

Monica C. Munoz-Torres, PhD

Phone: +1 (707) 723 4170 | Email: munoztmo@oregonstate.edu

Highly accomplished genomics scientist with extensive experience at the computer and at the bench. Exceptional ability to lead and carry research projects from inception, through execution, analysis, publication, and dissemination of resources. Experienced project manager, especially for bioinformatics software development and for genome curation efforts. Very successful in building and growing communities around common scientific interests.

PROFESSIONAL EXPERIENCE

2018 – present **Assistant Professor, Program Manager.** Oregon State University. Corvallis, OR, USA
2017 – 2018 **Project Manager, Staff Scientist.** Phoenix Bioinformatics. Fremont CA, USA
2013 – 2017 **Bioinformatics Scientist, Project Manager.** Lawrence Berkeley National Lab. Berkeley, CA, USA
2012 – 2012 **Postdoctoral Fellow - Computational Genomics.** Smithsonian Tropical Research Institute. Panama.
2009 – 2012 **Postdoctoral Fellow - Bioinformatics.** Dept of Biology, Georgetown University. Washington, DC, USA
2003 – 2008 **Graduate Research Assistant.** Clemson University Genomics Institute (CUGI). Clemson, SC. USA
2000 – 2001 **Agriculture Specialist.** The World Bank and Epcot Science Division, The Walt Disney World Company. Lake Buena Vista, FL. USA
1998 – 2002 **Research Assistant.** International Center for Tropical Agriculture (CIAT). Cali, Colombia.

EDUCATION

2009 **PhD. Genetics.** Clemson University. Clemson, SC. USA
1999 **BSc. Biology and Genetics.** Universidad del Valle, Cali, Colombia.

SERVICE, LEADERSHIP, MEMBERSHIPS

Ad Hoc Reviews

2011 – Present **Scientific Panel Reviewer.** United States National Science Foundation (NSF).
2018 – Present **Reviewer.** Scientific Reports (Nature Publishing Group)
2015 – Present **Reviewer.** BIOINFORMATICS (Oxford Journals).
2015 – Present **Reviewer.** Current Opinion in Insect Science (Elsevier).
2014 – Present **Reviewer.** DATABASE (Oxford Journals).
2011 – Present **Reviewer.** BMC Genomics. (BioMed Central).
2013 – 2017 **Scientific Panel Reviewer.** United States Department of Agriculture (USDA).
2010 – 2012 **Reviewer.** Nature Reader Panel. (Nature Publishing Group).

Leadership

2020 – Present **Director of Operations.** NIH/NCI Center for Cancer Data Harmonization (CCHD)
2019 – Present **Steering Committee.** Global Alliance for Genomics and Health (GA4GH)
2018 – Present **Organizing Committee.** International Plant and Animal Genome Conference (PAG)
2016 – 2017 **Chair.** International Society for Biocuration.
2015 – Present **Steering Committee.** Manakin Genomics. NSF-funded Research Coordination Network (RCN).
2017 – 2018 **Project Manager.** *Phylogenies* Development Team. Phoenix Bioinformatics.
2014 – 2017 **Project Manager.** *Apollo* Development Team. Lawrence Berkeley National Laboratory.
2013 – 2015 **Co-PI.** *Building non-model species genome curation communities.* Working Group at National Evolutionary Synthesis Center (NESCent).
2011 – 2019 **Steering Committee, Group Leader (Curation).** i5k - 5,000 Arthropod Genomes Sequencing Initiative.

