

# SAMUEL DAVID GAMBOA-TUZ

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## EDUCATION

### Doctor in Science (Biological Science: Biotechnology)

January 2016 – June 2020

Center for Scientific Research of Yucatan

Merida, Yucatan, Mexico

Advisor: Dr. Luis C. Rodríguez-Zapata.

Thesis: "Functional Analysis of TMBIM Genes from Papaya (*Carica papaya* L.) in Abiotic Stress Tolerance" (title translated from Spanish).

Professional license: 12227901 (MX)

### Master in Science (Biological Science: Biotechnology)

August 2013 – October 2015

Center for Scientific Research of Yucatan

Merida, Yucatan, Mexico

Advisor: Dr. Luis C. Rodríguez-Zapata.

Thesis: "Differential Expression of Bax Inhibitor 1-Like Protein-Coding Genes from *Carica papaya* in Response to Salinity and Water Stress" (title translated from Spanish).

Professional license: 11961706 (MX)

### Bachelor in Biology

August 2006 – February 2013

Faculty of Veterinarian Medicine and Zootechnics,  
Autonomous University of Yucatan

Merida, Yucatan, Mexico

Advisors: Dr. Karla Y. Acosta-Viana and Dr. Matilde Jiménez-Coello

Thesis: "Frequency of *Trypanosma rangeli* and *Trypanosoma cruzi* in DNA Samples from Humans, Reservoirs, and Vectors from Merida, Yucatan, Mexico" (title translated from Spanish).

Professional license: 8058226 (MX)

## PUBLICATIONS

Google Scholar profile: [bit.ly/sdgt-scholar](http://bit.ly/sdgt-scholar)

ORCID: <https://orcid.org/0000-0002-6863-7943>

### Peer-reviewed research articles

1. Zoghbi-Rodríguez, N.M.<sup>1</sup>, **Gamboa-Tuz, S.D.**<sup>1</sup>, Pereira-Santana, A., Rodríguez-Zapata, L. C., Sanchez-Teyer, L. F., Echeverría-Machado, I. \* (2021). Phylogenomic and microsynteny analysis provides evidence of genome arrangements of high-affinity nitrate transporter gene families of plants. *International Journal of Molecular Sciences*, 22(23), 13036. <https://doi.org/10.3390/ijms222313036>
2. Carrillo-Bermejo, E. A.<sup>1</sup>, **Gamboa-Tuz, S. D.**<sup>1</sup>, Pereira-Santana, A., Keb-Llanes, M. A., Castano, E., Figueroa-Yañez, L. J., & Rodríguez-Zapata, L. C.\* (2020). The SoNAP gene from sugarcane (*Saccharum officinarum* L.) is a senescence-associated NAC transcription factor involved in response to osmotic and salt stress. *Journal of Plant Research*, 133(6), 897-909. <https://doi.org/10.1007/s10265-020-01230-y>
3. Pereira-Santana, A.\*, **Gamboa-Tuz, S. D.**, Zhao, T., Schranz, M. E., Vinuesa, P., Bayona, A., Rodríguez-Zapata, L. C., & Castano, E.\* (2020). Fibrillar evolution through the tree of life: Comparative genomics and microsynteny network analyses provide new insights into the evolutionary history of Fibrillar. *PLOS Computational Biology*, 16(10), e1008318. <https://doi.org/10.1371/journal.pcbi.1008318>
4. **Gamboa-Tuz, S. D.**<sup>1</sup>, Pereira-Santana, A.<sup>1</sup>, Zamora-Briseño, J. A., Castano, E., Espadas-Gil, F., Ayala-Sumano, J. T., Keb-Llanes, M. A., Sanchez-Teyer, L. F., & Rodríguez-Zapata, L. C.\* (2018). Transcriptomics and co-expression networks reveal tissue-specific responses and regulatory hubs under mild and severe drought in papaya (*Carica papaya* L.). *Scientific Reports*, 8(1), 14539. <https://doi.org/10.1038/s41598-018-32904-2>
5. **Gamboa-Tuz, S. D.**<sup>1</sup>, Pereira-Santana, A.<sup>1</sup>, Zhao, T., Schranz, M. E., Castano, E., & Rodríguez-Zapata, L. C.\* (2018). New insights into the phylogeny of the TMBIM superfamily across the tree of life: Comparative genomics and synteny networks reveal independent evolution of the BI and LFG families in plants. *Molecular Phylogenetics and Evolution*, 126, 266–278. <https://doi.org/10.1016/j.ympev.2018.04.032>

