Abstract

Evolutionary innovations have shaped the diversity of animal and plant forms. The origin of these evolutionary innovations implies the origin of new regulatory pathways, which leads to a change in the development pattern. Most evolutionary innovations as shown by research in a variety of models have suggested that they are caused not by the appearance of new genes, but rather by the acquisition of new function by pre-existing genes. Understanding the genetic and molecular changes which lead to a shift in the developmental pattern leading to the regulation of the particular trait is therefore one of the key challenges of evolutionary developmental genetics. Sex comb in Drosophila is a sexually dimorphic morphological character, which serve as a good model system to understand how genetic modifications have taken place in the course of evolution leading to as an evolutionary innovation. Though genetic network controlling the development of this trait has been studied to some extent in D. melanogaster, and Sophophoran group, understanding of the changes that have lead to the origin of this new character from the primitive bristles remain to be dissected out. In this context the question asked in the present project is “What are the changes in the developmental genetic pathway underlying the evolution of the primitive bristles pattern of Drosophila in general to sex comb as in the Sophophoran group”. Studies in the present project explore the differences in the genetic regulators viz, Sex combs reduced, dachshund and bric-a-brac from the species cluster with primitive bristle to species with sex comb of Drosophila. Lower Sex combs reduced expression is associated with species primitively lacking sex
comb and higher *Sex combs reduced* expression with species bearing sex comb. Alteration of Dachshund could be witnessed from the species group primitively lacking sex comb to species with sex comb. Unaltered *bric-a-brac* expression could be seen in the two groups of species taken up for the study. Bioinformatics based predictions were also made for *dachshund* which displayed a difference from the group primitively lacking sex comb to the group with sex comb in its immunostaining property. Variations in the sequences and secondary structure are shown by the bioinformatics study. At the same time the study has also shown the interaction between the spatial patterning regulators with the regulators of the sex determining pathway. The study deciphers the role played by splice variants of *double sex* in shaping the morphogenesis of sex comb development. Details of the results are discussed.