

**Poster C-13**  
**RHOGAP DOMAIN-CONTAINING**  
**PROTEINS PHYLOGENY – AN**  
**BAYESIAN APPROACH**



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**Short Abstract:** Proteins containing a RHOGAP domain work as molecular switches involved in the regulation of diverse cellular functions. The ability of these GTPases to regulate a wide number of cellular processes comes from their interaction with multiple proteins, including their inhibitors, the RHOGAPs protein family, which stimulates their intrinsic GTPase activity.

**Long Abstract:**

Proteins containing a RHOGAP domain, defined by the presence of a 150-amino acid homolog region, work as molecular switches involved in the regulation of diverse cellular functions. The ability of these GTPases to regulate a wide number of cellular processes comes from their interaction with multiple proteins, including their inhibitors, the RHOGAPs protein family, which stimulates their intrinsic GTPase activity. Here, a phylogenetic approach was applied to study the evolutionary relationship among 59 RHOGAP domain-containing proteins. The sequences were aligned by their RHOGAP domain and the phylogenetic hypotheses were generated using Maximum Parsimony and Bayesian analyses. The character tracing of two traits, GTPase activity and presence of other domains, indicated a significant phylogenetic signal for both of them. Interaction between genomics, evolution and bioinformatics goes further than simply sequence alignment and elucidating relationships among species. Evolutionary analysis may help researchers design new strategies to understand proteins or genes interactions and their functionalities and might provide an insight for new experiments. In conclusion, a phylogenetics study of RHOGAP domain-containing proteins has demonstrated that there is a strong evolutionary relationship among the super-family members, especially when they share common motifs or GAP activity.