Genetics Of Partial Resistance In Lettuce Against Race 2 Of *Verticillium dahliae*

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Verticillium wilt in Lettuce

Verticillium dahliae causes wilt disease (Fig. 1a) in lettuce (2n=2x=18) in the Salinas Valley of California, the biggest production area in the USA.

The fungus is a soil-borne pathogen that initiates infection through the roots and causes root vascular discoloration (Fig. 1b), leaf wilting, and plant death.

The disease is distributed along the Salinas Valley as mostly race 1 but the presence of race 2 isolates are suspected to increase in the future.

Complete race 1 resistance is controlled by a single dominant gene (*Verticillium resistance 1 Vr1*). Race 1 is currently available in resistant breeding lines.

No complete resistance against race 2 is available. Four Plant introductions (PIs) were identified as sources of Partial Resistance (PR) against race 2 of *V. dahliae*.

The objectives of this research were to map Quantitative Trait Loci (QTL) in a biparental population developed from a cross between two Partial Resistant PIs and Identify possible transgressive segregants (families with better resistance than parents) that could be used in breeding.

Figure 1. a) Verticillium wilt in iceberg lettuce; b) healthy and infected lettuce taproots

Phenotyping and Genotyping

PI 204707 was crossed to PI 171674, 99 F_3 families were phenotyped for Root Discoloration Incidence (DI). Days to First Flower (DFF) was recorded to determine the relationship between earliness and disease resistance. Experiments were conducted twice in the greenhouse using the race 2 isolate VdLs17 of *V. dahliae* isolated from lettuce.

Genotyping by Sequencing was performed using the restriction enzyme *AvaII* and Single Nucleotide Polymorfisms (SNPs) were identified with TASSEL 3.0. A genetic map was constructed using JoinMap and QTLs were detected using QTL Network that calculates the QTL x Environment (E) interaction.
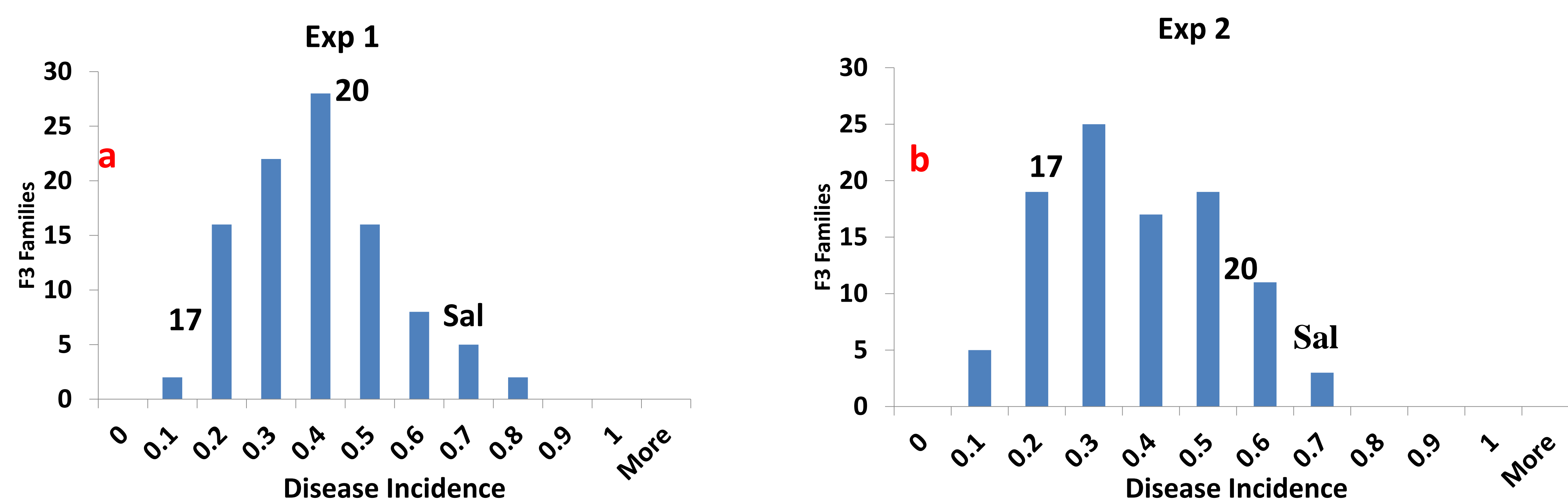

Figure 2. Distribution of 99 F_3 families for Disease Incidence in greenhouse test for population 171674x204707 in a) Experiment 1 (planted in January 2013) and b) Experiment 2 (planted in October 2013). 17 represents the DI of PI 171674, 20 represents the DI of PI 204707 and Sal the susceptible control Salinas.

Results

The 99 F_3 families followed a normal distribution in both experiments for DI and DFF (Fig. 2a and b). Significant differences were observed among families for DI (Exp 1 *P=0.00023* and Exp 2 *P<0.0001*) and DFF (Exp 1 *P<0.0001* and Exp 2 *P=0.0002*). A small but significant correlations (r=0.42 *P<0.0001*; r=0.32 *P=0.0012*) between experiments were observed for the DI indicating QTL × E interaction. A large correlation (r=0.86 *P<0.0001*) between experiments was detected for DFF.

