拟南芥LEAFY基因在花发育中的网络调控及其生物学功能

Regulation Network and Biological Roles of LEAFY in Arabidopsis thaliana in Floral Development

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重点综述了拟南芥花分生组织特征基因——LEAFY(LFY)基因及其同源基因在花发育中的网络调控及其 生物学功能。LFY基因广泛表达于高等植物的营养性和生殖性组织。LFY基因需要与其他基因相互作用,並且表达 量达到一定水平时才能促进成花。LFY基因处于成花调控网络的关键位置,不仅调控开花时间和花转变,而且在花▶文章反馈 序和花的发育中也起重要作用。碳源、植物激素等因子直接或间接地影响LFY基因的表达和作用。提示通过掌握 LFY基因的表达调控规律进一步探讨成花机理的可行性。

Abstract:Recent research progress on regulation network and biological roles of LFY gene in Arabidopsis thaliana and its homologue genes in floral development are reviewed emphatically in the ▶本刊中 包含"LFY基因"的 present paper. LFY gene expresses widely in both vegetative and reproductive tissues in different higher plants, therefore investigation on role of LFY gene on flowering is of general significance. LFY gene plays an important role to promote flower formation by interaction and coordination with other genes, such as TFL, EMF, AP1, AP2, CAL, FWA, FT, AP3, PI, AG, UFO, CO, LD, GA1 etc, and a critical level of LFY expression is essential.LFY gene not only controls flowering-time and floral transition, but also plays an important role in inflorescence and floral organ development. It was situated at the central site in gene network of flowering regulation, positively or negatively regulates the level or activities of flowering-related genes. Some physiological factors, such as carbon sources, phytohormones, affect directly or indirectly the expression and actions of LFY gene. This indicates that level of LFY expression can also be regulated with physiological methods. It is probable that we can explain the principal mechanism of flowering by regulation network of LFY gene.

LFY基因 基因网络 生理因子 花发育 Key words LFY gene gene network physiological factor flower development

分类号

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Abstract

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