

**PROFESSIONAL EXPERIENCE AND APPOINTMENTS**

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- Assistant Professor, School of Biological Sciences, Washington State University (WSU), 2013-present
- Adjunct Faculty School Global Animal Health & School Molecular Biosciences (WSU), 2013-present
- Postdoctoral Scholar, Stanford University, 2010-2013
- Postdoctoral Fellow, Cornell University, 2009-2010
- Statistics Consultant, Scharifker Consultores, 2003-2004

**RESEARCH PRODUCTIVITY AND GRANTSMANSHIP**

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- *Since WSU*: NSF-WSU (PI) \$3,750 2015-2016; NSF-MRI (co-PI) \$360,000 2015-2017; Illumina (PI) \$2,600; CORPOICA-Colombia (PI) \$10,271; WSU-CAS (PI) \$1,000. *Prior to WSU*: Complete Genomics (PI) \$30,000 2012, MARS (co-PI) \$850,659 2011-2012. **Total=\$1,258,280.**
- Pending: HFSP \$800,000 (co-PI); DOE \$2,608,828 (co-PI); CIFAR \$87,000 (PI); Agilent \$100,000 (PI); NIH-IREACH \$104,507 (PI; all allocated to PI).
- 28 peer review publications, 12 since WSU.
- Pub impact factor: high= 40.3, low=2.319, h-index= 17, 2 Nature, 1 Science, 1 PNAS, 2 PLOS Genetics, 3 Molecular Biology and Evolution; cited 1738 times.
- 5 WSU, 9 national and 3+ international research collaborators.
- 39 invited oral presentations, 11 posters and 4 oral presentations by grads/postdocs.

**TEACHING AND MENTORING**

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- Bio 418 (Fall 14, 15, 16, 17); Bio 534 Modern Methods in Population Genomics (Spring 15, 16, 18); Bio 593-2 Seminar (Spring 14); co-Lecture: Bio 571 (Spring 15, 16); Guest-Lecture: Bio 521 (Spring 17); Bio 474 (designed and approved for Spring 19). International Faculty at 2 week workshop Conservation Genetics (15, 16, 17, 18)
- 6 undergraduate research projects, 2 M.S. students (ABD 1) and 2 Ph.D. students. Committee member for 5 M.S. and 12 Ph.D. students.
- Average teaching rating 4.3/5.

**SERVICE**

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- *Washington State University*: Honors College Thesis advisor (2016-2017), Multicultural Team Mentoring Program (2016-present), Member of the advisory committee to Genomics Core at WSU Spokane (2015-current), Member of committee advising on strategies for the establishment of High Performance Computing on Campus (2014-2015).
- *College of Science*: Undergrad Research Training, Undergraduate Research Competition Judge, Faculty mentor for NSF sponsored Undergraduates in Biology and Mathematics (UBM).
- *School of Biological Sciences*: Panel for new graduate student recruitment (2015-2016), Co-authored prospectus for Data Analytics in SBS (2014-2015), *Ecology, Evolution, and Genetics Reading* (EEGR) group Organizer (2014-2015), contribute to student recruitment pickup (2016-2017).
- *Outside the University*: Organization of Session at Gordon Research Conference (2017), Panel member for NSF Division of Molecular and Cellular Biosciences (2015), reviewer for 12 international journals including PNAS, PLOS Genetics and Nature Microbiology. Thesis Opponent, University of the Arctic, Tromsø-Norway (2016). Core Faculty, Latin American Network for Conservation Genetics (2013-current).
- *Volunteer and Outreach*: Science after Hours (2017-current), active outreach to Latin American Institutions.

**HONORS AND AWARDS**

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- Outstanding Honors Thesis Advisor Award, WSU (2017), NSF- Advance Grant for External Mentorship Program, WSU (2015), Emory Division Scholar Fellowship (2004-2009), Programa Promocion al Investigador (PPI), Venezuela (2004-2006) and Orden Jose Felix Ribas en Tercera Clase, Venezuela (2004)

## CONTACT INFORMATION

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School of Biological Sciences  
Washington State University  
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Pullman, WA 99164-4236  
(509) 335-0179 omar.cornejo@wsu.edu

## EDUCATION

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Ph.D., Biological and Biomedical Sciences, 2009, Emory University, Atlanta GA Dissertation title: "Population Dynamics and Population Genetics of Recombination in Bacteria" (Advisor: Bruce Levin)  
MSc., Ecology and Population Biology, 2004, Instituto Venezolano de Investigaciones Científicas-IVIC, Caracas-Venezuela, Dissertation title: "Trends in the accumulation of AT in mitochondrial genomes of insects. A Comparative approach" (Advisor: Ananias A. Escalante)  
B.S., Biology, 2001, Universidad Simón Bolívar, Caracas-Venezuela, Dissertation Title: "Codon usage bias in *Helicobacter pylori*. Two genomes comparison" (Advisors: Moritz Benado and Ananias Escalante)

## PROFESSIONAL ACADEMIC EXPERIENCE

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Assistant Professor, School of Biological Sciences,  
Washington State University August 2013-Present  
Adjunct Faculty, Paul Allen School Global Animal Health,  
Washington State University, August 2013-Present  
Adjunct Faculty, School Molecular Biosciences,  
Washington State University, August 2013-Present  
Postdoctoral Fellow, Department of Genetics, School of Medicine,  
Stanford University, Stanford, CA. 2010-2013 (Advisor: Carlos D. Bustamante)  
Postdoctoral Fellow, Department of Biological Statistics and Computational Biology,  
Cornell University, Ithaca, NY, 2009-2010 (Advisors: Adam C. Siepel and Carlos D. Bustamante)  
Statistical Consultant, Independent consultant  
Scharifker Consultores, Caracas-Venezuela, 2003-2004  
Assistant Editor, Biology Department,  
Universidad Simón Bolívar, 2000

## FUNDING

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### Funded Grants since WSU (Total \$377,621)

