lachaud, L., Cotton, J.A., Sanders, M., Cuypers, B., Imamura, H., Dujardin, J.-C. Delputte, P., Cos, P., Caljon, G., Gamarro, F., Castanys, S. and Maes, L. 2016. Genomic and molecular characterization of miltefosine resistance in *Leishmania infantum* strains with either natural or acquired resistance through experimental selection of intracellular amastigotes. *PLoS One* 11:e0154101.
- Imamura, H., Downing, T., Van den Broeck F. (29 additional authors) and *Cotton, J.A. 2016. Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. *eLife* 5:e12613.
- Crellen, T., Allan, F., Durrant, C., Huckvale, T., Holroyd, N., Emery, A.M., Rollinson, D., Aanensen, D.M., Berriman, M., Webster, J.P. and *Cotton, J.A. 2016. *Schistosoma mansoni* genomes reveal population history and effects of selection. *Scientific Reports*. 6:20954.
- Hunt, V.L. et al. (Cotton 8th out of 38 authors). 2016. The genomic basis of parasitism in the *Strongyloides* clade of nematodes. *Nat Genet* 48(3):299-307.
- Shaw, C.D., Lonchamp, J., Downing, T., Imamura, H., Freeman, T.M., Cotton, J.A., Sanders, M., Blackburn, G., Dujardin, J.-C., Rijal, S., Khanal, B., Illingworth, C.J.R., Coombs, G.H. and Carter, K.C. 2016. In vitro selection of miltefosine resistance in promastigotes of *Leishmania donovani* from Nepal: genomic and metabolomics characterization. *Mol Microbiol*. 99(6):1134-1148.
- Laing, R., Martinelli, A., Tracey, A., Holroyd, N.E., Gilleard, J.G. and Cotton, J.A. 2016. *Haemonchus contortus*: genome structure, organization and comparative genomics. *Adv Parasitol* 93:569-598.
- Kuo, H.-C., Chen, S.F., Fang, Y.P., Cotton, J.A., Parker, J.D., Csorba, G., Lim, B.K., Eger, J.L., Chen, C.-H., Chou, C.-H. and Rossiter, S.J. 2015. Speciation processes in putative island endemic sister bat species: false impressions from mitochondrial DNA and microsatellite data. *Mol Ecol* 24:5910-1926.
- Lamberton, P.H.L., Crellen, T., Cotton J.A. and Webster, J.P. 2015. Modelling the effects of mass drug administration on the molecular epidemiology of schistosomes. *Adv Parasitol* 87:293-327.
- Dujardin, J.-C., Mannaert, A., Durrant, C., Cotton J.A. 2014. Mosaic aneuploidy in *Leishmania*: The perspective of whole genome sequencing. *Trends Parasitol*. 30:554-555.
- Foth B.J., Tsai I.J., Reid A.J., Bancroft A.J., Nichol S., Tracey A., Holroyd N., Cotton J.A., Stanley E.J., Zarowiecki M., Liu J.Z., Huckvale T., Cooper P.J., Grencis R.K., Berriman M. 2014. Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. *Nat Genet* 46: 693-700.
- International Glossina Genome Initiative. 2014. Genome sequence of the tsetse fly (*Glossina morsitans*): vector of African trypanosomiasis. *Science* 344:380-386.
- *Cotton, J.A., Lilley, C.J., Jones, L.M., Kikuchi, T., Reid, A.J., Thorpe, P., Tsai, I.J., Beasley, H., Blok, V., Cock, P.J., Eves-van der Akker, S., Holroyd, N., Hunt, M., Mantelin, S., Naghra, H., Pain, A., Palomares-Ruis, J.E., Zarowiecki, M., Berriman, M., Jones, J.T. and Urwin, P.E. 2014. The genome and life-stage specific transcriptomes of *Globodera pallida* elucidate key aspects of plant parasitism by a cyst nematode. *Genome Biology* 15:R43.
- Rogers, M.B., T. Downing, B.A. Smith, H. Imamura, M. Sanders, M. Svobodova, P. Volf, M. Berriman, J.A. Cotton* and D.F. Smith. 2014. Genomic confirmation of hybridization and recent inbreeding in a vector-isolated *Leishmania* population. *PLoS Genetics* 10:e1004092.
- Eberhard, M.L., E. Ruiz-Tiben, D.R. Hopkins, C. Farrell, F. Toe, A. Weiss, P.C. Withers Jr., M.H. Jenks, E.A. Thiele, J.A. Cotton, Z. Hance, N. Holroyd, M.A. Tahir and T. Mounda. 2014. The peculiar epidemiology of Dracunculiasis in Chad. *Am. J. Trop. Med. Hygiene* 90:61-70.

