The durability of a major resistance gene is affected by quantitative trait loci which also confer quantitative resistance to virus

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have to adapt to different constraints at the same time.

Our study will contribute to this objective for wheat leaf rust, caused by *Puccinia triticina*.

Eight wheat genotypes were selected and confronted in a greenhouse to three isolates, belonging to different pathotypes. A high diversity and variability was expressed in the host x isolate combinations investigated for five components of resistance: infection efficiency (IE), latent period (LP), lesion size (LS), spore production per lesion (SPL), and spore production per unit of sporulating tissue (SPS). Isolate-specificity was found for all these components.

The genomics regions involved in resistance components of two of the cultivars were characterised in a doubled haploid population by QTL analysis. From the eight QTLs found, four were associated to the resistance expressed on a single component, and three of them to the resistance expressed on two components. All these QTLs were also associated to global disease reduction in field epidemic conditions.

In order to estimate the impact of the different components, measured in controlled conditions, on the resistance level in field conditions, disease severity (DS) was measured at three different times of epidemic development in the field. Statistical models were developed to provide the estimations of each trait for each cultivar-isolate pair, and correlation between traits was tested. All the components, except for SPL, participated to quantitative resistance in field epidemic conditions in different ways. The effect of LP in resistance was cumulative over the epidemic, whereas sporulation components effect (LS and SPS) was more important at the beginning of the epidemic, and decreased as the epidemic progress. IE had a more important effect on resistance in the middle of the epidemic.

Measurements of resistance components in controlled conditions allowed us to reveal phenotypical and genetical diversity in quantitative resistance to wheat leaf rust. Combining QTLs identified in this study, which were associated to different components, will diversify the mechanisms of resistance, taking into account the pathogen specificity, and protecting plants at the different stages of the epidemic. Alltogether, this strategy should lower the risk of erosion of the available sources of quantitative resistance.

Keywords: Quantitative resistance, Wheat leaf rust, QTL analysis, Statistical modelisation

The durability of a major resistance gene is affected by quantitative trait loci which also confer quantitative resistance to virus.

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Abstract

Genetic resistance provides efficient control of crop diseases but is limited by pathogen adaptation to resistant cultivars. The durability of the *pvr2*^{3} allele, conferring resistance to *Potato virus Y* (PVY) in pepper (*Capsicum annuum*), was demonstrated to depend on the plant genetic background which modulates the frequency of *pvr2*^{3} resistance breakdown due to virus mutation. Our objective was to identify, in this genetic background, quantitative trait loci (QTLs) controlling the breakdown frequency of the *pvr2*^{3} major gene (resistance durability) and to compare them to the QTLs controlling quantitative resistance.

The QTL analysis was performed using a population of 310 doubled-haploid (DH) lines issued from the F1 hybrid between pepper line, 'Perennial' carrying *pvr2*^{3} in a partially resistant background, and 'Yolo

Wonder' carrying the susceptible *pvr2*$^{+}$ allele in a susceptible background. The DH lines were genotyped with 234 markers and the linkage map was established. The breakdown frequency of *pvr2*^{3} was assessed in the "*pvr2*^{3} sub-population" of 156 DH lines carrying the *pvr2*^{3} allele but segregating for the genetic background, after inoculation with a wild-type PVY cDNA clone avirulent (not infectious *per se*) towards *pvr2*^{3}. The quantitative resistance (PVY accumulation and area under disease progress curve (AUDPC)) was assessed using the same PVY clone inoculated to the "*pvr2*$^{+}$ sub-population" of 154 DH lines from the same progeny but carrying the *pvr2*$^{+}$ susceptibility allele. The same quantitative resistance traits were also assessed in the "*pvr2*^{3} sub-population" inoculated by a mutant of the previous PVY clone carrying a single mutation allowing the breakdown of *pvr2*^{3}.

Genotypic variance was highly significant for all traits with heritabilities of 0.87 for the breakdown frequency of *pvr2*^{3} and 0.47 to 0.62 for quantitative resistance traits. Two main QTLs, explaining 29% and 10% of the variance of *pvr2*^{3} breakdown frequency were identified on chromosomes 3 and 1. Considering the virus accumulation, 2 to 3 significant QTLs were detected, including the QTL on chromosome 3 which displayed a major effect on virus accumulation in the "*pvr2*^{3} sub-population" but a minor effect in the "*pvr2*$^{+}$ sub-population", suggesting an interaction between this QTL and the alleles at the *pvr2* locus. For the AUDPC trait, 3 to 4 QTLs were significant including the QTLs on chromosomes 1 and 3 previously detected for resistance breakdown frequency.

Comparative mapping of the different traits showed that the two QTLs controlling the breakdown frequency of the *pvr2*^{3} allele are also involved in quantitative resistance, indicating that QTLs for quantitative resistance in the genetic background have a pleiotropic effect on the durability of the major resistance gene. Interestingly, the amplitude of the effect on virus accumulation of the QTL on the chromosome 3 depends on the allele at the *pvr2* locus, suggesting functional interaction between these loci. This first mapping of QTLs directly affecting resistance durability opens the way for sustainable resistance breeding.

Keywords: Resistance durability, quantitative resistance, resistance breakdown, Capsicum, Potato virus Y, major resistance gene, QTL analysis, eukaryotic translation initiation factor 4E.

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