



Gautier Richard



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Team

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Direction

Gaël Le Trionnaire
Denis Tagu

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Epigenetic mechanisms involved in aphids sexual polyphenism



Social-economic context

Agro-ecosystems consist of organisms subject to variations in environmental factors (abiotic) to which they must adapt. Among the mechanisms involved in adaptation, phenotypic plasticity is a fast and efficient way to produce suitable alternative phenotypes. Aphids are major pests of agronomic crops that show a remarkable phenotypic plasticity during their life cycle. Indeed, asexual individuals that multiply very quickly during summer are able to perceive the autumnal decrease of the photoperiod to produce sexual individuals whose mate to produce cold-resistant eggs. This life-trait is defined as reproductive polyphenism.

Scientific context

Aphids genome plasticity allows them to quickly anticipate changes in environmental conditions in order to produce better adapted phenotypes. Understanding the molecular mechanisms that regulate this phenomenon is therefore essential to better explain the adaptive success of these pests. The phenotypic transition from asexual individuals to sexual individuals being quick, changes in the DNA sequence are probably not involved. This clue and several others strongly suggest the involvement of epigenetic mechanisms in the adaptation process of the aphid to the seasonal modification of environmental conditions.

Transcriptomic and post-transcriptomic studies suggest that, in response to photoperiod decrease, neuroendocrine signaling could target specific receptors in embryos germline. As a result of the perception of this signal, chromatin remodeling events may occur in the germline cells. This would allow an opening or a differential regulation of the expression of certain genomic regions containing genes and regulatory elements such as enhancers, silencers or insulators associated with the embryos fate. The control and regulation of reproduction polyphenism in aphids could thus involve a combination of neuroendocrine signaling and epigenetic mechanisms.

Objectives

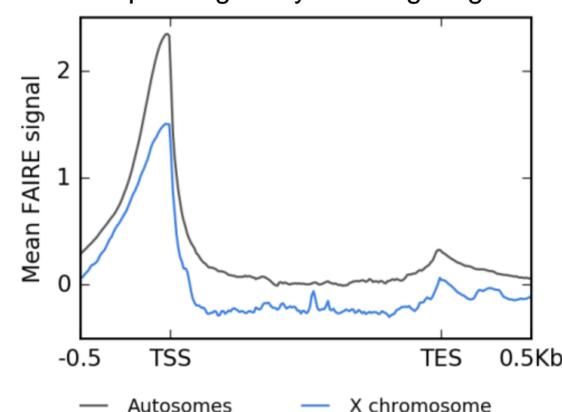
In order to verify this hypothesis, this PhD project proposes to identify aphids genomic regions potentially under epigenetic regulation during the seasonal reproduction switch in the pea aphid's (*Acyrtosiphon pisum*) sexual and asexual embryos and their germline. This PhD is separated in 3 distinct objectives :

1. Identification of genomic regions subject to chromatin remodelling during reproduction polyphenism. In order to study the chromatin state at the genome-wide scale, the Formaldehyde Assisted Isolation of Regulatory Elements methodology will be performed ; followed by genome-wide high-throughput sequencing (FAIRE-seq).
2. Characterization of histone post-translation modifications associated with differentially opened regions identified by FAIRE-seq. Chromatine Immunoprecipitation (ChIP) will be tuned and followed by Quantitative PCR to assess the enrichment of some histone marks at precise loci. A genome-wide analysis will be performed later.
3. Bioinformatic integration of the FAIRE-seq (and ChIP-seq) with RNA-seq and on-going Proteome-seq.

Results

- The FAIRE-seq methodology has been performed on whole *A.pisum* individuals in order to confirm its success for the first time on this non-model organism. Transcription Start Site (TSS) are known to be preferentially opened regions accross numerous organisms. Using the FAIRE we showed that it is also the case for *A.pisum*. These results will be soon the subject of a publication in an international journal.
- The FAIRE DNA of asexual and sexual embryos have been extracted and will soon be sequenced.

DNA opening analysis along all genes



Perspectives

- FAIRE Bioinformatic analyses of asexual and sexual embryos must be performed when the sequencing is finished.
- The Chromatine Immunoprecipitation (ChIP) will be set up on asexual and sexual embryos.