Outreach, Education, Community Engagement

2020 – Present **Equity, Diversity, and Inclusion Committee.** Global Alliance for Genomics and Health
2019 – Present **Equity, Diversity, and Inclusion Committee.** International Society for Biouration
2017 – Present **Equity, Diversity, and Inclusion Committee.** International Society for Computational Biology
2016 – 2017 **Web development:** i5k - 5,000 Arthropod Genomes <http://i5k.github.io/> (GitHub Pages)
2014 – 2017 **Web development:** The Gene Ontology <http://geneontology.org/> (Drupal)
2014 – 2017 **Web development:** International Society for Biocuration <http://biocuration.org/> (Word Press)
2013 – 2017 **Web development:** Apollo Genome Annotation Editor <http://genomearchitect.org/> (Drupal, GitHub Pages)
2015 **Interactive Exhibit:** *Annotation Café* at the Arthropod Genomics Symposium. Manhattan, KS. USA.
2017, 2018 **Booth:** *Entomological Society of America* at Science Fair. San Francisco, CA. USA.
2016 **Booth:** *i5k - 5,000 Genomes* at XXV International Congress of Entomology. Orlando, FL. USA.
2016 **Booth:** *Gene Ontology Consortium* at Allied Genetics Conference. Orlando, FL. USA.
2010 – 2017 **Newsletter Editor.** International Society for Biocuration (ISB).

Professional Memberships

- 2016 – Present **Member.** Entomological Society of America (ESA)
- 2015 – Present **Member.** Open Bioinformatics Foundation (OBF)
- 2015 – Present **Organizer.** Bioinformatics Open Source Conference (BOSC)
- 2010 – Present **Member.** International Society for Biocuration (ISB).
- 2009 – Present **Member.** Clemson University Alumni Association.
- 2008 – Present **Member.** Society for the Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS).
- 2008 – Present **Member.** American Association for the Advancement of Science (AAAS).

TEACHING

2012 - 2018 **Instructor** - Introduction to Manual Annotation Using Apollo for Distributed, Collaborative Genome Curation Efforts

- Assembly, Annotation & Analysis Winter School. ETH Zurich, Ascona, Switzerland. 2018.
- Roadshow through six nodes of the Australia Bioinformatics Resource (EMBL-ABR). Australia. 2017
- Arthropod Bioinformatics Workshop. X Arthropod Genomics Symposium. South Bend, IN, USA. 2017
- Tulane University. New Orleans, LA. USA. 2017.
- Assembly, Annotation & Analysis Winter School. ETH Zurich, Ascona, Switzerland. 2017.
- Stowers Institute for Medical Research. Kansas City, MO. USA. 2016.
- University of Tennessee, Knoxville. Knoxville, TN. USA. 2015.
- 2nd Workshop Bioinformatics and Genomics for Undergraduates. Reed College. Portland, OR. USA. 2015.
- Center for Bioinformatics and Computational Biology (BIOS). Manizales, Caldas, Colombia. 2015.
- Manakin Genomics Research Coordination Network. Smithsonian – George Mason University School of Conservation. Front Royal, VA. 2015.
- *Heliconius* Meeting. Smithsonian Tropical Research Institute. Gamboa Research Station. Panama. 2015.
- Citrus Psyllid Meeting. Arthropod Genomics Center, Kansas State University, Manhattan, KS, USA. 2015.
- University of Exeter, Exeter, UK. 2014.
- University of Illinois, Urbana/Champaign, IL, USA. 2014.
- Introduction for the i5k Pilot project. 2014.
- Inaugural i5k Workshop. Kansas City, MO. USA. 2012.

2009 - 2019

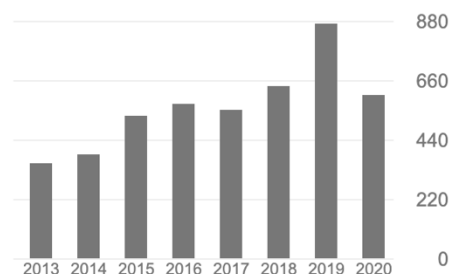
Instructor - various subjects

- Annotation Jamboree: functional curation. Plant and Animal Genome Conference. San Diego, CA, USA. 2018, 2019.
- Workshop on Bioinformatics Tools for Plant Genomics. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA. 2017.
- The Genome Train. IX Arthropod Genomes Symposium. Arthropod Genomics Center, Kansas State University, Manhattan, KS, USA. 2015.
- Data Visualization & Annotation. 8th International Biocuration Conference, Beijing, China. 2015.
- Next Generation Sequencing and Analysis. Hawkesbury Institute for the Environment. University of Western Sydney. Penrith, Sydney, Australia. 2015.
- Best Practices in Biocuration and Manual Annotation. Purdue University, West Lafayette, IN. USA. 2011.
- Next-gen sequencing: Data acquisition, comparative genomics, design and analysis for population genetics, systematics and development. National Evolutionary Synthesis Center (NESCent), Durham, NC. USA. 2011.
- Annotating your favorite gene family. Arthropod Genomics Center. Kansas State University. Manhattan, KS. USA. 2010
- Coral Genomics for the Non-Genomic Scientist. NOAA-NCRI. National Conservation Training Center. Shepherdstown, WV. USA. 2009

