Identification and characterization of pleiotropic and epistatic QDRL conferring partial resistance to *Pythium irregulare* and *P. sylvaticum* in soybean

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Abstract

**Key message** Pleiotropic and epistatic quantitative disease resistance loci (QDRL) were identified for soybean partial resistance to different isolates of *Pythium irregulare* and *Pythium sylvaticum*.

**Abstract** Pythium root rot is an important seedling disease of soybean [*Glycine max* (L.) Merr.], a crop grown worldwide for protein and oil content. *Pythium irregulare* and *P. sylvaticum* are two of the most prevalent and aggressive *Pythium* species in soybean producing regions in the North Central U.S. Few studies have been conducted to identify soybean resistance for management against these two pathogens. In this study, a mapping population (derived from E13390 x E13901) with 228 F4:5 recombinant inbred lines were screened against *P. irregulare* isolate MISO 11–6 and *P. sylvaticum* isolate C-MISO2–2–30 for QDRL mapping. Correlation analysis indicated significant positive correlations between soybean responses to the two pathogens, and a pleiotropic QDRL (*qPirr16.1*) was identified. Further investigation found that the *qPirr16.1* imparts dominant resistance against *P. irregulare*, but recessive resistance against *P. sylvaticum*. In addition, two QDRL, *qPsyl15.1*, and *qPsyl18.1* were identified for partial resistance to *P. sylvaticum*. Further analysis revealed epistatic interactions between *qPirr16.1* and *qPsyl15.1* for RRW and DRX, whereas *qPsyl18.1* contributed resistance to RSE. Marker-assisted resistance spectrum analysis using F6:7 progeny lines verified the resistance of *qPirr16.1* against four additional *P. irregulare* isolates. Intriguingly, although the epistatic interaction of *qPirr16.1* and *qPsyl15.1* can be confirmed using two additional isolates of *P. sylvaticum*, the interaction appears to be suppressed for the other two *P. sylvaticum* isolates. An ‘epistatic gene-for-gene’ model was proposed to explain the isolate-specific epistatic interactions. The integration of the QDRL into elite soybean lines containing all the desirable alleles has been initiated.

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Introduction

Soybean is a major crop around the world for its protein and oil content. In 2020, total world soybean production reached a historical record of 353.5 million tons with a production area of approximately 127.0 million hectares (FAOSTAT 2020). The U.S. soybean yield production in 2020 was 112.5 million tons, a 16% increase from the 96.7 million tons in 2019. Despite the continual increase in soybean production in the U.S. and the world, the impact of soybean diseases on yield cannot be ignored (Lin et al. 2022). For example, the soybean annual yield losses caused by diseases in the U.S. and Ontario, Canada ranged from 10.1 to 13.9 million tons from 2010 to 2014, accounting for 11.7–14.2% of total soybean production of the year (Allen et al. 2017). Allen

More than 35 soybean diseases have been considered economically important (Hartman et al. 2015) and seedling diseases are some of the most destructive diseases of soybean, causing 0.68 – 1.76 million tons (25.1 – 64.5 million bushels) of annual yield loss in the U.S. and Ontario, Canada (Allen et al. 2017).

Pythium spp., an oomycete pathogen, are some of the major causal agents of soybean seedling diseases (Griffin 1990; Arafa et al. 2020; Clevinger et al. 2021). Currently more than thirty Pythium species have been confirmed as soybean pathogens, causing seed rot, seedling damping-off and root rot (Zhang et al. 1998; Huzar-Novakowski and Dorrance 2018; Dorrance et al. 2004; Zitnick-Anderson and Nelson 2015; Broders et al. 2007; Radmer et al. 2017; Rojas et al. 2017; Li et al. 2019; Navarro and Krystel 2019; Clevinger et al. 2021). In a two-year survey of oomycete pathogens, more than 3,400 oomycete cultures were isolated from 11 major soybean producing states of the U.S and Ontario, Canada. Further analysis revealed that more than 86% of the recovered isolates were Pythium species, with P. sylvaticum and P. irregulare as two of the most prevalent and aggressive Pythium species (Rojas et al. 2017). Internal transcribed spacer (ITS) sequencing analysis indicated that P. irregulare and P. sylvaticum are phylogenetically close to each other and both belong to Clade F (Hyde et al. 2014; Rojas et al. 2017).

