

## **CHARACTERIZATION OF EXPRESSED *PGIP* GENES IN RICE AND WHEAT REVEALS SIMILAR EXTENT OF SEQUENCE VARIATION TO DICOT PGIPS AND IDENTIFIES AN ACTIVE PGIP LACKING AN ENTIRE LRR REPEAT**

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Polygalacturonase-inhibiting proteins (PGIPs) are leucine-rich repeat (LRR) proteins involved in plant defence. A number of PGIPs have been characterized from dicot species, whereas only a few data are available from monocots. Database searches and genome-specific cloning strategies allowed the identification of four rice (*Oryza sativa* L.) and two wheat (*Triticum aestivum* L.) *Pgip* genes. The rice *Pgip* genes (*Ospgip1*, *Ospgip2*, *Ospgip3* and *Ospgip4*) are distributed over a 30 Kbp region of the short arm of chromosome 5, whereas the wheat *Pgip* genes, *Tapgip1* and *Tapgip2*, are localized on the short arm of chromosome 7B and 7D, respectively. Deduced amino acid sequences show the typical LRR modular organization and a conserved distribution of the eight cysteines at the N- and C- regions. Sequence comparison suggests that monocot and dicot PGIPs form two separate clusters sharing about 40% identity and shows that this value is close to the extent of variability observed within each cluster. Gene-specific RT-PCR and biochemical analyses demonstrate that both *Ospgips* and *Tapgips* are expressed in the whole plant or in a tissue-specific manner, and that OsPGIP1, lacking an entire LRR repeat, is an active inhibitor of fungal polygalacturonases. This last finding can contribute to define the molecular features of PG-PGIP interactions and highlights that the genetic events that can generate variability at the *Pgip* locus are not only limited to substitutions or small insertions/deletions, as so far reported, but can also involve variation in the number of LRRs.