- Tsagkogeorga, G., J. Parker, E. Stupka, **J.A. Cotton** and S.J. Rossiter. 2013. Phylogenomic analyses elucidate the evolutionary relationships of bats. *Curr. Biol.* 23:2262-2267.
- Parker, J., G. Tsagkogeorga, **J.A. Cotton**, Y. Liu, P. Provero, E. Stupka and S.J. Rossiter. 2013. Genome-wide signatures of convergent evolution in echolocating mammals. *Nature* 502:228-231.
- Laing, R., T. Kikuchi, A. Martinelli, I.J. Tsai, R.N. Beech, E. Redman, N. Holroyd, D.J. Bartley, H. Beasley, C. Britton, D. Curran, E. Devaney, A. Gilabert, M. Hunt, F. Jackson, S.L. Johnston, I. Kryukov, K. Li, A.A. Morrison, A.J. Reid, N. Sargison, G.I. Saunders, J.D. Wasmuth, A. Wolstenholme, M. Berriman, J.S. Gilleard and **J.A. Cotton***. 2013. The genome and transcriptome of *Haemonchus contortus*, a key model parasite for drug and vaccine discovery. *Genome Biology* 14:R88.
- Davies, Kalina T.J., Paul J.J. Bates, Ibnu Martanto, **James A. Cotton** and Stephen J. Rossiter. 2013. The evolution of bat vestibular systems in the face of potential antagonistic selection pressures for flight and echolocation. *PLoS One* 8(4):e61998.
- Saunders, G.I., J.D. Wasmuth, R. Beech, R. Laing, M. Hunt, H. Naghra, **J.A. Cotton**, M. Berriman, C. Britton and J.S. Gilleard. 2013. Characterization and comparative analysis of the complete *Haemonchus contortus* β -tubulin gene family and implications for benzimidazole resistance in strongylid nematodes. *Int. J. Parasitol.* 43(6):465-475.
- Svinti, V., **J.A. Cotton** and J.O. McInerney. 2013. New approaches for unraveling reassortment pathways. *BMC Evolutionary Biology* 13(1):1.
- San Mauro, D., D.J. Gower, **J.A. Cotton**, R. Zardoya, M. Wilkinson and T. Massingham. 2012. Experimental design in phylogenetics: Testing predictions from expected information. *Systematic Biology* 61(4):661-674.
- Reid, Adam J., S. J. Vermont, **J.A. Cotton**, D. Harris, G.A. Hill-Cawthorne, S. Könen-Waisman, S.M. Latham, T. Mourier, R. Norton, M.A. Quail, M. Sanders, D. Shanmugam, A. Sohal, J.D. Wasmuth, B. Brunk, M.E. Grigg, J.C. Howard, J. Parkinson, D.S. Roos, A.J. Trees, M. Berriman, A. Pain and J.M. Wastling. 2012. Comparative genomics of the apicomplexan parasites *Toxoplasma gondii* and *Neospora caninum*: Coccidia differing in host range and transmission strategy. *PLoS Pathogens* 8(3):e1002567.
- Davies, Kalina T. J., **James A. Cotton**, John D. Kirwan, Emma C. Teeling and Stephen J. Rossiter. 2012. Parallel signatures of sequence evolution among hearing genes in echolocating mammals: an emerging model of genetic convergence. *Heredity* 108:480-489.
- Downing, Tim, Hideo Imamura, Saskia Decuyper, Taane G. Clark, Graham H. Coombs, **James A. Cotton**, James D. Hilley, Simonne de Doncker, Ilse Maes, Jeremy Mottran, Michael A. Quail, Suman Rijal, Gabriele Schöniar, Olivia Stark, Shyam Sundar, Manu Vanaerschot, Christiane Hertz-Fowler, Jean-Claude Dujardin and Matthew Berriman. 2011. Whole genome sequencing of multiple Leishmania donovani clinical isolates provides insights into the evolution and mechanisms of drug resistance. *Genome Research* 21:2143-2156.
