

Long non--coding RNA in the pea aphid; identification and comparative expression in sexual and asexual embryos

Fabrice Legeai, Thomas Derrien, Valentin Wucher, David Audrey, Gaël Le Trionnaire, Denis Tagu

▶ **To cite this version:**

Fabrice Legeai, Thomas Derrien, Valentin Wucher, David Audrey, Gaël Le Trionnaire, et al.. Long non--coding RNA in the pea aphid; identification and comparative expression in sexual and asexual embryos. Arthropod Genomics Symposium, Jun 2014, Urbana, United States. hal-01091304

HAL Id: hal-01091304
https://inria.hal.science/hal-01091304

Submitted on 5 Dec 2014

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Long non coding RNA (lncRNA) have been shown to be involved in multiple mechanisms in particular in epigenetic regulation such as control of DNA methylation patterns or chromatin remodeling.

Aphids have the ability to produce extremely divergent phenotypes in response to environmental stimuli. Reproductive modes are condition-dependent in aphids since they are able to switch from asexual to sexual reproduction in response to autumnal photoperiod shortening. This means that aphids produce embryos developing into either sexual adults or asexual parthenogenetic females. Our group already deciphered the transcriptomic and post-transcriptomic regulations associated with this process and as a general understanding of epigenetic regulatory mechanisms potentially mediating phenotypic plasticity, we investigated the role of lncRNA in sexual and asexual embryos of the pea aphid.

We established a new bioinformatics pipeline for the detection of lncRNAs from RNA-Seq data, and produced the first pan-genomics catalogue of aphids lncRNAs. Among 2,172 identified lncRNAs, 24 are differentially expressed between sexual and asexual embryos at different stages. Furthermore, we asserted for each lncRNA a classification of putative cis-interactions based on its genomic distance to neighboring mRNAs. Besides the identification of microRNAs and their putative targets, these results allow the constitution of a broad gene regulation network of the aphid phenotypic plasticity at the embryo level.

This workflow is available in Galaxy on the BioInformatics Platform for Arthopods of Agroecosystems (www.inra.fr/bipaa) and can be applied to any organism for which an annotated genome sequence and RNA-Seq data are provided.