

Hongyu Jin

 JIN-HY |  hjin5 |  jinhy2191@gmail.com |  4029376983

EDUCATION

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- 2019 - present Ph.D. student at **University of Nebraska-Lincoln** (GPA: 3.88/4.0)
Advisors: Dr. James Schnable and Dr. Jinliang Yang
Relevant Courses: Computer Vision, Data Mining, Multivariate Statistics
- 2014 - 2018 Bachelor's Degree at **China Agricultural University** (GPA: 3.64/4.0)

WORK EXPERIENCE

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- Graduate Research Assistant at University of Nebraska-Lincoln** Aug 2019 - present
– Process genomic data, including SNP calling, population genetics analysis, GWAS and genomic prediction.
– Perform high throughput phenotyping. Use computer vision and deep learning algorithms to extract plant phenotypes from plant images taken in field and greenhouse.
- Mentor of 2022 Summer Research Program at University of Nebraska-Lincoln** Jun 2022 - Aug 2022
– Guide the intern through a high-throughput phenotyping experiment.
– Teach the intern basic machine learning algorithm and application on hyperspectral image segmentation.
- Research Intern at Duke University, Durham NC** Sep 2018 - Mar 2019
– Phenotype and cross pollinate *Ipomea* plants.
– Genotype *Ipomea* plants for gene fine mapping.
- Research Intern at Syngenta Biotechnology in Beijing, China** Sep 2017 - Feb 2018
– Construct vectors for gene editing experiment
– Conduct quality control test for the gene editing vectors

PUBLICATIONS

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- Ma, C., B. Li, L. Wang, M. Xu, L. E. **H. Jin**, Z. Wang, and J. Ye (May 2019). "Characterization of phytohormone and transcriptome reprogramming profiles during maize early kernel development". In: *BMC Plant Biology* 19.1. DOI: [10.1186/s12870-019-1808-9](https://doi.org/10.1186/s12870-019-1808-9). URL: <https://doi.org/10.1186/s12870-019-1808-9>.
- Shen, L., T. Zhong, L. Wang, Q. Zhang, **H. Jin**, M. Xu, and J. Ye (Sept. 2019). "Characterization the role of a UFC homolog, AtAuxRP3, in the regulation of Arabidopsis seedling growth and stress response". In: *Journal of Plant Physiology* 240, p. 152990. DOI: [10.1016/j.jplph.2019.152990](https://doi.org/10.1016/j.jplph.2019.152990). URL: <https://doi.org/10.1016/j.jplph.2019.152990>.
- A.H.M. Nipuna Chamara, K. Alkady, **H. Jin**, F. Bai, A. Samal, and Y. Ge (2021). *A Deep Convolutional Neural Network Based Image Processing Framework for Monitoring the Growth of Soybean Crops*. DOI: [10.13031/aim.202100259](https://doi.org/10.13031/aim.202100259). URL: <http://doi.org/10.13031/aim.202100259>.
- Boatwright, J., S. Sapkota, **H. Jin**, J. Schnable, Z. Brenton, R. Boyles, and S. Kresovich (July 2022). "Sorghum Association Panel whole-genome sequencing establishes cornerstone resource for dissecting genomic diversity". In: *The Plant Journal* 111.3, pp. 888–904. DOI: [10.1111/tpj.15853](https://doi.org/10.1111/tpj.15853). URL: <https://doi.org/10.1111/tpj.15853>.
- Grzybowski, M., M. Zwiener, **H. Jin**, N. Wijewardane, A. Atefi, M. Naldrett, S. Alvarez, Y. Ge, and J. Schnable (2022). *Variation in morphophysiological and metabolic responses to low nitrogen stress across the sorghum association panel*. DOI: [10.1101/2022.06.08.495271](https://doi.org/10.1101/2022.06.08.495271). URL: <http://doi.org/10.1101/2022.06.08.495271>.
- Mural, R., G. Sun, M. Grzybowski, M. Tross, **H. Jin**, C. Smith, L. Newton, C. Andorf, M. Woodhouse, A. Thompson, B. Sigmon, and J. Schnable (2022). "Association mapping across a multitude of traits collected in diverse environments in maize". In: *GigaScience*. DOI: [10.1093/gigascience/giac080](https://doi.org/10.1093/gigascience/giac080). URL: <http://doi.org/10.1093/gigascience/giac080>.

PRESENTATIONS

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- Hongyu Jin**, Michael Tross, Ravi V. Mural, Ruijuan Tan, Christine Smith, Linsey Newton, Jinliang Yang, Addie M. Thompson, James C. Schnable: Cross environment yield prediction using genomic and phenotypic data in maize. Poster presented at: 64rd Annual Maize Genetics Meeting, in St. Louis, MO, March 2022.
- Hongyu Jin**, Michael Tross, Ravi V. Mural, Ruijuan Tan, Christine Smith, Linsey Newton, Jinliang Yang, Addie M. Thompson, James C. Schnable: Cross environment yield prediction using genomic or phenotypic data in maize. Poster presented at: 2022 NAPB Annual Meeting, in Ames IA.
- Hongyu Jin** and Jinliang Yang. Pollen-sequencing: A rapid and cost-effective method to construct genetic map using sequencing data from the hybrid pollens. Poster presented at: 63rd Annual Maize Genetics Meeting, 2021 Virtual.
- Hongyu Jin**, Michael Tross, Ravi V. Mural, Ruijuan Tan, Christine Smith, Linsey Newton, Jinliang Yang, Addie M. Thompson, James C. Schnable. Benchmarking cross environment yield prediction in maize. Recorded long talk at Third International Workshop on Machine Learning for Cyber-Agricultural Systems (MLCAS2021)
- A.H.M. Nipuna Chamara**, **Khalid Alkady**, **Hongyu Jin**, Frank Bai, Ashok Samal and Yufeng Ge. Deep Convolutional Neural Network Based Image Processing Framework for Monitoring the Growth of Soybean Crops. Recorded talk at 2021 ASABE Annual International Virtual Meeting

SKILLS

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- Computing tools Python, R, bash, Matlab, and high performance computing
Data analysis tools Scikit-learn, Pytorch, Keras and OpenCV
Miscellaneous Field work, cross pollination, DNA extraction, PCR and molecular cloning