**Plant Promoter Prediction Tool and Isolation of a Promoter from Porteresia coarctata**

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**Abstract**

In silico identification of promoters is complicated by the hierarchical, modular and diverse nature of their architecture. Tools developed for prediction of eukaryote promoters produce acceptable results for certain species but are not as specific for plants. An algorithm to predict plant-promoters is described. The programme was trained on 255 plant promoters and verified with 50 promoters. The tool was able to accurately identify 72% of the test sequences. A promoter sequence designated as Pccp was identified from the genomic sequences of Porteresia coarctata. The tool was validated with laboratory results. Cloning of Pccp upstream to gusA and introduction of the fusion-construct into plant tissues revealed GUS expression confirming predicted sequence as the promoter.

**References**


