

## Laboratory of Crop Breeding

### Department of Agronomy, National Chung Hsing University

#### 實驗室主持人 PI



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#### Education :

**PhD in Agriculture** (Graduate School of Environmental and Life Science, Okayama Univ, JAPAN)

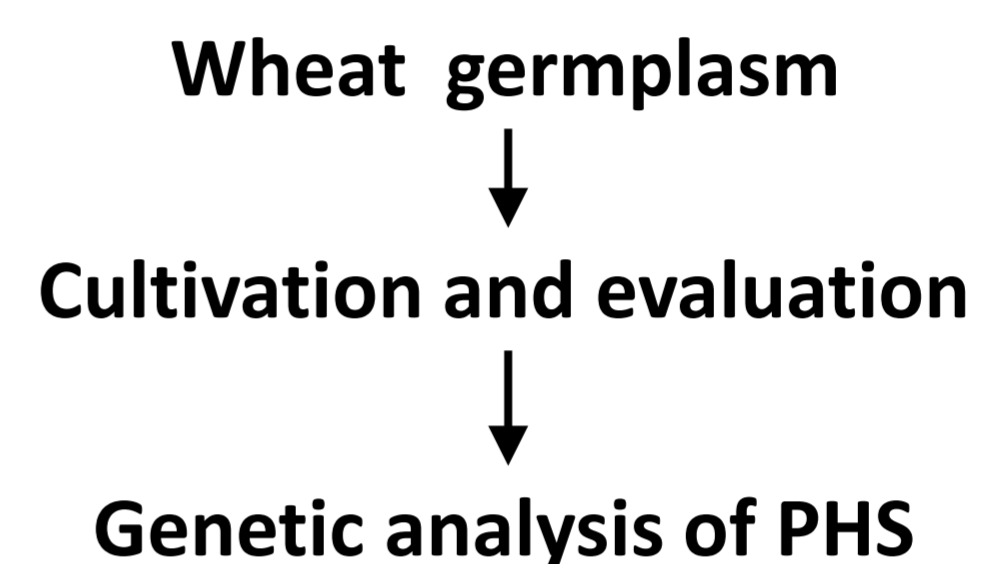
**MSc in Agronomy** (Department of Agronomy, NCHU, Taichung, TAIWAN)

**BSc in Agronomy** (Department of Agronomy, NCHU, Taichung, TAIWAN)

#### 研究主題 Research topic

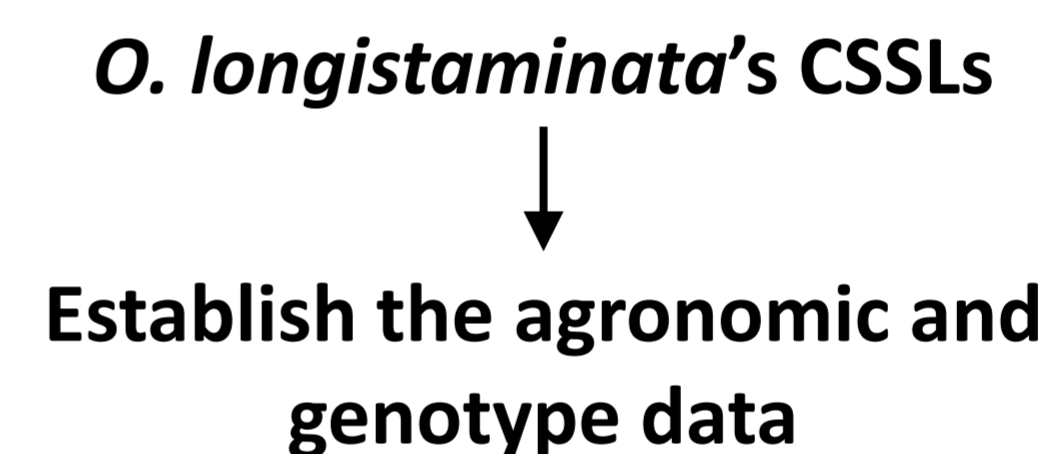
##### WHEAT

Wheat (*Triticum* spp.) is one of the major staple food of the world. In order to achieve high and stable wheat production in Taiwan, it is necessary to increase and evaluate the wheat genetic resources, improving current varieties, and developing diverse varieties. In addition, the wheat harvest time overlaps with the Spring raining season that could lead to pre-harvest sprouting (PHS) occur, resulting in huge damage in yield and quality. Therefore, it is crucial to investigation the PHS resistance of the wheat varieties in Taiwan.



