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**Professional Experience**

1. Research Scientist. University of Florida, Department of Plant Pathology. April 2018 to present
2. Postdoctoral Associate, University of Florida, Department of Plant Pathology. April 2012 to February 2018.
3. Postdoctoral Associate, Cornell University, Department of Plant Pathology 2010-March 2012.
4. Graduate Research Assistant, Cornell University, Department of Microbiology 2003-2009
5. Assistant Researcher, National of Institute of Health-Peru (NIH-Peru) 1998-2002

**Education**

1. Ph.D. in Microbiology, **Cornell University (2009)**
2. B.Sc. in Microbiology, Research Thesis with Honors**, Universidad Nacional Mayor de San Marcos**, Peru (1998)

**Selected Relevant Publications**

1. Oliva R, Ji C, Atienza-Grande, **Huguet-Tapia JC**, Pérez-Quintéros A, Li T, J Eom J, Li C, Nguyen H, Liu B, Auguy F, Sciallano C, Luu VT,. Dossa GS, Cunnac S, Schmidt SM, Slamet-Luedin IH, Vera Cruz C, Szurek B, Frommer WB, White FF and Yang B. Genome-editing for broad-spectrum resistance against rice bacterial blight. **Nature Biotech. 2019** Oct 28. doi: 10.1038/s41587-019-0267-z. **Equal contribution author.**
2. Eom JS, Luo D, Atienza-Grande G, Yang J, Ji C, Thi Luu V, **Huguet-Tapia JC**, Char SN, *Liu B, Nguyen H, Schmidt SM, Szurek B, Vera Cruz C, White FF, Oliva* R, Yang B, Frommer WB. [Diagnostic kit for rice blight resistance.](https://www.ncbi.nlm.nih.gov/pubmed/31659338) **Nat Biotechnol. 2019 Oct 28. doi: 10.1038/s41587-019-0268-y**
3. Peng Z, Hu Y, Zhang J, **Huguet-Tapia JC**, Block AK, Park S, Sapkota S, Liu Z, Liu S, White FF.. [*Xanthomonas translucens* commandeers the host rate-limiting step in ABA biosynthesis for disease susceptibility.](https://www.ncbi.nlm.nih.gov/pubmed/31575748) **Proc. Natl. Acad. Sci. U. S. A**. 2019 Oct 15;116(42):20938-20946. doi: 10.1073/pnas.1911660116. Epub 2019 Oct 1.
4. Chenhao Li, Ji C, **Huguet-Tapia JC**, White FF, Dong H, Yang, B. An efficient method to clone TAL effector genes from *Xanthomonas oryzae* using Gibson assembly. **Mol. Plant Pathol. 2019.**Oct;20(10):1453-1462. doi: 10.1111/mpp.12820.
5. Newberry EA, Gaber M, Timilisina S, Blagojevic N, Obradovic A, Bull CT, Goss EM, **Huguet-Tapia JC**, Paret ML, Jones JB Potnis N. Inference of Convergent Evolution Among *Pseudomonas syringae* strains Isolated from Watermelon, Cantaloupe, and Squash. **Frontiers in Microbiol. 2019**. Feb 19. doi: 10.3389/fmicb.2019.00270.
6. Ascunce MS, Shin K, **Huguet-Tapia JC**, Poudel R, Garrett KA, van Bruggen AHC, Goss EM. Penicillin Trunk Injection Affects Bacterial Community Structure in Citrus Trees. **Microb. Ecol**. **2018** Dec 1. doi: 10.1007/s00248-018-1302-1.
7. Sapp A, **Huguet-Tapia JC**, Sánchez-Lamas M, Atienza-Grande GT, Primo ED, Rinaldi J, Klinke S, Goldbaum FA, Bonomi HR, Christner BC, Otero LH. Draft Genome Sequence of Methylobacterium sp. Strain V23, Isolated from Accretion Ice of the Antarctic Subglacial Lake Vostok. **Genome Announc. 2018** Mar 8;6(10). pii: e00145-18. doi: 10.1128/genomeA.00145-18.
8. Gochez AM, **Huguet-Tapia JC**, Minsavage GV, Shantaraj D, Jalan N, Strauß A, Lahaye T, Wang N, Canteros BI, Jones JB, Potnis N. Pacbio sequencing of copper-tolerant *Xanthomonas citri* reveals presence of a chimeric plasmid structure and provides insights into reassortment and shuffling of transcription activator-like effectors among *X. citri* strains. **BMC Genomics**. Jan **2018** doi: 10.1186/s12864-017-4408-9.
9. Lapaz MI, **Huguet-Tapia JC**, Siri MI, Verdier E, Loria R, and Pianzzola MJ. Genotypic and phenotypic characterization of Streptomyces species causing potato common scab in Uruguay. **Plant Disease**. **2017**, Volume 101, Number 8. doi.org/10.1094/PDIS-09-16-1348-RE.
10. Zhang Y, Bignell DRD, Zuo R, Fan Q, **Huguet-Tapia JC**, **Ding Y**, Loria R. Promiscuous pathogenicity islands and phylogeny of pathogenic *Streptomyces* spp. **Mol. Plant. Microbe Interact**. **2016** Aug;29(8):640-50. doi: 10.1094/MPMI-04-16-0068-R. .
11. **Huguet-Tapia JC**, Lefebure T, Badger JH, Guan J, Pettis GS, Stanhope MJ, Loria R. Genome content and phylogenomics reveals both ancestral and lateral evolutionary pathways in plant pathogenic *Streptomyces*. **Appl. Environ. Microbiol**. **2016** Jan 29;82(7):2146-55. doi: 10.1128/AEM.03504-15.
12. **Huguet-Tapia JC**, Peng Z, Yang B, Yin Z, Liu S, White FF. Complete genome sequence of the African strain AXO1947 of *Xanthomonas oryzae* pv. Oryzae. **Genome Announc**. **2016** Feb 11;4(1). pii: e01730-15. doi: 10.1128/genomeA.01730-15.
13. Zuo R, Zhang Y, **Huguet-Tapia JC**, Mehta M, Dedic E, Bruner SD, Loria R, Ding Y. [An artificial self-sufficient cytochrome P450 directly nitrates fluorinated tryptophan analogs with a different regio-selectivity.](http://www.ncbi.nlm.nih.gov/pubmed/26743860) **Biotechnol. J.** **2016** May;11(5):624-32. doi: 10.1002/biot.201500416.
14. Ascunce MS**, Huguet-Tapia JC**, Braun EL, Ortiz-Urquiza A, Keyhani NO, Goss EM. . [Whole genome sequence of the emerging oomycete pathogen Pythium insidiosum strain CDC-B5653 isolated from an infected human in the USA.](http://www.ncbi.nlm.nih.gov/pubmed/26981361) **Genom. Data**. 2015 Nov 23;7:60-1.

**Professional activities**

**Society Memberships:**

American Society for Microbiology (ASM)

American Phytopathological Society (APS)

International Society of Computational Biology (ISCB)

**Editorial Services**

**Peer Review Activities:**

Scientific Reports. Nature publishing group.

Genome Announces. American Society for Microbiology.

Crop Science. Crop Science Society of America.