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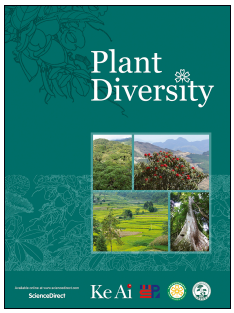

Plant phylogenomics based on genome-partitioning strategies: progress and prospects

Xiang-Qin Yu, Dan Yang, Cen Guo, Lian-Ming Gao

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Plant phylogenomics based on genome-partitioning strategies: progress and prospects

Xiang-Qin Yu [a], Dan Yang [a,c], Cen Guo [b,c], Lian-Ming Gao [a*]

[a] Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan 650201, China

[b] Germplasm Bank of Wild Species, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan 650201, China

[c] Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, Yunnan 650201, China

* Corresponding author. Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, 132# Lanhei Road, Kunming 650201, Yunnan, China. Fax: +86 0871 65225286

E-mail address: gaolm@mail.kib.ac.cn (L. M Gao).

Abstract

The rapid expansion of next-generation sequencing (NGS) has generated a powerful array of approaches to address fundamental questions in biology. Several genome-partitioning strategies to sequence selected subsets of the genome have emerged in the fields of phylogenomics and evolutionary genomics. In this review, we summarize the applications, advantages and limitations of four NGS-based genome-partitioning approaches in plant phylogenomics: genome skimming, transcriptome sequencing (RNA-seq), restriction site associated DNA sequencing (RAD-Seq), and targeted capture (Hyb-seq). Of these four genome-partitioning approaches, targeted capture