Cited by

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	All	Since 2015
Citations	5547	3784
h-index	29	26
i10-index	40	38



PUBLICATIONS

1. Michael E Sparks, Raman Bansal, Joshua B Benoit, Michael B Blackburn, Hsu Chao, Mengyao Chen, Sammy Cheng, [...] **M Munoz-Torres et al.** 2020. Brown marmorated stink bug, *Halyomorpha halys* (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. *BMC Genomics* 21(1) doi: 10.1186/s12864-020-6510-7
2. Thomas G W C, E Dohmen, D S T Hughes, S C Murali, M Poelchau, [...] **M Munoz-Torres et al.** 2020. Gene content evolution in the arthropods. *Genome Biol* 21(15) doi: 10.1186/s13059-019-1925-7
3. Oeyen J P, P Baa-Puyoulet, J B Benoit, L W Beukeboom, E Bornberg-Bauer, A Buttstedt, [...] **M Munoz-Torres et al.** 2020. Sawfly genomes reveal evolutionary acquisitions that fostered the mega-radiation of parasitoid and eusocial Hymenoptera. *Genome Biol Evol* 12(7):1099-1188. <https://doi.org/10.1093/gbe/evaa106>
4. De Vega J J, R P Davey, J Duitama, D Escobar, M A Cristancho-Ardila, G J Etherington, A Minotto, N E Arenas-Suarez, J D Pineda-Cardenas, J Correa-Alvarez, A V Camargo Rodriguez, W Haerty, J P Mallarino-Robayo, E Barreto-Hernandez, **M Muñoz-Torres**, N Fernandez-Fuentes, F Di Palma, Colombian Cyberinfrastructure Consortium for Biodiversity. 2020. Colombia's cyberinfrastructure for biodiversity: Building data infrastructure in emerging countries to foster socioeconomic growth. *Plants People Planet* <https://doi.org/10.1002/ppp3.10086>
5. Shefchek KA, N L Harris, M Gargano, N Matentzoglou, D Unni, [...] **M Munoz-Torres**, D Osumi-Sutherland. 2020. The Monarch Initiative in 2019: an integrative data and analytic platform connecting phenotypes to genotypes across species. *Nucl Acids Res* 48(Database issue): D704–D715. doi:10.1093/nar/gkz997
6. Gourdine JP F, M H Brush, N A Vasilevsky, K Shefchek, S Köhler, N Matentzoglou, **M C Munoz-Torres**, J A McMurry, X A Zhang, P N Robinson, M A Haendel. 2019. Representing glycophenotypes: semantic unification of glycobiology resources for disease discovery. *Database* <https://doi.org/10.1093/database/baz114>
7. Tang YA, K Pichler, A Füllgrabe, J Lomax, J Malone, **M C Munoz-Torres**, D V Vasant, E Williams, M Haendel. 2019. Ten quick tips for biocuration. *PLoS Comp Bio* <https://doi.org/10.1371/journal.pcbi.1006906>
8. Hosmani P, T Shippy, S Miller, J B Benoit, **M Munoz-Torres**, M Flores-Gonzalez, L A Mueller, H Wiersma-Koch, T D'Elia, S J Brown, S Saha. 2019. A quick guide for student-driven community genome annotation. *PLoS Comp Bio* <https://doi.org/10.1371/journal.pcbi.1006682>
9. Dunn N, D R Unni, C Diesh, **M Munoz-Torres et al.** 2019. Apollo: Democratizing genome annotation. *PLoS Comp Bio* doi.org/10.1371/journal.pcbi.1006790
10. Panfilio K A, I M Vargas Jentzsch, J B Benoit, D Erezylmaz; [...] **M Munoz-Torres et al.** 2019 Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. *Genome Biology*. 20:64 doi: 10.1186/s13059-019-1660-0.
11. Armisen D, R Rajakumar, M. Friedrich, J Benoit, H Robertson, [...] **M Munoz-Torres et al.** 2018. The genome of the water strider *Gerris buenoi* reveals expansions of gene repertoires associated with adaptations to life on the water. *BMC Genomics* doi:10.1186/s12864-018-5163-2.
12. Harper L, J Campbell, EKS Cannon, S Jung, M Poelchau, [...] **M Munoz-Torres et al.** 2018. AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. *Database*, Volume 2018, 1 January 2018, bay088, doi:10.1093/database/bay088.
13. Schoville SD, Y Chen, MN Anderson, JB Benoit, A Bhandari [...] **M Munoz-Torres et al.** 2018. A model species for agricultural pest genomics: the genome of the Colorado potato beetle *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae). *Scientific Reports. Article number 1938*. doi: 10.1038/s41598-018-20154-1.
14. Poynton HC, S Hasenbein, JB Benoit, MS Sepulveda, MF Poelchau, [...] **M Munoz-Torres et al.** 2018. The Toxicogenome of *Hyalomma azteca*: A Model for Sediment Ecotoxicology and Evolutionary Toxicology. *Environ. Sci. Technol* 52 (10), pp 6009–6022 doi:10.1021/acs.est.8b00837.
15. Adema C, L Hillier, C Jones, E Loker, M Knight, [...] **M Munoz-Torres et al.** 2017. Whole genome analysis of a schistosomiasis-transmitting freshwater snail. *Nat Commun.* 8:15451. doi: 10.1038/ncomms15451.
16. Saha, S, PS Hosmani, K Villalobos-Ayala, S Miller, T Shippy, A Rosendale, [...] **M Munoz-Torres**, D Nelson, MF Poelchau, JB Benoit, H Wiersma-Koch, T D'elia, SJ Brown. 2017. Improved annotation of the insect vector of Citrus greening disease: Biocuration by a diverse genomics community. *Database (Oxford)*, Volume 2017, bax032, doi:10.1093/database/bax032.
17. Putman, TE, S Lelong, S Burgstaller-Muehlbacher, A Waagmeester, C Diesh, N Dunn, **M Munoz-Torres**, GS Stupp, C Wu, AI Su, BM Good. 2017. WikiGenomes: an open web application for community consumption and curation of gene annotation data in Wikidata. *Database (Oxford)* 2017 (1): bax025 doi.org/10.1093/database/bax025
18. Papanicolaou, A, MF Schetelig, P Arensburger, PW Atkinson, JB Benoit, [...] **M Munoz-Torres et al.** 2017. The whole genome sequence of the Mediterranean fruit fly, *Ceratitis capitata* (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. *Genome Biol.* 18:11 DOI 10.1186/s13059-017-1155-9
19. **Munoz-Torres, MC**, SJ Carbon. 2016. "Get GO! Retrieving GO data using AmiGO, QuickGO, API, Files, and Tools." *In The Gene Ontology Handbook. Vol 1446 Methods in Molecular Biology* pp 149-160. Book Chapter. *Springer Humana* 1st ed.

