

Protein domain analysis from genomic sequence data revealed the regulation of LRR related domains in plant transpiration in Ficus

Tiange Lang¹, Jinyu Liu¹, Kunfang Cao¹ and Charles H. Cannon^{1,2}

¹Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, PR China

²Department of Biological Sciences, Texas Tech University, USA

We developed a pipeline which can predict protein domains directly from genomic sequence data without a reference genome. The pipeline avoided some complex problems of *de novo* assembly such as micro reads and small single repeats. We used the pipeline on Ficus genomic data and found that the combination of LRRNT_2 and LRR_8 domains is related to hydrophobic process in Ficus. From the view of protein sequence, all those domains have leucine-rich repeats where leucine is a hydrophobic amino acid.

langtiange@xtbg.org.cn