

Transcriptomic analysis of seasonal photoperiodism in the pea aphid using international genomic resources

By Denis Tagu

INRA, Agrocampus Rennes, UMR 1099 BiO3P (Biology of Organisms and Populations applied to Plant Protection), F-35653 LE RHEU, France (denis.tagu@rennes.inra.fr)

Aphids are able to change their reproductive mode in response to photoperiodism through the expression of phenotypic plasticity called reproductive polyphenism. Under long-day conditions (spring and summer), aphids reproduce by parthenogenesis. However, the shortening of photoperiod induces a switch to sexual reproduction that occurs by the end of summer. Males and females are thus produced and after mating, over-wintering eggs are laid. The mechanisms of perception of the shortening of photoperiod and its consequences on egg development and morph orientation are misunderstood, but they probably involve early modifications in the neuroendocrine response. Our goal is to identify genes regulated by the shortening of day-length responsible for reproductive switch.

In this talk, I will first present the different genomic resources developed on the pea aphid (*Acyrtosiphon pisum*) in the frame of the International Aphid Genomics Consortium. This concerns Expressed Sequence Tag (EST), genomic databases (AphidBase), RNAi and the whole genome sequenced by the Baylor College of Medicine (Houston, Tx).

In a second part, I will describe the use of these genomic resources to study seasonal photoperiodism in the pea aphid. A microarray containing 3000 cDNAs (corresponding to 1700 unigenes) was constructed and used for competitive hybridizations between RNAs extracted from heads of aphids (third instars) reared under long or short photoperiod. Analysis revealed that 59 genes were significantly up- or down-regulated by the shortening of photoperiod. A third of these genes encoded cuticular proteins while 15 % encoded proteins involved in cellular differentiation or signaling as wunen – a lipid phosphate phosphatase- and HDD11 – a protease containing a reeler domain that plays a pivotal role in the development of the central nervous system. Quantitative PCR experiments performed on 5 transcripts confirmed microarray results. Complementary experiments eliminated molting and circadian rhythms as putative confounding effects.