National Science Foundation – WSU: "NSF Advance Grant for External Mentor support" \$3,750 (PI: **Cornejo**, mentor: Clark – Cornell University) 2015-2016  
National Science Foundation - MRI: Development: "Acquisition of an Integrated Data-Assisted Research and Training Scalable Storage System (IDARTs3) at Washington State University" \$360,000 (PI: Mailhot, **co-PI: Cornejo**) (Cost sharing additional \$154,285) 2015-2017  
Illumina – WSU: "Disentangling the genetic basis of color in *Anthurium spp* flowers" \$2,600 (PI: **Cornejo**) 2015  
CORPOICA, Colombia: "Training on genotyping by sequencing techniques for the characterization of agricultural plant resources" \$10,271 (PI: **Cornejo**) 2015  
WSU – CAS, travel award \$1,000 (PI: **Cornejo**) Not Used. 2014

Pending

Human Frontier Science Program (HFSP): LOI - “Ancient genomics analysis of coevolutionary processes of 1:n species in space and time” (PI: Sikora, **co-PI: Cornejo**)  
Department of Defense, RC19-C2-1019: “Source, transport, and fate of environmental DNA in aquatic ecosystems to inform species detection” \$2,608,828 (PI: Fremier, **co-PI: Cornejo et al.**)  
Canadian Institute for Advanced Research (CIFAR): “Human microbiome research” \$87,000 (**co-PI: Cornejo**)  
Agilent (Company): “Human microbiome research” \$100,000 (**co-PI: Cornejo**)  
National Institutes of Health, IREACH 17-003 \$104,507 (PI: Buchwald, **co-PI: Cornejo**)  
National Institutes of Health, Director’s New Innovator Award Program (DP2): “Integrative analysis of heterogeneity in pathogen genome architecture and host adaptive immune system” \$1,500,000 (**PI: Cornejo**)

Grants submitted while at WSU (not funded)

Mallinckrodt Foundation (Proposal after winning internal nomination): “Host Genetic determinants of the microbial composition” \$180,000 (**PI: Cornejo**) Selected applicant from WSU 2017  
WSU Seed: “Integrated analysis of diversifying selection in highly differentiated natural populations of Theobroma cacao, the chocolate plant” \$30,000 (**PI: Cornejo**) 2017  
National Science Foundation - Division of Environmental Biology: Preliminary Proposal: “Integrated analysis of diversifying selection and phenotypic differentiation in natural populations” (**PI: Cornejo**) 2017  
National Science Foundation - Division of Environmental Biology: Preliminary Proposal: “Understanding processes that contribute to the accumulation of deleterious mutations in the genome of natural populations” (**PI: Cornejo**) 2017  
Human Frontier Science Program (HFSP): “Multi-scale dynamics of infectious diseases. Malaria evolution from individuals to populations” (**PI: Cornejo**, co-PI: Sikora) 2016  
National Science Foundation - Division of Environmental Biology: Preliminary Proposal: “Identifying genomic hotspots of coevolution” (**PI: Cornejo**, co-PIs: Dybdahl and Nuismer) 2016  
National Institutes of Health, Maximizing Investigators' Research Award (R35): “The genomic architecture of deleterious mutation accumulation in natural populations” \$1,902,139 (**PI: Cornejo**) 2016  
WSU seed “High throughput system characterization of the immune repertoire in humans” \$30,000 (**PI: Cornejo**) 2015  
National Science Foundation - Division of Environmental Biology: “Collaborative Research: Identifying genomic hotspots of coevolution” \$937,149 (**PI: Cornejo**, co-PIs: Dybdahl and Nuismer) 2015  
National Science Foundation – Integrative Organismal Systems (PGRP) “Research-PGR: Transcriptomic unraveling of the genetic basis of differential disease susceptibility in the arboreal crop Theobroma cacao” \$4,200,000 (**PI: Cornejo**, co-PIs: Udhayakumar - University of West Indies - and Eilertson - Penn State -) 2015  
Silicon Mechanics: “Computing for Genomics, Genetics and Bioinformatics Research and Training” \$190,000 (**co-PIs: Kelley/Cornejo**) 2015  
National Institutes of Health, National Institute of Allergies and Infectious Diseases: “The impact of the flea vector microbiome on plague transmission” \$151,000 (PI: Vadyvaloo, **co-PI: Cornejo**) 2015  
National Institutes of Health, Director’s New Innovator Award Program (DP2): “Inferring changes in the genomic architecture of malarial parasites driven by host-immune factors” \$1,500,000 (**PI: Cornejo**) 2014  
WSU, CEREO (Internal): “A chemical genetic approach to elucidate the root response towards pathogen attack” \$14,958 (PI: Kunz, **co-PI: Cornejo**) 2014  
National Science Foundation – Integrative Organismal Systems (PGRP) “Research-PGR: Transcriptomic unraveling of the genetic basis of differential disease susceptibility in the arboreal crop Theobroma cacao” \$3,495,999 (**PI: Cornejo**, co-PIs: Udhayakumar - University of West Indies - and Eilertson - Penn State -) 2014

National Science Foundation - Division of Environmental Biology: *Preliminary Proposal: "Ploidy or sex as the target of parasite-mediated selection under the Red Queen hypothesis"* (PI: Dybdahl, **co-PIs: Cornejo** and Nuismer) 2014

National Science Foundation - Division of Environmental Biology: *Preliminary Proposal: "Ecology and Evolution of Clonal Suicide: when is the cost of bacteriocin production not too high?"* (**PI: Cornejo**) 2014

Silicon Mechanics: *"Computing for Genomics, Genetics and Bioinformatics Research and Training"* \$190,000 (**co-PIs: Cornejo/Kelley**) 2014

WSU Internal Keck Foundation: *"Inferring changes in the genomic architecture of malarial parasites driven by host-immune factors"* (**PI: Cornejo**) 2014

WSU internal for NRT—DESE: *"GenOmics and PHeNomics data—Enabled Research Training (GOPHERT)"* (PI: Cousins, **co-PI: Cornejo** et al.) 2014

WSU Internal, PEW: *"Longitudinal transcriptomic and metagenomic analysis of children nasopharyngeal cavity aimed at understanding the relevant factors associated to the development of invasive pneumonia"*, (**PI: Cornejo**) 2014

