**Genomic changes shaping domestication traits of soybean**

Lam HM1, Wang Z1, Wang X1, Duan S1, Xie M1, Wong FL1, Yung WS1, Li MW1

*honming@cuhk.edu.hk*

1 School of Life Sciences and Center for Soybean Research of the State Key Laboratory of Agrobiotechnology, The Chinese University of Hong Kong, Hong Kong SAR, China

During soybean domestication, genetic variations were selected to improve agronomic traits such as growth habit, flowering time, and crop yield. Genomic studies in crops not only advance our understanding about crop domestication, but also enable the identification of novel alleles for crop improvement.

To understand domestication-related events using wild germplasms, we have constructed a reference-grade genome of wild soybean W05. By comparing between the wild and cultivated soybean genome, a complex structural rearrangement which led to the expression of a subtilisin-anti-CHS1 chimeric transcript was found to cause the seed coat color change during domestication. Using a recombinant inbred population between wild soybean W05 and cultivated soybean C08, we have performed QTL mapping and successfully identified genomic variations regulating different domestication traits. Making use of the optical mapping data, a copy number variation region of the *gibberellin 2-oxidase 8* genes was found to be strongly selected during domestication to repress trailing growth and long shoots. Also, several QTLs for root system architecture-related traits was found to co-localize with flowering-time loci in soybean. Knocking down the maturity gene *E1* led to a diminished root system, suggesting that the selection for flowering time has indirectly shaped the root system architecture in soybean. We also identified that a loss-of-function allele of a transcriptional repressor, GmbHLH113, contributed to a longer root hair that has potential beneficial effect on nutrient acquisition. To facilitate breeding, we also developed a universal panel of DNA markers including domestication traits-associated markers based on the genomic data from popular soybean varieties.

***References:***

[1] Xie M. et al, ‘A reference-grade wild soybean genome’, Nat Commun, vol. 10, 2019, p. 1216.

[2] Wang X. et al, ‘Increased copy number of gibberellin 2-oxidase 8 genes reduced trailing growth and shoot length during soybean domestication’, Plant J, vol. 107, 2021, p. 1739-1755.