

CURRICULUM VITAE

Cymon J. Cox

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Date of birth: 26th May 1966

Nationality: British

Educational History

October, 1994 - September, 1998. **Ph.D.** University of Reading, Whiteknights, Reading, UK. Phylogenetic relationships of the Eubryalean mosses (Bryineae, Musci). Advised by Dr. T. A. Hedderson.

September, 1992 - June, 1994. **BSc. (Hons.) Botany (Upper Second Class).** University College North Wales, Bangor, Gwynedd, North Wales, UK. The Taxonomy of *Polypodium* L. as evidenced by R.A.P.D.S. Advised by Dr. A. J. E. Smith and Dr. A. Shirsat.

Professional Employment

June, 2013 - present. **Coordinating Researcher (FCT Investigador)**

Group Leader of the Plant Systematics and Bioinformatics Research Group, Centro de Ciencias do Mar, Universidade do Algarve, Faro, Portugal.

June, 2008 - June, 2013. **Auxiliary Investigador (Research Fellow, Ciencia 2007)**

Group Leader of the Plant Systematics and Bioinformatics Research Group, Centro de Ciencias do Mar, Universidade do Algarve, Faro, Portugal.

June, 2005 - June, 2008. **Post Doctoral Research Fellow**

Natural History Museum, London, U.K. Investigating deep phylogeny using better methods. PI Dr. P. Foster (NHM, London).

December, 2001 - May, 2005. **Research Associate**

Department of Biology, Duke University, Durham, NC, USA. Moss Diversity Project. PI's: Dr. A. J. Shaw (Duke University) and Dr. B. Goffinet (University of Connecticut).

December, 2003 - May, 2005. **Research Associate**

Department of Biology, Duke University, Durham, NC, USA. Assembling the Fungal Tree of Life (AFTOL). PI: Dr. F. Lutzoni (Duke University).

November, 1999 - November, 2001. **Mellon Research Fellow**

Department of Biology, Duke University, Durham, NC, USA. Molecular phylogenetics of the moss family Mniaceae.

January, 1999 - October, 1999. **Research Associate**

Natural History Museum, London, UK. Phylogenetic relationships among the pleurocarpous mosses. PI: Dr. A. Newton (NHM, London).

January, 1998 - December, 1998. **Research Assistant**

The Natural History Museum, London, UK. Population biology and phylogenetics of the fern genus *Asplenium* and related taxa. PI: Dr. J. Vogel (NHM, London).

Research Interests

As a phylogenetic systematist my primary research aim is the reconstruction of ancestral relationships among organisms using molecular and morphological character data. The resulting evolutionary trees allow us to trace the temporal trajectories of organismal traits and to identify key evolutionary developments: both of which enable us to reconstruct important aspects of the paleo-biosphere. This knowledge provides us with the context for the understanding of our place within the modern biosphere and to devised informed strategies to contend with future changes in our environment.

Since the '60s the application of molecular methods to evolutionary systematics - especially DNA and protein sequences analysis - has had a profound effect on our understanding of the relationships among organisms. Today we can trace the evolutionary lineages linking bacteria to whales and we realistically speak about knowing, at one extreme, the relationships among the major groups in the Tree of Life, and at the end of the spectrum, about relationships among individuals and populations within a single species. However, the pace at which molecular sequence data can now be gathered (whole bacteria genomes take but minutes to sequence) has out-stripped our ability to effectively analyse the data due to computational constraints and often the difficulty is in determining what data are most appropriate to answer a question rather than what data are available. Moreover, the enormous growth in the availability of genetic data, and the increasing ease in which new data are obtainable in an era where genomic sequencing is routine, has meant that systematists are becoming increasingly reliant on bioinformatic frameworks to manage and manipulate the large amounts of data they employ.