Host resistance has been considered the most efficient and environmental-friendly method to manage plant diseases, and partial resistance has, at this point, been identified as the only type of host resistance against P. irregulare and P. sylvaticum (Bates et al. 2008; Ellies et al. 2013; Stasko et al. 2016; Lin et al. 2018; Klepadlo et al. 2019; Scott et al. 2019; Lerch-Olson et al. 2020; Lin et al. 2020; Wu et al. 2020; Clevinger et al. 2021). Ellis et al. (2013) identified 6 quantitative disease resistance loci (QDRL) on soybean chromosomes 1, 6, 8, 10, 11, and 13, with 4.4–17.7% of phenotypic variations explained (PVE).

Stasko et al. (2016) identified two QDRL on chromosomes 14 and 19 from ‘Sloan’ soybean, which explained 6.6% and 5.5% of partial resistance to P. irregulare. Lin et al. (2018) reported two QDRL on chromosomes 11 and 20, respectively, explaining 15.4% and 12.7% of phenotypic variations from two improved soybean lines ‘E05226-T’ and ‘E09088’. Using the same mapping population, 5 QDRL were identified on soybean chromosomes 10, 18, and 20, conferring 9.5%—16.5% of partial resistance to P. sylvaticum (Lin et al. 2020).

Remarkably, pleiotropic QDRL have been frequently identified for resistance to different Pythium species. For example, using six nested association mapping (NAM) populations, Scott et al. (2019) identified two pleiotropic QDRL on chromosomes 13 and 17, respectively, conferring resistance to both P. irregulare and P. ultimum var. ultimum. In another study, a major QDRL was identified on Chr. 8 imparting resistance to P. irregulare (16.7–24.1% of PVE), P. sylvaticum (4.9–21.4% of PVE), and P. torulosum (66.6% of PVE) (Clevinger et al. 2021). In addition, another large effect QDRL was identified on Chr. 6 for resistance to P. sylvaticum (26.2–26.9% of PVE) and P. irregulare (6.1–26.6% of PVE) (Clevinger et al. 2021).

E13390 and E13901 are improved soybean lines from the Michigan State University soybean breeding program. Two QDRL with epistatic interactions for partial resistance to Phytophthora sansomeana were identified from a F4:5 mapping population (150029) derived from E13901 x E13390 in our previous study (Lin et al. 2021). Further investigation indicated that E13901 also imparts significantly higher level of partial resistance to P. irregulare and P. sylvaticum than E13390. Therefore, the objectives of this study aim to 1) identify and develop molecular markers for the QDRL imparting partial resistance to P. irregulare and P. sylvaticum and QDRL on chromosomes 10, 18, and 20, conferring 9.5%—16.5% of partial resistance to P. sylvaticum (Lin et al. 2020).

Materials and methods

Plant materials and preparation of Pythium inoculum

The mapping population (150,029) consisted of 228 F4:5 recombinant inbred lines which were used for linkage map and QDRL mapping as described in Lin et al. 2021. Briefly, the MSU improved soybean line E13901 was crossed with E13390 in 2015 for F1, which was self-pollinated in the field in 2016. The F2 population was subjected to self-pollination using the single seed decent method for two generations in
the greenhouse to obtain F4 seeds, which were subsequently planted next year in the field for F4:5 families. These F4:5 families were used for QDRL mapping. The F4:5 families were then advanced two generations using single seed decent to obtain F6:7 families, which were used for marker-assisted resistance spectrum (MARS) analysis.

*P. irregulare* isolate MISO 11–6 and *P. sylvaticum* isolate C-MISO2–2–30, from symptomatic soybeans in Michigan, were used for QDRL mapping (Rojas et al. 2017). There additional isolates of *P. irregulare* (ILSO 3–48C, AR-127.S.2.S.A, and C-MISO2_5-14) and four isolates of *P. sylvaticum* (NESO 2–13, INSO 1–10c, O_14–6, and MISO 6–2) were used in MARS analyses. The inoculum of *P. irregulare* isolate MISO 11–6 was prepared by placing 1200 ml of white millet and 500 ml of water into a 0.5 micron ventilated 3 mil polypropylene 20.3 cm L × 12.7 cm W × 50.8 cm D spawn bag (FungiPerfecti, Shelton, WA), rolled with the vent-side facing upward and placed into autoclavable pans and autoclaved for 275 min. The sterilized white millet was allowed to cool to room temperature for 24 h. Isolate MISO 11–6 was grown on CMA-PARP medium for 3–7 days, after which five colonized plates and five non-colonized CMA-PARP plates were aseptically placed in a sterile stainless-steel blender (Waring, VWR International) and 500 ml of sterile water added to the carafe. The contents were blended until a thick slurry developed. Approximately 100 ml of the *P. irregulare* slurry was poured in each spawn bag. After addition of the slurry, spawn bags were sealed three times with heat sealer, then incubated for 14 days at 20–22°C (room temperature). To enhance uniform millet colonization, the spawn bags were mixed every other day.