National Science Foundation - MRI: *Development: A High-Performance Scientific and Data-Intensive Computing Initiative at WSU* \$319,777 (PI: Mailhot, **co-PI: Cornejo et al.**) 2013

#### Funded grants listed as a collaborator

National Science Foundation, CISE: *"PMU: CC\*IIE Networking Infrastructure: A High Speed Scalable Research Core at Washington State University"* \$498,066 (**Key personnel**) 2014-2016

National Science Foundation – Integrative Organismal Systems: *"What is Normal Milk? Sociocultural, Evolutionary, Environmental, and Microbial Aspects of Human Milk Composition"* \$950,00 (**Key personnel**, PI: McGuire) 2013-2018

#### Funded grants prior to WSU (Total Funded: \$880,659):

Complete Genomics (Company), \$30,000 (**PI: Omar E. Cornejo**) 2011-2012

MARS (Company), \$850,659 (PI: Bustamante, **co-PI: Omar E. Cornejo**) 2011-2012

**PUBLICATIONS** 28 pubs (12 since WSU), cited 1738 times, \*Corresponding, #WSU students or postdocs, &Undergrads

h-index = 17, Impact factor: high = 40.137 and low = 2.319

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#### Currently in review

32. **Cornejo O.E.**, #Quanckenbush, C., Gopaulchan, D. and Umaharan, P. (2018) Comparative transcriptomic analysis reveals key components controlling spathe color in *Anthurium andraeanum* Hort. (reviewing manuscript)
31. **Cornejo O.E.**, Yee M.-C., Mockaitis K., Adams A., Strandberg R., Livingston D., Stack C., Umaharan P., Royaert S., Tawari N.R., Ng P., Schnell R., Phillips W., Bustamante C.D., Motamayor J.C. (2018) Genomic insights into the natural and domesticated evolutionary history of the chocolate tree, *Theobroma cacao*. (in review *Communications Biology - Nature*). Available in BioRxiv doi: <https://doi.org/10.1101/223438>
30. McCoy, R.C., Newnham, L.J., Ottolini, C., Hoffmann, E., Chatzimeletiou, K., **Cornejo, O.E.**, Petrov, D.A., Demko, Z.P., Sigurjonsson, S., Handyside, A.H. (2018) Tripolar mitosis drives the association between maternal genotypes of PLK4 and aneuploidy in human preimplantation embryos. (in review *Human Molecular Genetics*) . Available in the BioRxiv doi: <https://doi.org/10.1101/182303>

29. Xia, C., Wang, M., Yin, C., **Cornejo, O.E.**, Hulbert, S.H., Chen, X. (2018) Gene loss provides genomic basis for host adaptation in cereal stripe rust fungi. (in review *PLOS Genetics*)

#### Published

28. **Cornejo O.E.**, Hickey, R.J., Suzuki, H. and Forney, L.J. (2017) Focusing the diversity of *Gardnerella vaginalis* through the lens of ecotypes. *Evolutionary Applications* 00:1–13. <https://doi.org/10.1111/eva.12555> (\*co-corresponding authors)
27. Livingstone III, D., Stack, C., Mustiga, G., Rodezno, D., Suarez, C., Amores, F., Feltus, A., Mockaitis, K., **Cornejo, O.E.**, Motamayor, J.C. (2017) A large chocolate chip – development of a 15K *Theobroma cacao* L. SNP array to create high-density linkage maps. *Frontiers in Plant Science* 8:2008. doi.org/10.3389/fpls.2017.02008.
26. Xia, C., Wang, M., **Cornejo, O.E.**, Jiwan, D.A., See, D.R., Chen, X. (2017) Secretome characterization and correlation analysis reveal putative pathogenicity mechanisms in the wheat stripe rust fungus *Puccinia striiformis* f. sp. *tritici*. *Frontiers in Microbiology* 00-12. doi: 10.3389/fmicb.2017.02394.
25. Miller E.L., Evans, B.A., **Cornejo, O.E.**, Roberts, I.S., and Rozen, D.E. (2017) Phenotype polymorphism in *Streptococcus pneumoniae* and its effects on population structure and recombination. *Genome Biology and Evolution* 9(10): 2546 - 2559. doi.org/10.1093/gbe/evx188
24. McManus, K.F., Tavarella, A., Henn, B., Bustamante, C.D., Sikora, M., and **Cornejo, O.E.\*** (2017) Population genetic analysis of the DARC locus (Duffy) reveals complex evolutionary history of a malaria resistance locus. *PLOS Genetics* 13(3): e1006560 doi: 10.1371/journal.pgen.1006560. **Highlighted in the Science (March 2017) (doi: 10.1126/science.aal0950)**
23. Chaurio, R.A., Pacheco, M.A., **Cornejo, O.E.**, Stanley, C.E., Castillo, A.I., Herrera, S., and Escalante, A.A. (2016) Evolution of the transmission-blocking vaccine candidates Pvs28 and Pvs25 in *Plasmodium vivax*: differentiation of the parasite populations from The Americas. *PLOS Neglected Tropical Diseases* 10(6): e0004786. doi:10.1371/journal.pntd.0004786
22. Jaimes, Y.Y., Gonzalez, C., Rojas, J., **Cornejo, O.E.**, Mideros, M.F., Restrepo, S., Cilas, C., and Furtado, E.L. (2016) Geographic differentiation and genetic structure of *Moniliophthora roreri* in the principal Cocoa production areas in Colombia. *Plant Disease* 100(8): 1548-1558. doi:10.1094/PDIS-12-15-1498-RE
21. Cooke, T.F., Yee, M.C., Muzzio, M., Adams, A., Bell, R., **Cornejo, O.E.**, Kelley, J.L., Bailliet, G., Bravi, C.M., Bustamante, C.D., and E.E. Kenny. (2016) GBStools: A unified approach for reduced representation sequencing and genotyping. *PLOS Genetics* 12(2): e1005631. doi:10.1371/journal.pgen.1005631
20. **Cornejo, O.E.\***, Fisher, D. and Escalante A.A. 2015. Genome-wide patterns of genetic polymorphism and signatures of selection in *Plasmodium vivax*. *Genome Biology and Evolution* 7(1): 106-119. doi:10.1093/gbe/evu267. **Highlighted in the News and Analysis / Genome Watch section of Nature Reviews in Microbiology (March 2015) (doi:10.1038/nrmicro3458)**
19. Raghavan M, ..., **Cornejo O.E.**, et al. one of 71 authors. (2015) Genomic evidence for the Pleistocene and recent population history of Native Americans. *Science* 349:6250.
18. Raghavan, M., ..., **Cornejo, O.E.**, et al. one of 56 authors. (2014) The genetic prehistory of the New World Arctic. *Science* 345:6200.
17. Rasmusen, M., ..., **Cornejo, O.E.**, et al. one of 42 authors. (2014) The genome of a Late Pleistocene human from a Clovis burial site in western Montana. *Nature* 506 (7487): 225 – 229.
16. Pepperell, C.S., Casto, A.M., Kitchen, A., Granka, J.M., **Cornejo, O.E.**, Holmes, E.C., Birren, B., Galagan, J., and Feldman, M.W. (2013) The role of selection in shaping diversity of natural *M. tuberculosis* populations. *PLOS Pathogens* 9(8): e1003543.
15. Utro, F., Haiminen, N., Livingstone, D., **Cornejo, O.E.**, Royaert, S., Schnell, R.J., Motamayor, J.C., Kuhn, D.N. and Parida, L. (2013) iXora: Exact Haplotype inferencing and trait association. *BMC Genetics* 14: 48.