Modeling of the molecular evolutionary process is an integral part of organismal systematics and increasing computational power has enabled us to apply evermore complex models. In this regard, I am particularly interested in the modeling of different forms of substitution process heterogeneity in maximum likelihood and Bayesian analytical analyses. Although often ignored by phylogeneticists, process heterogeneity is present at all levels of the Tree of Life and its accommodation in our models is having an increasingly profound impact on phylogenetic systematics. Indeed, it is becoming increasingly apparent that some of our long-standing and strongly supported ideas about the evolution of major groups may be wrong because of the use of poorly-fitting models that result in biases. I have focused much of my research on two examples that fall into this category: 1) the three-domains hypothesis for the tree of life, which states that there are 3 major lineages of life, namely bacteria, archaea, and eukaryotes, and 2) that vascular land plants (e.g. ferns and seeds plants) are derived from non-vascular bryophytes (e.g. mosses and liverworts). While both of these hypotheses routinely appear in biology textbooks, the work myself and colleagues have been doing show that they are both most likely wrong. Our analyses suggest that eukaryotes are derived from archaea and that therefore there are only 2 domains of Life (the so-called eocyte hypothesis), and that the vascular plants and bryophytes are both derived from the same ancestor and neither is the direct ancestor of the other.

Besides these over-arching themes of my research programme, I have worked on many diverse taxa from *Candida* (the fungus causing "thrush" infections) to *Sphagnum* peatmosses, the stuff used to mulch a garden, and used a wide variety of methods and disciplines from phylogenomics to population biology. In parallel with these research aims I also write and deploy software and manage a UNIX-based computational cluster that facilitates my research and that of my colleagues at CCMAR. The importance of bioinformatics skills as part of my research (as with many biologists today) cannot be overstated as it enables me to perform novel analyses that would otherwise be impossible.

Current research projects

- ***Determining the causes of inter-genomic conflict in the land plant phylogeny. Principal Investigator, FCT Portugal PTDC/BIA-EVF/1499/2014***

Recently published phylogenetic analyses have contradicted the long-established idea that vascular plants evolved from bryophyte ancestors - a conclusion that provides the theoretical foundation for the many comparative studies in plant evolution. Our re-analyses of the chloroplast data from the pivotal studies supporting the canonical early-evolving (paraphyletic) bryophytes hypothesis have shown the methodologies used in the original studies to be flawed and their conclusions due to inadequate modelling of substitutions in protein-coding genes. This result has important implications for all phylogenetic analyses of protein-coding genes but especially those at deep (ancient) phylogenetic levels. Our analyses concluded that, contrary to established theory, bryophytes are in fact monophyletic and the sister-group to tracheophytes (vascular plants), and therefore bryophytes are not the ancestors of tracheophytes but a more recently diverged group. However, almost simultaneously, two new studies (one in collaboration with our group) of nuclear and mitochondrial land plant data, respectively, were published that supported the established bryophytes-paraphyletic tree, although they differed in detail of which groups were the earliest-diverging. In this project we will determine the causes of the conflict among the current best phylogenies derived from each of the three genomes of land plants and their algal ancestors. While it is possible that each of the three genome phylogenies is correct and the conflict due evolutionary processes (e.g. lateral gene transfer), it is highly unlikely, and we hypothesise that the conflict is most likely the result of inadequate modeling (i.e. systematic error).

Past research projects

- *The conquest of land: a phylogenetic study of charophyte and land plant chloroplast evolution using data- and time-heterogeneous substitution models. Principal Investigator, FCT Portugal PTDC/BIA-EVF/113129/2009*
- *EXTANT: Extant or extinct tipping points as climate changes drive genetic diversity and dynamics of range edge populations as evolutionary hotspots. Collaborator, PI Ester Serrao funded by FCT Portugal EXCL/AAG-GLO/0661/2012*
- *Evolution of early eukaryotes. Collaborator*

Computing Expertise

The enormous growth in the availability of genetic data, and the increasing ease in which new data are obtainable, has meant that systematists are becoming increasingly reliant on bioinformatic frameworks to manage and manipulate the large amounts of data they employ. Moreover, the proliferation of phylogenetic software has necessitated that systematists are able to interpret the utility of new algorithms and software, as well as implement their own ideas in novel analyses. I am particularly interested in the development of new bioinformatic software for the manipulation and analysis of phylogenetic data.