The inoculum of all other isolates was prepared by transferring a 5-mm agar plug from an actively growing isolate to 60 mm × 15 mm petri dish plates containing corn meal agar (CMA). The plates were then incubated at room temperature for 10–14 days until the pathogen fully colonized the plates. The inoculum was chopped into 4 mm × 4 mm pieces before use.

**Evaluation of soybean resistance to *Pythium* pathogens**

A modified layer test assay (Dorrance et al. 2008; Lin et al. 2018; Lin et al. 2020, 2021) was used for disease evaluation at the Michigan State University greenhouse facilities, with environmental conditions controlled at 24 °C—27 °C and 12-h photoperiod. The inoculation starts by filling seed starting trays (3.81 cm L × 2.54 cm W × 5.72 cm D) (cell, T.O. Plastics, Inc.) with medium size vermiculite and soaked in tap water until the vermiculite was fully saturated. Then two 2 cm-deep, 1 cm-wide holes were made in each cell and 2 g of *MISO11-6* inoculum, or one 4 mm × 4 mm piece of all other isolates was placed at the bottom of each hole. Two soybean isolates were then placed on top of the inoculum and softly pressed to ensure each seed was adhered to the inoculum.

Twelve seeds were planted as a single replicate for each line, with a total of three replicates for the inoculated group and three replicates for the non-inoculated treatment. After planting, all the trays were transferred to greenhouse benches covered with waterproof plastic for water retention. The benches were watered until the water reached the level of the inoculum. After that, the benches were watered every other day to maintain a consistent water level until the day before data collection. Fourteen days after planting, the number of germinated seeds was counted, and the fresh root weight was measured using an electronic balance (Scout Pro, SP 4001; Ohaus Corp, Pine Brook, NJ). The responses of each soybean line challenged with *P. irregulare* and *P. sylvaticum* isolates were evaluated using the ratio of seedling emergence (RSE), the ratio of fresh root weight (RRW), and the disease resistance index (DRX) (Lin et al. 2021), where:

\[ \text{RSE} = \frac{\text{number of germinated seeds of an inoculated replicate}}{N}, \]

\[ \text{RRW} = \frac{\text{total fresh root weight of an inoculated replicate}}{\text{mean of RWC}}, \]

where RWI = total fresh root weight of an inoculated replicate/N, N represents the number of vigorous seedlings of each inoculated replicate and is estimated using the mean of germinated seeds across all the non-inoculated replicates. To ensure high quality of seeds, a cutoff of N ≥ 10 in each replicate was applied, and.

\[ \text{RWC} = \frac{\text{total fresh root weight of a non-inoculated replicate}}{\text{number of germinated seeds of the replicate}}, \]

\[ \text{DRX} = \frac{\sqrt{\text{RRW} \times \text{RSE} \times 100}}{100} \]

DRX ranges from 0 to 100, with 0 for complete susceptibility and 100 for complete immunity.

**DNA extraction and linkage map**

For each F4:5 family, leaf samples from 12 F5 seedlings were bulk collected and used for DNA extraction as described in Lin et al. 2021. Briefly, the leaf samples were collected, and then placed at − 80 °C freezer for storage and subsequently lyophilized before DNA extraction. DNA samples were extracted using a standard Cetyl Trimethyl Ammonium Bromide (CTAB) method and the resulting DNA pellet was dissolved in 200 μl 10 mM Tris–HCl buffer. DNA samples were quantified using an ND-1000 Spectrophotometer (NanoDrop Technologies, Inc., Wilmington, DE, USA) for chip analysis. The genotyping of the population...
was carried out using Illumina Infinium BARCSoySNP6K iSelect BeadChip genotyping array (Illumina, San Diego, USA) (Song et al. 2013), which yielded 978 polymorphic markers for linkage map construction using Joinmap software (v4.0, Ooijen 2006) with an independence LOD = 4.0 and a max recombination frequency of 0.5 (Lin et al. 2021). A total of 23 linkage groups were obtained, corresponding to the 20 chromosomes of soybean (Lin et al. 2021).