## Book chapters

1. Carrillo-Bermejo, E. A., Herrera-Alamillo, M. A., **Gamboa-Tuz, S. D.**, Keb-Llanes, M. A., Castano, E., Robert, M. L., & Rodríguez-Zapata, L. C. (2017). Transcriptome, genetic transformation and micropropagation: Some biotechnology strategies to diminish water stress caused by climate change in sugarcane. In V. Andjelkovic (Ed.). *Plant abiotic stress and responses to climate change* (pp. 89-108). *IntechOpen*.  
<https://doi.org/10.5772/intechopen.72438>

## RESEARCH EXPERIENCE

### Ph.D. student

January 2016 – June 2020

*Yucatan Center for Scientific Research*

*Merida, Yucatan, Mexico*

- Application of phylogenetics, syteny networks, and orthology analyses to infer the molecular evolution of protein families: TMBIM, Fibrillarín, and nitrate transporters.
- RNA-seq transcriptomic analysis of papaya plant tissues under drought stress.
- Use of transgenic tobacco plants for the functional analysis of papaya TMBIM genes in NaCl stress tolerance.

### M.Sc. student

August 2013 – October 2015

*Yucatan Center for Scientific Research*

*Merida, Yucatan, Mexico*

- Molecular cloning and differential expression analysis of papaya TMBIM genes in response to abiotic stress.

### Undergraduate research assistant

January 2011 – December 2012

*Regional Research Center Dr. Hideyo Noguchi*

*Merida, Yucatan, Mexico*

- Molecular detection of trypanosomes in humans, reservoirs, and vectors.

### Undergraduate research Assistant

June 2010 – August 2010

*Technological Institute of Merida*

*Mérida, Yucatán, Mexico*

- Characterization of the gene expression patterns of papaya fruit in response to 1-Methylcyclopropene (an ethylene/ripening inhibitor) using the differential display technique.

## TEACHING EXPERIENCE

### Collaborator teacher (invited)

November 2021

*Center for Research and Assistance in Technology and Design of the State of Jalisco* *Guadalajara, Jalisco, Mexico*

- Module: Introduction visualization and manipulation of data in R (10 h).
- Course: Computational Biology.
- Program: Master of Science in Biotechnology Innovation.

### Collaborator teacher (invited)

November 2020

*Center for Research and Assistance in Technology and Design of the State of Jalisco* *Guadalajara, Jalisco, Mexico*

- Module: Introduction to data visualization and manipulation in R (8 h).
- Course: Computational Biology.
- Program: Master of Science in Biotechnology Innovation.

## SCHOLARSHIPS

- National scholarship (Ph.D.), 2016-2019 - National Council of Science and Technology, Mexico.
- National scholarship (M.Sc.), 2013-2015 - National Council of Science and Technology, Mexico.

## PROFESSIONAL DEVELOPMENT

- Workshop: How to Build and Create Tidy Tools (in R), 2019.
- Workshop: Genome Assembly and Annotation, 2018.

## TECHNICAL SKILLS

- **GNU/Linux OS.** Use of the command line for data parsing and extraction, and application of different bioinformatics tools.
- **Programming:**
  - **Bash.** A few scripts that I've written and shared: [https://github.com/sdgamboa/bash\\_scripts](https://github.com/sdgamboa/bash_scripts)
  - **R** (Rstudio, Base, Tidyverse, Bioconductor).
- **Version control.** Git and GitHub; my site: <https://github.com/sdgamboa>
- **Preferred text editor:** Vim.
- **Network analysis.** Clustering and visualization of networks (Igraph, CFinder, Cytoscape, Gephi).
- **RNA-seq data analysis.** Quality check and filtering, assembly, annotation, read mapping, differential expression.
- **Molecular evolution.** Homology search, alignment, model testing, phylogenetic inference, orthology, syntenic networks.
- **Molecular biology.** Purification of nucleic acids, PCR, molecular cloning (restriction enzymes and Gateway technology), genetic transformation (bacteria and plants).