- Proficiency in the use of Unix (Linux)/OSX operating systems. All my research and desktop computing has been performed using a Linux operating system since 1999.
- Installation and administration of computer clustering technologies. My laboratory purchased, installed, and maintains a 128 CPU cluster facility primarily to meet the group's computational needs, but also as a resource for other research groups at CCMAR. <http://gyra.ua1g.pt>
- Experience with relational (SQL) databasing (PostGres, MySQL) and web content management frameworks (Zope).
- Programming and application pipeline development using the Python programming language. I am a contributor to the Biopython project.
- Proficiency in the use of a wide range of phylogenetic software, e.g. P4, MrBayes, Paup*, Phylip, MacClade, Mesquite, Phylobayes, PAML, PhyML, RAxML, Beast, GARLI, Prottest, Modeltest, Muscle, ClustalW, Se-AL, Seaview, Seq-Gen, Tree-Puzzle, & Consel.

Research Grants

- 2016-2018. Principal Investigator. Foundation for Science and Technology, Ministry of Education and Science, Portugal. PTDC/BIA-EVF/1499/2014 - *Determining the causes of inter-genomic conflict in the land plant phylogeny.*
- 2014. Named researcher. Foundation for Science and Technology, Ministry of Education and Science, Portugal. EXPL/MAR-EST/1664/2013 - *Illuminating the metabolism of foundational and elusive microbial symbionts in benthic ecosystems: a cultivation-independent quest for Hahellaceae (Gammaproteobacteria, Oceanospirillales) genomes*
- 2010-2013. Principal Investigator. Foundation for Science and Technology, Ministry of Education and Science, Portugal. PTDC/BIA-EVF/113129/2009 - *The conquest of land: a phylogenetic study of charophyte and land plant chloroplast evolution using data and time-heterogeneous substitution models.*
- 2010-2013. Principal Investigator. Foundation for Science and Technology, Ministry of Education and Science, Portugal. PTDC/BIA-BCM/102395/2008 - *The origin and early diversification of plants: a phylogenomic approach employing novel composition-heterogeneous methods.*

- 2010-2013. Named researcher. Foundation for Science and Technology, Ministry of Education and Science, Portugal. PTDC/MAR/101431/2008 - *Unlocking the bacterial diversity encrypted in the metagenomes of marine sponges*
- 2003-2005. Named researcher. Assembling the Fungal Tree of Life (AFTOL), National Science Foundation, USA. Contributed the bioinformatics portion of the grant application.
- 2001-2005. Named researcher. Moss Diversity Project. National Science Foundation, USA. Contributed to all aspect of the writing of the application.
- 1999-2001. Mellon Research Fellow. Duke University, USA. Molecular phylogenetics of the moss family Mniaceae.

Other funding awards

- 2017. EMBO Practical Course: Tree building: advance concepts and practice of phylogenetic systematics, October 2018, Faro, Portugal
- 2016. EMBO Practical Course: Tree building: advance concepts and practice of phylogenetic systematics, 24-29 April 2017, Faro, Portugal
- 2016. EuroMarine Foresight Workshop: The application of genomics to fisheries management, 26-28th April 2017, Faro, Portugal
- 2013-2018. FCT Investigador Research Position, Coordinating Researcher
- 2008-2013. Ciencia 2007 Fellow Research Position, Auxiliary Researcher

Teaching Experience

- 2011. *MSc. Marine Genomics, University of the Algarve, Faro, Portugal.* Invited lecturer in phylogenetics and bioinformatics.
- 2010. *MSc. Marine Genomics, University of Aveiro, Aveiro, Portugal.* Invited lecturer on phylogenetics and bioinformatics.
- 2006. *MSc, Plant Taxonomy and Biodiversity, Royal Botanic Gardens, Edinburgh, UK.* Invited lecturer in maximum likelihood and Bayesian approaches to systematics.
- 2004. *Duke University, USA.* Invited speaker on Bayesian approaches to systematics on the graduate course in molecular systematics.
- 1999. *The Centre for Plant Diversity and Systematics, Reading University, UK.* Demonstrator and advisor on the Intensive Course in Molecular Systematics.
- 1994-1996. *Department of Botany, Reading University, UK.* Undergraduate tutoring and practical demonstrations to second and third year students.

