Functional analysis of the reproductive mode switch in pea aphid

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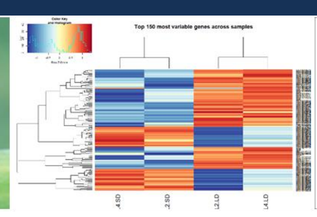
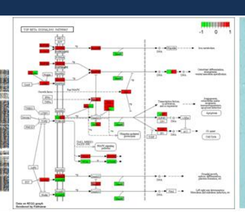
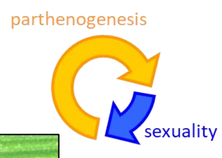


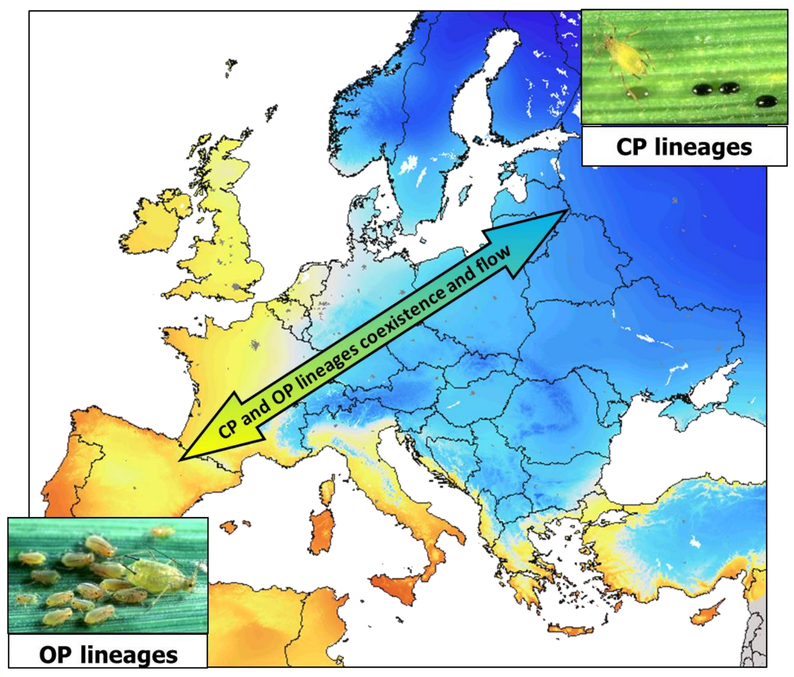


Social-economic context

Aphids feed from plant phloem sap and can transmit plant viruses. Their ability to switch of reproductive mode during their annual life cycle in response to photoperiod explain their success as major crop pests. Phenotypic plasticity in aphids is characterized by a clonal reproduction (viviparous parthenogenesis) in spring and summer, and a production of sexual individuals at autumn arrival when photoperiod decreases. This plasticity allows a rapid colonization of agroecosystems in spring and summer and cold-resistance over winter by the production of diapausing eggs.

In nature, some lineages of the pea aphid - the model organism used for this study (IAGC, 2010) - have lost this ability to respond to photoperiodic cues. Two types of lineages thus coexist in european temperate regions: CP lineages (Cyclical Parthenogenesis) are able to respond to photoperiod and OP lineages (Obligate Parthenogenesis) that have lost the capacity to respond. OP lineages are more abundant in regions with soft winters (South-West) whereas CP lineages are predominant in regions with harsh winters (North-East).





Scientific context

Approaches of population genomics have shown that a region under divergent selection genetically differentiates CP lineages from OP lineages (Jaquiéry *et al.*, 2014). It is hypothesized that the inability of OP lineages to respond to photoperiod is due to mutations in the coding sequence of genes within this region. These mutations would prevent OP lineages to produce sexual individuals. Some candidate genes share homologies with *Drosophila* genes known to be involved in embryogenesis or nervous and visual system development and signalisation. It is also hypothesized that some genes are differentially expressed in response to photoperiod between the two types of lineages as a consequence of the causal mutations. These genes are likely to be involved in the neuroendocrine signalling in response to photoperiod or in the determinism of embryos germline.

Objectives

My PhD project aims at:

1) Identifying cellular functions affected by the causal mutations in OP lineages using RNA-seq approaches to compare OP and CP lineages transcriptomes in various tissues

2) Characterizing the spatio-temporal expression - using ISH and qRT-PCR approaches - of the best candidate genes (selected from the region under selection and the RNA-seq) in OP and CP lineages

3) Validating or not the function of candidate genes in the switch of reproductive mode using directed mutagenesis approaches (CRISPR-Cas9)

Results and perspectives

The first months were dedicated to the conception of the experimental design necessary for the collection of heads (from different developmental stages) and embryos (before and after the switch) samples from CP and OP lines for latter RNA-seq analysis. Preliminary experiments were necessary to optimize the synchronization of the developmental stages of larvae and embryos from the two types of lineages. The main experiment for sample collection is now underway and should allow the obtention of RNA-seq results within three months.

References

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