

Curriculum Vitae of Ahmed Moustafa

Post-Doctoral Research Fellow, Microbial & Environmental Genomics, J. Craig Venter Institute

Education

- PhD, Computational Genetics, University of Iowa (2005 – 2009)
 - Thesis: Evolutionary and functional genomics of photosynthetic eukaryotes
- BS, Computer Science, Alexandria University (1993 – 1998)
 - Thesis: Code mobility & intelligent software agents

Appointments

- **Post-Doctoral Research Fellow**, J. Craig Venter Institute (2010 – Present)
- **Post-Doctoral Research Associate**, Rutgers University (2009 – 2010)
- **Graduate Research Assistant**, University of Iowa (2005 – 2009)
- **Senior Software Engineer**, Kaiser Permanente (2000 – 2005)
- **Software Engineer**, Scientific Computation Center, Alexandria University (1998 – 2000)

Publications

- **Ahmed Moustafa**, Deana L. Erdner, David M. Kulis, Donald M. Anderson, Debashish Bhattacharya. Exceptionally rich gene repertoire in a toxic red tide dinoflagellate. *PLoS ONE*.
- Adrian Reyes-Prieto, Hwan Su Yoon, **Ahmed Moustafa**, Eun Chan Yang, Robert A. Andersen, Sung Min Boo, Takuro Nakayama, Ken-ichiro Ishida, Debashish Bhattacharya. Differential gene retention in plastids of common recent origin. *Molecular Biology and Evolution*.
- **Ahmed Moustafa**, Bánk Beszteri, Uwe G. Maier, Chris Bowler, Klaus Valentin, Debashish Bhattacharya. Genomic footprints of a cryptic plastid endosymbiosis in diatoms. *Science*. 2009 Jun 26;324(5935):1724-6.
 - Featured and reviewed in the same issue of *Science*
 - Evaluated and rated as “**Must Read**” by *Faculty of 1000* (Post-publication peer-review)
 - Ranked among the “**Top 10**” Evolutionary Biology articles by *Faculty of 1000*
 - Ranked among the “**Top 10**” Microbiology articles by *Faculty of 1000*
 - Cited 12 times
- **Ahmed Moustafa**, Jeannette E. Loram, Jeremiah D. Hackett, Donald M. Anderson, F. Gerald Plumley, Debashish Bhattacharya. Origin of saxitoxin biosynthetic genes in cyanobacteria. *PLoS ONE*. 2009 Jun 1;4(6):e5758.
- Mary E. Rumpho, Jared M. Worful, Jungho Lee, Krishna Kannan, Mary S. Tyler, Debashish Bhattacharya, **Ahmed Moustafa**, James R. Manhart. Horizontal gene transfer of the algal nuclear gene *psbO* to the photosynthetic sea slug *Elysia chlorotica*. *PNAS*. 2008 Nov 18;105(46):17867-71.
 - Featured on the cover
 - Ranked among the “**most-read**” articles during November and December 2008
 - Cited 11 times
- **Ahmed Moustafa**, CX Chan, Megan Danforth, David Zear, Hiba Ahmed, Nagnath Jadhav, Trevor Savage, Debashish Bhattacharya. A phylogenomic approach for studying plastid endosymbiosis. *Genome Informatics*. 21: 165-176 (2008) 165.

- Adrian Reyes-Prieto, **Ahmed Moustafa**, Debashish Bhattacharya. Multiple genes of apparent algal origin suggest ciliates may once have been photosynthetic. *Current Biology*. 2008 Jul 8;18(13):956-62.
 - Cited 22 times
- **Ahmed Moustafa**, Adrian Reyes-Prieto, Debashish Bhattacharya. Chlamydiae has contributed at least 55 genes to Plantae with predominantly plastid functions. *PLoS ONE*. 2008 May 21;3(5):e2205.
 - Cited 11 times
- William Lanier, **Ahmed Moustafa**, Debashish Bhattacharya, Josep Comeron. EST analysis of *Ostreococcus lucimarinus*, the most compact eukaryotic genome, shows an excess of introns in highly expressed genes. *PLoS ONE*. 2008 May 14;3(5):e2171.
- **Ahmed Moustafa**, Debashish Bhattacharya. PhyloSort: a user-friendly phylogenetic sorting tool and its application to estimating the cyanobacterial contribution to the nuclear genome of *Chlamydomonas*. *BMC Evolutionary Biology*. 2008 Jan 15;8:6.
 - Ranked as “**highly accessed**” publication
 - Cited 12 times
- Naomi Phillips, Calhoun Sam, **Ahmed Moustafa**, Debashish Bhattacharya, Edward Braun. Genomic insights into evolutionary relationships among heterokont lineages emphasizing the phaeophyceae. *Journal of Phycology*. 44 (1), 15.18 (2008)
- **Ahmed Moustafa**. JAligner: an open-source efficient implementation of the Smith-Waterman algorithm. *SourceForge*. (2003)
 - Cited about 60 times

