

## Academic History

**Postdoctoral Scholar (Advisor: James C. Schnable)** October 2021 - present  
**University of Nebraska** Lincoln, NE, USA

- Identification of candidate genes using large gene expression and genetic variants datasets for Maize and Sorghum.
- Recognition and correction for signals that can add bias or noise to large gene expression analysis.
- Call of Single nucleotide polymorphisms (SNPs) from approximately 800 Maize RNA-Seq libraries using GATK.
- Application of molecular tools to identify alleles with a putative loss-of-function phenotype to study candidate genes previously identified.

**PhD - Plant Biotechnology** March 2017 - August 2021  
**LANGEBIO-CINVESTAV** Irapuato, Mexico

- Elucidation of the effect of nitrogen deficiency on the molecular phosphorus starvation response in Maize using transcriptional, ionic and phenotypic data.
- Identification of parental regions within crosses using Single nucleotide polymorphisms (SNPs) and simple sequence repeats (SSRs).
- Generation of Maize populations.
- Manual phenotyping of Maize plants in multiple fields and greenhouses.

**MSc - Plant Biotechnology** September 2014 - February 2017  
**LANGEBIO-CINVESTAV** Irapuato, Mexico

- Selection of lines with teosinte (*Zea mays ssp. parviglumis*) introgression based on molecular markers
- Correction for environmental effects in phenotypes using linear mixed models.
- Collection of plant tissue in greenhouse and laboratory (root and aerial parts).

**BSc - Agricultural engineering** August 2009 - June 2013  
**Universidad Autónoma Chapingo** Texcoco, México

## Leadership & Activities

**President** 2023 – 2024  
**Collective Research Organization of Plant Science (CROPS)** University of Nebraska-Lincoln

- Promote scientific events to help students develop ideas and network with scientists outside the university.
- Help the community to develop soft skills in a supportive environment.
- Guide younger scientist.

## Skills

**Personal:** Teamwork, Active listening, Leadership, Optimization

**Technical:** R language (advanced), Bash command line (intermediate), Data analysis and management, Writing and summarizing results for publications and reports

**Language:** English (advanced), Spanish (Native)

**Laboratory:** Real-time-PCR analysis, Molecular marker application

## Presentations

- “Inferring gene function from expression levels in maize” North Dakota State University. March 12<sup>th</sup> 2024. Invited lecture (Online)
- “Population-Level Gene Expression Can Repeatedly Link Genes to Functions in Maize” Plant and Animal Genome 2024 conference. January 11<sup>th</sup> - 17<sup>th</sup> 2024. Invited talk
- “Inferring gene function from expression levels in maize” Plant Science Innovation department (Internal talk). November 20<sup>th</sup> 2023. Invited talk
- “Employing environmental indices to augment cross-environment prediction accuracy in diverse maize populations. Machine Learning for Cyber-Agricultural Systems (MLCAS2023). July 2<sup>nd</sup> 2023. Invited talk
- “Measurement of expression from a limited number of genes is sufficient to predict flowering time in maize”. Maize Genetic Conference 2023. March 16<sup>th</sup> - 19<sup>th</sup>. Invited talk
- “A small subset of genes can predict flowering time with high accuracy in maize” MLCAS2022. October 10<sup>th</sup> - 11<sup>th</sup>. Invited talk

## Preprints

- Engelhorn J, Snodgrass S, Kok A, Seetharam A, Schneider M, Kiwit T, Singh A, Banf M, Khaipho-Burch M, Runcie D, Camargo V, **Torres-Rodríguez, J. V.**, Sun G, Stam M, Fiorani F, Schnable JC, Bass H, Hufford M, Stich B, Frommer W, Ross-Ibarra J, Hartwig T. (2023). Phenotypic variation in maize can be largely explained by genetic variation at transcription factor binding sites. bioRxiv doi: 10.1101/2023.08.08.551183

## Publications

- **Torres-Rodríguez, J. V.**, Li, D., Turkus, J., Newton, L., Davis, J., Lopez-Corona, L., ... & Schnable, J. C. (2023). Population-level gene expression can repeatedly link genes to functions in maize. *The Plant Journal* [Accepted].
- Tross, M. C., Grzybowski, M. W., Jubery, T. Z., Grove, R. J., Nishimwe, A. V., **Torres-Rodríguez, J. V.**, ... & Schnable, J. C. (2023). Data-driven discovery and quantification of hyperspectral leaf reflectance phenotypes across a maize diversity panel. *The Plant Phenome Journal* [Accepted].
- Sun, G., Wase, N., Shu, S., Jenkins, J., Zhou, B., **Torres-Rodríguez, J. V.**, ... & Schnable, J. C. (2022). Genome of *Paspalum vaginatum* and the role of trehalose mediated autophagy in increasing maize biomass. *Nature Communications*, 13(1), 1-20.
- Alonso-Nieves, A. L., Salazar-Vidal, M. N., **Torres-Rodríguez, J. V.**, Pérez-Vázquez, L. M., Massange-Sánchez, J. A., Gillmor, C. S., & Sawers, R. J. (2022). The *pho1; 2a0-m1. 1* allele of *Phosphate1* conditions misregulation of the phosphorus starvation response in maize. *Plant Direct*, 6(7)
- **Torres-Rodríguez, J. V.**, Salazar-Vidal, M. N., Chávez Montes, R. A., Massange-Sánchez, J. A., Gillmor, C. S., & Sawers, R. J. (2021). Low nitrogen availability inhibits the phosphorus starvation response in maize (*Zea mays* ssp. *mays* L.). *BMC plant biology*, 21(1), 1-18.
- Crow, T., Ta, J., Nojoomi, S., Aguilar-Rangel, M. R., **Torres-Rodríguez, J. V.**, Gates, D., ... & Runcie, D. (2020). Gene regulatory effects of a large chromosomal inversion in highland maize. *PLoS genetics*, 16(12), e1009213.