- Kikuchi, T., **James A. Cotton**, Jonathan J. Dalzell, Koichi Hasegawa, Natsumi Kanzaki, Paul McVeigh, Takuma Takanashi, Isheng J. Tsai, Samuel A. Assefa, Peter J.A. Cock, Thomas Dan Otto, Martin Hunt, Adam J. Reid, Alejandro Sanchez-Flores, Kazuko Tsuchihara, Toshiro Yokoi, Mattias C Larsson, Johji Miwa, Aaron G Maule, Norio Sahashi, John T. Jones and Matthew Berriman. 2011. Genomic insights into the origin of parasitism in the emerging plant pathogen Bursaphelenchus xylophilus. *PLoS Pathogens* 7(9):e1002219.
- Johnson, Louise J., **James A. Cotton**, Conrad P. Lichtenstein, Greg S. Elgar, Richard A. Nichols, P. David Polly and Steven C. LeComber. 2011. Stops making sense: Translational trade-offs and stop codon reassignment. *BMC Evolutionary Biology* 11:227.
- Loader, Simon P., Mark Wilkinson, **J.A. Cotton**, G. John Measey, Michele Menegon, Kim M. Howell, Hendrik Muller and David J. Gower. 2011. Molecular phylogenetics of *Boulengerula* (Amphibia:Gymnophiona:Caeciliidae) and implications for taxonomy, biogeography and conservation. *Herpetological Journal* 21:5-16
- Cotton, J.A.*** and James O. McInerney. 2010. Eukaryotic genes of archaeobacterial origin are more important than the more numerous eubacterial genes, irrespective of function. *Proceedings of the National Academy of Sciences, USA* 37:13959-13964.
- Yang Liu, Stephen J. Rossiter, Xiuqun Han, **J.A. Cotton** and Shuyi Zhang. 2010. Cetaceans on a molecular fast track to ultrasonic hearing. *Current Biology* 20:1834-1839.
- Yang Liu, **J.A. Cotton***, Bin Shen, Xiuqun Han, Stephen J. Rossiter and Shuyi Zhang. 2010. Convergent sequence evolution between echolocating bats and dolphins. *Current Biology* 20:R53-R54.
- San Mauro, D., Gower, D., Massingham, T., Wilkinson, M., Zardoya, R. and **J.A. Cotton***. 2009. Experimental design in Caecilian systematics: phylogenetic information of mitochondrial genomes and nuclear rag1. *Systematic Biology* 58(4):425-438.
- Zhao, H., Rossiter, S.J., Teeling E.C., Li, C., **Cotton, J.A.** and S. Zhang. 2009. The evolution of color vision in nocturnal mammals. *Proceedings of the National Academy of Sciences of the USA* 106:8980-8985.
- Gold, K., **Cotton, J.A.** and A. Stollewerk. 2009. The role of Notch signalling and numb function in mechanosensory organ formation in the spider *Cupiennis salei*. *Developmental Biology* 327:121-131.
- Cotton, J.A.*** and M. Wilkinson. 2009. Supertrees enter the mainstream of phylogenetics. *Trends in Ecology and Evolution* 24:1-3.
- McCann, A., **Cotton, J.A.** and J.O. McInerney. 2008. The Tree of Genomes: An Empirical Comparison of Genome Phylogeny Reconstruction Methods. *BMC Evolutionary Biology* 8:312.
- Li, G., Wang, J., Rossiter, S.J., Jones, G., **Cotton, J.A.** and S. Zhang. 2008. The hearing gene Prestin reunites echolocating bats. *Proceedings of the National Academy of Sciences of the USA* 37:13959-13964.
- McInerney, J.O., **J.A. Cotton** and D. Pisani. 2008. The Tree of Life: Past, present...and future? *Trends in Ecology and Evolution* 23:276-281.