14. Motamayor, J.C., Mockaitis, K., Schmutz, j., Haiminen, N., Livingstone, D., **Cornejo O.E.**, Findley, S., Zheng, P., Utro, F., Royaert, S., Saski, C., Jenkins, J., Podicheti, R., Zhao, M., Scheffer, B., Feltus, A., Gutierrez, O., Amores, F., Phillips, W., Marelli, J.P., May, G.D., Bretting, P., Shapiro, H., Ma, J., Bustamante, C.D., Schnell, R.J., Main, D., Gilbert, D., Parida, L., and Kuhn, D.N. (2013) The genome sequence of the most cultivated cacao type and its use in the mapping of oligogenic traits: pod color as an example. *Genome Biology* 14: R53
13. **Cornejo, O.E.**, Lefébure, T., Pavinski-Bitar, P.D., Lang, P., Richards, V.P., Eilertson, Do, T., K., Beighton, D., Zeng, L., Ahn, S-J, Burne, R.A., Siepel, A.C., Bustamante, C.D., and M. Stanhope. (2013) Evolutionary and population genomics of the cavity causing bacteria *Streptococcus mutans*. *Molecular Biology and Evolution*, 30(4): 881-893.  
**\*Highlighted in Science News & Analysis (February 2013) doi: 10.1126/science.339.6122.896**
12. Utro, F., **Cornejo, O.E.**, Livingstone, D., Motamayor, J.C., and Parida, L. (2012) ARG-Based genome-wide analysis of cacao cultivars. *BMC Bioinformatics* 13 (Supp19): S17.
11. Pacheco, M.A., Battistuzzi, F.U., Junge, R.E., **Cornejo, O.E.**, Williams, C.V., Landau, I., Ravonisoarimalala, L.R., Snounou, G., Jones-Engel, L., and Escalante A.A. (2011). Timing the origin of human malaria: the lemur puzzle. *BMC Evolutionary Biology* 11: 299.
10. Dewey F., Chen, R., Cordero, S., Ormond, K., Caleshu, C., Karczewski, K., Carrillo, M., Wheeler, M., Dudley, J., Byrnes, J., **Cornejo, O.E.**, Knowles, J., Woon, M., Sungkuhl, K., Gong, L., Thorn, C., Hebert, J., Capriotti, E., David, S., Pavlovic, A., West, A., West, J., Thakuria, J., Ball, M., Zaranek, A., Rehm, H., Church, G., Bustamante, C.D., Snyder, M., Altman, R., Klein, T., Butte, A., and E. Ashley. (2011). Phased whole genome genetic risk in a family quartet using a major allele reference sequence. *PLoS Genetics* 7(9): e1002280.
9. **Cornejo, O.E.\***, McGee, L., and Rozen, D.E. (2010). Polymorphism in the competence peptide does not limit recombination in *Streptococcus pneumoniae*. *Molecular Biology and Evolution* 27: 694-702.
8. Krief, S., Escalante, A.A., Pacheco, M.A., Mugisha, L., Andre, C., Halbwax, M., Fischer, A., Krief, J-M., Kasenene, J., Crandfield, M., **Cornejo, O.E.**, Chavatte, J-M, Lin, C., Letourneur, F., Gruner, AC, McCutchan, T., Renia, L., Snounou G. (2010). On the diversity of malaria parasites in African Apes and the origin of *Plasmodium falciparum* from Bonobos. *PLoS Pathogens* 6(2): e1000765.
7. Levin BR, **Cornejo, O.E.** (2009). The Population and Evolutionary Dynamics of Homologous Gene Recombination in Bacteria. *PLoS Genetics* 5(8): e1000601.
6. Leung, S.W., Apponi, L.H., **Cornejo, O.E.**, Kitchen, C.M., Valentini, S.R., Pavlath, G.K., Dunham, C.M., and Corbett, A.H. (2009). Splice Variants of the Human ZC3H14 Gene Generate Multiple Isoforms of a Zinc Finger Polyadenosine RNA Binding Protein. *Gene* 439(1-2):71-78.
5. **Cornejo, O.E.**, Rozen, D.E., May, R.M., and Levin, B.R. (2009). Oscillations in Continuous Culture Populations of *Streptococcus pneumoniae*: Population Dynamics and the Evolution of Clonal Suicide. *Proceedings of the Royal Society, London. B series*, 276(1659): 999-1008.
4. **Cornejo, O.E.**, and Escalante, AA. (2006). The origin and age of *Plasmodium vivax*. *Trends in Parasitology*, 22(12): 558-563.
3. Escalante, A.A., **Cornejo, O.E.**, Freeland, A., Poe, A.E., Durrego, E., Collins, W.E., and Lal, A.A. (2005). A monkey's tale: The origin of *Plasmodium vivax* as a human malaria parasite. *Proceedings of the National Academy of Sciences (USA)* 102(6): 1980-1985. (**Master Thesis work**)
2. Escalante, A.A., **Cornejo, O.E.**, Rojas, A., Udhayakumar, V., and Lal, A.A. (2004). Assessing the effect of natural selection in malaria parasites. *Trends in Parasitology*, 20(8): 388-395.
1. Sebastiani, M., Aponte, C., Andara, C., **Cornejo, O.E.**, Esclasans, D., Marquez, E., Moscarella, R., Ponte, A. y Vizcaino, D. (2000). El enfoque de las evaluaciones de impacto ambiental en el ordenamiento territorial. Caso: Reserva Forestal Imataca, Venezuela (Impact assessment