20. Buels, R, E Yao, C Diesh, R Hayes, **M Munoz-Torres**, G Helt, D Goodstein, C Elsik, S Lewis, L Stein, I Holmes. 2016. JBrowse: a dynamic web platform for genome visualization and analysis. *Genome Biol.* 17: 66. doi: 10.1186/s13059-016-0924-1
21. Engel, P, W Kwong, Q McFrederick, KE Anderson, S Barribeau, [...] **M Munoz-Torres et al.** 2016. The bee microbiome: impact on bee health and model for evolution and ecology of host-microbe interactions. *mBio* vol. 7 no. 2 e02164-15. doi: 10.1128/mBio.02164-15.
22. Harris, NL, PJA Cock, H Lapp, B Chapman, R Davey, C Fields, K Hokamp, **M Munoz-Torres**. 2016. The 2015 Bioinformatics Open Source Conference (BOSC 2015). *PLoS Comput Bio.* 12(2):e1004691. doi: 10.1371/journal.pcbi.1004691.
23. Sadd, Ben M, SM Barribeau, G Bloch, DC de Graaf, P Dearden, CG Elsik, J Gadau, [...] **M Munoz-Torres et al.** 2015. The genomes of two key bumblebee species with primitive eusocial organisation. *Genome Biol* 16(1):76.
24. The Gene Ontology Consortium, **MC Munoz-Torres** (Corresponding Author). 2015. The Gene Ontology: Going Forward. *Nucl Acids Res* 43(Database issue):D1049-56. doi: 10.1093/nar/gku1179
25. Terrapon, N, C Li, HM Robertson, L Ji, X Meng, W Booth, Z Chen, [...] **M Munoz-Torres et al.** 2014. Molecular traces of alternative social organization in a termite genome. *Nat Commun.* 5:3636. doi: 10.1038/ncomms4636.
26. Elsik, CG, KC Worley, AK Bennett, M Beye, F Camara, CP Childers, DC de Graaf, [...] **MC Munoz-Torres, et al.** 2014. Finding the missing honey bee genes: lessons learned from a genome upgrade. *BMC Genomics* 15:86.
27. Lee, E, G Helt, J Reese, **MC Munoz-Torres**, C Childers, RM Buels, L Stein, IH Holmes, C Elsik, and SE Lewis. 2013. Web Apollo: A Web-based Genomic Annotation Editing Platform. *Genome Biol:* 14:R93.
28. **i5K Consortium***. 2013. The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture and the Environment. ***MC Munoz-Torres** is part of the i5K Consortium. *J of Heredity.* 104 (5): 595-600.
29. Gaudet, P, **M Munoz-Torres**, M Robinson-Rechavi, T Attwood, A Bateman, JM Cherry, R Kania, C O'Donovan, C Yamasaki. 2013. DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration. *Database (Oxford);* 2013: bat077
30. Gaudet, P, C Arighi, F Bastian, A Bateman, J Blake, JM Cherry, P D'Eustachio, R Finn, M Giglio, L Hirschman, R Kania, W Klimke, MJ Martin, I Karsch-Mizrachi, **MC Munoz-Torres**, D Natale et al. 2012. Recent advances in Biocuration: Meeting Report from the fifth International Biocuration Conference. *Database (Oxford):* bas036. doi:10.1093/database/bas036
31. Blair, MW, CH Galeano, E Tovar, **MC Munoz-Torres**, A Velasco Castrillon, SE Beebe, IM Rao. 2012. Development of a Mesoamerican intra-genepool genetic map for quantitative trait loci detection in a drought tolerant× susceptible common bean (*Phaseolus vulgaris* L.) cross. *Molecular Breeding* 29:71–88