Other Duties

- Coordinator of the **Advanced Technologies and Training** programme. The ATT programme is CC-MAR's institutional training programme for graduate students and paying participants. As part of the programme I organise an annual Marine Genomics Workshop that in 2016 was attended by 20 participants from 15 European and African countries. <http://att.ccmr.ualg.pt>
- Institutional liason for ELIXIR.pt and ELIXIR EXCELERATE projects.

Presentations

Invited Papers

- 2013. Relationships among the freshwater charophyte algae and land plants. *Society for Molecular Biology and Evolution, Annual Conference, Chicago, IL, USA, 7-11 July.*
- 2012. Genes versus proteins: conflict and consensus among land plant relationships. *3rd International Symposium on the Molecular Systematics of Bryophytes, The New York Botanical Garden, NY, USA, 20-22 June.*
- 2010. Investigating the archaeobacterial origin of Eukaryotes. *Annual Meeting of the Society for Molecular Biology and Evolution (SMBE 2010) - Lyon, France - 4-8 July.*
- 2009. Plenary: Phylogenetic analyses of the chloroplast proteomes of charophytes and the major land plant groups using methods to account for non-stationary composition heterogeneity. *International Association of Bryology - Cape Town, South Africa - 16-21 August.*
- 1999. Phylogeny of diplolepidous alternate mosses. *Green Plant Phylogeny Research Coordination Group Meeting, Xalapa, Veracruz, Mexico. 9-11 March.*
- 1999. Phylogenetic relationships among the diplolepidous-alternate mosses (Bryidae) inferred from nuclear and chloroplast DNA sequences. *Green Plant Phylogeny Research Coordination Group Meeting - St. Louis, Missouri: International Botanical Congress - 1-7 August.*

Professional affiliations

- Member of the Society for Molecular Biology and Evolution.
- Member of the Society of Systematic Biologists, and member of the editorial board of *Systematic Biology* (the journal of the Society of Systematic Biologists).

Publications

Peer-Reviewed Articles in Professional Journals and Books

1. Louro, B. G. De Moro, C.M. Garcia, C.J. Cox, A. Veríssimo, S.J. Sabatino, António, M. Santos, & A.V.M. Canario. 2018 A haplotype-resolved draft genome of the European sardine (*Sardina pilchardus*) *bioRxiv* 441774.
2. Fernández, I., J.M.O. Fernandes, V.P. Roberto, M. Kopp, C. Oliveira, M.F. Riesco, J. Dias, C.J. Cox, M.L. Cancela, E. Cabrita, & P. Gavaia. 2018. Circulating small non-coding RNAs provide new insights into vitamin K nutrition and reproductive physiology in teleost fish. *Biochimica et Biophysica Acta (BBA)-General Subjects* 1863: 39-51. doi:10.1016/j.bbagen.2018.09.017
3. Cox, C.J. 2018. Land plant molecular phylogenetics: a review with comments on evaluating incongruence among phylogenies. *Critical Reviews in Plant Sciences* 1-15. doi:10.1080/07352689.2018.1482443
4. Puttick, M.N., J.L. Morris, T.A. Williams, C.J. Cox, D. Edwards, P. Kenrick, S. Pressel, C.H. Wellman, H. Schneider, D. Pisani, & P.C.J. Donoghue. 2018 The interrelationships of land plants and the nature of the ancestral embryophyte *Current Biology* 28:733-745. doi:10.1016/j.cub.2018.01.063
5. Rosa, J., C.J. Cox, M.L. Cancela & V. Laizé. 2017. Identification of a fish short-chain dehydrogenase/reductase associated with bone metabolism. *Gene* 645: 137-145. doi:10.1016/j.gene.2017.12.021
6. Lu, L., C.J. Cox, S. Mathews, W. Wang, J. Wen, & Z. Chen. 2017. Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). *Cladistics* 34: 57-77. doi:10.1111/cla.12191
7. Califano, G., S. Castanho, F. Soares, L. Ribeiro, C.J. Cox, L. Mata, & R. Costa. 2017. Molecular taxonomic profiling of bacterial communities in a gilthead seabream (*Sparus aurata*) hatchery. *Frontiers in Microbiology* 8: 204. doi:10.3389/fmicb.2017.00204