approach in land use ordering. Case study: Imataca Forstal Reserve in Venezuela) *Revista Geografica Venezolana*, 41(2): 187-213.

#### Non-refereed

**Cornejo, O.E.** Benado, M. 2000. Lack of mite parasitism in natural populations of *Drosophila* of the cactophilic *D. martensis* cluster (*D. repleta* group). *Drosophila Information Service*. Volume: 83 Pages: 13-14

#### Books

Aguilera, M., Azocar, A., and Gonzalez Jimenez, E. (2003) *Biodiversidad en Venezuela, Volume I (Biodiversity in Venezuela, Vol I)*. Impresion Editorial ExLibris, 534 pp. (**Omar E. Cornejo, Assistant Editor**)

Aguilera, M., Azocar, A., and Gonzalez Jimenez, E. (2003) *Biodiversidad en Venezuela, Volume II (Biodiversity in Venezuela, Vol II)*. Impresion Editorial ExLibris, 543 pp. (**Omar E. Cornejo, Assistant Editor**)

#### **RESEARCH PUBLICITY**

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Scientific American “*Oral Mystery: Are Agriculture and Rats Responsible for Tooth Decay?*” (took on my article on the evolution of cavities causing bacteria), Feb 2013.

#### **COLLABORATIONS**

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##### Washington State University

Asaph Cousins, SBS  
Charlie Robbins, SBS  
Mark Dybdahl, SBS  
Xianming Chen, PP  
Viveka Vadyvaloo, GAH

##### National

Juan Carlos Motamayor, MARS  
Marc Lucia, Stanford University  
Elizabeth Eagan, Stanford University  
MC Yee, Stanford University  
Ananias A. Escalante, Temple University  
Luis Barreiro, University of Chicago  
Larry Forney, University of Idaho  
Shirley Luckhart, University of Idaho  
Che-Hong Chen, Stanford University

##### International

Martin Sikora, Natural History Museum, Copenhagen-Denmark  
Daniel Rozen, Leiden University, Netherlands  
***Anopheles gambiae* 1000 genomes project Consortium (Ag1000). My lab is a partner lab of the Ag1000 project steered by the Wellcome Trust Foundation. My lab is in charge of developing the fine scale recombination map and contribute to the design of studies that will make use of the resource.**

#### **PRESENTATIONS**

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a. *Invited and contributed talks at professional meetings*

- Cornejo, O.E.** (2017) Host/pathogen genetic variability impact on the outcome of their interaction. Gordon Conference in Population Microbiology, NH (**Organizer of a session for the conference**).
- Cornejo, O.E.** (2017) Selection on the DARC locus in humans was Soft, yet Strong. Society for the Study of Evolution, Portland, OR
- Cornejo, O.E.** (2017) The evolution of the DARC locus (Duffy) reveals complex evolutionary history of a malaria resistance locus. The Institute for Bioinformatics and Evolutionary Studies, Moscow, ID, contributed
- Cornejo, O.E.** (2016) How relevant are the Pan and Core Genome in the evolution of pathogenic bacteria? North-West Branch American Society for Microbiology, Seattle, WA, invited
- Cornejo, O.E.** (2016) Comparative transcriptomic analysis reveals genes involved in color determination in *Anthurium* spp. Illumina Users Group, Pullman, WA, invited
- Cornejo, O.E.** (2016) Genome-wide patterns of genetic polymorphism and signatures of selection in *Plasmodium vivax*. EVO-WIBO (Evolution in Washington, Idaho, British Columbia, and Oregon), Port Townsend, WA, invited
- Cornejo, O.E.** (2015) Population Genomics in health and disease and the evolution of genomic architecture. Illumina User Group Meeting 2015, Seattle, WA, invited
- Cornejo, O.E.** (2014) Taller: Introduccion a las nuevas tecnologias de secuenciacion (Introduction to next generation sequencing techniques). I LatinAmerican Congress in Conservation Genetics, Macuto, Venezuela, invited
- Cornejo, O.E.** (2014) Genomica Evolutiva de Cacao: historias de demografia, endocruza y color (Evolutionary Genomics in Cacao: stories of demographics, inbreeding and color). I LatinAmerican Congress in Conservation Genetics, Macuto, Venezuela, invited
- Cornejo, O.E.** (2014) Usos potenciales de tecnicas de secuenciacion de proxima generacion para resolver problemas en genetica para la conservacion (Potential uses of next generation sequencing techniques to address problems in conservation genetics). I LatinAmerican Congress in Conservation Genetics, Macuto, Venezuela, invited

*Prior to WSU*

- Cornejo O.E.** (2013) Impact of selfing in the reconstruction of the demographic history of *Theobroma cacao*. Plant and Animal Genomes (Workshop of Cacao Genomics), San Diego, CA, invited
- Cornejo O.E.** (2013) Building genomic resources for *Theobroma cacao*. Plant and Animal Genomes (Workshop on Genomes and GeneBanks), San Diego, CA, invited
- Cornejo O.E.** (2012) Assessing the evolutionary history of *Theobroma cacao* from re-sequenced genomes. Plant and Animal Genomes (Workshop of Cacao breeders), San Diego, CA, invited
- Cornejo O.E.** (2011) Building a Next Generation Platform for Association Studies in Cacao. Plant and Animal Genomes (Workshop of Cacao breeders), San Diego, CA
- Cornejo O.E.** (2009) Competence peptide polymorphism does not limit recombination in *Streptococcus pneumoniae*. NSF/NIH Ecology and Evolution of Infectious Diseases Annual Meeting, Park City, UT

