

# **ABSTRACT of My Master Thesis**

Each developmental process consists of a series of divisions, regulations, and decisions. Throughout different series of developmental instructions, a fertilized egg of each species develops into distinct multicellular organism, which may be totally different from each other. Various evo-devo models have been proposed to describe the similarities and differences among developmental processes. The funnel model and hourglass model are the most well-known among them.

The funnel model states that the development proceeds from general features to species-specific patterns. On the other hand, the hourglass model states that higher similarity exists during the formation of body plan among the embryogenesis of different species. The stage with the highest conservation is referred as the phylotypic stage. By comparing the transcriptomic data among different species, several studies have been reported to support the idea of hourglass model. Although pieces of evidence indicate an evolutionary constraint during phylotypic stage, the evolutionary explanation and molecular mechanism behind this phenomenon, however, are not fully understood yet.

In our study, we aimed to tackle the problem via network and pathway analyses. Using the gene association network information and gene expression data, we first measured the stochasticity within the biological network during the developmental process. Such analysis enables us to trace and compare the changes of network randomness among developmental processes of different species. Next, we sketched out the pathway dynamics during developmental process in order to narrow down our study from global network connections to detailed molecular regulations. With the systematic network view of developmental process, our results provided an alternative aspect of comparative embryology.