8. **Shaw, A.J., N. Devos, Y. Liu, C.J. Cox, B. Goffinet, K.I. Flatberg, & B. Shaw. 2016** Organellar phylogenomics of an emerging model system: Sphagnum (peatmoss) *Annals of Botany* 118: 185-196. doi:10.1093/aob/mcw086
9. **Civáň, P., H. Craig, C.J. Cox, & T.A. Brown. 2016.** Multiple domestications of Asian rice. *Nature Plants* 2: 16037. doi:10.1038/nplants.2016.37
10. **Laenen, B., A. Machac, S.R. Gradstein, B. Shaw, J. Patiño, A. Désamoré, B. Goffinet, C.J. Cox, A.J. Shaw, & A. Vanderpoorten. 2016.** Increased diversification rates follow shifts to bisexuality in liverworts. *New Phytologist* 210: 1121-1129. doi:10.1111/nph.13835
11. **Martínez-Garrido, J., E.A. Serrão, A.H. Engelen, C.J. Cox, P. García-Murillo, & M. González-Wangüemert. 2016.** Multilocus genetic analyses provide insight into speciation and hybridization in aquatic grasses, genus *Ruppia*. *Biological Journal of the Linnean Society* 117(2): 177-191. doi:10.1111/bij.12666
12. **Marques, C.L., I. Fernández, M.N. Viegas, C.J. Cox, P. Martel, J. Rosa, M.L. Cancela, & V. Laizé. 2016.** Comparative analysis of zebrafish bone morphogenetic proteins 2, 4 and 16: molecular and evolutionary perspectives *Cellular and Molecular Life Sciences* 73(4): 841-857. doi:10.1007/s00018-015-2024-x
13. **Rathore, O.S., A. Faustino, P. Prudêncio, P. Van Damme, C.J. Cox, & R.G. Martinho. 2016** Absence of N-terminal acetyltransferase diversification during evolution of eukaryotic organisms *Scientific reports* 6: 21304. doi:10.1038/srep21304
14. **Civáň, P., J. Craig, C.J. Cox, & T.A. Brown. 2015.** Three geographically separate domestications of Asian rice. *Nature Plants* 1: 15164. doi:10.1038/nplants.2015.164
15. **Pearson, G.A., A. Lago-Leston, F. Cánovas, C.J. Cox, F. Verret, S. Lasternas, C.M. Duarte, S. Agusti, & E.A. Serrão. 2015.** Metatranscriptomes reveal functional variation in diatom communities from the Antarctic Peninsula *The ISME journal* 9: 2275-2289. doi:10.1038/ismej.2015.40
16. **Ramos, A.A., A. Weydmann, C.J. Cox, A.V.M. Canario, E.A. Serrão, & G.A. Pearson. 2015.** A transcriptome resource for the copepod *Calanus glacialis* across a range of culture temperatures. *Marine Genomics* 23: 27-29. doi:10.1016/j.margen.2015.03.014
17. **Hardoim, C.C.P., M. Cardinale, A.C.B. Cuccio, A.I.S. Esteves, G. Berg, J.R. Xavier, C.J. Cox, & R.S. Costa. 2014.** Effects of sample handling and cultivation bias on the specificity of bacterial communities in keratose marine sponges. *Frontiers in Microbiology* 5: 611. doi:10.3389/fmicb.2014.00611
18. **Laenen, B., B. Shaw, H. Schneider, B. Goffinet, E. Paradis, A. Désamoré, J. Heinrichs, J.C. Villarreal, S.R. Gradstein, S.F. McDaniel, D.G. Long, L.L. Forrest, M.L. Hollingsworth, B. Crandall-Stotler, E.C. Davis, J. Engel, M. Von Konrat, E.D. Cooper, J. Patiño, C.J. Cox, A. Vanderpoorten, & A.J. Shaw. 2014.** Extant diversity of bryophytes emerged from successive post-Mesozoic diversification bursts. *Nature Communications*, 5: 5134. doi:10.1038/ncomms6134
19. **Cox, C.J., B. Li, P.G. Foster, T.M. Embley, & P. Civáň. 2014.** Conflict among phylogenies of early land plants is caused by heterogeneous compositions among synonymous substitutions. *Systematic Biology*, 63(2): 272-279. doi:10.1093/sysbio/syt109
20. **Silva, I.A.L., C.J. Cox, R.B. Leite, M.L. Cancela, & N. Conceição. 2014.** Evolutionary conservation of TFIIF subunits: Implications for the use of zebrafish as a model to study TFIIF function and regulation *Comparative Biochemistry and Physiology Part B: Biochemistry and Molecular Biology*, 172: 9-20. doi:10.1016/j.cbpb.2014.03.007
21. **Liu, Y., C.J. Cox, W. Wang, & B. Goffinet. 2014.** Mitochondrial phylogenomics of early land plants: Mitigating the effects of saturation, compositional heterogeneity, and codon-usage bias *Systematic Biology*, 63: 862-878. doi:10.1093/sysbio/syu049
22. **Li, B. J.S. Lopes, P.G. Foster, T.M. Embley, & C.J. Cox. 2014.** Compositional biases among synonymous substitutions cause conflict between gene and protein trees for plastid origins. *Molecular Biology and Evolution*, 31(7): 1697-1709. doi:10.1093/molbev/msu105

