**Integrated single-nucleus and spatial transcriptomics captures transitional states in soybean nodule maturation**

Liu J1, Kong X2,3,4, Long YP1, Zhang H1, Jia JB1, Qiu LJ2, Zhai JX1,Yan Z2,3

*[zhaijx@sustech.edu.cn](mailto:zhaijx@sustech.edu.cn)*

*[yanzhe@caas.cn](mailto:yanzhe@caas.cn)*

*1 Department of Biology, School of Life Sciences, Southern University of Science and Technology, Shenzhen , China*

*2 The National Key Facility for Crop Gene Resources and Genetic Improvement (NFCRI), Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, P.R. China*

*3  Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Changchun, China*

*4  University of Chinese Academy of Sciences, Beijing, China*

Legumes form symbiosis with rhizobium leading to the development of nitrogen-fixing nodules. Nodule development begins with the differentiation of cortex of infected root and involves interplays of both nodules and rhizobia. However, our understanding of cellular heterogeneity and developmental lineage of nodule is still limited. By integrating single-nucleus and spatial transcriptomics, we established a cell atlas of soybean nodules and roots. In central infected zones of nodules, we found that uninfected cells specialize into functionally distinct subgroups during nodule development, and revealed a transitional subtype of infected cells with enriched nodulation-related genes. Further functional analysis revealed the important role of cell-type-specific genes in regulating nodule development and nitrogen fixation.

***References:***

[1] Liu J. et al., 2023, Nat Plants. 9(4):515-524.