32. **Munoz-Torres, MC**, JT Reese, CP Childers, AK Bennett, JP Sundaram, KL Childs, N Milshina, J Anzola, CG Elsik. 2011. Hymenoptera Genome Database: integrated community resources for species of insects of the order Hymenoptera. *Nucl Acids Res* 39(supl 1): doi:10.1093/gkq1145.
33. Blair, MW, N Hurtado, CM Chavarro, **MC Munoz-Torres**, MC Giraldo , F Pedraza , J Tomkins and R Wing. 2011. Gene-based SSR markers for common bean (*Phaseolus vulgaris* L.) derived from root and leaf tissue ESTs: an integration of the BMc series. *BMC Plant Biol* 11:50 doi: 10.1186/1471-2229-11-50.
34. Suen, G, C Teiling, L Li, C Holt, E Abouheif, E Bornberg-Bauer, P Bouffard, [...] **MC Muñoz-Torres et al.** 2011. The Genome Sequence of the Leaf-Cutter Ant *Atta cephalotes* Reveals Insights into Its Obligate Symbiotic Lifestyle. *PLoS Genet* 7(2): e1002007. doi:10.1371/journal.pgen.1002007.
35. Smith, CR, CD Smith, HM Robertson, M Helmkamp, A Zimin, M Yandell, C Holt, [...] **MC Munoz-Torres, et al.** 2011. Draft genome of the red harvester ant *Pogonomyrmex barbatus*. *PNAS* doi: 10.1073/pnas.1007901108.
36. Smith, CD, A Zimin, C Holt, E Abouheif, R Benton, E Cash, V Croset, CR Currie, E Elhaik, CG Elsik, [...] **MC Muñoz-Torres et al.** 2011. Draft genome of the globally widespread and invasive Argentine ant (*Linepithema humile*). *PNAS* doi: 10.1073/pnas.1008617108.
37. **Munoz-Torres, MC.** 2011. Comparative Genomics and Molecular Evolution: New Genomic Resources for the Hymenoptera and Evolutionary Studies on the Genes of the *Nasonia vitripennis* HOX Complex. *Proquest, Umi Dissertation Publishing.* ISBN: 1244008001, 9781244008007. 222pp.
38. Werren, JH, S Richards, CA Desjardins, O Niehuis, J Gadau, J Colbourne, and The Nasonia Genome Working Group*. 2010. Functional and Evolutionary Insights from the Genomes of Three Parasitoid Nasonia Species. * **M Muñoz Torres** is part of The Nasonia Genome Working Group. *Science* 327: 343-348.
39. Loehlin DW, DC Oliveira, R Edwards, JD Giebel, ME Clark, MV Cattani, L van de Zande, EC Verhulst, LW Beukeboom, **M Muñoz-Torres**, JH Werren. 2010. Non-coding changes cause sex-specific wing size differences between closely related species of Nasonia. *PLoS Genet* 6(1):e1000821.
40. **Munoz-Torres, M**, C Sasaki, B Blackmon, J Romero-Severson, JH Werren. 2010. Development of BAC library resources for parasitoid Hymenoptera (*Nasonia vitripennis* and *Nasonia giraulti*. Pteromalidae). *Insect Mol Biol* 19: Suppl 1,181-7.
41. **Munoz-Torres, MC**, J Reese, C Childers, A Bennett, J Sundaram, D Vile and C Elsik. 2010. The Hymenoptera Genome Database. Available from *Nature Precedings* at <http://dx.doi.org/10.1038/npre.2010.5182.1>