Statistics and QDRL mapping

SPSS software (IBM SPSS Statistics, IBM Corporation, Chicago, IL) was used in this study for statistical analysis. The software QTL Cartographer V2.5 (Wang et al. 2012) was used for composite interval mapping (CIM) with window size of 5 cM and the walking speed of 1 cM. The threshold of LOD score for statistical significance of QDRL effects was determined by 1000 permutations, and the LOD value corresponding to an experiment-wise Type I error rate of 5% (α = 0.05) was considered the threshold of significance (Churchill and Doerge 1994). The position of each QDRL was estimated as the point of maximum LOD score in the region under consideration.

Results

Response of soybean lines to \textit{P. irregulare} and \textit{P. sylvaticum}

As expected, E13901 conferred significantly higher level of partial resistance to \textit{P. irregulare} and \textit{P. sylvaticum} than those of E13390. The RSE of E13901 against \textit{P. irregulare} ranged from 0.67 to 0.92, with the mean of 0.81 ± 0.07, which was significantly higher than that of E13390, which ranged from 0.17 to 0.42, with the mean of 0.31 ± 0.07; The RRW of E13901 ranged from 0.39 to 0.52 with the mean of 0.44 ± 0.04, which was significantly higher than that of the other parent, which ranged from 0.04 to 0.19 with the mean of 0.12 ± 0.04. The DRX of the resistant parent ranged from 51.14 to 68.94 with the mean of 59.47 ± 5.17 and was significantly higher than the susceptible parent which ranged from 8.19 to 28.40, with the mean of 19.01 ± 5.86 (Table 1). The same pattern was observed for the partial resistance to \textit{P. sylvaticum}. The mean of RSE, RRW, and DRX of E13901 were 0.97 ± 0.03, 0.71 ± 0.04, and 82.81 ± 3.45, respectively, which were significantly than those of E13390, which were 0.89 ± 0.07, 0.42 ± 0.08, and 61.25 ± 8.29, respectively (Table 2). Both lines conferred higher level of partial resistance against \textit{P. sylvaticum} than \textit{P. irregulare}.

The partial resistance of F4:5 lines in population 150,029 to \textit{P. irregulare} mostly ranged between the parental lines, with the means of RSE, RRW, and DRX at 0.59 ± 0.01, 0.25 ± 0.05, and 37.89 ± 0.64, respectively. The histogram analysis indicated that the distribution of partial resistance of 150,029 to \textit{P. irregulare} appeared normal distribution (Fig. 1A, 1B, and 1C for RSE, RRW, and DRX, respectively). For resistance to \textit{P. sylvaticum}, the means of RSE, RRW, and DRX of F4:5 lines in 150,029 were 0.97 ± 0.03, 0.69 ± 0.01, and 81.64 ± 0.41, respectively. The histogram of RRW and DRX appeared normal distribution, while that of RSE was left-skewed. Transgressive segregation was obviously observed as nearly half of the lines exhibited a higher level of partial resistance than the resistant parent (Fig. 1D, 1E, and 1F).

Considering the close relationship of \textit{P. irregulare} and \textit{P. sylvaticum}, we were interested to explore if the partial resistance against the two pathogens were correlated. Pearson’s correlation test was therefore applied as shown in Table 3 and Fig. 2. The correlation coefficients of RSE, RRW, and DRX between the partial resistance to \textit{P. irregulare} and \textit{P. sylvaticum} were 0.252, 0.172, and 0.163, respectively, all significantly correlated at $p < 0.05$ or $p < 0.01$ level.