Three QTLs for disease traits were identified in linkage groups (LG) 5, 6 and 8 explaining a small proportion of the phenotypic variance (R^2 = 4%, 12% and 6%, respectively) (DI in Fig. 3 in red). QTL × E approached significance on LG6 (P=0.051 and 0.0538) for the additive component.

A large (R^2 = 30%) effect QTL in LG7 and small ((R^2 = 4%) effect QTL in LG4 were identified for DFF (Fig. 3 in green).
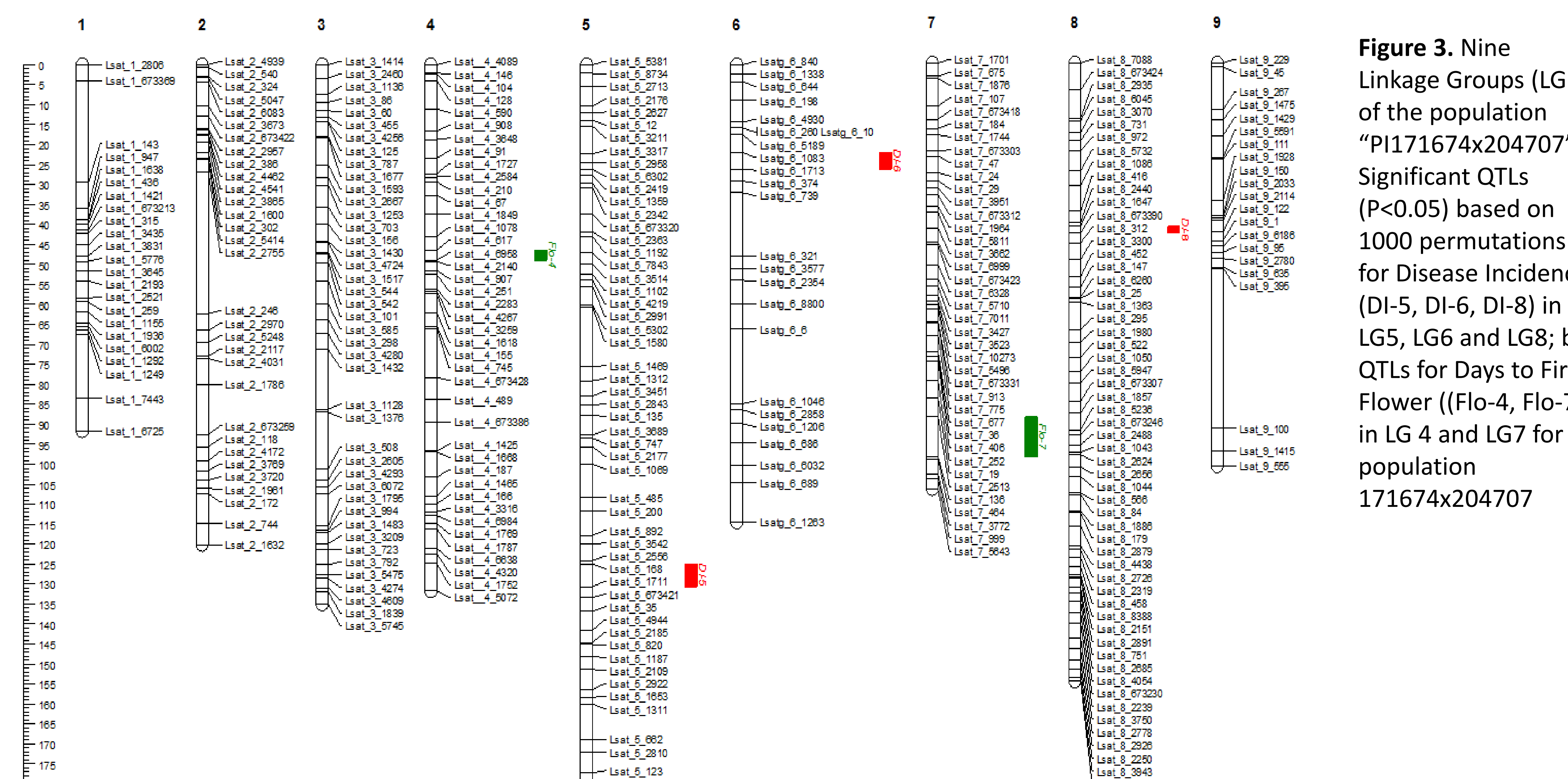

Figure 3. Nine Linkage Groups (LG) of the population "PI171674x204707". Significant QTLs (P<0.05) based on 1000 permutations a) for Disease Incidence (DI-5, DI-6, DI-8) in LG5, LG6 and LG8; b) QTLs for Days to First Flower ((Flo-4, Flo-7) in LG 4 and LG7 for population 171674x204707

Conclusions and future directions

No family (transgressive segregants) with superior performance to the most resistant parent (PI 171674) was detected.

PI 171674 (PR) had consistently less root discoloration compared to PI 204707 (PR) but both PIs had less root discoloration than the susceptible control 'Salinas'.

Disease traits are controlled by several QTLs with small effects that interact with the environment. Other environmentally specific QTLs were detected in LG 3, 4 and 5 (no reported here).

Genes controlling DI and DFF are in different LG. No relationship between flowering and resistance was identified showing that both traits can be independently breed.

Breeding lettuce for resistance to race 2 of Verticillium wilt should be done using methods for quantitatively inherited traits.