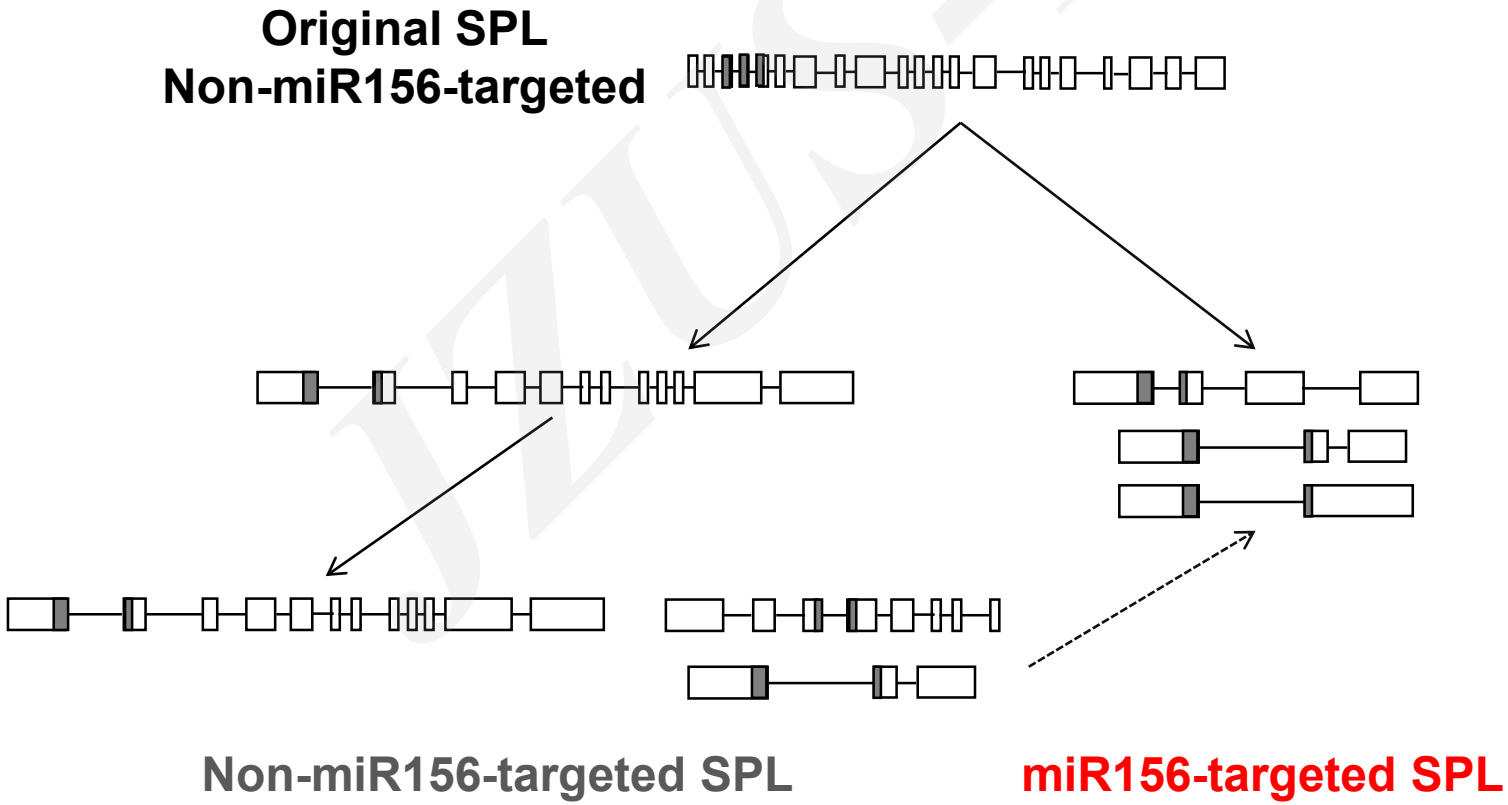
Cite this as: Erkui YUE, Hua TAO, Jianhong XU. Genome-wide analysis of microRNA156 and its targets, the genes encoding SQUAMOSA promoter-binding protein-like (SPL) transcription factors, in the grass family Poaceae[J]. *Journal of Zhejiang University Science B*, 2021, 22(5): 366-382.
https://doi.org/10.1631/jzus.B2000519