*b. Invited university seminars*

- Cornejo, O.E.** (2017) What can the genome tell us about the evolution of hosts and microbes? Walla Walla University, Walla Walla, WA,
- Cornejo, O.E.** (2017) A population genetics approach to the study of Host/Microbe Interactions. CIRC-WSU High performance computing at WSU, Pullman, WA,
- Cornejo, O.E.** (2017) A population genetics approach to the study of Host/Microbe Interactions. JCVI, San Diego, CA
- Cornejo, O.E.** (2017) What can the genome tell us about the evolution of hosts and microbes? Department of Entomology, Pullman, WA
- Cornejo O.E.** (2016) From Genomes to Metagenomes and Back. The Arctic University of Norway, Trømsø, Norway (International invitation)



- Cornejo O.E.** (2015) Evolutionary genomics in health and disease. External review of WSU's condominium institutional research computing at WSU (Institutional support for the development of the university-wide initiative on High Performance Computing at WSU), Pullman, WA
- Cornejo O.E.** (2015) Evolutionary genomics in health and disease. WSU Vancouver campus (seminar series), Vancouver, WA
- Cornejo O.E.** (2015) Evolutionary genomics of infectious diseases: understanding microbial chromosome evolution in time and space. Center of Infectious Disease Dynamics (CIDDD) seminar series, Penn State University, State College, PA
- Cornejo O.E.** (2014) Desarrollo de herramientas genómica para el establecimiento de planes de mejoramiento genético en cacao (Development of genomic resources to establish genetic breeding plans in cacao). Corpoica-Colombia agricultural research center, Mosquera/Bogota (Colombia) (Invited talk as part of an initiative to establish a partnership between Cornejo lab and Corpoica)
- Cornejo O.E.** (2014) Evolutionary genomics of sweets and cavities. Fred Hutchinson Center for Cancer Research, Seattle, WA
- Cornejo O.E.** (2013) Evolutionary genomics of sweets and cavities. University of Idaho, Biology Department, Moscow, ID
- Cornejo O.E.** (2013) On the evolutionary genomics of *Theobroma cacao* and the genetic basis of phenotypic variation. Carnegie Institution for Science, Stanford, CA
- Cornejo O.E.** (2013) Population Genetics in the Genomic era. *Washington State University*, workshop on "A Scientific Computing Initiative at WSU: Building the Capacity to Lead", Pullman, WA

*Prior to WSU*

- Cornejo O.E.** (2013) Variant Discovery of SNPs in a wide panel of Amerindian individuals. special seminar NGS Bioinformatics at Stanford Center for Genomics & Personalized Medicine, School of Medicine, Stanford University, Stanford, CA
- Cornejo O.E.** (2013) Evolution and Population Genomics of Pathogens. Santa Clara University, Biology Department. Santa Clara, CA
- Cornejo O.E.** (2013) Ecology and evolutionary biology of microorganisms: from short oscillations to long-term expansions. School of Molecular Biosciences (SMB), Washington State University, Pullman, WA
- Cornejo O.E.** (2013) The value of genomic information: from demographic inference to disentangling the genetic basis of diversity and adaptation. *School of Biological Sciences, Washington State University*, Pullman, WA
- Cornejo O.E.** (2013) Evolutionary Genomics of the cavity causing bacteria: *Streptococcus mutans*. *School of Pharmacology, The Arctic University of Norway*, Tromsø, Norway
- Cornejo O.E.** (2007) Clonal Suicide in *Streptococcus pneumoniae*: Mathematical models and experiments informing each other. Integrative Biology Department Seminar Series *ETH Zurich*. Zurich, Switzerland
- Cornejo O.E.** (2006) Recombination and assisted suicide in *Streptococcus pneumoniae*. *Hopital Necker - Enfants Malades Assistance Publique - Hopitaux de Paris*. Evolutionary Biology of Infectious Diseases, Paris, France

*c. Additional contributed talks (Student authors, \*Undergraduate, #Graduate)*

- #Jimenez Schwarzkopf, E. (2018) Recombination in *Theobroma cacao*. *WSU Biology Graduate Student Symposium*, Pullman WA.
- #Saxton, M., Quackenbush, C., Hutzenbiler, B., **Cornejo, O.E.**, Jansen, H., Robbins, C., Kelley, J.L. Differential RNA expression across seasons in brown bears (*Ursus arctos*) can provide novel insight into hibernation physiology and benefits to human health, *International Association for Bear Research and Management*, Quito, Ecuador
- #Nelson, J.T., **Cornejo, O.E.** (2017) Genome-wide patterns of divergent selection among populations of *Theobroma cacao*. *Evolution*, Portland, OR

#Jimenez Schwarzkopf, E., **Cornejo, O.E.** (2017) Recombination in *Theobroma cacao*. *Evolution* Portland, OR

*d. Posters (\*Undergraduate, #Graduate)*

#Harding, C.J., Sikora, M., **Cornejo, O. E.** (2017) Exploring the oral microbiome of ancient humans. *Evolution* 2017, Portland, OR

#Nelson, J.T., **Cornejo, O. E.** (2017) Widespread signatures of divergent selection among highly differentiated populations of *Theobroma cacao*. *WSU Biology Graduate Student Symposium*, Pullman, WA

\*Huynh, A., Quackenbush, C.R., **Cornejo, O.E.** (2017) Characterizing the oral microbiome of East Africans in association with their oral health status. Showcase for Undergraduate Research and Creative Activities (SURCA), Pullman, WA **received Crimson award**

Kolbe A., Studer A., **Cornejo O.E.**, Cousins A.B. (2016) Transcriptional response of maize carbonic anhydrase mutants to CO<sub>2</sub> limitation. *C<sub>4</sub> Photosynthesis Conference*, Canberra, Australia

