and annotator-Apollo. As apoptotic genes have an important role in embryonic development, cell differentiation and overall survival of an organism, sequencing and annotating these genes will be very helpful for understanding the complex processes of apoptosis as well as cell differentiation in Hessian fly. Computational tools and experimental approaches were used for annotating genes. The *in-silico* predictions were tested and validated by an experimental approach. Based on the data available in public databases for other characterized species in the dipteral order, as of now, we have identified 97 genes regulating apoptosis in *Drosophila melanogaster* and *Aedes aegypti* and based on homology prediction, we were able to uniquely identify 20 genes in *Mayetiola destructor* genome. The remaining genes were currently considered absent or missing in prediction. The predictions were validated both computationally and experimentally. Experimentally, the putative genes were validated by the conventional PCR and sequencing method.

B 3

Diversity analysis based on BIOLOG and 16S rDNA sequencing of *Bacilli* from rhizosphere of coconut palms growing in acidic soils of Kerala and Karnataka

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PCR targeting the 16S rDNA has been used extensively to study prokaryote diversity and allows identification of prokaryotes as well as the prediction of phylogenetic relationships. It is the basic molecular tool for amplified rDNA fragments (ARDRA) which detects interspecies and inter-strainal variability and provides accurate genetic diversity information on microbes. Although aerobic endospore-forming bacteria, typically *Bacillus* and its derived genera, are one of the major types of soil bacteria, investigations concerning diversity of *Bacillus* in extreme acidic rhizosphere soils were least studied. Hence the present study was conducted and *Bacillus* spp. were isolated from the rhizosphere of coconut, growing in acidic soils of Kerala and Karnataka(soil pH varying from 2.18- 4.99) with a focus to study their diversity. Carbon source utilization pattern based on BIOLOG and ARDRA analysis of these isolates using twelve Fast digest® restriction enzymes *viz*., *Hae*III, *Hinf*I, *Alu*I, *Taq*I, *Msp*I, *Rsa*I, *Hha*I, *EcoR*I , *Hpa*II, *Hind*III, *Bga*III and *Xba*I was employed for diversity studies. The identification of acid tolerant bacterial isolates through Microbial Identification System (BIOLOG) and 16S rDNA sequencing revealed *B. subtilis, B. amyloliquefaciens*, *B. megaterium, B. cereus, Lysinibacillus sphaericus* and *B. tequilensis*as the major species. The digestion of 16S rDNA product with *Taq*I, *Alu*I and *Hha*I endonucleases gave 29, 23 and 17 restriction patterns respectively. The present results suggest diverse population of acid-tolerant *Bacillus* spp. in rhizosphere region of coconut palms.