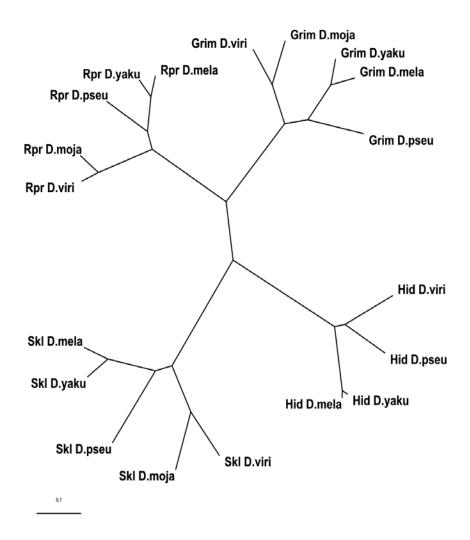
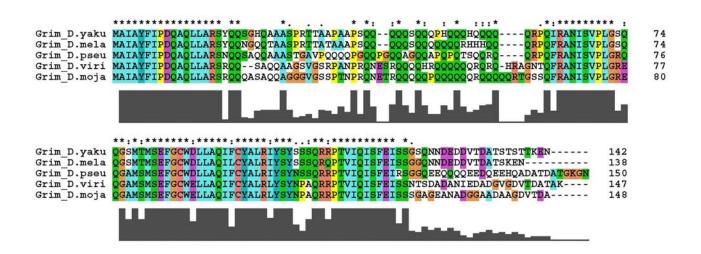
Supplementary Information:

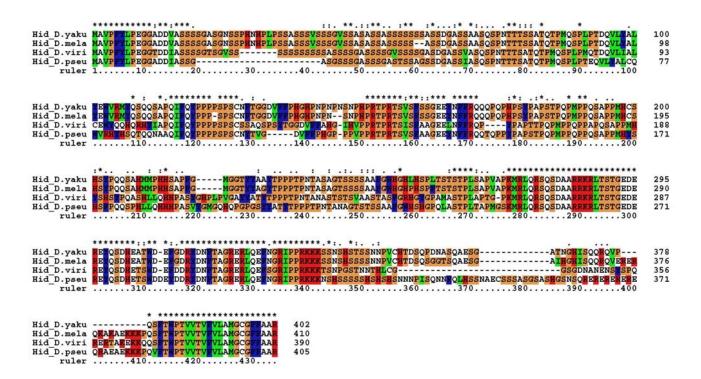
I.) **Distance Tree of RGH Proteins From The Five Species**. Sequences were aligned using ClustalX and the Neighbor-Joining tree was bootstrapped for 2000 trials. The resulting distance tree were displayed and outputted with TreeView (Page 1996). Scale is for the rate of nucleotide substitution per site.



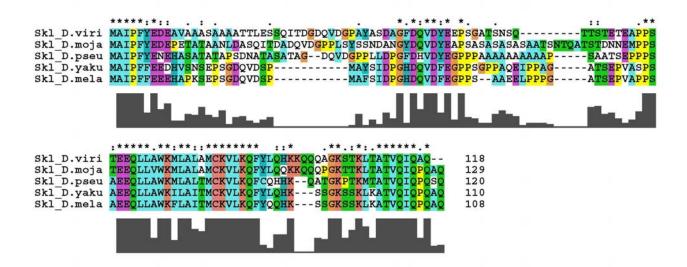
II.) Alignment of Orthologs of Grim.



III.) Alignment of Orthologs of Hid.



IV.) Alignment of Orthologs of Sickle (Skl).



References:

Page, R. D. (1996). TreeView: an application to display phylogenetic trees on personal computers. *Comput Appl Biosci*, **12**(4), 357-8.