

Genome-wide characterization and expression patterns of chitinase genes in the pigeonpea (*Cajanus cajan* (L.) Millsp.) genome

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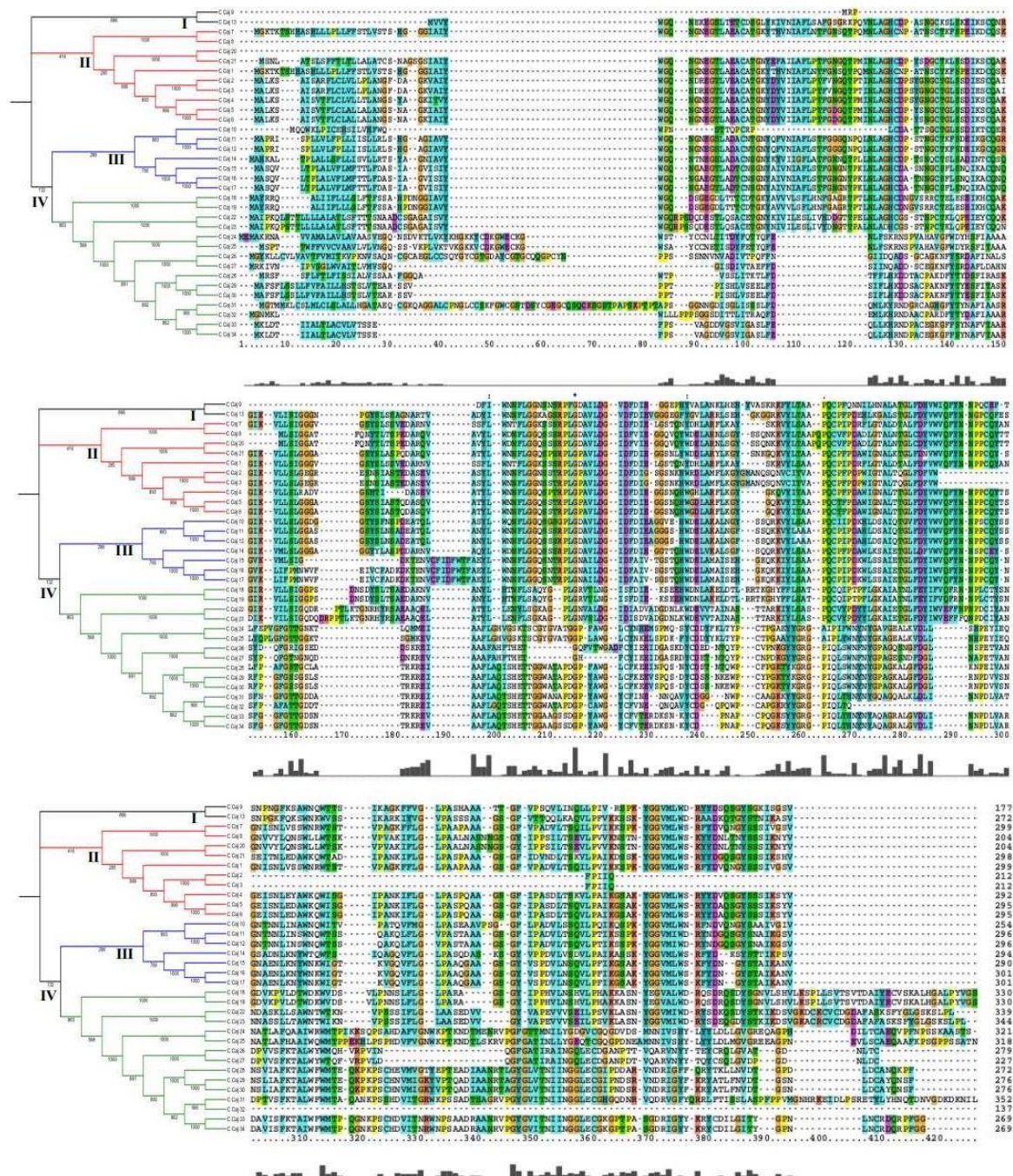


Fig S1. The neighbor-joining phylogenetic tree of 34 pigeonpea chitinase genes and their multiple sequence alignment generated using MUSCLE and ClustalW via their amino acid sequence. The clustering of 34 pigeonpea chitinase genes in to four distinct cluster shows high degree of sequence conservation among the respective gene clusters.



Fig S2. Alignment of selected species-specific chitinase genes from each sub-clade to showing protein sequence conservation in each clade and sub-clade of GH-18, GH-19 and PR-4 chitinase families in across the 14-plant species.