

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

Results

The 99 F₃ 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.

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.

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

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).

No complete resistance against race 2 is available. Four Plant introductions (PIs) were	ʰ Ĥ
No complete resistance against race 2 is available. Four Plant introductions (Pls) were identified as sources of Partial Resistance (PR) against race 2 of <i>V. dahliae</i> .	10 15 20

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

Lsat_1_3831 Lsat_2_5414 Lsat_3_156 Lsat_4_617 Lsat_5_2363 Lsat_1_5776 Lsat_2_2755 Lsat_3_1430 Lsat_4_6958 Isat_5_1192 Lsat_6_321 Lsat_7_3662 Lsat_8_452 Lsat_8_452 Lsat_1_3645 Lsat_3_1517 Lsat_4_907 Lsat_5_3514 Lsat_6_3577 Lsat_7_673423 Lsat_8_6260 Lsat_8_6260 Lsat_1_2193 Lsat_3_544 Lsat_4_2283 Lsat_5_1102 Lsat_6_8800 Lsat_7_6328 Lsat_8_1363 Lsat_1_259 Lsat_2_246 Lsat_3_101 Lsat_4_267 Lsat_5_291 Lsat_6_8800 Lsat_7_701 Lsat_8_1363	1	2	3	4	5	6	1	8	9
	Lsat_1_673369	Lsat_2_540 Lsat_2_324 Lsat_2_5047 Lsat_2_6083 Lsat_2_3673 Lsat_2_673422 Lsat_2_957 Lsat_2_386 Lsat_2_4482 Lsat_2_4482 Lsat_2_4482 Lsat_2_4482 Lsat_2_3885 Lsat_2_3885 Lsat_2_302 Lsat_2_302 Lsat_2_5414 Lsat_2_2755	Lsat_3_2460 Lsat_3_1136 Lsat_3_86 Lsat_3_60 Lsat_3_4258 Lsat_3_4258 Lsat_3_125 Lsat_3_125 Lsat_3_1677 Lsat_3_1693 Lsat_3_1693 Lsat_3_1253 Lsat_3_1253 Lsat_3_1253 Lsat_3_156 Lsat_3_156 Lsat_3_1430 Lsat_3_1517 Lsat_3_544 Lsat_3_542 Lsat_3_542 Lsat_3_101	Lsat_4_148 Lsat_4_104 Lsat_4_128 Lsat_4_590 Lsat_4_908 Lsat_4_91 Lsat_4_1727 Lsat_4_1727 Lsat_4_2584 Lsat_4_210 Lsat_4_67 Lsat_4_67 Lsat_4_1849 Lsat_4_617 Lsat_4_617 Lsat_4_6958 Lsat_4_2140 Lsat_4_2140 Lsat_4_2283 Lsat_4_2283 Lsat_4_2283 Lsat_4_2283 Lsat_4_4267	Lsat_5_8734 Lsat_5_2713 Lsat_5_2176 Lsat_5_2827 Lsat_5_2827 Lsat_5_3211 Lsat_5_3317 Lsat_5_2958 Lsat_5_2419 Lsat_5_2419 Lsat_5_1359 Lsat_5_2342 Lsat_5_2363 Lsat_5_2363 Lsat_5_7843 Lsat_5_7843 Lsat_5_7843 Lsat_5_3514 Lsat_5_4219 Lsat_5_2991	Lsatg_6_1338 Lsatg_6_644 Lsatg_6_198 Lsatg_6_280 Lsatg_6_10 Lsatg_6_5189 Lsatg_6_1083 Lsatg_6_1713 Lsatg_6_374 Lsatg_6_374 Lsatg_6_739	Lsat_7_675 Lsat_7_1876 Lsat_7_107 Lsat_7_673418 Lsat_7_673418 Lsat_7_1744 Lsat_7_673303 Lsat_7_47 Lsat_7_24 Lsat_7_29 Lsat_7_29 Lsat_7_3951 Lsat_7_673312 Lsat_7_673312 Lsat_7_673423 Lsat_7_673423 Lsat_7_673423 Lsat_7_673423 Lsat_7_673423 Lsat_7_673423 Lsat_7_673423 Lsat_7_673423	Lsat_8_673424 Lsat_8_2935 Lsat_8_6045 Lsat_8_3070 Lsat_8_731 Lsat_8_972 Lsat_8_5732 Lsat_8_1086 Lsat_8_1086 Lsat_8_416 Lsat_8_416 Lsat_8_2440 Lsat_8_1647 Lsat_8_673390 Lsat_8_312 Lsat_8_3300 Lsat_8_452 Lsat_8_147 Lsat_8_6260 Lsat_8_25 Lsat_8_1363 Lsat_8_295	