Manuscripts in Progress

- **Ahmed Moustafa**, Adrian Reyes-Prieto, Alexandra Z. Worden, Debashish Bhattacharya. Genome reduction and its impact on endosymbiotic transferred genes.
- **Ahmed Moustafa**, Aurora M. Nedelcu, Debashish Bhattacharya. Estimating the contribution of photosynthetic microbes to the choanoflagellate *Monosiga brevicollis*.
- Adrian Reyes-Prieto, **Ahmed Moustafa**, Debashish Bhattacharya. Green algae contributed to the chromalveolate membrane transporter repertoire.

Teaching Experience

- **Teaching Fellow**, *Molecular Phylogenetics*, University of Iowa (Spring 2009)
- **Teaching Assistant**, *Statistics for Bioinformatics*, University of Iowa (Spring 2008)
- **Teaching Assistant**, *Bioinformatics*, University of Iowa (Fall 2006)
- **Teaching Assistant**, *Introduction to Programming*, Alexandria University (Fall 2000)

Awards

- Received a predoctoral fellowship in Genetics from the *National Institute of Health* (July 2008)
- Received a grant from the *Marine Genomics Europe* to talk at the Marine Environmental Genomics and Gene Expression workshop, Germany (May 2008)
- Received a grant from the *Woods Hole Center for Oceans and Human Health* to talk at the Fourth Symposium on Harmful Algae in the US (October 2007)
- Received a membership to the *American Association for the Advancement of Science/Science Program for Excellence in Science* (February 2007)

Memberships & Professional Activities

- Journal peer-reviewer, *PLoS ONE*
- Journal peer-reviewer, *BMC Genomics*
- Journal peer-reviewer, *BMC Evolutionary Biology*
- Journal peer-reviewer, *Molecular Biology and Evolution*
- Journal peer-reviewer, *Evolutionary Bioinformatics*
- Journal peer-reviewer, *Genomics Insights*
- Member, *International Society for Computational Biology*
- Member, *IEEE Computer Society*
- Member, *American Society for Microbiology*
- Member, *Bioinformatics Organization*

Computational Skills

- **Programming languages:** Java/J2EE, Perl, Tcl, C/C++, Ruby, Python
- **Web development:** HTML/XHTML/DHTML, CSS, JavaScript, AJAX, PHP
- **Development tools:** Eclipse, NetBeans, WebSphere, Emacs, Visual Studio
- **Database systems:** MySQL, PostgreSQL, DB2, Oracle
- **Operating systems:** Linux, Unix, Mac OS, Windows, Mainframe
- **Biological and statistical platforms:** BioPerl, BioRuby, BioSQL, R, MATLAB

Open-Source Activities

- Designed and developed the open source **JAligner**, an efficient and clean implementation of the Smith-Waterman algorithm, for biological local pairwise sequence alignment. JAligner has been incorporated into many academic, open-source, and commercial applications such as STRAP (structure-based sequence alignment), Argo (genome browser), BioWeka (biological data mining framework), SeqFEATURE (structure-based function prediction), and ApolloRNA (non-coding RNA identification). Additionally, JAligner has been used as a model to teach dynamic programming and sequence alignment in many universities across the world such as Institute of Informatics and Telematics (Italy), National Yang-Ming University (Taiwan), University of Blumenau (Brazil), University of Copenhagen (Denmark), University of Maryland (USA), University of Otago (New Zealand), University of Tokyo (Japan), and Virginia Tech (USA).
 - Cited more than 60 times in journal articles and book chapters
 - Downloaded more than 10,000 times with a monthly average of 150 downloads
 - Accepted by the National Institute of Standards and Technology as a representative implementation of the algorithm
 - Rated Top “25%” by JARS
- Designed and developed the open source **PhyloSort** to sort phylogenetic trees by searching for subtrees that contain a monophyletic group of interest defined by operational taxonomic units. PhyloSort has been incorporated into PhyloGena (phylogenomic pipeline).
 - Cited more than 10 times
 - Rated Top “25%” by JARS
- Participated in porting packages from ArsDigita Community System (ACS) to OpenACS.