23. **Civáň, P., P.G. Foster, M.T. Embley, A. Sèneca, C.J. Cox. 2014.** Analyses of charophyte chloroplast genomes help characterize the ancestral chloroplast genome of land plants. *Genome Biology and Evolution*, 6(4): 897-911. doi:10.1093/gbe/evu061
24. **Williams, T.A, P.G. Foster, C.J. Cox, & T.M. Embley. 2013.** An archaeal origin of eukaryotes suggests there are only two primary domains of life. *Nature*, 504: 231-236. doi:10.1038/nature12779
25. **Cox, C.J., & P.G. Foster. 2013.** A 20-state empirical amino-acid substitution model for green plant chloroplasts. *Molecular Phylogenetics and Evolution*, 68: 218-220. doi:10.1016/j.ympev.2013.03.030
26. **Hardoim, C.P.P, C.J. Cox, R.S. Peixoto, A.S. Rosado, R. Costa, & J.D. va Elsas. 2013.** Diversity of the candidate phylum Poribacteria in the marine sponge *Aplysina fulva*. *Brazilian Journal of Microbiology*, 44: 329-334. doi:10.1590/S1517-83822013000100048
27. **Williams, T.A, P.G. Foster, T.M.W. Nye, C.J. Cox, & T.M. Embley. 2012.** A congruent phylogenomic signal places eukaryotes within the Archaea. *Proceedings of the Royal Society B*, 279: 4870-4879. doi:10.1098/rspb.2012.1795
28. **Hardoim, C.P.P, A.I.S. Esteves, F.R. Pires, J.M.S. Gonçãlves, C.J. Cox, J.R. Xavier, & R. Costa. 2012.** Phylogenetically and spatially close marine sponges harbour divergent bacterial communities. *PLoS ONE*, 7(12): e53029. doi:10.1371/journal.pone.0053029
29. **Huttunen, S., N. Bell, V.K. Bobrova, V. Buchbender, W.R. Buck, C.J. Cox, B. Goffinet, L. Hedenäs, B.-C. Ho, M.S. Ignatov, O. Kuznetsova, I.A. Milyutina, A. Newton, S. Olsson, L. Pokorný, A.J. Shaw, M. Stech, A. Troitsky, A. Vanderpoorten, & D. Quandt. 2012.** Disentangling knots of rapid evolution: origin and diversification of the moss order Hypnales. *Journal of Bryology*, 34: 187-211. doi:10.1179/1743282012Y.0000000013
30. **Forrest, L.L., N. Wickett, C.J. Cox & B. Goffinet. 2011.** Deep sequencing of Ptilidium (Ptilidaceae) suggests evolutionary stasis in liverwort plastid genome structure. *Plant Ecology & Evolution*, 144: 1-15. doi:10.5091/plecevo.2011.535
31. **Cox, C.J., B. Goffinet, N.J. Wickett, S.B. Boles & A.J. Shaw. 2010.** Moss diversity: a molecular phylogenetic analysis of genera. *Phytotaxa*, 9: 175-195. doi:10.11646/phytotaxa.9.1.10
32. **Conceição, N., C.J. Cox, B. Simões, M. Viegas & M.L. Cancela. 2010.** Comparative promoter analysis and its application to the identification of candidate regulatory factors of cartilage-expressed genes. *The Journal of Applied Ichthyology*, 26: 245-250. doi:10.1111/j.1439-0426.2010.01415.x
