



HAL
open science

Identification of major genes involved in rapeseed quantitative resistance to *Leptosphaeria maculans* by an innovative effectoromics approach.

Camille Rabeau, Sébastien Faure, Audren Jiquel, Isabelle Fudal

► To cite this version:

Camille Rabeau, Sébastien Faure, Audren Jiquel, Isabelle Fudal. Identification of major genes involved in rapeseed quantitative resistance to *Leptosphaeria maculans* by an innovative effectoromics approach.. Journées Jean Chevaugeon, Jan 2024, Aussois, France. hal-04485957

HAL Id: hal-04485957

<https://hal.science/hal-04485957>

Submitted on 1 Mar 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

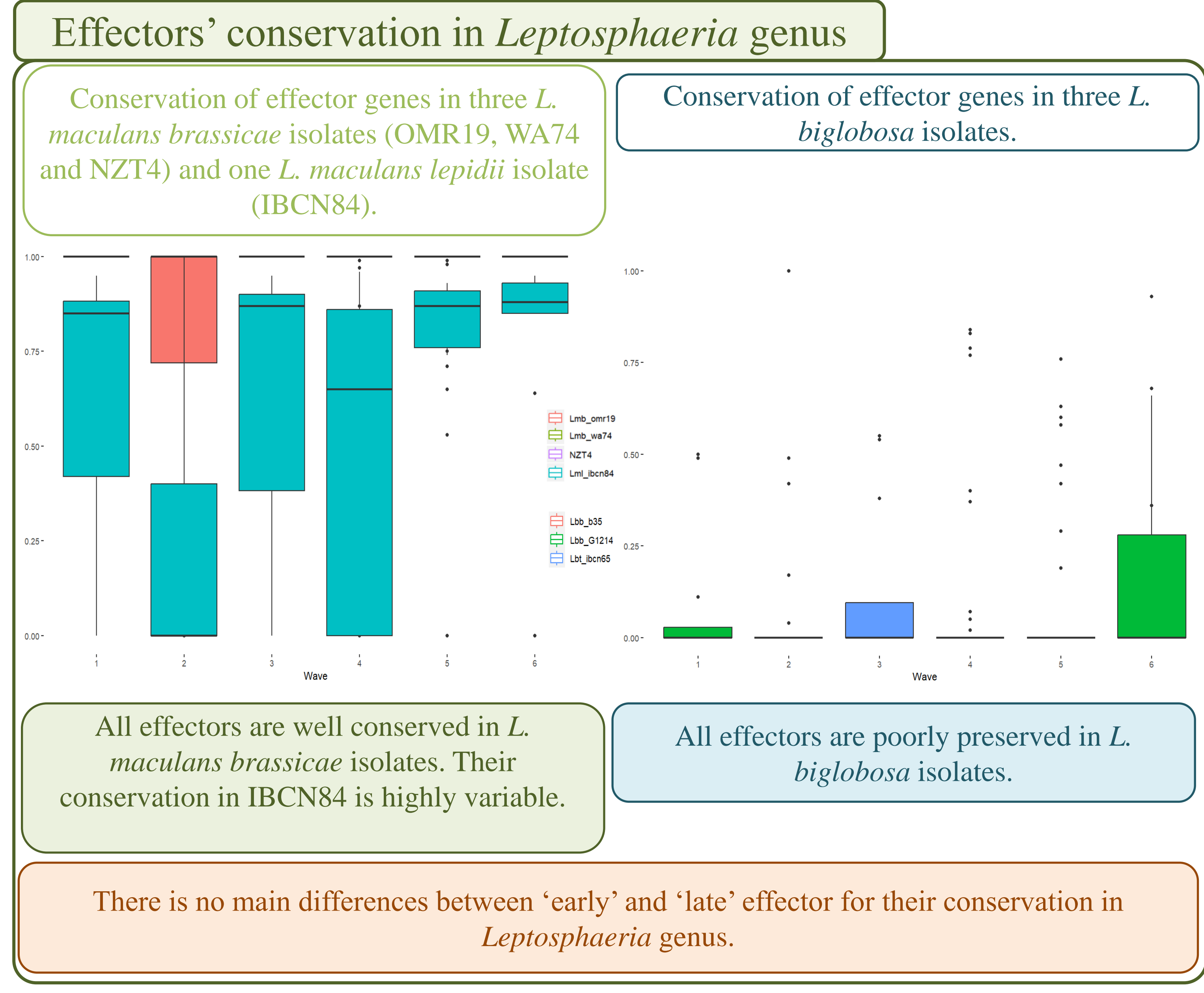
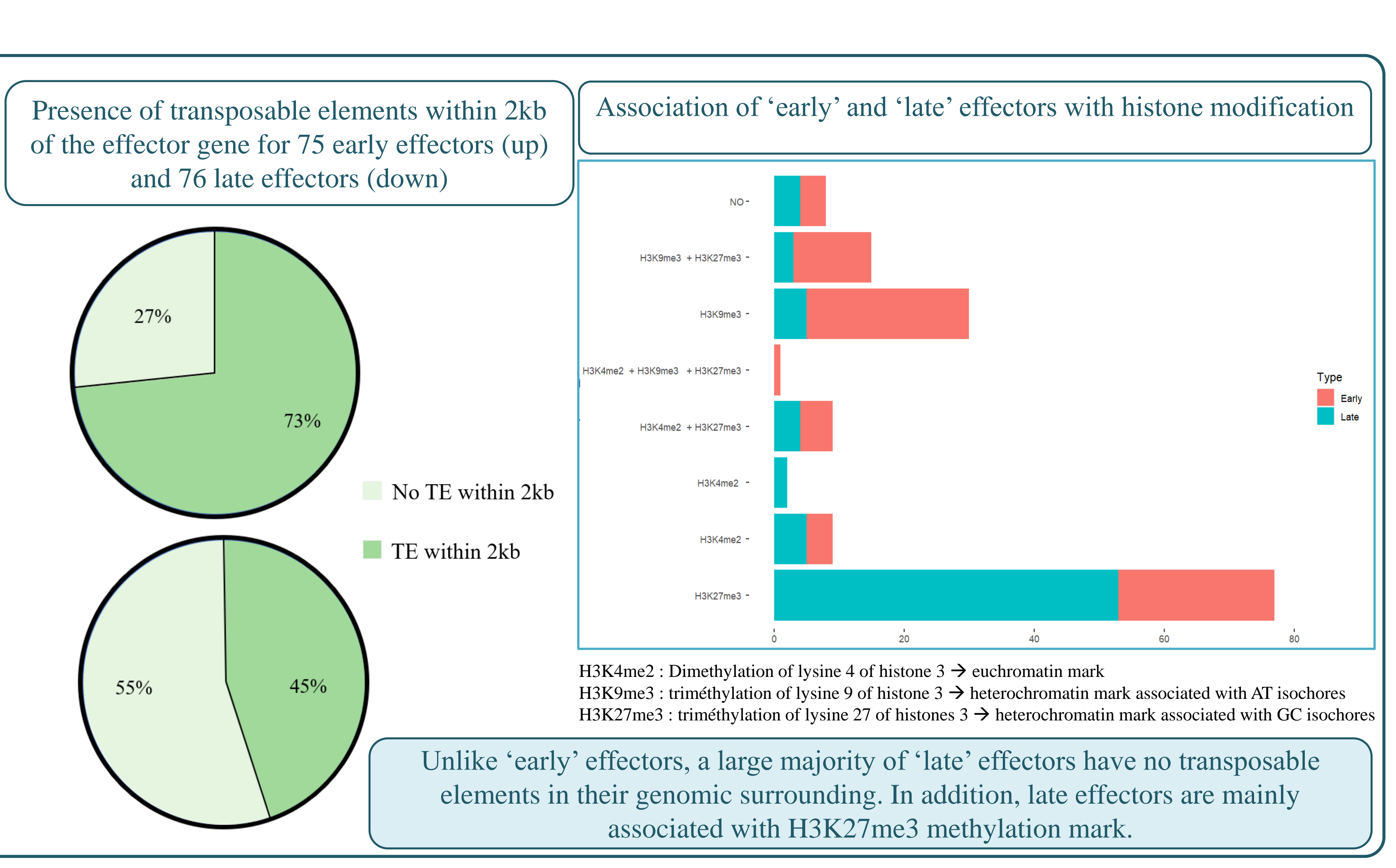
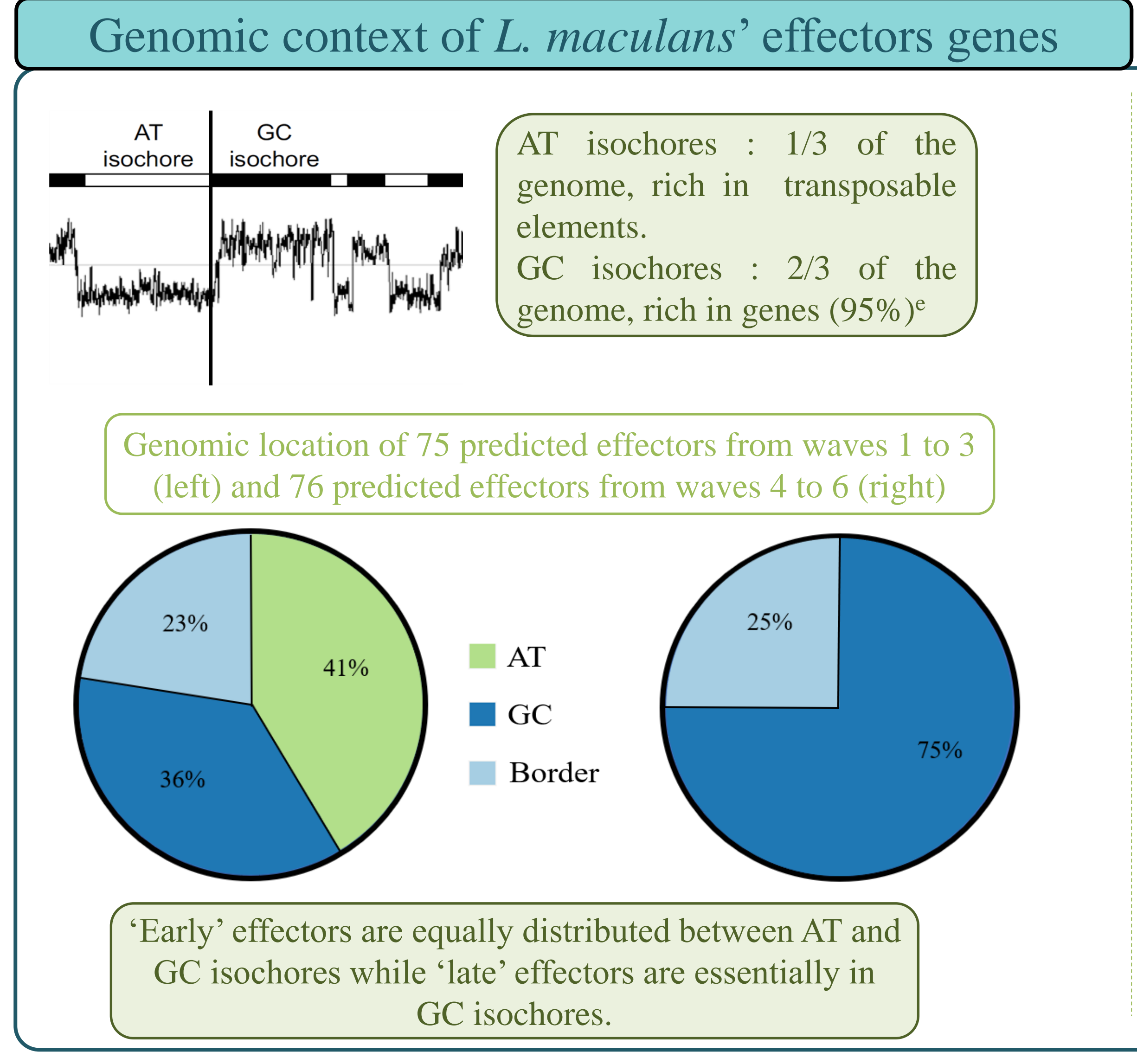