QDRL mapping for partial resistance to \textit{P. irregulare} and \textit{P. sylvaticum}

Using the 228 F4:5 lines, one QDRL (dubbed \textit{qPirr16.1}) was detected for both RRW and DRX for resistance to \textit{P. irregulare} (isolate MISO 11–6) using CIM method. \textit{qPirr16.1} was located at 1.91 cM on soybean chromosome 16, flanked by SNP markers Gm16_7743486_G_T and Gm16_7851145_G_A. The LOD scores of \textit{qPirr16.1} were 3.64 and 3.52 for RRW and DRX, respectively, which were higher than the LOD threshold of 3.30 and 3.20,

| Table 1 Statistics of soybean lines to \textit{P. irregulare} (isolate MISO 11–6) |
|---------------------------------|-----------------|-----------------|-----------------|
|                                | RSE             | RRW             | DRX             |
|                                | Mean ± SE       | Range           | Mean ± SE       | Range           | Mean ± SE       | Range           |
| E13390                          | 0.31a ± 0.07    | 0.17–0.42       | 0.12a ± 0.04    | 0.04–0.19       | 19.01a ± 5.86   | 8.19–28.40      |
| E13901                          | 0.81a ± 0.07    | 0.67–0.92       | 0.44a ± 0.04    | 0.39–0.52       | 59.47a ± 5.17   | 51.14–68.94     |
| 150,029 F4:5                   | 0.59c ± 0.01    | 0.23–0.97       | 0.25c ± 0.05    | 0.07–0.47       | 37.89c ± 0.64   | 12.91–65.96     |

Different letters indicate significant differences at $a = 0.05$ level
RSE: ratio of seedling emergence; RRW: ratio of root weight; DRX: disease resistance index
The QDRL could explain 5.96% and 5.72% of RRW and DRX variations, respectively, with additive effects of –0.019 and –2.255 for RRW and DRX, indicating that the allele of E13901 contributed to the higher value of RRW and DRX exhibiting a higher level of resistance (Fig. 3A, Table 4).

Using CIM method, two QDRL were detected for soybean partial resistance to *P. sylvaticum* (dubbed *qPsy15.1* and *qPsy18.1*, respectively). *qPsy15.1* was located at 2.81 cM on soybean Chr. 15, between SNP markers Gm15_4315169_T_C and Gm15_4264903_C_T. The QDRL was detected using both RRW and DRX, with LOD scores of 4.02 and 4.07, respectively. The QDRL explained the RRW and DRX variations of 6.66% and 6.49%, respectively, and the additive effects were -0.024 and -1.742, respectively, indicating that the desirable-resistant allele was from E13901 (Fig. 3B, Table 4).

*qPsy18.1* was identified through RSE alone, with a LOD score of 3.68. *qPsy18.1* was located at 0.001 cM on Chr. 18, flanked by SNP markers Gm15_4315169_T_C and Gm15_4264903_C_T. The QDRL explained 6.51% of RSE variations with an additive effect of 0.011, which

### Table 2

|        | RSE          | RRW          | DRX          |
|--------|--------------|--------------|--------------|
|        | Mean ± SE    | Range        | Mean ± SE    | Range        | Mean ± SE    | Range        |
| E13390 | 0.89a ± 0.07 | 0.75–1.00    | 0.42a ± 0.08 | 0.28–0.56    | 61.25a ± 8.29 | 46.01–74.60  |
| E13901 | 0.97b ± 0.03 | 0.92–1.00    | 0.71b ± 0.04 | 0.63–0.76    | 82.81b ± 3.45 | 76.03–87.39  |
| 150,029| 0.97b ± 0.03 | 0.82–1.00    | 0.69b ± 0.01 | 0.47–0.93    | 81.64b ± 0.41 | 62.47–96.33  |

Different letters indicate significant differences at a = 0.05 level

RSE: ratio of seedling emergence; RRW: ratio of root weight; DRX: disease resistance index

### Table 3

| P. irregulare | RSE         | RRW          | DRX          |
|---------------|-------------|--------------|--------------|
| P. sylvaticum  | RSE         | RRW          | DRX          |
| RSE           | 0.252 **    | –            | –            |
| RRW           | –           | 0.172 **     | –            |
| DRX           | –           | –            | 0.163 *      |

* and ** indicated significant correlation at *P*<0.05 and *P*<0.01 level, respectively

respectively. The QDRL could explain 5.96% and 5.72% of RRW and DRX variations, respectively, with additive effects of –0.019 and –2.255 for RRW and DRX, respectively, indicating that the allele of E13901 contributed to the higher

### Fig. 1

Response of soybean lines to *P. irregulare* A–C and *P. sylvaticum* D–F
Fig. 2 Scatter plot for correlation of partial resistances to *P. irregulare* and *P. sylvaticum*. x-axis: *P. irregulare*; y-axis: *P. sylvaticum*. A RSE; B RRW; C DRX

