

Homology Modeling and Characterization Studies on Gamma Subunits of Heterotrimeric G Proteins in *Oryza sativa* and *A.thaliana*

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Heterotrimeric G proteins, composed of alpha, beta, and gamma subunits, act as molecular switches to turn on intracellular signaling upon arrival of external stimuli at membrane receptors. In plants they participate in multiple developmental processes from seed germination, early seedling development to organ shape determination, as well as and in defense mechanisms, hormone perception and ion-channel regulation.

Recently, it was demonstrated that the components of G proteins and intrinsic signaling and network mechanisms in plants are significantly different from those in the animal counterparts. One of these differences is the complex family of plant gamma subunits which may be directly involved in signaling and is likely to play a role in the specificity of signaling. The present study involves computational analyses for modeling the structures RGG1 and AGG1, the gamma subunits from rice and Arabidopsis respectively, and the biochemical and biophysical characterization of the two purified proteins. Homology modeling yielded an extended helical structure for both RGG1 and AGG1 proteins. In experimental characterization studies, RGG1, RGG2 and additionally AGG1 were expressed in *E. coli*. and purified from bacteria for dynamic light scattering (DLS) and circular dichroism spectroscopy (CD). Stability of structures was investigated in thermal denaturation experiments. Comparative results will be presented and discussed in the context of plant gamma subunit function(s).