



# Regulation of ATG6/Beclin-1 homologs by abiotic stresses and hormones in rice (*Oryza sativa* L.)

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**ABSTRACT.** Autophagy, a complex and conserved mechanism, serving as a defense response in all eukaryotic organisms, is regulated by several proteins, among which ATG proteins are the most important due to their involvement in autophagosome formation. ATG6/Beclin-1 proteins, reported to be essential for autophagosome formation and assigned as a conserved domain, were subjected to database searches. We found three homologs in the rice (*Oryza sativa*) genome. A phylogeny tree was constructed to establish their across species relationship, which divided them into three distinct groups; two for plants, i.e., monocots and dicots, and one for animals. Evolutionary study of this family by critical amino acid conservation analysis revealed significant functional divergence. The finding of important stress-related *cis*-acting elements in the promoter region of rice *ATG6* genes demonstrated their involvement in

abiotic stress responses. Furthermore, expression profiling of rice *ATG6* genes based on microarray data, as well as by semi-quantitative RT-PCR, showed differential expression when subjected to different stresses suggesting the involvement of *OsATG6* genes in abiotic stresses (heat, cold and drought) and hormone (abscisic acid) responses. Analysis of co-expressed genes showed that most of them annotated to DNA repair pathways and proteolysis, etc. Collectively, these results suggest the involvement of *OsATG6* genes in different stresses, and provide a basis for further functional studies to investigate the biological mechanism of action of these genes under abiotic stresses.

**Key words:** Autophagy; Abiotic stress; Phylogeny; Rice