Genome-wide analysis of microRNA156 and its targets, the genes encoding SQUAMOSA promoter-binding protein-like (SPL) transcription factors, in the grass family Poaceae

Key words: miR156, SPL genes, DNA methylation, Gene expression, Grass genomes

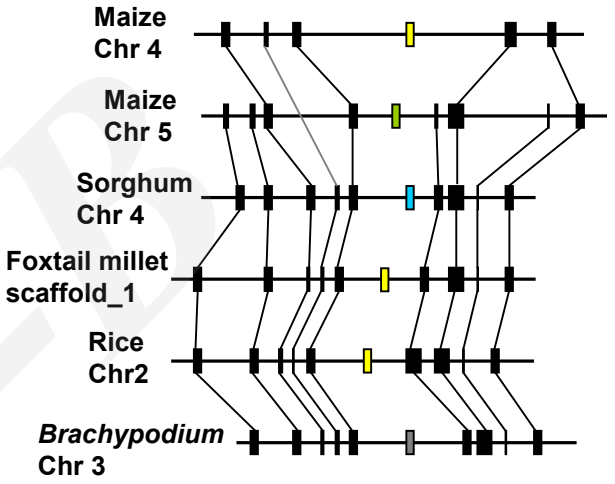
Research Summary

This study mainly focused on the origin and evolution of *MIR156* and *SPL* genes, the SPLs appear to have resulted from vertical evolution, whereas MIR156s appear to have resulted from strong evolutionary selection on mature sequences.

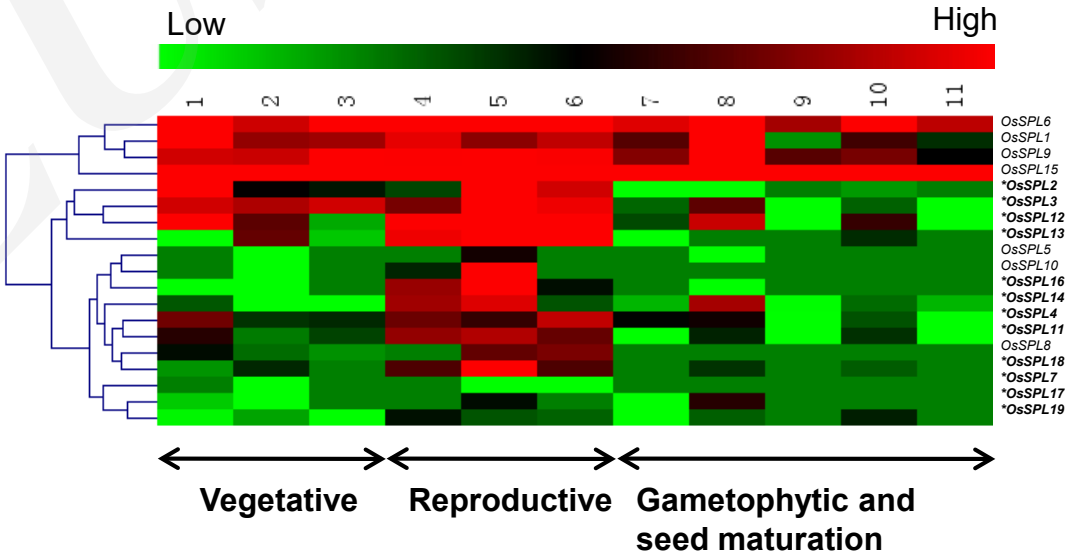


Innovation points

- **Identified** multiple copies of *MIR156* and *SPL* in the grass genomes. Sequence and chromosomal synteny analysis showed that both *MIR156s* and *SPLs* are conserved across species in the grass family.



- **Four** non-miR156-targeted genes were highly expressed and three miR156-targeted genes were only slightly expressed in all tissues/developmental stages. The remaining *SPLs* were highly expressed in the juvenile stage, but their expression was lower in the adult stage.



Innovation points

- **DNA methylation profiles of *SPLs* and *MIR156s* in different rice tissues showed diverse methylation patterns, and hypomethylation of non-CG sites was observed in rice endosperm.**