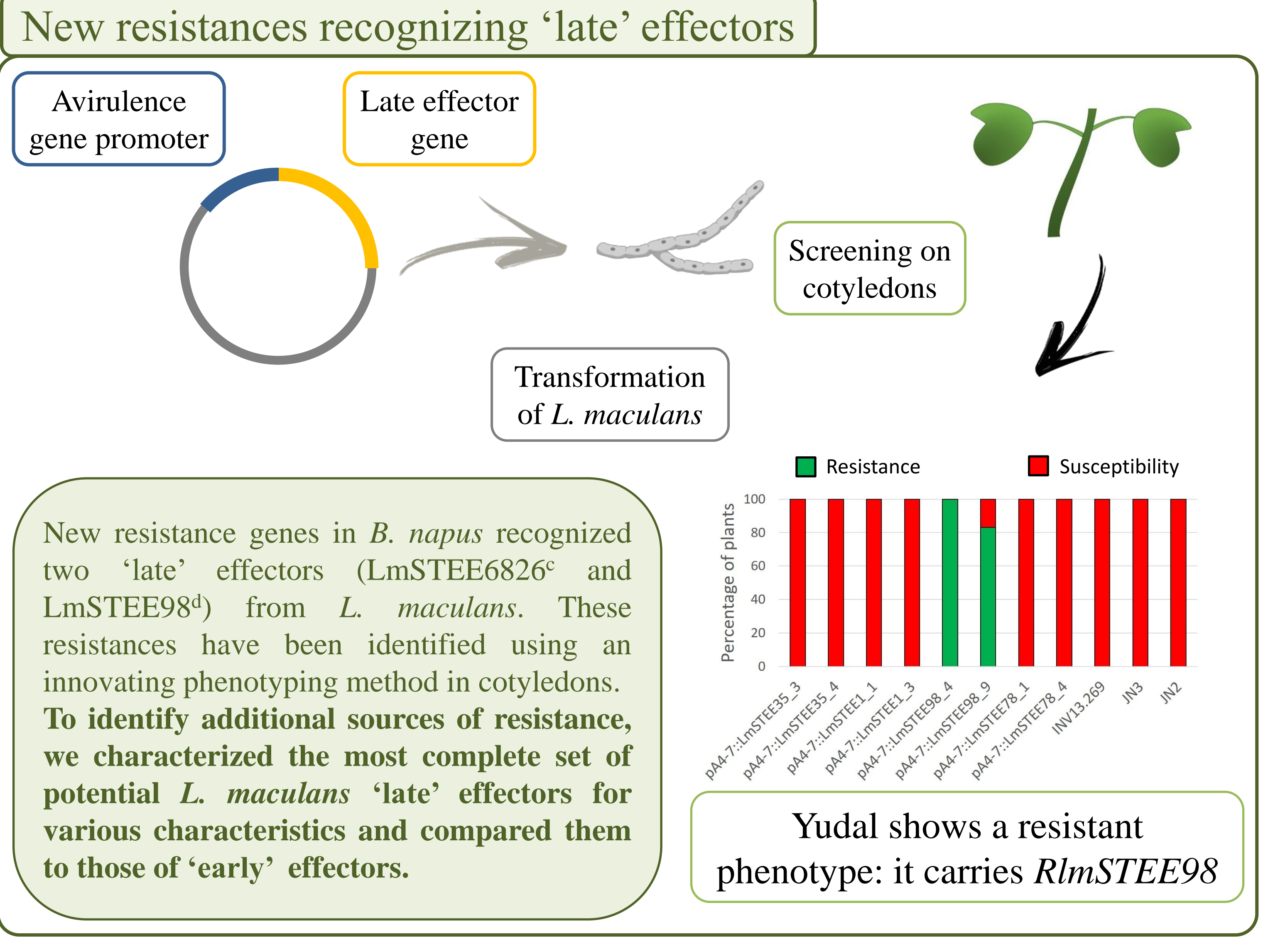
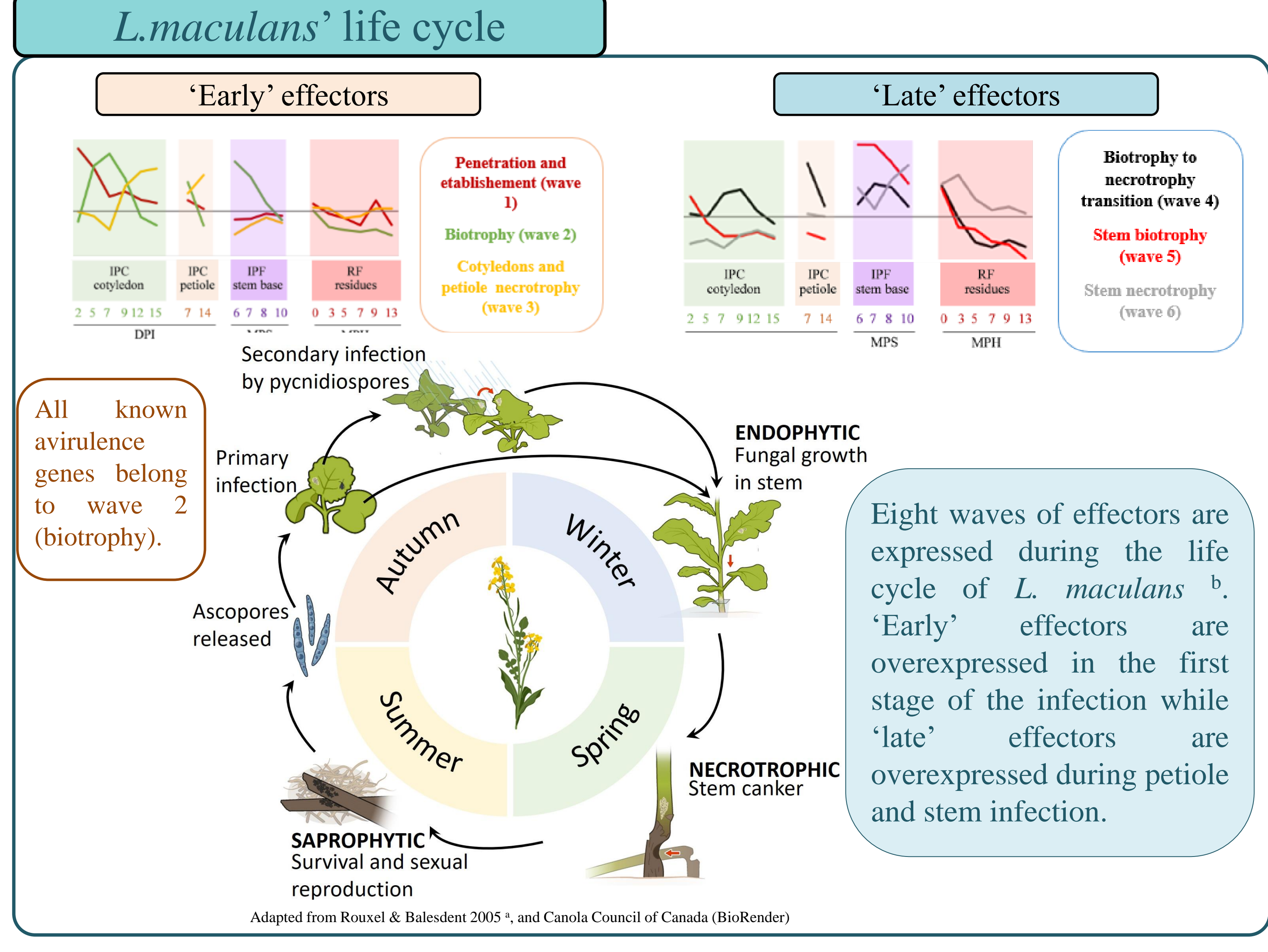
L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Identification of major genes involved in rapeseed quantitative resistance to *Leptosphaeria maculans* by an innovative effectomics approach.