33. **Shaw, A.J., C.J. Cox, W.R. Buck, N. Devos, A.M. Buchanan, L. Cave, R. Seppelt, B. Shaw, J. Larrain, R. Andrus, J. Greilhuber, & E. M. Tensch. 2010.** Newly resolved relationships in an early land plant lineage: Bryophyta class Sphagnopsida (peat mosses). *American Journal of Botany*, 97: 1511-1531. doi:10.3732/ajb.1000055
34. **Shaw, A.J., N., Devos, C.J. Cox, S.B. Boles, B. Shaw, A.M. Buchanan, L. Cave, & R. Seppelt. 2010.** Peatmoss (Sphagnum) diversification associated with Miocene Northern Hemisphere climatic cooling? *Molecular Phylogenetics and Evolution*, 55: 1139-1145. doi:10.1016/j.ympev.2010.01.020
35. **Foster, P.G., C.J. Cox, & T.M. Embley. 2009.** The primary divisions of Life: a phylogenomic approach employing composition-heterogeneous methods. *Philosophical Transactions of the Royal Society (B)*, 364: 2197-2207. doi:10.1098/rstb.2009.0034
36. **Cock, P.J.A., T. Antao, J.T. Chang, B.A. Chapman, C.J. Cox, A. Dalke, I. Friedberg, T. Hamelryck, F. Kauff, B. Wilczynski, and M.J.L. de Hoon. 2009.** Biopython: freely available Python tools for computational molecular biology and bioinformatics. *Bioinformatics*, 25: 1422-1423. doi:10.1093/bioinformatics/btp163
37. **Waeschenbach, A., C.J. Cox, D.T.J. Littlewood, J.S. Porter, P.D. Taylor. 2009.** First molecular estimate of cyclostome bryozoan phylogeny confirms extensive homoplasy among skeletal characters used in traditional taxonomy. *Molecular Phylogenetics and Evolution*, 52: 241-251. doi:10.1016/j.ympev.2009.02.002

38. Cox, C.J., P.G. Foster, R.P. Hirt, S.R. Harris, & M.T. Embley. 2008. The archaeobacterial origins of eukaryotes. *Proceeding of the National Academy of Sciences U.S.A.*, 105: 20356-20361. doi:10.1073/pnas.0810647105
39. Shaw, A.J., I. Holz, C.J. Cox, & B. Goffinet. 2008. Phylogeny, character evolution and biogeography of the Gondwanic moss family *Hypopterygiaceae*. *Systematic Botany*, 33: 21-30. doi:10.1600/036364408783887311
40. Kauff, F., C.J. Cox, & F. Lutzoni. 2007. WASABI: An automated sequence processing system for multi-gene phylogenies. *Systematic Biology*, 56(3): 523-531. doi:10.1080/10635150701395340
41. Goffinet, B., N.J. Wickett, O. Werner, R.M. Ros, C.J. Cox, & A.J. Shaw. 2007. Distribution and phylogenetic significance of the 71-kb inversion in the plastid genome in Funariidae (Bryophyta). *Annals of Botany*, 99: 747-753. doi:10.1093/aob/mcm010
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