

林木基因編輯技術之進展和未來前景

最新的基因組編輯技術 CRISPR (clustered, regularly interspaced, short palindromic repeats, 群聚且有規律間隔的短重複序列) 正在革新生物學的各個方面, 包括農業和林業。它能夠以前所未有的精確度和效率生成轉基因無效突變體, 這對於生育週期長的異交樹種而言是一項可喜的突破。在這次演講將介紹 CRISPR 基因組編輯在楊樹中的多基因家族成員的標的基因操作和串聯排列基因突變的案例研究。異交物種中的序列多態性對有效的基因組編輯會導致被低估的障礙。雖然序列多態性數據通常無法通過當前基因組網站, 且未被廣泛運用在 gRNA 程序設計中所考慮。演講中將討論我們所開發的基因組資源和敏感變異體生物資訊的研究, 以解決異交、雜交或多倍體物種的基因組編輯挑戰。還將討論我們利用 CRISPR 的強大技術在基因編輯外與關鍵技術缺口的新興應用, 可以增益森林生物學。結合早期開花策略, 利用一個育種代就能將 CRISPR 產生的無效突變體以雜交方式產生非轉基因後代。利用此技術可培育出具有攜帶突變目標基因而無外源 DNA 的精英營養系來生產遺傳工程農產品, 此一模式最終可能有助於公眾提高對基改產品的接受度。

GENOME EDITING IN FOREST TREES: PROGRESS AND FUTURE PROSPECTS

The latest genome editing technology, called CRISPR, is revolutionizing all facets of biology including agriculture and forestry. It enables generation of transgenic null mutants with unprecedented precision and efficiency—a welcoming breakthrough for outcrossing tree species with long generation cycles. In this talk, I will present case studies of CRISPR genome editing in *Populus* for targeted manipulation of multigene family members, and for mutation of tandemly arrayed genes. Sequence polymorphisms in outcrossing species pose an underappreciated obstacle to efficient genome editing. However, sequence polymorphism data are usually inaccessible via current genome portals, and are not considered in popular gRNA design programs. I will discuss genomic resources and variant-sensitive bioinformatics pipelines that we have developed to address the genome editing challenges of outcrossing, hybrid or polyploid species. I will also discuss emerging applications of CRISPR beyond gene editing, and critical gaps in our ability to harness this powerful technology to advance forest biology. In conjunction with early flowering strategies, it will be possible to cross CRISPR null mutants to generate transgene-free progenies in one breeding generation. Elite clones carrying targeted gene mutation(s) without foreign DNA may ultimately help increase public acceptance of bioengineered agricultural products.