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Change of paradigm for breeding disease resistant cultivars robust to varying environments: estimators of the robustness of plant immunity and promising genes for the future

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Oral communication

Summary

To drastically reduce the use of chemical pesticides to control crop pathogens, breeding of immune cultivars is a sustainable and effective solution that should be included in integrated management approaches (Lefebvre *et al.*, 2020). However, the immune response of plants to a pathogen attack depends on the environment. Plants with an efficient immunity to a pathogen in a given environment commonly have a decreased or suppressed immunity in another environment. This observation is accentuated by the current context of climate change, which is responsible for a strong increase in environmental variability via the rise in average global temperatures and the higher frequency and intensity of extreme weather events, such as heat waves, floods and droughts (Berthomé *et al.*, 2021). It is therefore crucial to select cultivars with stable immunity to pathogens in changing environments.

The stability of immunity echoes the concept of robustness, which is defined by the stable expression of a trait in response to a genetic or environmental perturbation. Two main types of robustness are distinguished: type I robustness is associated with the stability of the mean of a trait, while type II robustness is associated with the stability of the variance of a trait (Félix & Barkoulas, 2015). Originally identified in animals, robustness has seldom been studied in plants. To create cultivars with stable immunity in changing environments, breeding programs often look for genes that confer an effective immunity in a few contrasting environments. This method is effective for the tested environments but does not ensure stable immunity in other environmental conditions. Identifying the genetic determinants that control the robustness of a trait, independently of the genetic determinism of the trait itself, would therefore be a major breakthrough in plant breeding to control crop pathogens.

Our research focuses on the robustness of plant immunity. Our main objectives are to (i) define methods for estimating the robustness of a trait, and (ii) identify the genetic architecture responsible for robustness. To this end, we characterised the immunity of a set of almost 300 accessions of pepper (*Capsicum annuum* L.), constituting a core-collection representative of *C. annuum* genetic diversity, to two major pathogens independently: the oomycete *Phytophthora capsici* and *Potato virus Y*. For each pathogen, several quantitative immunity parameters were assessed in two environments contrasted for temperature, to simulate a temperature-related environmental perturbation. From these immunity parameters obtained under each temperature environment, we estimated new quantitative parameters associated with the type I and type II robustness of immunity. We analysed their relevance by studying their correlations and their performance according to two criteria: experimental heritability (*i.e.* reproducibility of the measurement) and discriminatory power (*i.e.* ability to separate accessions according to their robustness level).

Type I and type II robustness parameters are weakly correlated, proving the necessity to analyse each type independently. Within each type of robustness, the parameters are split into two groups corresponding to two ways of analysing robustness for a given accession. One corresponds to the deviation from the hypothesis of perfect stability of the trait in response to the perturbation. The other corresponds to the deviation from the reaction norm of the whole core-collection to the perturbation. The different parameters within each group are highly correlated but vary in terms of performance.

In parallel, we genotyped at a high-density the core-collection by specific allelic capture. For each pathogen, genome-wide association studies (GWAS) of the parameters of immunity and robustness identified several single-nucleotide polymorphisms (SNPs) associated with (i) the immunity under each of the two environments tested and (ii) the robustness of immunity to temperature change.

No SNPs common to both pathogens were identified, indicating that immunity and robustness of immunity between the two tested environments are pathogen-specific. A few significant SNPs identified for immunity are common to both environments but all are distinct from those identified for the robustness of immunity. Intriguingly, the majority of candidate genes within the confidence intervals of quantitative trait loci (QTLs) determining robustness of immunity are associated with immunity mechanisms. A gene encoding a heat shock protein (HSP) is of particular interest since studies in different organisms have demonstrated a link between HSPs and the robustness of developmental traits (Félix & Barkoulas, 2015).

To go further, we explored several other issues, such as the trade-off between the robustness of immunity and immunity itself, the link between robustness of immunity and robustness of plant development, and the genericity of robustness of immunity to different environmental perturbations. To this end, measurements related to plant development were carried out and immunity was measured for both pathogens with different watering conditions simulating drought and flood.

Keywords: robustness, immunity, environmental perturbation, pepper (*Capsicum annuum* L.), *Phytophthora capsici*, *Potato virus Y*

Literature

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