

VALERIA VELASQUEZ-ZAPATA

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SUMMARY

My research currently focuses on developing mathematical models and methods for understanding disease emergence. I study pathogenic mechanisms and host immune responses through the combination of statistical modeling and wet lab approaches, such as the production and analysis of high-throughput data (like Y2H-Seq and RNA-Seq), the use of systems biology to build biological networks, and the integration multi-omics data. Multidisciplinary collaborations have led me to interact with molecular biologists, geneticists, statisticians, and computer scientists in the development of solutions in the field. I hope to find opportunities where I can find fulfillment in my work by continuing to expand my understanding of biological systems and apply my data analysis expertise.

EDUCATION

PhD, Bioinformatics and Computational Biology (minor in Statistics) Iowa State University, USA	GPA: 4/4 July 2021
MS, Biomedical Research University of Valladolid, Spain	GPA: 9.2/10 July 2015
BS, Biology University of Antioquia, Colombia	GPA: 4.4/5 October 2013
BS, Biological Engineering National University of Colombia	GPA: 4.1/5 July 2010

PROJECTS

Y2H-SCORES: [Y2H-SCORES](#) is a software developed to rank protein-protein interactions from yeast two-hybrid next generation interaction screening (Y2H-NGIS) data. Besides the software, I developed a [Y2H-NGIS simulator](#) to generate Y2H-NGIS data, and a [Benchmarking](#) section that proves the performance of the software across published datasets.

Interact-omics: I developed [Interact-omics](#), a series of workflows to integrate interactome data with omics like eQTL, RNASeq and Y2H-NGIS. Different network analyses are presented and applied to characterize the *Mla* receptor signaling.

TranscriptoNET: I am developing different data analysis workflows for transcriptome data. [TranscriptoNET](#) include generation and integration of Gene Regulatory Networks (GRNs), prioritization of transcription factors for their role in regulating expression, data visualization and epistatic analysis of gene effects on gene expression.

SKILLS

Proficient: R, Python, MATLAB, L^AT_EX, Git, BASH, Slurm, Excel, Benchling, Biorender

Familiar: SQL, SAS, Adobe illustrator

Languages: Spanish (native), English (C2), Portuguese (A2)

PUBLICATIONS

- **Velásquez-Zapata V**, Elmore J, Banerjee S, Dorman K, Wise R. *Next-generation yeast-two-hybrid analysis with Y2H-SCORES identifies novel interactors of the MLA immune receptor*. PLoS Computational Biology (2021).
- Banerjee S, **Velásquez-Zapata V**, Fuerst G, Elmore J, Wise R. *NGPINT: A Next-generation protein-protein interaction software*. Briefings in Bioinformatics (2020).
- Chapman A, Hunt M, Surana P, **Velásquez-Zapata V**, Xu W, Fuerst G, Wise R. Disruption of barley immunity to powdery mildew by an in-frame Lys-Leu deletion in the essential protein SGT1. GENETICS (2020).
- **Velásquez-Zapata V**, Palacio K, Gaviria A, Cano LE. *Assessment of genotyping markers in the molecular characterization of a population of clinical isolates of Fusarium in Colombia*. Biomedica (2021).
- Reyes-Herrera P, Muñoz-Baena L, **Velásquez-Zapata V**, Patiño L, Delgado O, Díaz-Diez C, Navas-Arboleda A, Cortés A. *Inheritance of Rootstock Effects in Avocado (Persea americana Mill.) cv. Hass*. Frontiers in Plant Science (2020).

- Gemmell N, **et al.** *The tuatara genome reveals ancient features of amniote evolution*. Nature (2020).
- Fraile E, Díez B, **Velásquez-Zapata V**, Acedo A, Sanz D, Velasco E. *Functional classification of DNA variants by hybrid minigenes: Identification of 30 spliceogenic variants of BRCA2 exons 17 and 18*. PLOS Genetics (2017).
- **Velásquez-Zapata V**, Ochoa R, Muskus C. *Detection of molecular targets in the phosphatidylinositol signaling pathway in Leishmania spp. through bioinformatics tools and mathematical modeling*. Biomedica (2015).

EXPERIENCE

2021-present: Postdoctoral Research Scientist, Wise Laboratory, Plant Pathology and Microbiology Department, Iowa State University. USA. Project: Temporal control of immunity to powdery mildew in barley.

2017-2021: Research Assistant, Wise Laboratory, Plant Pathology and Microbiology Department, Iowa State University. Project: Host and pathogen signalling in cereal fungal interactions.

2015-2016: Research Professional, Colombian Corporation of agricultural research (Agrosavia), Colombia. Project: Technological, productive, and commercial development of avocado in Antioquia.

2014-2015: Research Assistant, Splicing and Cancer susceptibility Laboratory, Molecular Biology and Genetics Institute (IBGM), University of Valladolid, Spain.

2012: Biotechnology Advisor, Microplast S.A. Colombia. Project: Establishment of a controlled breeding system of *Sitophilus oryzae* for repellency bioassays

TALKS

Multi-layered characterization of the barley interactome links MLA immune receptor signaling with defense gene expression, 2021, IS-MPIM conference

Multi-layered characterization of the barley interactome links MLA immune receptor signaling with defense gene expression, 2021, Powdery mildew workshop, IS-MPIM conference

Modeling effector-host interactions in the context of the barley protein interactome, 2019, Colombian Conference in Bioinformatics and Computational Biology

Next-Generation Screening for Host Interactors of Fungal Effectors in Cereal Immunity, 2018, Predictive Plant Phenomics symposium. Iowa State University

FELLOWSHIPS AND ACADEMIC AWARDS

2021: Research Excellence Award. Iowa State University.

2019: Brown Graduate Fellowship. Iowa State University.

2018-2020: Faculty for The Future Ph.D. Fellowship. The Schlumberger Foundation.

2016: Diane Brandt scholarship. Iowa State University.

2015-2021: Fulbright-Minciencias Ph.D. Fellowship.

2014, 2015: Enrollment of honor. Universidad de Valladolid, Spain.

2014, 2015: Asia-Iberoamerica Master Scholarship. Universidad de Valladolid- Banco Santander. Spain.

2012: Iberoamerica Scholarship. Undergraduates. Banco Santander. Spain.

WORKSHOP AWARDS

2022: Genetics Society of America DeLill Nasser award.

2021: Genetics Society of America Presidential Membership.

2019: Sponsorship for attendance to the Grace Hopper Celebration. Anita.org.

2019, 2021: SACNAS conference travel award.

2019, 2021: Sponsorship for attendance to the CRA IDEALS and CRA-W Grad Cohort Workshops.

2018: Bioinformatics Analysis for Conservation Genomics. Smithsonian-Mason School for conservation scholarship.

201e: Centro Argentino Brasileiro en Biotecnologia CABBIO and Colciencias course scholarship.

2015: Universidad Internacional de Andalucía Summer course scholarship. Spain.