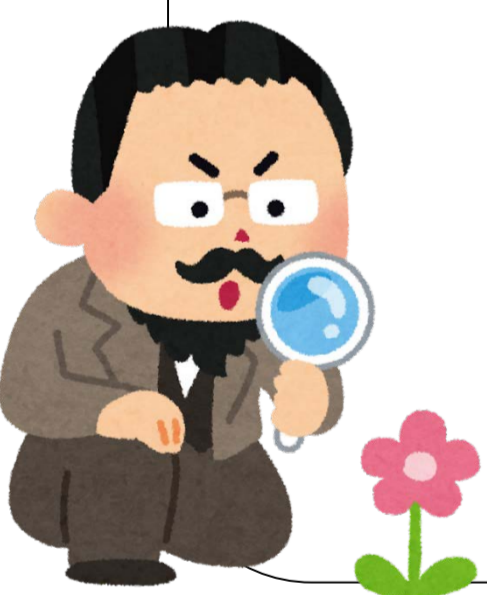
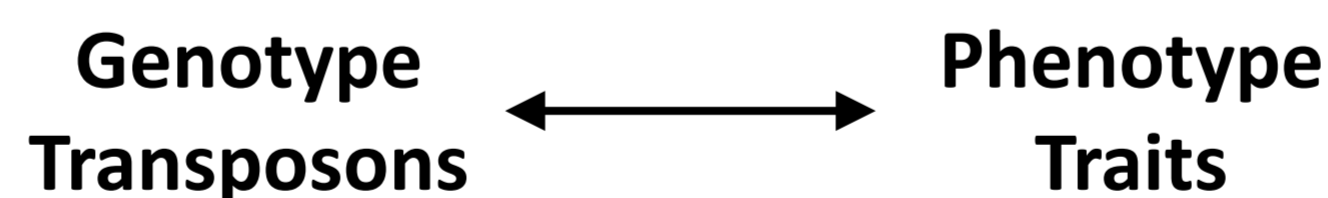
##### RICE

Wild relatives of rice (*Oryza sativa*) have the potential for improving agronomic traits and enlarging the genetic variability in modern varieties. *O. longistaminata* is grown in Africa tropical area, perennial, with rhizomes, high biomass, and resistance to biotic and abiotic stresses. It's a powerful tool to identify and apply the useful traits from wild species through their chromosome segment substitution lines (CSSLs), those were selected by molecular markers covering the whole genome.



##### TRANSPOSON

Transposable elements (TEs) provide genetic diversity and structural variation in genomes and play a key role in the study of plant genomes. By studying the copy number, locations and transposition abilities of TEs and the relation with important traits could reveal the lineage and genetic factors for regulating traits.



#### 研究成果 Publication

- Huang, Y.-H., Lin, T.-C., **Chiou, W.-Y.**, Cheng, Y.-M. (2021). The *r-X1* deletion induces terminal deficiencies in the maize B chromosome. *Chromosome Research* 29: 351–360.
- Wu, C.-C., Wei, F.-J., **Chiou, W.-Y.**, Tsai, Y.-C., Wu, H.-P., Gotarkar, D., Wei, Z.-H., Lai, M.-H., Hsing, Y.-I.C. (2020). Studies of rice *Hd1* haplotypes worldwide reveal adaptation of flowering time to different environments. *PLoS ONE* 15: e0239028.
- Chiou, W.-Y.**, Kawamoto, T., Himi, E., Rikiishi, K., Sugimoto, M., Hayashi-Tsugane, M., Tsugane, K., and Maekawa, M. (2019). *LARGE GRAIN* Encodes a Putative RNA-Binding Protein that Regulates Spikelet Hull Length in Rice. *Plant Cell and Physiology* 60: 503–515.
- Chiou, W.-Y.**, Tsugane, K., Kawamoto, T., and Maekawa, M. (2018). Easy sectioning of whole grain of rice using cryomicrotome. *Breeding Science* 68: 381–384.
- Wei, F.-J., Kuang, L.-Y., Oung, H.-M., Cheng, S.-Y., Wu, H.-P., Huang, L.-T., Tseng, Y.-T., **Chiou, W.-Y.**, et al. (2016). Somaclonal variation does not preclude the use of rice transformants for genetic screening. *The Plant Journal* 85: 648–659.