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43. Blair, MW, **M Muñoz Torres**, F Pedraza, MC Giraldo, HF Buendia, and N Hurtado. 2009 Development of microsatellite markers for common bean (*Phaseolus vulgaris* L.) based on screening of non-enriched small insert genomic libraries. *Genome* 52(9): 772-782.
44. Bonet, J, EL Girona, DJ Sargent, **MC Muñoz-Torres**, A Monfort, AG Abbott, P Arús, DW Simpson, J Davik. 2009. The development and characterisation of a bacterial artificial chromosome library for *Fragaria vesca*. *BMC Res Notes* 2:188 DOI:10.1186/1756-0500-2-188.
45. Blair, MW, **M Muñoz Torres**, MC Giraldo, F Pedraza. 2009. Development and diversity of Andean-derived, gene-based microsatellites for common bean (*Phaseolus vulgaris* L.) *BMC Plant Biol* 9:100 DOI:10.1186/1471-2229-9-100
46. **M Muñoz Torres***, Wilfert, L*, C Reber, R Schmid-Hempel, J Tomkins, J Gadau, P Schmid-Hempel, 2008. Construction and characterization of a BAC-library for a key pollinator, the bumblebee *Bombus terrestris* L. *These authors contributed equally to this work. *Insect Soc* DOI 10.1007/s00040-008-1034-1.
47. Schlueter, JA, JL Goicoechea, K Collura, N Gill, J Lin, Y Yu, D Kudrna, A Zuccolo, CE Vallejos, **M Muñoz-Torres**, MW Blair, J Tohme, J Tomkins, P McClean, RA Wing, SA Jackson. 2008. BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (*Phaseolus vulgaris* L.) *Genome. Trop Plant Biol* 1;1:40-48.
48. Dunning-Hotopp, JC, ME Clark, DCSG Oliveira, JM Foster, P Fischer, **MC Muñoz Torres**, JD Giebel, N Kumar, N Ishmael, S Wang, J Ingram, RV Nene, J Shepard, J Tomkins, S Richards, DJ Spiro, E Ghedin, BE Slatko, H Tettelin, JH Werren. 2007. Widespread Lateral Gene Transfer from Intracellular Bacteria to Multicellular Eukaryotes. *Science* 317 (5845):1753 – 1756. **Faculty of 1000 Article FFa10**
49. Blenda AV, I Verde, LL Georgi, GL Reighard, SD Forrest, **M Muñoz-Torres**, WV Baird, AG Abbott. 2007. Construction of a genetic linkage map and identification of molecular markers in peach rootstocks for response to peach tree short life syndrome. *Tree Genet Genomes* 3:341-350.
50. Islam FMA, S Beebe, **M Muñoz Torres**, J Tohme, RJ Redden and KE Basford. 2004. Using molecular markers to assess the effect of introgression on quantitative attributes of common bean in the Andean gene pool. *Theor Appl Genet* 108:243–252.
51. Hernandez G, M Ramírez, MW Blair, M Lara, L Blanco, **M Muñoz Torres**, S Barazesh, E Verdoorn, M Graham, CP Vance. 2004. Comparative analysis of common bean (*Phaseolus vulgaris* L.) nodule, root, pod and leaf expressed sequence tag (ESTs) libraries: a platform for "Phaseomics" research. *Proceedings of the 5th AEP- 2nd ICLGG Conference*, June 8-12, Dijon, France.
52. **Muñoz Torres, MC.** 2001. Integration of three genomic maps from advanced lines populations of common bean (*Phaseolus vulgaris* L.) belonging to the Andean and Mesoamerican collections of the International Center for Tropical Agriculture, using molecular markers. *Report on COLCIENCIAS Young Scientist Fellowship at CIAT.* 93p.
53. **Muñoz Torres, MC.** 1999. Molecular Characterization of Germplasm from cultivated accessions of common bean (*Phaseolus vulgaris* L.) from CIAT's core collection through Randomly Amplified Polymorphic DNA (RAPD) markers. *Thesis presented as requisite to obtain the degrees of BSc in Biology and Genetics.* 153 p.

