國立陽明交通大學應用數學系
學術演講公告

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講　題：Single-cell transcriptomics unveils xylem cell development and evolution

時　間：112 年 11 月 28 日(星期二) 下午 2:00 –3:00

地　點：(光復校區) 科學一館 223 室

Abstract

As the most abundant tissue on Earth, xylem is responsible for lateral growth in plants. Typical xylem has a radial system composed of ray parenchyma cells and an axial system of fusiform cells. In most angiosperms, fusiform cells are a combination of vessel elements for water transportation and libriform fibers for mechanical support, while both functions are performed together by tracheids in other vascular plants. However, little is known about the developmental programs and evolutionary relationships of these xylem cell types. Through both single-cell and laser-capture microdissection transcriptomic profiling, here we demonstrate the developmental lineages of ray and fusiform cells in stem-differentiating xylem across four divergent woody angiosperms. Cross-species analyses of single-cell trajectories reveal highly conserved ray, yet variable fusiform, lineages across angiosperms. Core eudicots Populus trichocarpa and Eucalyptus grandis share nearly identical fusiform lineages. The tracheids in the basal eudicot Trochodendron aralioides, an evolutionarily reversed character, exhibit strong transcriptomic similarity to vessel elements but not libriform fibers, suggesting that water transportation, instead of mechanical support, is the major feature. We also found that the more basal angiosperm Liriodendron chinense has a fusiform lineage distinct from that in core eudicots. This evo-developmental framework provides a comprehensive understanding of the formation of xylem cell lineages across multiple plant species spanning over a hundred million years of evolutionary history. Within the past one and half years, four research groups have published their studies in the top 5% journals on elucidating stem-differentiating xylem development. Yet, these four articles led to four conflicting models. In an attempt to sort out this puzzle, we reached out to the other corresponding authors to determine the current most plausible model.

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