Biological analyses of transcriptional regulators in *Drosophila*

TANAKA Ryo

Gene expression is accurately and dynamically modulated by various mechanisms including epigenetic regulation and transcription DNA to RNA. These regulations are fundamental mechanism for development, tissue homeostasis and behavior.

1. Functional analysis of Smallish during *Drosophila* development

Smallish (Smash), the *Drosophila* homologue of human LMO7, was reported as a key regulator of *Drosophila* embryogenesis associated with actomyosin contractility. Although *smash* mRNA is expressed throughout *Drosophila* development, only Smash function at the adherence junction in embryonic epithelial cells has been revealed. Here, I demonstrated that the eye imaginal disc-specific *smash* knockdown induced eye morphological aberrations associated with increased apoptosis. Moreover, immunohistochemical analyses revealed that Smash mainly localized to the nucleus in several tissues, including eye imaginal discs. As is the case with LMO7, the *smash* knockdown in eye imaginal discs decreased the expression of the *ote* and *bocks* genes known as the *Drosophila* homologue of the *emerin* gene. Furthermore, down-regulated *ote* and *bocks* expression induced apoptosis. Taken together, these results indicate that Smash functions in proper *Drosophila* eye development mediated by the regulation of *ote* and *bocks* gene expression.

2. G9a is a key regulator of the starvation-induced behaviors in *Drosophila melanogaster*

Organisms are exposed to starvation stress in nature. In spite of the importance of behavioral strategies under the starvation, the underlying mechanisms have not been fully understood. Here, I revealed that *Drosophila* G9a (dG9a), one of histone methyltransferases, plays a key role for the starvation-induced behaviors. RNA-seq and RT-qPCR analysis revealed that the expression of gustatory receptor genes for sensing sugar are increased in *dG9a* null mutant under the starvation condition. Consistent with its up-regulation, proboscis extension reflex tests indicated that the sucrose sensitivity under starvation conditions was significantly increased. Moreover, the locomotion activity was promoted in starved *dG9a* null mutant. This hyperactivity is caused by down-regulation of *insulin-like peptide* genes expression under the *dG9a* depletion, which genes are required for the suppression of starvation-induced hyperactivity. Moreover, refeeding of wild type flies after starvation conditions restores these phenotypes. These data suggest that dG9a functions as a key regulator for the decision of behavioral strategies under starvation conditions.