



## Structural and phylogenetic analysis of Pto-type disease resistance gene candidates in *Hevea brasiliensis*

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**ABSTRACT.** The tomato *Pto* gene encodes a serine/threonine kinase (STK) whose molecular characterization has provided valuable insights into the disease resistance mechanism of tomato. Therefore, *Pto* is considered as a promising candidate for engineering broad-spectrum pathogen resistance in this crop. In this study, a pair of degenerate primers based on conserved subdomains of plant STKs similar to the tomato *Pto* protein was used to amplify similar sequences in a hevea cultivar (*Hevea brasiliensis* Muell. Arg). A fragment of ~550 bp was amplified, cloned, and sequenced. The sequence analysis of several clones revealed 12 distinct sequences highly similar to STKs. Based on their significant similarity with the tomato *Pto* protein (BLASTX *E* value < 3e-53), seven sequences were classified as *Pto* resistance gene candidates (*Pto*-RGCs). Multiple sequence alignment of the hevea *Pto*-RGC products revealed that these sequences contain several conserved subdomains present in most STKs, as well as several conserved residues that are crucial for *Pto* function. Moreover, phylogenetic analysis

showed that the hevea Pto-RGCs clustered with Pto, suggesting a common evolutionary origin with this resistance gene. The Pto-RGCs isolated in this study represent a valuable sequence resource that could assist in the development of disease resistance in hevea.

**Key words:** Disease resistance gene; Pto; Serine/threonine kinase; *Hevea brasiliensis*