Fig. 3 Molecular mapping of QDRL conferring partial resistance to *P. irregulare* A, *P. sylvaticum* B and C, and joint phenotype analysis D using 228 soybean F4:5 families. The LOD threshold was determined by 1000 permutations at *p* < 0.05

Table 4 QDRL detected in 150,029 for partial resistance to *P. irregulare* and *P. sylvaticum*

| Trait       | Chr | Position (cM) | Planking markers | $R^2$ (%) | LOD Threshold | Additive Effect |
|-------------|-----|---------------|------------------|-----------|---------------|----------------|
| *qPirr16.1* | RRW | Gm16 1.91     | Gm16_7743486_G_T and Gm16_7851145_G_A | 5.96      | 3.64          | −0.019         |
|             | DRX | Gm16 1.91     | Gm16_7743486_G_T and Gm16_7851145_G_A | 5.72      | 3.53          | −2.255         |
| *qPsy15.1*  | RRW | Gm15 2.81     | Gm15_4315169_T_C and Gm15_4264903_C_T | 6.66      | 4.02          | −0.024         |
|             | DRX | Gm15 2.81     | Gm15_4315169_T_C and Gm15_4264903_C_T | 6.49      | 4.07          | −1.742         |
| *qPsy18.1*  | RSE | Gm18 0.01     | Gm18_61528293_C_T and Gm18_61065114_G_A | 6.51      | 3.68          | 0.011          |
| Pleiotropic QDRL | DRX | Gm16 1.91 | Gm16_7743486_G_T and Gm16_7851145_G_A | 6.85      | 4.04          | −1.597         |

*a* LOD threshold of significance is determined by permutation tests of 1000 iterations (*p* ≤ 0.05) (Churchill and Doerge 1994)

*b* Positive value of additive effect indicates that the E13390 allele increases the trait value
indicated that the desirable allele of resistance was from E13390 (Fig. 3C, Table 4).

**qPirr16.1 is a pleiotropic QDRL conferring resistance to both *P. irregulare* and *P. sylvaticum* in different manners**

Because of the significant correlations of phenotypic responses to *P. irregulare* and *P. sylvaticum*, we hypothesized that a pleiotropic QDRL could be detected contributing resistance to both pathogens. To test this hypothesis, a joint phenotype was calculated by averaging the value of each index of each line for both pathogens. CIM mapping using the joint phenotypes identified a pleiotropic QDRL for DRX at 1.91 cM on chromosome 16, flanked by Gm16_7743486_G_T and Gm16_7851145_G_A, which overlaps with the *qPirr16.1* locus (Fig. 3D, Table 4). The pleiotropic QDRL explained 6.85% of the variation of the joint DRX with LOD of 4.04 and its additive effect was -1.597, indicating that E13901 is the resistance donor (Fig. 3D, Table 4).

Interestingly, although *qPirr16.1* was identified for resistance to *P. irregulare*, it was not detected in QDRL mapping for *P. sylvaticum*. Therefore, to verify the resistance of *qPirr16.1* to *P. sylvaticum*, different genotypic groups (R, S, and H) were identified in the F4:5 mapping population using the flanking markers Gm16_7743486_G_T and Gm16_7851145_G_A. 71 lines with E13901 genotype were marked as R group, 97 lines with E13390 genotype were identified as S group, and 48 heterozygous genotypes on both marker loci were included in H group (Table S1).

Multiple comparisons between different genotypic groups against the *P. irregulare* isolate MISO 11–6 indicated that the R group was significantly higher than the S group in all RSE, RRW and DRX, confirming the partial resistance of *qPirr16.1* to *P. irregulare*. The H group also showed a similar level of resistance as the R group and was significantly higher than the S group in all three traits, indicating that the resistance of *qPirr16.1* is dominant to *P. irregulare* (Fig. 4A, 4B, and 4C). For *P. sylvaticum*, the RSE of the R group was not significant compared with S group, however, R group was significantly higher than the S group in RRW and DRX, confirming the partial resistance of *qPirr16.1* to *P. sylvaticum*. Interestingly, the H group was as susceptible as the S group in both RRW and DRX, and was significantly lower than the R group, suggesting that the partial resistance from *qPirr16.1* was recessive against *P. sylvaticum*. Therefore, *qPirr16.1* is a pleiotropic QDRL which contributes dominant and recessive resistance to *P. irregulare* and *P. sylvaticum*, respectively.

