**Yingni Xiao**

Visiting Adjunct Scholar

Prof. Erich Grotewold Lab

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Research Experiences

**Associate Researcher, Sweet corn Lab, Crops Research Institute, Guangdong Academy of Agricultural Sciences (2017.11-present)**

* Investigating the candidate genes associated with the nutritional quality of sweet corn kernels, including vitamin E and folate.
* Employing multi-omics approaches to dissect the complex genetic traits in sweet corn.
* Developing molecular markers to improve the nutrition quality in sweet corn.

**Post-doctoral Associate, Prof. Yang Xiaohong Lab, China Agricultural University (2016.01-2017.10)**

* Exploring the candidate genes associated with kernel weight or size ( embryo size, embryo weight, and so on) in maize kernel by GWAS.
* Exploring the candidate genes associated with kernel composition (starch, protein and oil) in maize kernel by GWAS.

**Graduate Research Associate, China Agricultural University (2009.09- 2015.12)**

* Fine mapping a major QTL associated with starch content in maize kernel.
* Transcriptome analysis of a pair of near-isogenic lines provides molecular insights into starch biosynthesis in maize kernel.

**Education**

Ph.D., Plant Genetics and Breeding, China Agricultural University, Beijing, China(2009.9-2015.12), supervised by Prof. Jiansheng Li & Prof. Xiaohong Yang.

Thesis: Fine mapping and clone a major QTL (qHS3) associated with starch content in maize kernel.

B.S., Agronomy, China Agricultural University, Beijing, China (2005.9-2009.6), supervised by Prof. Zhiyong Liu.

Thesis: Identification and Genetic Mapping of Powdery Mildew Resistance Gene.

**Professional Skills**

* **Molecular genetics**: Extensive wet lab experiences including mutant characterization, gene cloning, genotyping and marker development, etc;
* **Quantitative trait locus (QTL) genetics**: linkage and association mapping;
* **Plant breeding and related work**: pollination, field design, sampling, harvesting etc;
* **Bioinformatics and Statistics:** familiar with designing bioinformatics analysis pipelines using R;
* **Project Management and Communication:** Good experience in team collaboration and project management; writing scientific manuscripts independently.

**Publications:**

1. Jingyan Liu#, **Yingni Xiao**#, et al., Integrated Transcriptome and Metabolome Analysis Reveals Mechanism of Flavonoid Synthesis During Low-Temperature Storage of Sweet Corn Kernels. *Foods*. 2024. 13: 4025.(# co-first author)
2. **Yingni Xiao**, Lihua Xie, et al., Impact of low temperature on the chemical profile of sweet corn kernels during post-harvest storage. *Food Chemistry*. 2024(431): 137079.
3. **Yingni Xiao**, Yongtao Yu, Lihua Xie, et al., A genome-wide association study of folates in sweet corn kernels. *Frontiers in plant science*. 2022: 1004455.
4. **Yingni Xiao**, Yongtao Yu, Gaoke Li, et al. Genome-wide association study of Vitamin E in sweet corn kernels. *Crop Journal*. 2020. 8:341-350.
5. **Yingni Xiao**, Shawn Thatcher, Min Wang, et al. Transcriptome analysis of near-isogenic lines provides molecular insights into starch biosynthesis in maize kernel. *Journal of integrative plant biology*, 2016. 8: 713-723.
6. Yin P, Fu X, Feng H, Yang Y, Xu J, Zhang X, Wang M, Ji S, Zhao B, Fang H, Du X, Li Y, Hu S, Li K, Xu S, Li Z, Liu F, **Xiao Y**, Wang Y, Li J, Yang X. Linkage and association mapping in multi-parental populations reveal the genetic basis of carotenoid variation in maize kernels. *Plant Biotechnol J*. 2024 22(8):2312-2326.
7. Chen W., Chen L., Zhang X., Yang N., Guo J., Wang M., Ji S., Zhao X., Yin P., Cai L., Xu J, Han Y, **Xiao Y.**, et al. Convergent selection of a WD40 protein that enhances grain yield in maize and rice. *Science*. 2022. 375(6587): abg7985.
8. Hu S., Wang M.#, Zhang X., Chen W., Song X., Fu X., Fang H., Xu J., **Xiao Y.,** et al. Genetic basis of kernel starch content decoded in a maize multi-parent population. *Plant Biotechnology Journal*. 2021(19): 2192-2205.
9. Wang T, Wang M, Hu S, **Xiao Y.,** et al. Genetic basis of maize kernel starch content revealed by high-density single nucleotide polymorphism markers in a recombinant inbred line population. *BMC plant biology,* 2015, 15(1): 288.