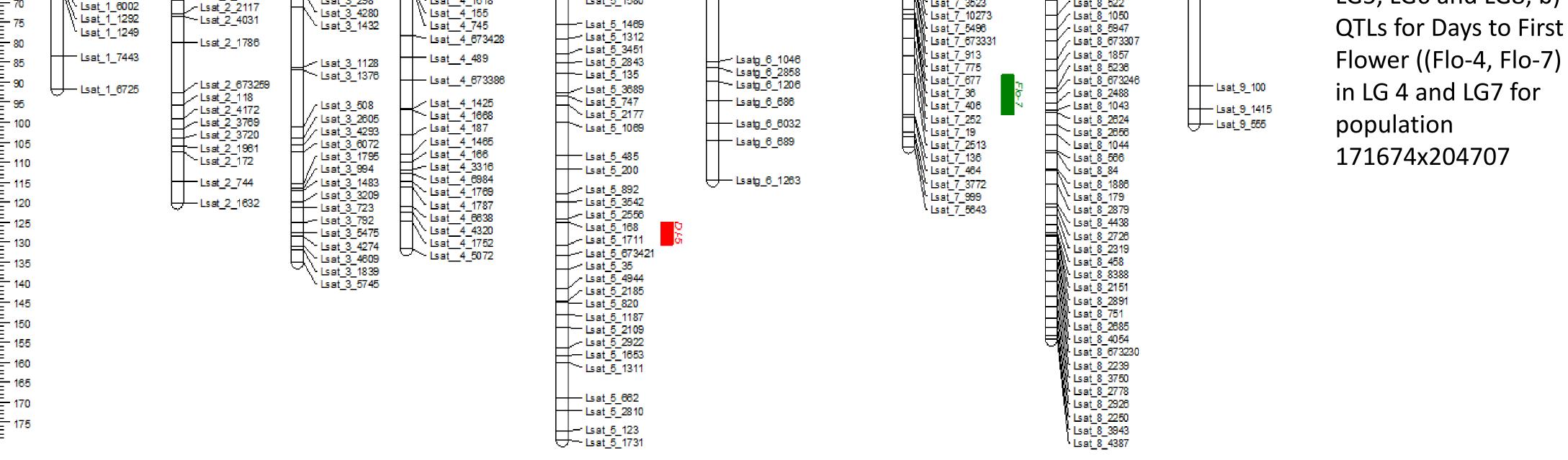
Figure 3. Nine Linkage Groups (LG) of the population "PI171674x204707". Significant QTLs (P<0.05) based on 1000 permutations a) for Disease Incidence (DI-5, DI-6, DI-8) in LG5, LG6 and LG8; b)

be used in breeding.

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 Avall 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.



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'.

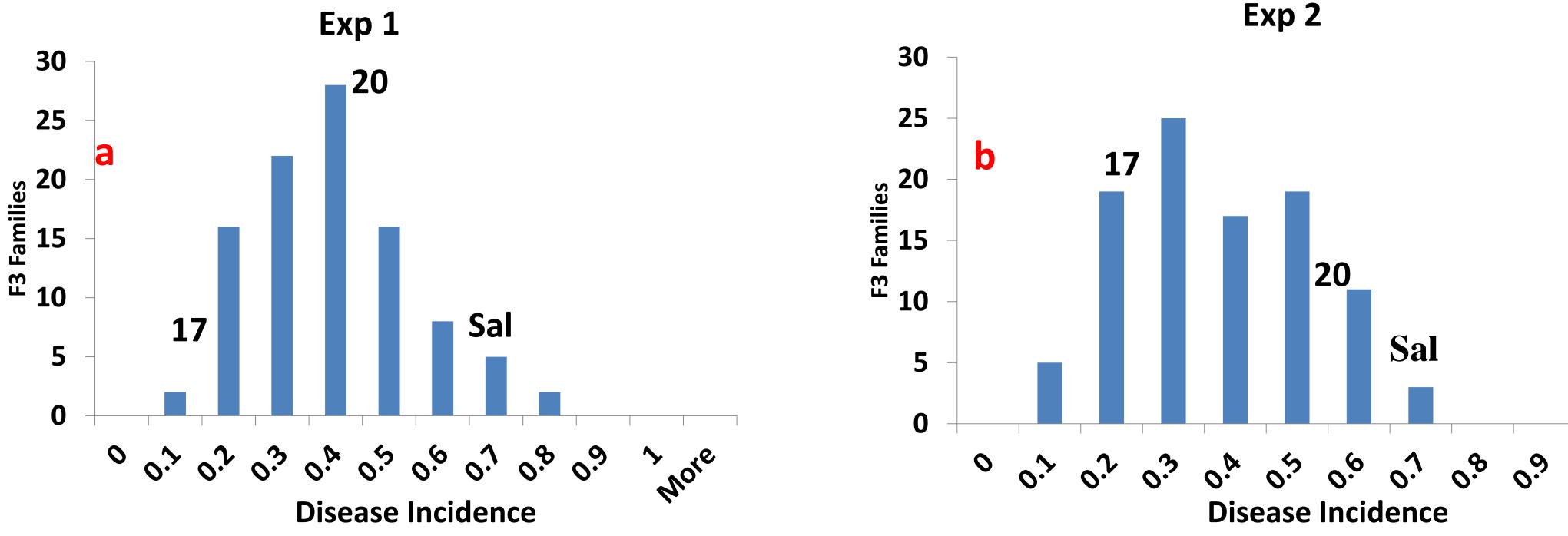


Figure 2. Distribution of 99 F₃ families for Disease Incidence in greenhouse test for population 171674x204707 in a) Experiment 1 (planted in January 2013) and b) Experiment 2 (planted in October 2013). 17 represents the DI of PI 171674, 20 represents the DI of PI 204707 and Sal the susceptible control Salinas.

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.

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