SELECTION OF INVITED PRESENTATIONS

- **Workshop on Equity, Diversity and Inclusion: how can we do better as a scientific society?** Online Workshop for the members of the International Society for Biocuration. 2020.
- **The Monarch Initiative, Closing the knowledge gap with semantics-based tools.** Bioinformatics Open Source Conference (BOSC) at Intelligent Systems in Molecular Biology (ISMB). Basel, Switzerland. 2019.
- **Diverse Perspectives on Data Licensing.** Workshop at the International Biocuration Conference. Cambridge, UK. 2019.
- **Evaluating utility of patient-centered deep phenotyping.** Personal Genomes: accessing, sharing and interpretation. Wellcome Genome Campus, Hinxton, Cambridge, UK. 2019.
- **Annotation Jamboree: a hands-on workshop on genome curation.**
 - XXVII & XXVIII Plant and Animal Genome Conference, San Diego, CA, USA, 2019 and 2020
- **Keynote “Roadshow” – a series of talks and workshops for the nodes of the Australia Bioinformatics Resources of the European Molecular Biology Laboratory (EMBL-ABR).** Australia. 2017
Topics:
 - Primer on Genome Annotation.
 - The Importance of Open Science.
- **Genome Curation: Harnessing the Power of the Crowd.**
 - Departmental Seminar. Dept. Ecology and Evolutionary Biology, Tulane University, New Orleans, LA, USA. 2017
 - Environmental Genomics and System Biology Division Retreat. LBNL. Lafayette, CA. USA. 2016
 - Departmental Seminar. Stowers Institute for Medical Research. Kansas City, MO. USA. 2016
- **Keynote “This is Bioinformatics: Computer Wizardry for the Biological Sciences.”** Bioinformatics Bootcamp.

