

Ancestral developmental mechanisms in insects revealed by RNAi analysis of cricket genes

Taro Mito, Taro Nakamura, Tetsuya Bando, and Sumihare Noji

Department of Life Systems, University of Tokushima, Japan

The RNAi approach has been widely used on insects in several fields, including embryogenesis, pattern formation, reproduction, biosynthesis and behavior. The increasing availability of insect genomes has made the RNAi technique an indispensable technique for characterizing gene functions in insects.

Mechanisms of embryonic patterning in insects have been extensively studied in *Drosophila melanogaster*. However, the mode of embryogenesis in *Drosophila* is highly derived and recent studies on other insects have revealed that there exist new developmental paradigms. In the past decade, we have been studying developmental gene networks in the cricket *Gryllus bimaculatus*, a phylogenetically basal insect, using RNAi. Our RNAi and transgenesis-based studies are revealing conserved and divergent aspects of anterior-posterior (AP) patterning system in *Gryllus*. The anterior head region of the cricket embryo is suggested to be specified by *orthodenticle* earlier than the gnathal and thoracic region. The gnathal and thoracic gap genes are activated by zygotically expressed *caudal*, which is under regulation of Wg/Arm signaling in the posterior germband. RNAi analyses also suggest that Wg/Arm and Notch/Delta signalings regulate posterior elongation of the germband. The evolution of AP patterning mechanisms in insects will be discussed based on recent progress in the study of *Gryllus* development.