

AGL80.5和FPA.3的自然变异通过生长素合成通路影响杨树萌芽时间

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摘要: 多年生木本植物的物候特征对其生态功能和适应复杂环境至关重要。然而, 这些性状背后的遗传基础尚不清楚。在此, 我们探讨了毛白杨 (*Populus tomentosa*) 春季芽萌芽的遗传结构和调控机制。通过物候性状和气候环境因素的全基因组关联分析, 我们鉴定了在光周期途径中调控萌芽时间的关键基因: *PtoAGL80.5* 和 *PtoFPA.3*。利用在人工气候箱中的转基因杨树以及在两个不同纬度下自然条件的生长实验, 我们验证 *PtoAGL80.5* 和 *PtoFPA.3* 在春季萌芽中的作用。萌芽阶段的动态转录组分析和分子实验揭示了 *PtoAGL80.5* 和 *PtoFPA.3* 的表达受到杨树典型物候模块 (即, *PtoEBB1-PtoSVP*) 的调控。此外, *PtoFPA.3* 的特定单倍型结合 *PtoAGL80.5* 的 RNA, 通过影响其蛋白含量差异激活生长素合成基因 *PtoTAR2.1* 的转录, 从而影响春季萌芽时间。此外, 到 21 世纪末, *PtoAGL80.5* 和 *PtoFPA.3* 的晚芽单倍型增加, 减少了毛白杨在不同纬度上的萌芽时间差异。我们的研究为理解多年生植物物候机制提供了更深入的认识, 并支持在气候变化中发展目标育种和保护策略。

Natural variants of AGL80.5 and FPA.3 contribute to bud break timing in poplar by controlling auxin biosynthesis

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Abstract: The phenological characteristics of perennial woody plants contribute to their ecological functions and adaptation to complex environments. However, the underlying genetic basis of these traits remains unclear. Here we explored the genetic architecture and regulatory mechanisms of spring bud break (BB) in *Populus tomentosa*. Through genome-wide association studies of phenological traits and climate-environment factors, we identified *AGAMOUS-LIKE 80* (*PtoAGL80.5*) and *FLOWERING TIME CONTROL* (*PtoFPA.3*) as causative genes within the photoperiod pathway that regulate BB timing. Using transgenic poplar in growth chambers and two different latitudes, we demonstrated the roles of these genes in earlier BB. Dynamic transcriptome analysis during the BB stage and molecular experiments revealed that the expressions of *PtoAGL80.5* and *PtoFPA.3* are regulated by the canonical phenological module (i.e., *EARLY BUD BREAK 1*, *SHORT VEGETATIVE PHASE-like*). Furthermore, a specific haplotype of *PtoFPA.3* binds to the RNA of *PtoAGL80.5*, affecting its protein content and subsequently activating the transcription of auxin synthesis gene *PtoTAR2.1*, which influence BB. Moreover, an increase in late bud haplotypes of *PtoAGL80.5* and *PtoFPA.3* by the end of the 21st century, which reduce the time difference in BB of *P. tomentosa* across latitudes. Our study provides a deeper understanding of the mechanisms underlying phenology in perennial plants and supports the development of target breeding and conservation strategies amid climate change.