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# Analysis of Genetic and Metabolomic Factors Involved in Resistance to Flea Beetles in Diploid Brassica Germplasm



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## CONTEXT & OBJECTIVES

Cabbage Stem Flea Beetle (CSFB) is an increasing threat to winter oilseed rape (*Brassica napus*) growers in Europe. Declining efficiency and regulatory bans on chemical protection in the European context have recently highlighted the urgent need to develop efficient combinations of agronomic practices, biocontrol and varietal resistance. To date, no strong oligogenic resistance to CSFB has been identified in *Brassica* germplasm. However, the reservoir of variability for partial resistance to CSFB in oilseed rape and in their diploid parental species could make it possible to envisage breeding solutions in the short to medium-term.

Here we present some of the approaches we are conducting to identify the **genetic and metabolomic factors** involved in **resistance to flea beetle damage in *Brassica* species**. Screening and genetic analysis of partial resistance are carried out on a panel comprising wild, feral and landrace accessions of *B. rapa* and *B. oleracea*, in order to exploit the largest genetic diversity in these two parental species of the allotetraploid cultivated species *B. napus*. We also present the strategy for initiating **introgression of resistance factors in oilseed rape**.

## STRATEGY

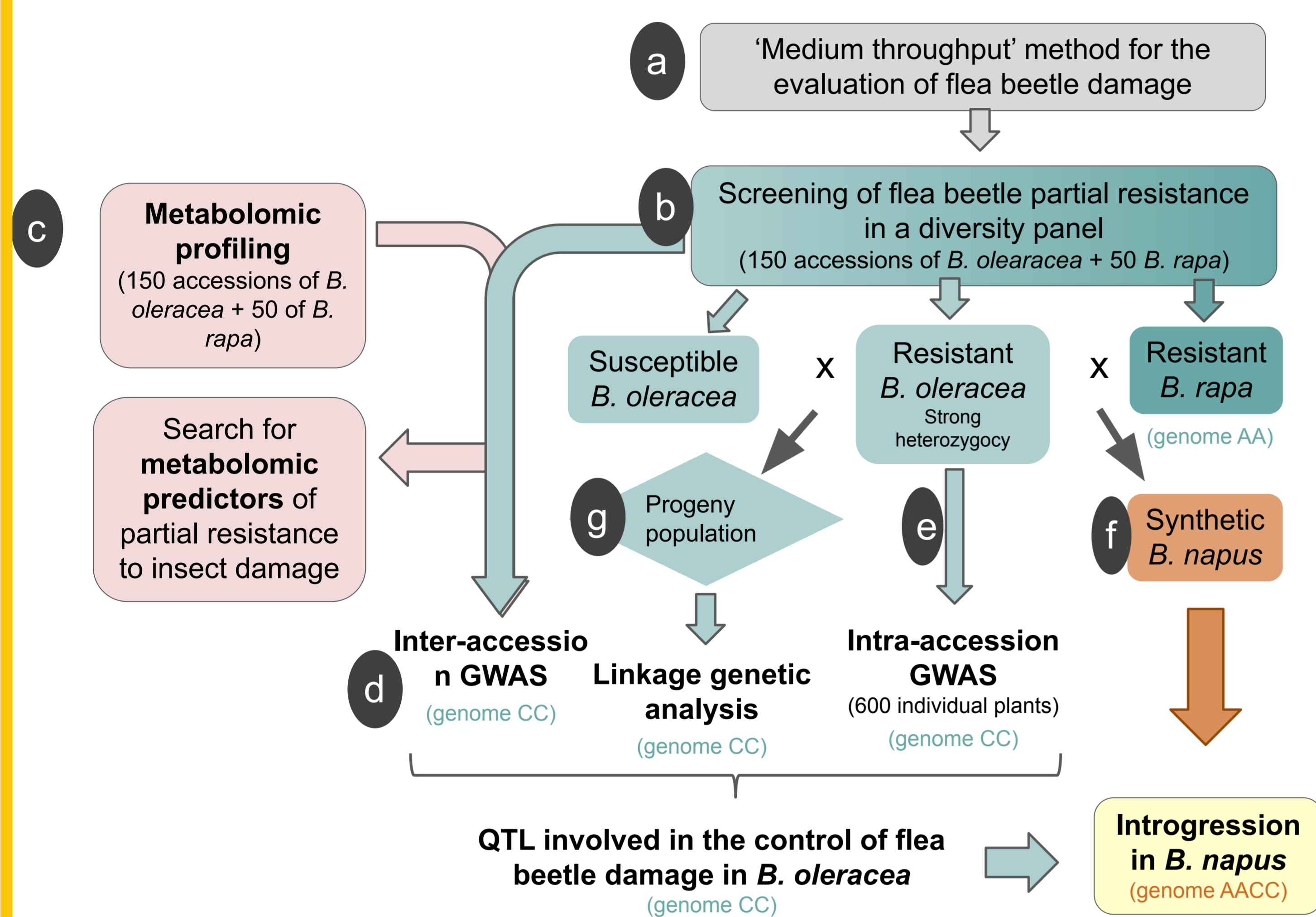


Fig. 1. Genetic strategies underway to identify and introgress genetic factors involved in partial flea beetle resistance

## PHENOTYPING METHOD

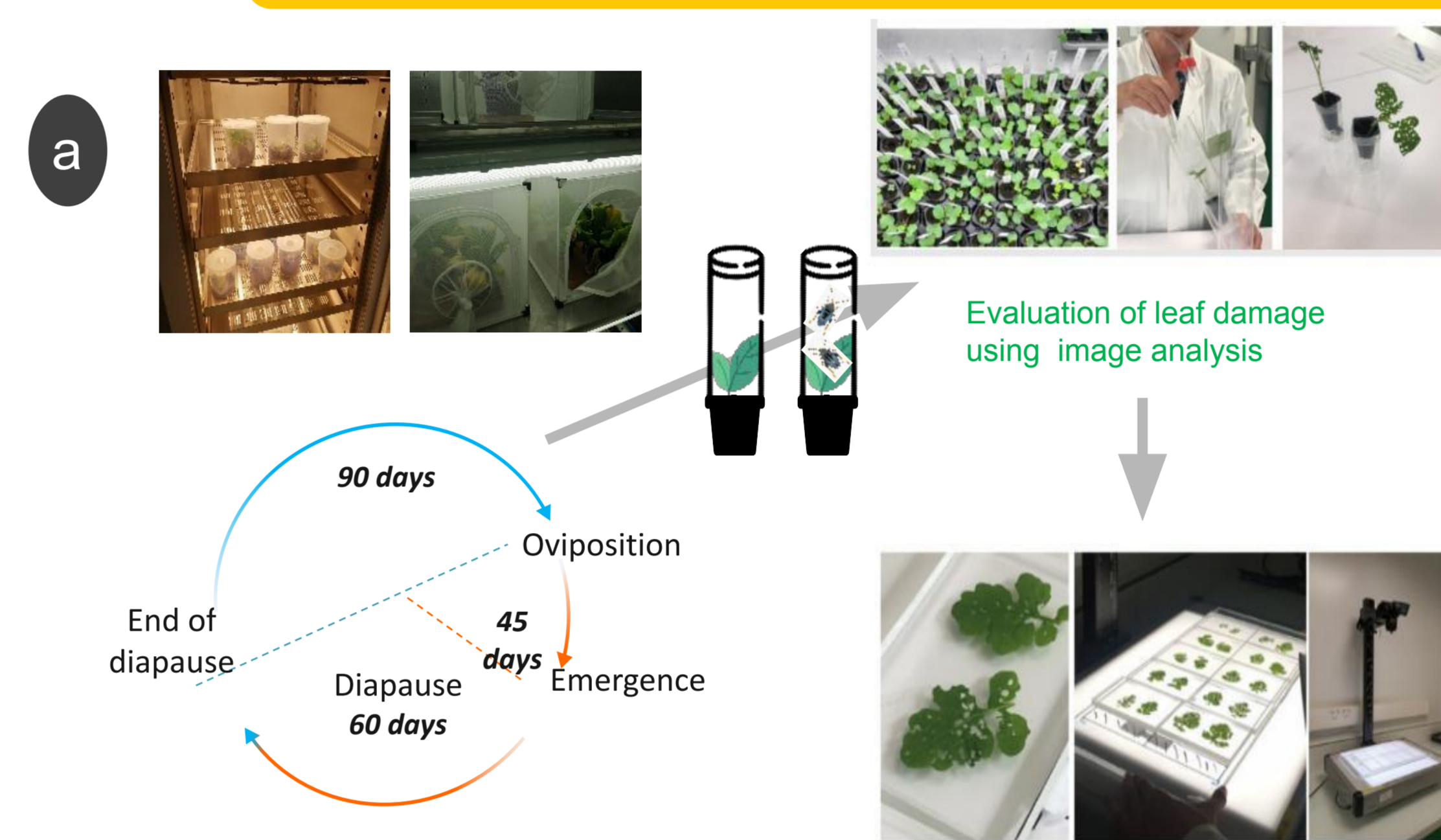


Fig. 2. Overview of the method designed for screening leaf damage caused by flea beetles. Following diapause, each plant is exposed for 48 hours to two adult insects that had previously fasted for 48 hours. Ten to 30 plants are evaluated (independent replicates) per accession.