- Peterson, K.J., **J.A. Cotton**, J.G. Gehling and D. Pisani. 2008. The Ediacaran emergence of bilaterians: congruence between the genetic and geologic fossil records. *Philosophical Transactions of the Royal Society Series B* 363:1435-1443.
- Day, J.J., **J.A. Cotton** and T.G. Barraclough. 2008. Tempo and mode of diversification in Lake Tanganyika cichlid fishes. *PLoS One* 3:e1730.
- Cotton, J.A.*** and M. Wilkinson. 2008. Quantifying the potential utility of phylogenetic characters. *Taxon* 57:131-136.
- Loader, S.P., D. Pisani, **J.A. Cotton**, D.J. Gower, J.J. Day and M. Wilkinson. 2007. Relative timescales reveal multiple origins of parallel disjunct distributions of African caecilian amphibians. *Biology Letters* 3:505-508.
- Pisani, D., **J.A. Cotton** and J.O. McInerney. 2007. Supertrees disentangle the chimeric origin of eukaryotic genomes. *Molecular Biology and Evolution* 24:1752-1760.
- Cotton, J.A.*** and M. Wilkinson. 2007. Majority-rule supertrees. *Systematic Biology* 56:445-452.
- Wilkinson, M., **J.A. Cotton**, F.-J. Lapointe and D. Pisani. 2007. Properties of supertree methods in the consensus setting. *Systematic Biology* 56:330-337.
- Cotton, J.A.*** and R.D.M. Page. 2006. The shape of human gene family phylogenies. *BMC Evolutionary Biology* 6:66. [4.45]
- Cotton, J.A.***, C.S.C. Slater and M. Wilkinson. 2006. Discriminating supported and unsupported relationships in supertrees using triplets. *Systematic Biology* 55:345-350
- Pfister, K., P.R. Shah, H. Hummerich, A. Russ, **J.A. Cotton**, A.A. Annuar, S.M. King and E.M.C. Fisher. 2006. Genetic analysis of the cytoplasmic dynein subunit families. *PLoS Genetics* 2:1.
- Wilkinson, M., D. Pisani, **J.A. Cotton**, and I. Corfe. 2005. Measuring support and finding unsupported relationships in supertrees. *Systematic Biology* 54:419-431.
- Wilkinson, M., **J.A. Cotton**, C. Creevey, O. Eulenstein, S.R. Harris, F.-J. Lapointe, C. Levasseur, J.O. McInerney, D. Pisani and J.L. Thorley. 2005. The shape of supertrees to come: tree-shape related properties of fourteen supertree methods. *Systematic Biology* 54:419-431.
- Cotton, J.A.*** and R.D.M. Page. 2005. Rates and patterns of gene duplication and loss in the human genome. *Proceedings of the Royal Society of London, Series B* 272:277-285.
- Cotton, J.A.** 2004. Analytical methods for detecting paralogy in molecular datasets. *Methods in Enzymology* 395:700-724
- Wilkinson, M., **J.A. Cotton** and J.L. Thorley. 2004. The information content of trees and their matrix representations. *Systematic Biology* 53:989-1001.
- Cotton, J.A.*** and R.D.M. Page. 2003. Gene tree parsimony vs. uninode coding for phylogenetic reconstruction. *Molecular Phylogenetics and Evolution* 29:298-308.
- Cotton, J.A.*** and R.D.M. Page. 2002. Going nuclear: vertebrate phylogeny and gene family evolution reconciled. *Proceedings of the Royal Society of London, Series B* 269:1555-1561.
- J.A. Cotton.** 2001. An unusual genetic system allows recombination to be recognized in an animal mitochondrial genome. *Genome Biology* 2(10):reports0034.
- J.A. Cotton.** 2001. Techniques commonly applied to the discovery of unknown prokaryotes have been used to identify new eukaryotic lineages within picoplankton. *Genome Biology* 2(7):reports0016.
- J.A. Cotton.** 2001. Invertebrate retroelements have borrowed diverse viral envelopes for infection. *Genome Biology* 2(2):reports0006.
- J.A. Cotton.** 2000. A new division of the Archaea could be the most ancient living lineage. *Genome Biology* 1(6):reports0076.
- J.A. Cotton.** 2000. Genome structure confirms the chastity of some ancient asexuals. *Genome Biology* 1(3):reports0068.
- J.A. Cotton.** 2000. DNA libraries from uncultured microbes reveal insights into the functional and genomic diversity of soil bacteria. *Genome Biology* 1(2):reports0060.