Talks

- **Ahmed Moustafa**, Deana L. Erdner, David M. Kulis, Donald M. Anderson, Debashish Bhattacharya. Deep transcriptomics of tFebruaryoxic red tide dinoflagellate *Alexandrium tamarense*. Fifth Symposium on Harmful Algae in the US. Ocean Shores, Washington, USA (November 15, 2009)
- Debashish Bhattacharya, Adrian Reyes-Prieto, **Ahmed Moustafa**, Hwan Su Yoon, Robert A. Andersen, CX Chan, Jeferson Gross. The evolution of photosynthesis on the tree of life. *Plant Biology 2009.* Honolulu, Hawaii, USA (July 18, 2009)
- Naomi Phillips, Edward Braun, **Ahmed Moustafa**, Debashish Bhattacharya, Donald Kapraun, Samantha Calhoun, Teresa Coaxum. Comparative genomics of photosynthetic Heterokonts. *Plant Biology 2009.* Honolulu, Hawaii, USA (July 18, 2009)
- **Ahmed Moustafa**, Jeannette E. Loram, David M. Kulis, Jeremiah D. Hackett, Deana L. Erdner, Donald M. Anderson, F. Gerald Plumley, Debashish Bhattacharya. Harmful algal blooms: origin of the saxitoxin biosynthetic pathway and high throughput transcriptomics of a toxic dinoflagellate. *Annual retreat of the Genetics Program.* University of Iowa, Iowa City, Iowa, USA (November 10, 2008)
- Naomi Phillips, Edward Braun, **Ahmed Moustafa**, Debashish Bhattacharya. Phylogenomic investigations within Brown Algae. *Combined Meeting of the International Society of Protistologists and the International Society for Evolutionary Protistology.* Dalhousie University, Halifax, Canada (July 25, 2008)
- **Ahmed Moustafa**, Debashish Bhattacharya. Phylogenomics and insights into algal genome evolution. *Marine Environmental Genomics and Gene Expression Workshop.* Alfred Wegener Institute, Bremerhaven, Germany (June 6, 2008) (**Awarded a travel voucher**)
- Klaus Valentin, Bánk Beszteri, **Ahmed Moustafa**, Debashish Bhattacharya. Two primary and one secondary endosymbiosis and the origin of the diatoms. *56th British Phycological Society Annual Meeting.* Bristol, UK (January 3, 2008)
- Jeannette E. Loram, **Ahmed Moustafa**, Debashish Bhattacharya, Jeremiah D. Hackett, Shelly Brandsrud, Deana L. Erdner, Donald M. Anderson, F. Gerald Plumley. A genomic approach for identifying the saxitoxin synthesis genes. *Fourth Symposium on Harmful Algae in the US.* Woods Hole, Massachusetts, USA (October 30, 2007)
- **Ahmed Moustafa**, Debashish Bhattacharya. Computational tools to facilitate the understanding of genome evolution of microalgae and the formation of toxic red tides. *Fourth Symposium on Harmful Algae in the US.* Woods Hole, Massachusetts, USA (October 30, 2007) (**Awarded a travel voucher**)
- Debashish Bhattacharya, **Ahmed Moustafa**, Tetyana Nosenko, Adrian Reyes-Prieto. Using comparative genomic approaches to unravel the complex evolutionary history of chromalveolates. *German Botanical Society Annual Meeting.* Hamburg, Germany (September 2007)
- Naomi Phillips, Calhoun Sam, **Ahmed Moustafa**, Debashish Bhattacharya, Edward Braun. Genomic insights into evolutionary relationships among Heterokont lineages. *Botany & Plant Biology Joint Congress.* Chicago, Illinois, USA (July 7, 2007)
- **Ahmed Moustafa**, Nicholas Rorick, Akira Kinoshita, Margaret I. Malik, Brian C. Schutte. Computational approach to predict Interferon regulatory factor 6 (Irf6) targets. *Sixth annual Joint Bioinformatics Symposium.* Iowa State University, Ames, Iowa, USA (July 14, 2006)