Camille Rabeau^{1,2}, Sébastien Faure², Audren Jiquel¹ and Isabelle Fudal¹
¹ UR BIOGER, INRAE, Université Paris-Saclay, 22 place de l'Agronomie, Palaiseau 91120, France
² Innolea, 6 Chemin des Panedautes, Mondonville 31700, France

L. maculans is a phytopathogenic fungus responsible for stem canker on rapeseed (*Brassica napus*). Its infectious cycle is going through an 'early' phase of leaf infection and a 'late' phase of asymptomatic colonization of the stem, finally leading to stem canker. Genetic resistance is the main way to control this disease, with several qualitative resistance genes recognizing avirulence genes mainly expressed during the 'early' stage of infection. We opted to focus on 'late' effectors expressed during stem colonization as we hypothesized that those effectors could trigger quantitative resistance in the stem, which would exert less selection pressure on the pathogen and be more durable.

Journées Jean Chevaugnon - 2024



Conclusions and perspectives

To identify additional sources of quantitative resistance, we characterized the most complete set of potential *L. maculans* 'late' effectors for their expression kinetics during rapeseed infection, their conservation within the *Leptosphaeria* genus and among fungi, their location in the *L. maculans* genome and their enrichment in epigenetic marks

We then selected six new effectors :

- specifically expressed during petiole or stem infection,
- conserved in *Leptosphaeria maculans*,
- located in gene-rich regions, enriched in heterochromatin marks associated with genes,

The selected 'late' effectors will be used to identify new resistances in *B. napus* genotypes that could be introduced into modern cultivars adapted to the agronomic context in France.

^a Rouxel & Balesdent, 2005 (MPP) DOI: 10.1111/J.1364-3703.2004.00282.X
^b Gay *et al.*, 2021 (BMC Biology) DOI: 10.1186/s12915-021-00989-3
^c Jiquel *et al.*, 2022 (Plant Direct) DOI: 10.1002/pld3.435
^d Jiquel *et al.*, 2021 (New Phytol) DOI: 10.1111/nph.17292
^e Rouxel *et al.*, 2011 (Nat Commun) DOI: 10.1038/ncomms1189