

Les paramètres nécessaires sont manquants ou erronés.

UNIVERSITY: LILLE , Faculty of Sciences and Technologies

Scientific field : Science de la matière, du rayonnement et de l'environnement

Title of the thesis: Identification of genes involved in cold response in pea at QTL WFD 3.1 and QTL WFD6.1

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Laboratory: Institut Charles Viollette, UMRT EcoBioAgro

Related research project (international/national/regional): for ex. labex, ERC, H2020, I-Site, etc...

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ABSTRACT (about half a page)

Pea (*Pisum sativum*) is a legume that owes its agronomic interest to its ability to develop symbiotic fixation of atmospheric nitrogen and to the high protein content of its seeds. Pea cultivation developed in France in the early 1970s and was revived in 2020, in the context of a European efforts to produce protein-rich materials able to replace soybean. Breeding programmes have therefore been implemented to develop winter varieties offering the possibility of higher and more stable yields, thanks to a longer development cycle.

During the low-temperature phases preceding frost, mechanisms are developed to avoid or tolerate frost: this is cold acclimation. Knowledge of the effects of cold acclimation on frost tolerance is therefore a central issue in the adaptation of plants to climate.

Previous studies of bi-parental populations have made it possible to detect 5 main QTLs involved in frost tolerance. Two of these zones are priority targets for the cloning of the underlying genes.

The first of these 2 QTLs is QTLWFD6.1, homologous to a frost tolerance QTL previously cloned in *Medicago truncatula* (Tayeh et al. 2013). Under this QTL are a large number of copies of CBF genes, transcription factors considered as major integrators of the cold response in several species (*Arabidopsis*, barley...). Studies on these different species have raised a recurring question: what is the impact on cold tolerance of the number of copies of these genes and their cluster structure? In order to answer these questions, the candidate will have to look at the sequences of these different genes, their pairing and the identification of orthologs with already known CBFs. The second QTL that will be investigated is QTL WFD 3.1. Under this QTL is the Hr locus involved in photoperiod floral initiation. It turns out that the candidate gene Hr is an ortholog of AtELF3 (EARLY FLOWERING 3), a gene involved in the circadian clock (Weller et al. 2012) as well as a copy of ICE1, a gene involved in the regulation of IVC. The candidate will therefore be interested in the interactions between genes controlling acclimation and those controlling circadian regulation.

Planned recruitment date : september 2021

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Additional remarks/comments :