



Screening oilseed rape for resistance to the pollen beetle (*Meligethes aeneus*), from metabolomics to the field

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Social-economic context

Farmers use pesticides to control insect pests but the use of these chemical compounds is becoming increasingly controversial because of their impact on human health and environment. New ways of dealing with these pests need to be developed. Plant breeding for resistance to insects could be an interesting answer to this issue. We have chosen to study oilseed rape (*Brassica napus*), an economically important crop which is attacked by a wide range of insects against which an important amount of insecticides is currently used. This work focusses on the main herbivore damaging oilseed rape: the pollen beetle (*Meligethes aeneus*).

Scientific context

Plant breeding for insect resistances is a difficult process, especially for insects that can not be reared. However, chemical ecology studies indicate that plant chemical compounds are essential drivers of interactions between plants and insect herbivores. Understanding the chemical mechanisms underlying these interactions could open the way for an indirect approach of plant screening for insect resistance. Previous studies carried out at IGEPP under controlled conditions and based on a limited set of oilseed genotypes, were able to link damages to plant buds by the pollen beetle to 5 chemical compounds. These results now need to be validated on a larger set of genotypes and under field conditions.

Objectives

The first objective of this PhD is to develop methods for phenotyping oilseed rape resistance to pollen beetle. These methods will allow to evaluate resistances to this insect on a small set of genotypes at various scales (laboratory, greenhouse, field). The second objective is to link damages observed to plant composition and find markers of resistances to this pest. The third objective is to evaluate how these biomarkers are affected by environmental conditions.

Perspectives

If resilient biomarkers are identified a wide range of genotypes grown under different environmental conditions could be analyzed for their composition and thereby indirectly screened for resistance to the pollen beetle. Identifying these compounds could allow further location of QTLs of their expression and ultimately open the way for new breeding strategies of oilseed rape crops resistant to the pollen beetle.