Chapters in Books

- Schönian, G., Lukeš, J., Stark, O. and **Cotton, J.A.** 2018. Molecular Evolution and Phylogeny of *Leishmania*. In Drug Resistance in *Leishmania* Parasites (Ponte-Sucre, A. and Padrón-Nieves, eds). Springer.
- J.A. Cotton.** 2016. From sequence reads to evolutionary inferences. In Next Generation Systematics. (Olson, P.D., Hughes, J. and J.A. Cotton, eds). Cambridge University Press.
- J.A. Cotton.** 2008 The impact of gene duplication on human genome evolution. In Encyclopedia of Life Sciences (ELS). John Wiley & Sons, Ltd. Chichester.
- Wilkinson, M. and **J.A. Cotton.** 2006. Supertree methods for building the tree of life: divide-and-conquer approaches to large phylogenetic problems, in Towards the tree of life: taxonomy and systematics of large and species-rich taxa (Hodkinson, T., J. Parnell and S. Waldron, eds.). CRC Press.
- Cotton, J.A.** and R.D.M. Page. 2004. Tangled tales from multiple markers: reconciling conflict between phylogenies to build molecular supertrees, in Phylogenetic supertrees: combining information to reveal the tree of life (Bininda-Emonds, O.R.P., ed.) Kluwer Academic, Dordrecht, The Netherlands.
- Page, R.D.M. and **J.A. Cotton.** 2000. GeneTree: A tool for exploring gene family evolution, in Comparative genomics: empirical and analytical approaches to gene order dynamics, map alignment and the evolution of gene families (Sankoff, D. and J.H. Nadeau, eds). Kluwer Academic Press, Dordrecht, The Netherlands.

Edited book

- Olson, P.D., Hughes, J. and **J.A. Cotton** (eds). 2016. Next Generation Systematics. Cambridge University Press.

Peer-reviewed Conference Contributions

Page, R.D.M. and J.A. Cotton. 2001. Vertebrate phylogenomics: reconciled trees and gene duplications, *in* Proceedings of the pacific symposium on biocomputing 2002 (Altman, R.B., A.K. Dunker, L. Hunter, K. Lauderdale and T.E. Klein, eds). World Scientific Press, Singapore.

Representative Presentations (* = invited speaker)