## CONCLUSION & PERSPECTIVES

We have developed **methods for assessing plant resistance to flea beetles damage**, which we can now deploy on medium-size panels (>100 accessions). This includes **1/ leaf damage** caused by adult flea beetles (Fig. 2) **2/ petiole damage** caused by larvae.

The results of our screening approach revealed **substantial genetic variability in leaf-damage symptoms** between accessions of *B. oleracea* and *B. rapa* (Fig 3). Several accessions of *B. oleracea* display interesting levels of partial resistance to adult insect herbivory, close to those observed in the resistant accession of *Sinapis alba* used here as a reference.

Preliminary results from metabolomic profiling of 200 *Brassica* accessions (Fig. 4) indicate a high diversity of specialized metabolites that will be used in the search for predictors of insect resistance.

No resistance QTL were detected in this analysis, due to the strong genetic structure of the panel, the relatively small number of accessions and the putative polygenic control of the resistance trait. However, the calculated heritability of 0.21 indicates that partial resistance to leaf damage has a genetic component, that we may have a better chance of capturing through the genetic approaches developed as part of this project.

As most accessions in the Brassica panel studied are highly heterozygous, **intra-accession variability will be exploited** in the near future for an extended intra-accession GWAS analysis.

## RESISTANCE SCREENING

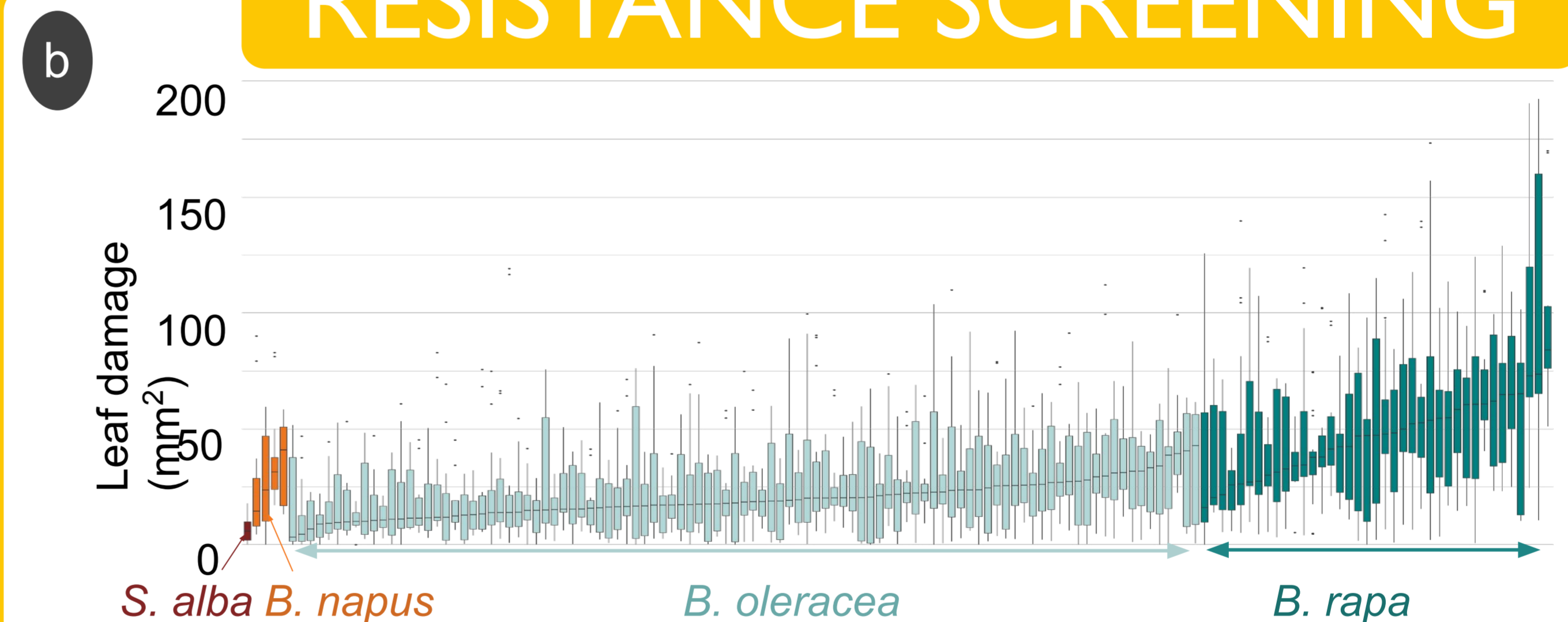


Fig. 3. Diversity of leaf damage levels in plantlets after 48-H exposure to two adult flea beetles, within a panel of *Brassica* accessions. The panel was mainly based on european accessions (Falentin et al. 2024 Genetic Ressources, 5, 61-71). It included wild, feral and landrace accessions of *B. oleracea* (150 accessions) and *B. rapa* (50 accessions). One accession of *Sinapis alba* (previously identified as resistant), and four accessions of *B. napus* were included as reference. For each accession, data presented here come from 10 independent replicates.

## METABOLOMICS

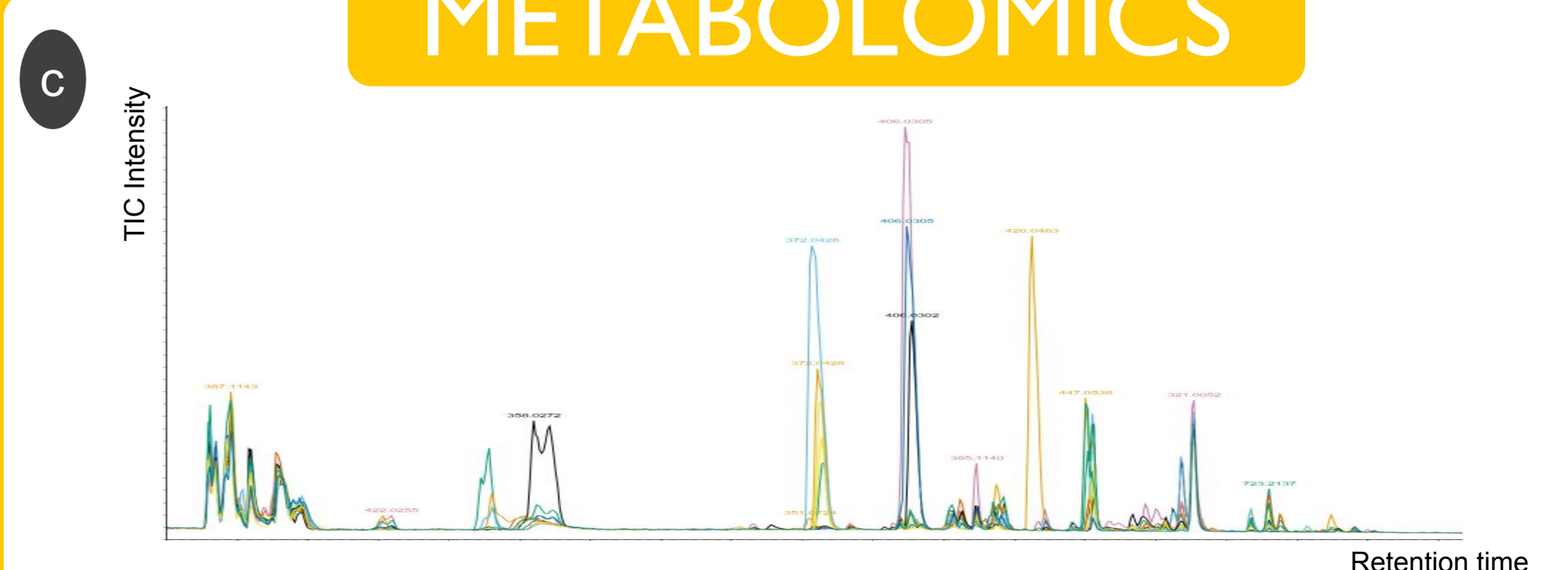


Fig. 4 Example of contrasted metabolomic profiles within the Brassica panel. Here are superimposed the UHPLC-HRMS TIC (Total-Ion Chromatograms) obtained from samples from 6 *Brassica* accessions (indicated with different colors). Numbers above peaks indicates m/z values for the most abundant ion at a given retention time. The ions with the highest peaks on this figure are associated with glucosinolates and phenolic compounds. Detailed analysis of the chromatograms typically leads to >3000 metabolic features.