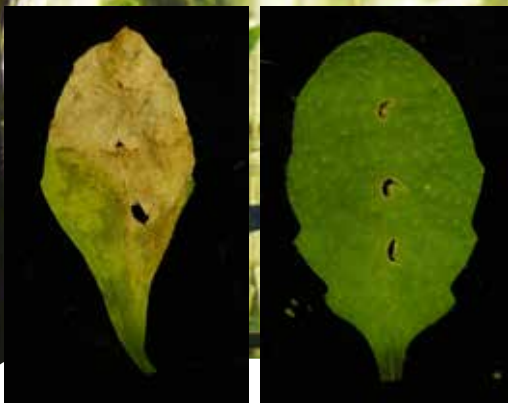


An atypical kinase under balancing selection confers broad-spectrum disease resistance in *Arabidopsis*

During the evolution of plant-pathogen interactions, plants have evolved the capability to defend themselves from pathogen infection by different overlapping mechanisms. Disease resistance is constituted by an elaborate, multilayered system of defense. Among these responses, quantitative resistance is a prevalent form of resistance in crops and natural plant populations, for which the genetic and molecular bases remain largely unknown. Thus, identification of the genes underlying quantitative resistance constitutes a major challenge in plant breeding and evolutionary biology, and might have enormous practical implications for human health by increasing crop yield and quality.

Our work contributes to understanding the molecular bases of quantitative resistance to the vascular pathogen *Xanthomonas campestris* (*Xc*), which is responsible for black rot, an important disease of crucifers worldwide. By multiple approaches, we demonstrate that RKS1 is a quantitative resistance gene in *Arabidopsis thaliana* conferring broad-spectrum resistance to *Xc* and that this resistance mechanism in plants is associated with regulation of RKS1 expression. We also provide evidence that RKS1 allelic variation is a major component of quantitative resistance to *Xc* at the species level. Finally, the long-lived polymorphism associated with RKS1 suggests that evolutionary stable broad-spectrum resistance to *Xc* may be achieved in natural populations of *A. thaliana*.



Left : Infected leaf of *A.thaliana* by *X.campestris* with RSK1 low resistance.
Right : same but with RSK1 high resistance.
Black spots marks entry points of infection