

Single-cell transcriptome atlas reveals spatiotemporal developmental trajectories in the basal roots of Moso bamboo (*Phyllostachys edulis*)

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Abstract: **【Objective】** Roots are essential for plant growth and development. Bamboo is a large Poaceae perennial with 1,642 species worldwide. Root system is the basis of bamboo forest growth and development, and plays an important role in the long-term maintenance of bamboo forest ecosystem function and productivity. The anatomical and morphological characteristics of bamboo roots are different from those of model plants such as *Arabidopsis* and rice. However, little is known about the transcriptional atlas that underpin root cell-type differentiation. **【Result】** Here, we set up a modified protocol for protoplast preparation and reported single-cell transcriptomes of 14,279 filtered single cells derived from the basal root tips of Moso bamboo. We identified four cell types and defined new cell type-specific marker genes for the basal root. We reconstructed the developmental trajectories of the root cap, epidermis, and ground tissues and elucidated critical factors regulating cell fate determination. According to *in situ* hybridization and pseudotime trajectory analysis, the root cap and epidermis originated from a common initial cell lineage, revealing the particularity of bamboo basal root development. We further identified key regulatory factors for these cells differentiation and indicated divergent root developmental pathways between Moso bamboo and rice. Additionally, *PheWOX13a* and *PheWOX13b* ectopically expressed in *Arabidopsis* inhibited primary root and lateral root growth by mediating the auxin pathway, which was different from *WOX13* orthologs in *Arabidopsis*. **【Conclusion】** The first single-cell resolution transcriptome atlas of Moso bamboo root was constructed, the developmental trajectories of root cap, epidermis, and ground tissues were reconstructed, and the important regulatory factors of bamboo root development were mined. Taken together, our results offer an important resource for investigating the mechanism of root cell differentiation and root system architecture in perennial woody species of Bambusoideae.

Keywords: Moso bamboo; scRNA-seq; transcriptional atlas; *WOX*; basal root development; cell differentiation