#Jimenez Schwarzkopf, E., Bustamante, C.D., Motamayor, J.C., **Cornejo, O.E.** (2016) Recombination in the chocolate factory: A fine-scale recombination map for *Theobroma cacao*. *Evolution*, Austin, TX

Chaurio, et al. **Cornejo, O.E.**, and Escalante. A.A. (2016) Evolution of the transmission-blocking vaccine candidates Pvs28 and Pvs25 in *Plasmodium vivax*: differentiation of the parasite populations from The Americas. *American Society of Tropical Medicine and Hygiene*, Atlanta, GA

*Prior to WSU*

**Cornejo, O.E.** (2013) Evolutionary genomics of *Theobroma cacao* and the genetic basis underlying phenotypes. *Meeting of the Society for the Study of Molecular Biology and Evolution*, Chicago, IL

**Cornejo O.E.** (2012) Assessing the evolutionary history of *Theobroma cacao* from re-sequenced genomes. *Meeting of the Society for the Study of Molecular Biology and Evolution*, Dublin, Ireland

**Cornejo O.E.** (2011) Genomic evidence of population genetic structure associated with differential recombination in *Streptococcus mutans*. *Gordon Conference in Microbial Population Biology*, Andover, NH

**Cornejo O.E.** (2009) Evolutionary Dynamics of Recombination in bacteria. *Gordon Conference in Microbial Population Biology*, Andover, NH

**Cornejo O.E.** (2007) Recombination and Clonal Suicide in *Streptococcus pneumoniae*: Mathematical models and experiments informing each other. *Gordon Conference in Microbial Population Biology*, Andover, NH

**Cornejo O.E.** (2007) Recombination and Clonal Suicide in *Streptococcus pneumoniae*. *Meeting Society for the Study of Evolution*, Seattle, WA

**Cornejo O.E.** (2005) Why to be tempered? Population Dynamics of a Lysogenic/Lytic phage. *Gordon Conference in Microbial Population Biology*, Andover, NH

Escalante AA, Durrego E, Chaurio R, **Cornejo O.E.**, Poe AC, Collins WE, Lal AA. (2004) Evolution of the genes encoding the transmission-blocking vaccine candidates Pv25 and Pv28 of *Plasmodium vivax*. *Annual Meeting, American Society of Tropical Medicine and Hygiene*, Miami, FL

Escalante AA, **Cornejo O.E.**, Freeland DE, Poe AC, Durrego E., Collins WE, Lal AA. (2004) Monkey's Tale: The Origin of *Plasmodium vivax* as a Human Malaria Parasite. *Annual Meeting, American Society of Tropical Medicine and Hygiene*, Miami, FL

## TEACHING

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### Washington State University

Lecturer, Biology 418 Parasitology (59 – 131 students)

Fall 2014, 2015, 2016 & 2017

Lecturer, Biology 534 Modern Methods Population Genomics (6 – 15 students)

Spring 2015, 2016 & 2018

Lecturer, Biology 593-2 Seminar Current Topics in Population Genetics (5 students)

Spring 2014  
Co-Lecturer, Biology 571 Quantitative Tools (20 – 25 students)  
Spring 2015, 2016  
Guest lecturer, Biology 521 Quantitative Genetics,  
Spring 2017  
New Course developed, Biology 474 Computational Biology  
Spring 2019

#### International Teaching

Lecturer and Organizer (reception and evaluation of projects), Workshop in Conservation Genetics – Latin American Network for Conservation Genetics (2 Weeks workshop - 10 Hours a day): **2015** (*Chile, 26 students from 6 countries*), **2016** (*Argentina, 25 students from 8 countries*), **2017** (*Bolivia, 22 students from 7 countries*), **2018** (*Colombia, TBD*)

I am in charge or evaluating projects (*usually 5 students project proposals, continued evaluation through the course*) and I teach 2 full days of course.

#### As Postdoc or graduate student

Teaching Assistant, Population Dynamics of Disease,  
Emory University, Spring 2006  
Teaching Assistant, Bioinformatics,  
Emory University, Fall 2008  
Instructor, Molecular Epidemiology,  
Universidad de los Andes, Merida, Venezuela., Spring 2004 (*35 students from 8 countries*)  
Instructor, Advanced Ideas in Phylogenetics,  
Institute for Advanced Ideas, Spring 2004 (*23 students*)

#### **ADVISEES**

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##### *Undergraduate Research Projects*

Hannah Wilson (2018-current)  
Darby Fox (2018-current)  
Sarah Kerr (2016-current)  
Daltan Boucher (2016)  
Ali Hakkami (2016)  
Jason Su (2015-2016)  
Taven Shumaker (2015)  
Nicholas Howard (2014-2015)  
Morgan Frank (2014-2015)  
Jack Bonnington (2013-2015)

##### *Honors Thesis Students*

Marlow Schulz (2017-2018)  
Ashley Huynh (2016-2017) **Pass with Distinction and recipient of Honors' Deans Award**  
(Accepted in Dental School at UW).

##### *Graduate Students*

Kaija Broders, MS SBS (2018-current)  
Joel Nelson, PhD SBS (2016 - current)  
Carlie Jo Harding, MS SBS (2016-current), ABD  
Enrique Jimenez Schwarzkopf, PhD SBS (2015-current)  
Kimberly McManus, Phd Stanford (co-advised with Carlos Bustamante, 2011-2015)

*Rotation Students (Graduate)*

Roxana Hickey, PhD University of Idaho (2014-2015)  
 Savannah Sanchez, PhD (2015)  
 Johannetsy Avillan, PhD (2017)

*Postdoctoral Scientist*

Farrakh Mehboob (2016)

*Visiting Scientist*

MC Yee, Stanford University (once a year since 2014)  
 Jaime Osorio, CORPOICA, Colombia (2016)

*Research Technician*

Corey Quackenbush (2013-2017)