- *Department of Parasitology, Charles University Prague (remotely). April 2020. Genomic approaches to anthelmintic drug resistance.
- *University of Glasgow, UK. May 2019. IBAHCM seminar. Population genomics of Guinea worm eradication.
- *Molecular Helminthology: An integrated approach, San Antonio, TX. April 2019. Genomic approaches to anthelmintic drug resistance.
- *Amhara Public Health Institute leishmaniasis symposium. Bahir Dar, Ethiopia. January 2019. Genomic insights into Leishmania population genomics.
- *ASTMH, New Orleans, October 2018: Population genomics of Guinea worm eradication.
- *ICOPA, Daegu, Korea, August 2018: Genomic approaches to anthelmintic resistance.
- *Royal Veterinary College. CEEED-Anwar guest lecture, July 2018: Genome-wide approaches to anthelmintic resistance.
- *London School of Hygiene and Tropical Medicine, Dept of Pathogen Molecular Biology seminar, June 2018: Genomic insights into the unusual genetics of *Leishmania*.
- British Society for Parasitology, Aberystwyth, April 2018: Population genomics of Guinea worm eradication.
- *University of Virginia School of Medicine, Division of infectious diseases, Sept 2017: Genomics of drug resistance in parasites: three roads to finding loci.
- *NIH global neglected infectious diseases lecture, Sept 2017: Genomics of drug resistance in parasites: three roads to finding loci.
- British Society for Parasitology, Dundee, April 2017: Population genomics of *Leishmania donovani*: from macroevolution to direct sequencing of clinical samples.
- London Center for Neglected Tropical Disease Research, Jan 2017: Population genomics of reduced efficacy of praziquantel against *Schistosoma mansoni*.
- *Wellcome Trust Center for Molecular Parasitology, Young Investigators' Symposium; August 2016. Invited speaker: Population genomics of *Leishmania* from local to global scales.
- British Society for Parasitology, London, April 2016: An assembly of the *Onchocerca volvulus* genome – a first look at filarial chromosomes
- British Society for Parasitology, Modelling 'speed dating', Lonon, April 2016: How can population genomics data for visceral leishmaniasis contribute to a quantitative understanding of epidemiology and control?
- *WAAVP, Liverpool, August 2015. Keynote speaker: Comparative genomics of 70 helminth genomes
- *CARS symposium, Liverpool, August 2015. Invited speaker: Helminth genomes: Filling in the gaps
- WorldLeish, Puerto Gallinha, Brazil, May 2013: Genomic confirmation of hybridisation and recent inbreeding in a vector-isolated *Leishmania* population
- British Society for Parasitology, Bristol, April 2013: Genomic confirmation of hybridisation and recent inbreeding in a vector-isolated *Leishmania* population
- 7th Biennial of the Systematics Association, Queens University, Belfast, July 2011: Convergent evolution at the sequence level: some batty and malarial examples
- 5th Biennial of the Systematics Association, Royal Botanic Gardens, Edinburgh, August 2007: Quantifying the potential utility of phylogenetic characters
- Society for Molecular Biology and Evolution, Tempe, AZ, June 2006: Understanding and evaluating the performance of supertree methods
- Virtual Institute of Bioinformatics Éire, Dublin, Ireland, April 2006: Will we ever have enough data to build the tree of life?
- Society for Molecular Biology and Evolution, Auckland NZ, June 2005: Inferring trees from trees: investigating properties of supertree methods
- Invited, Bioinformatics seminar series, Trinity College, Dublin, Nov 2004: Models of gene duplication and loss: two links between pattern and process
- 4th Biennial of the Systematics Association, Trinity College, Dublin, August 2003: The shape of human gene family phylogenies
- Evolution 2002, University of Illinois, Urbana-Champaign, IL, 28 June-2nd July 2002: A molecular timescale for vertebrate gene family evolution
- Pacific Symposium on Biocomputing, Hawai'i, 3rd-7th January 2002: Vertebrate Phylogenomics: Reconciled Trees and Gene Duplications
- 3rd Young Systematists Forum, Natural History Museum, December 2001: The evolutionary dynamics of gene families: phylogenetic methods reveal the birth and death of gene lineages
- Evolution 2001 University of Tennessee, Knoxville, TN, 26-30th June 2001: Nuclear gene duplications support a traditional view of vertebrate phylogeny

2nd Young Systematists Forum, Natural History Museum, November 2000: A phylogenetic approach to studying gene duplications, and what it tells us about vertebrate phylogeny
DCAF, Hotel Le Chantecler, St Adele, Quebec, 22-25th September 2000: GeneTree: A tool for exploring gene family evolution