- Auburn University, Auburn, AL. 2016
- **Essential Requirements for Community Annotation Tools.** 9th International Biocuration Conference. Geneva, Switzerland. 2016
 - **Collaborative Genome Curation: Precision and Depth in the Annotation Process.** Seminar Series. Department of Entomology and Plant Pathology. University of Tennessee, Knoxville, TN. USA. 2015
 - **Genome Cartography – Annotation with Precision and Depth** (Original Title in Spanish: Cartografía de Genomas - anotación con precisión y profundidad). 3rd Colombian Congress for Computational Biology and Bioinformatics. Universidad de Antioquia. Medellín, Colombia. 2015
 - **Apollo: Web-based, Scalable, Collaborative, Interactive Genome Curation Platform**
 - Bioinformatics Open Source Conference (BOSC), Orlando, FL. USA. 2016, and Dublin, Ireland. 2015
 - Phenotype Research Coordination Network. Biosphere 2, Oracle, AZ. USA. 2016
 - XXIII & XXIV Plant and Animal Genome Conference, San Diego, CA, USA, 2016 and 2015
 - Smithsonian Tropical Research Institute, Naos Island Laboratories. Panama City, Panama. 2015
 - Smithsonian National Museum for Natural History. “Genomics Tools” seminar series. Washington, DC. USA. 2015
 - International Biocuration Conference, Beijing, China, 2015 and Cambridge, UK. 2013
 - Genome10K, Santa Cruz, CA, USA (Poster). 2015
 - Intelligent Systems in Molecular Biology (ISMB). Orlando, FL. USA 2016, and Dublin, Ireland, 2015
 - Genome Informatics Conference. Cambridge, UK. 2014
 - The Vertebrate Annotation Group (HAVANA). Wellcome Trust Sanger Institute. Hinxton, UK. 2014
 - GMOD Meeting. Cambridge, UK. 2013 and Washington, DC. USA. 2012
 - 7th Arthropod Genomics Symposium, Notre Dame, IN. USA. 2013
 - FlyBase Team Meeting, Harvard University. Cambridge, MA. USA. 2013
 - **The Gene Ontology – Outreach & User Advocacy.** Gene Ontology Consortium Meetings.
 - Oregon State University, Corvallis, OR. USA. 2017
 - University of Geneva, Geneva, Switzerland. 2016
 - George Washington University, Washington, DC. USA. 2015
 - Centre for Genomic Regulation. Barcelona, Spain. 2014
 - **Three’s a crowd-source: The Collaborative Nature of Genome Annotation.**
 - 8th Arthropod Genomics Symposium, Institute for Genomic Biology, University of Illinois Urbana Champaign, Champaign, IL, USA. 2014
 - 7th International Biocuration Conference. Toronto, Canada. 2014
 - **Lessons learned from community-based biocuration efforts.** sbv IMPROVER. Lagonissi, Greece. 2013
 - **Annotating Genomes and Training the Annotators.** 6th Annual Arthropod Genomics Symposium and Inaugural i5k Workshop. Kansas City, MO. USA. 2012
 - **The Hymenoptera Genome Database.**
 - 5th International Biocuration Conference. International Society for Biocuration (ISB). Washington, DC. USA. 2012
 - International Nasonia Meeting. Nashville, TN. USA. 2011 and Tokyo, Japan. 2010
 - Annual Arthropod Genomics Symposium. Kansas City, MO. USA. 2009, 2010, and 2011
 - 2nd Honey Bee Genomics and Biology Meeting. Cold Spring Harbor Laboratory. Cold Spring Harbor, NY. USA. 2011
 - XIX Plant and Animal Genome Conference. San Diego, CA. USA. 2010
 - **Computational Tools for Insect Biology: Genomics and Biocuration.** 2011.
 - Seminar Series. Depts. of Entomology and Biological Sciences. Purdue University. West Lafayette, IN.
 - Seminar Series. Depts. of Entomology and Bioinformatics. Colombian National Coffee Research Center (CENICAFE). Chinchiná, Colombia.