*Graduate student committee service*

Carly Prior, PhD (16-current)	Elisabetta Luci, PhD (14-current)
Savannah Sanchez, PhD (16-current)	Kimberly Lackey PhD (14-current)
Mark Smithson, PhD (15-current)	Allison Kolbe, PhD (14-2016)
Xia Chongjing, PhD (15-current)	Rui Li, PhD (14-2016)
Krysten C. Huddleston, MS (15-current)	Richard E III Berl PhD (14-2015)
Lanie Smith, MS (16-17)	Hymas Tatton, MS (15)
Kari Ferolito, MS (15-17)	Therese Jones, MS (13-14)
Vidar Sørnum, PhD (16)	
Clayton Bailes, PhD (15-current)	
Josh Brindley (13-current)	

**AWARDS**


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Outstanding Honors Thesis Advisor Award, WSU	2017
Gordon Conference Financial Award	2017
Advance Grant for External Mentorship Program, WSU	2015
Travel Award to SMBE Satellite Symposium on Phylomedicine, SMBE	2012
Travel Award. Marine Biology Labs, Woods Hole, MA	2005
Emory Division Scholar Fellowship	2005-2009
Programa Promocion al Investigador (PPI), Venezuela	2004-2006
Orden Jose Felix Ribas en Tercera Clase, Venezuela	2004
NSF Travel Award, Panamerican Institute of Advances Studies	2004
Scholarship by the Fondo Nacional de Ciencia y Tecnologia, DIB	2002-2004
UNESCO-ICTP Travel Award	2002

**PROFESSIONAL AFFILIATIONS**


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Society for the Study of Evolution	2016-current
Genetics Society of America	2016-current
Society for Molecular Biology and Evolution	2009-current
Core Faculty, Latin American Network for Conservation Genetics	2013-current

**PROFESSIONAL SERVICE***Washington State University*

Honors College Thesis advisor (2017 & 2018)  
 For Ashley Huynh & Marlow Schulz

Showcase for undergraduate research and creative activities, WSU (2016-2018)

Poster judge

Search committee director of Facility core on Functional Genomics (Grand Challenges Initiative at WSU), WSU, 2016

Office of Multicultural Student Services Team Mentoring Program, 2016-present

Student mentor

Member of the advisory committee to Genomics Core at WSU Spokane, WSU (2015-current)

Search committee for new IT specialist for High Performance Computing (HPC) equipment, WSU 2015

Search committee for new HPC administrator, WSU 2015

Member of committee advising on strategies for the establishment of High Performance Computing on Campus (2014-2015)

Member of expert panel presenting relevant research at WSU that requires the investment on HPC infrastructure (2015)

Consultant to WSU Functional Genomics Core in Spokane (2015)

Member of committee for High Performance Computing acquisition on campus (2013-2015)

#### *College of Arts and Science*

Faculty mentor for NSF sponsored Undergraduates in Biology and Mathematics (UBM) program (2015)

Student research mentor (Nicholas Howard)

#### *School of Biological Sciences*

Panel for new graduate students, "Computing Resources available at WSU" (2015)

Co-authored prospectus for Data Analytics in SBS (2014-2015)

*Ecology, Evolution, and Genetics Reading* (EEGR) group Organizer, 2014-2015

Hosted regional discussion group: *Palouse Ecology, Evolution, and Systematics (PEES)* 2014

Panel for new graduate students, "How to prepare for a career in biology" (2014-2015)

Coordinate the pick-up of graduate student recruits at Spokane (2017-2018)

#### *National*

Organization of Session at Gordon Research Conference (2017)

Microbial Population Biology GRC, Andover, NH.

Panel member

NSF Division of Molecular and Cellular Biosciences, 2015

*Ad hoc* journal reviewer:

PLOS Genetics

PLOS Computational Biology

Proceedings of the National Academy of Sciences (USA)

Molecular Biology and Evolution

Genome Biology and Evolution

PLOS One

PLOS Pathogens

PLOS Neglected Tropical Diseases

Nature Microbiology

eLife

Infection, Genetics and Evolution,

Journal of Theoretical Biology

*Ad hoc* grant reviewer:

National Science Foundation (2016-2017)

#### *International*

Co-Organizer and teaching faculty at the Biology of Vector-borne Diseases six-day training course, Moscow, ID (2018) (<http://www.uidaho.edu/cals/center-for-health-in-the-human-ecosystem/education/vector-borne-diseases>)

Core Faculty, Latin American Network for Conservation Genetics (2013-current, <http://regenec.org/>)

Thesis Opponent, University of the Arctic, Tromsø-Norway

### **INDUSTRY INTERACTIONS**

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Consultant for MARS, Inc. “Genetic analysis of *Theobroma cacao*” 2013-present

Consultant through Gerson Lehrman Group, 2017-present

### **VOLUNTEER AND OUTREACH**

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Science After Hours Best of Series, talks to the community (2018)

Science After Hours Best of Series, talks to the community (2017)

Team Mentoring Program – how to engage with science presentation 10/5/17

Virtual Seminars to the undergrad students of Universidad del Norte de Santander (Colombia) to introduce the potential uses of genomics in agriculture (2014-2017)

Scientific consultant, I am part of a large community of more than 1,000 Venezuelan scientists working to develop a nation-wide plan for the development of the Scientific and Technological apparatus in

Venezuela after the exit of the current government. An initiative led by Dr. Gioconda San Blas

Contributions to a popular science magazine for children (2002)

### **RESEARCH FOCUS**

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I am a population geneticist whose research focuses on the study of basic evolutionary processes that shape genetic variation in pathogenic populations and contribute to their adaptive evolution. My group uses a combination of computer simulations, simple mathematical models and statistical analysis on genomic data to infer the evolutionary history of populations, to map genetic bases of characters and to perform inferences on the impact of selection in pathogens and hosts. My current focus is on working at the intersection of the discovery of variants in the genomes of pathogen and hosts that result from the interaction of organisms and can largely impact the outcome of infection at the population level. The long-term goal is to translate these genetic discoveries into improved public health measurements aimed at reducing disease burden and the disparities caused by disease in human populations.

1. Evolutionary population genetics/genomics of pathogens.
2. Impact of Recombination to bacterial/host populations structure and adaptive evolution.
3. Genetic inference of human population history and the evolution of disease related traits.