PHYTOCYSTATINS: NEW INSIGHTS AFTER THE ARABIDOPSIS, RICE AND POPLAR GENOMES.

Rogério Margis^{1,2}, Giancarlo Pasquali¹ and Márcia Margis-Pinheiro³

¹Centro de Biotecnologia, Universidade Federal do Rio Grande do Sul; ²Departamento de Bioquímica, Universidade Federal do Rio Grande do Sul and ³Departamento de Genética, Universidade Federal do Rio Grande do Sul. Email: rogerio.margis@ufrgs.br

Plant protease inhibitors play an important role controlling proteolytic activities, which are essential for plant development and survival. A comparative analysis of genes from rice, arabidopsis and poplar revealed the presence of four main cystatin groups. One corresponds to the standard cystatin inhibitors, the second group has a Cterminal extension and was probably originated from the duplication of an ancestral gene related to the group I. The most divergent genes where clustered in group III, while members from group IV present a sequence insertion between the -helix and the QxVxG motifs. Multicystatins, with more than two cystatin domains, were not identified in the genomes of these three plants. Analysis of poplar ESTs allow the identification of different phytocystatins spliced forms. Phytocystatins from group II represent an example of combined mechanisms of gene duplication and alternative splicing, which may have conferred new functions not vet determined to these proteins. Our results show that this family of protein presents a dynamic evolutionary pattern, operated by gene duplication and differential alternative splicing. Keywords: phytocystatins, alternative splicing, cysteine proteinase inhibitors. Work supported by CNPa.