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Body Axis Segmentation in the Common House Spider *Parasteatoda tepidariorum*: Identification of Gene Expression Waves That Pattern Conserved Stripes in a Cell-based Field*

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The common house spider *Parasteatoda tepidariorum* (Chelicerata) has emerged as a non-insect arthropod model for studying developmental and evolutionary mechanisms (Oda and Akiyama-Oda, 2008; Hilbrant et al., 2012). Its genome has been sequenced by the Baylor College of Medicine Human Genome Sequencing Center and the international *P. tepidariorum* genome consortium (Schwager et al., 2017). Our group also accumulated genomic and transcriptomic sequences from our laboratory stocks of the spider isolated in Japan (Oda et al., 2007; Sasaki et al., 2017), which are available at our data resource site (http://www.brh2.jp) as well as at the DDBJ/EMBL/GenBank Nucleotide Sequences Databases. Besides these sequence resources, there are a number of benefits associated with the use of *P. tepidariorum*. Its phylogenetic position, distant from insects within the Arthropoda phylum, may help conduct comparative studies of looking deep into the evolutionary root of arthropod animals. In contrast to most insect embryos, which are syncytia at early stages, spider embryos undergo patterning in a cellular environment from the early stages (Kanayama et al., 2010), which could enhance the significance of the comparative studies. Experimental techniques available in this spider, such as parental and embryonic RNA interference (RNAi), facilitate in-depth analyses of developmental mechanisms at the cell and molecular levels. Parental RNAi can silence target gene activity in early whole embryos (Akiyama-Oda and Oda, 2006), and embryonic RNAi enables one to analyze gene function in cell clones in the normal background (Kanayama et al., 2011), as in mosaic analysis in *Drosophila* larvae. More importantly, the RNAi techniques can be effectively combined with genome-wide, non-biased gene discovery analysis based on next-generation sequencing techniques (Yasuko Akiyama-Oda and H. Oda, in prep.). Therefore, we believe that the *P. tepidariorum* embryo provides an ideal cell-based platform with which to study mechanisms of pattern formation and their evolution in arthropods.

One of the major patterning events observed among all arthropod embryos is body axis segmentation, in which stripes of gene expression develop dynamically in the embryonic field through processes varied among regions of the field, although the output stripe patterns of gene expression (e.g., stripes of segment polarity gene expression) are highly conserved irrespective of insect or non-insect arthropods. However, little is understood about the basis of molecular and genetic mechanisms that generate a diversity of stripe-forming processes in a cell-based field of an arthropod embryo. This issue may be associated with one of the biggest questions in the EVO-DEVO field, what ancestral state of development enabled the evolution of a diversity of patterning processes in a phylum.

To pursue our research in this direction using the *P. tepidariorum* model, we conducted a quantitative study of stripe-forming processes as well as genome-wide identification of genes whose expression levels are regulated by Hedgehog signaling pathway components, which were previously shown to be involved in axis formation in the spider embryo (Akiyama-Oda and Oda, 2010). In this talk, based on data we obtained in previous and present studies (Akiyama-Oda and Oda, 2010; Kanayama et al., 2011), we suggest that mechanisms that operate waves of gene expression are fundamental to spider body axis segmentation in all regions of the embryonic field.

References

Akiyama-Oda, Y. and H. Oda (2006) Axis specification in the spider embryo: *dpp* is required for radial-to-axial symmetry transformation and *sog* for ventral patterning. Development, **133**, 2347–2357.

Akiyama-Oda, Y. and H. Oda (2010) Cell migration that orients the dorsoventral axis is coordinated with anteroposterior patterning mediated by Hedgehog signaling in the early spider embryo. Development, **137**, 1263–1273.

Hilbrant, M., W.G. Damen and A.P. McGregor (2012) Evolutionary crossroads in developmental biology: the spider *Parasteatoda tepidariorum*. Development, **139**, 2655–2662.

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Kanayama, M., Y. Akiyama-Oda, O. Nishimura, H. Tarui, K. Agata and H. Oda (2011) Travelling and splitting of a wave of hedgehog expression involved in spider-head segmentation. Nature communications, **2**, 500.

Kanayama, M., Y. Akiyama-Oda and H. Oda (2010) Early embryonic development in the spider *Achaearanea tepidariorum*: microinjection verifies that cellularization is complete before the blastoderm stage. Arthropod structure & development, **39**, 436–445.

Oda, H., O. Nishimura, Y. Hirao, H. Tarui, K. Agata and Y. Akiyama-Oda (2007) Progressive activation of Delta-Notch signaling from around the blastopore is required to set up a functional caudal lobe in the spider *Achaearanea tepidariorum*. Development, **134**, 2195–2205.

Oda, H. and Y. Akiyama-Oda (2008) Differing strategies for forming the arthropod body plan: lessons from Dpp, Sog and Delta in the fly *Drosophila* and spider *Achaearanea*. Development, growth & differentiation, **50**, 203–214.

Sasaki, M., Y. Akiyama-Oda and H. Oda (2017) Evolutionary origin of type IV classical cadherins in arthropods. BMC evolutionary biology, **17**, 142.

Schwager, E.E., P.P. Sharma, T. Clarke, D.J. Leite, T. Wierschin, M. Pechmann, Y. Akiyama-Oda, L. Esposito, J. Bechsgaard, T. Bilde, A.D. Buffry, H. Chao, H. Dinh, H. Doddapaneni, S. Dugan, C. Eibner, C.G. Extavour, P. Funch, J. Garb, L.B. Gonzalez, V.L. Gonzalez, S. Griffiths-Jones, Y. Han, C. Hayashi, M. Hilbrant, D.S.T. Hughes, R. Janssen, S.L. Lee, I. Maeso, S.C. Murali, D.M. Muzny, R. Nunes da Fonseca, C.L.B. Paese, J. Qu, M. Ronshaugen, C. Schomburg, A. Schönauer, A. Stollewerk, M. Torres-Oliva, N. Turetzek, B. Vanthournout, J.H. Werren, C. Wolff, K.C. Worley, G. Bucher, R.A. Gibbs, J. Coddington, H. Oda, M. Stanke, N.A. Ayoub, N.M. Prpic, J.F. Flot, N. Posnien, S. Richards and A.P. McGregor (2017) The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC biology, **15**, 62.