**qPirr16.1 work together with qPsy15.1 for resistance to *P. sylvaticum* isolate C-MISO2-2–30**

To characterize the interaction between *qPirr16.1* and *qPsy15.1*, four genotypic groups (RR, RS, SR, and SS) were identified using the flanking markers of *qPirr16.1* and *qPsy15.1*, respectively. The RR group contained 22 F4:5 lines with E13901 genotype at both loci; the RS group consisted of 29 lines with E13901 locus at *qPirr16.1* locus and E13390 genotype at *qPsy15.1* locus; the SR group included 28 F4:5 lines with E13390 genotype at *qPirr16.1* locus and E13901 genotype at *qPsy15.1* locus; and the SS group contained 71 F4:5 lines with E13901 genotype at both loci; the S group is E13390 genotype containing 97 F4:5 lines, the H group is heterozygous with 48 F4:5 lines.
The four genetic groups were identified from the F4:5 population using the flanking markers of *qPsy15.1* and *qPirr16.1* in Table 4. The RR group included 22 lines which were both E13901 alleles on both loci; The RS group included 28 lines with E13901 allele on *qPsy15.1* locus and E13901 allele on *qPirr16.1* locus; The SR group included 29 lines with E13900 alleles on both loci; The SS group included 39 lines with E13900 genotype on both loci. The multiple comparisons among groups were carried out using least square difference (LSD) with significance level at p < 0.05.

Multiple comparisons using Least Square Difference (LSD) post hoc test indicated that neither *qPirr16.1* nor *qPsy15.1*, or the combination of both QDRL contributed to the RSE for partial resistance to *P. sylvaticum* isolate C-MISO2-2–30 (Fig. 5A), which was consistent with the QDRL mapping results (Table 4, Fig. 4). For RRW, the RR group was significantly higher than the SS group at p < 0.05 and p < 0.055. For DRX, the differences between the RR and RS groups were not significant at p < 0.05 but the RR group was significantly higher than the SS group at p < 0.01 (p = 0.055). For DRX, the differences between the RR and RS or SS groups were not significant at p < 0.05, but the RR group was significantly higher than the SS group at p < 0.01 (p = 0.077) (Figure S2 B1-B3).

The response of the two QDRL against O_14-6 was identical to that against C-MISO2-2–30 with an epistatic pattern, where the combination of *qPirr16.1* and *qPsy15.1* conferred significantly higher resistance for RRW and DRX, but not for RSE, whereas each QDRL alone did not contribute resistance (Figure S2 A1-A3).

However, the two QDRL behaves differently for isolates NESCO 2–13 and MISO_6-2. For NESCO 2–13, the SR group was significantly higher than the SS group for RSE, RRW,
and DRX, indicating that qPsyl15.1 confer partial resistance to the isolate. However, the resistance of both the RR and the RS groups were significantly lower than the SR and SS group, suggesting that qPirr16.1 enhanced soybean susceptibility to the isolate, and may inhibited the resistance of qPsyl15.1 (Figure S2 C1-C3). The RR, RS, and SR groups did not show significant differences compared to the SS group against MISO_6-2, suggesting that neither qPirr16.1 nor qPsyl15.1, nor the combination of the two QDRL contribute resistance to the isolate. Instead, qPirr16.1 may play an inhibitor role against qPsyl15.1 since the RSE and DRX of the RR group were significantly lower than the SR group against MISO_6-2.

Discussion

In this study, a novel QDRL, qPirr16.1, was identified conferring partial resistance to P. irregulare, which was further confirmed with three additional isolates of P. irregulare (ILSO 3-48C, AR-127.S.2.3.A, and C-MISO2_5-14) using a MARS test. Further analysis found that qPirr16.1 is a pleiotropic QDRL and works together with another novel QDRL, qPsyl15.1, for partial resistance to three isolates of P. sylvaticum (C-MISO2-2–30, O_14-6, and INSO 1-10c). Interestingly, qPirr16.1 confers dominant resistance against P. irregulare but recessive resistance against P. sylvaticum. Pleiotropic QDRL are not uncommon for partial resistance to Pythium diseases, suggesting there is likely some similarity of resistance mechanisms against different species of Pythium pathogens. For example, two QDRL were identified on chromosomes 13 and 17 that both confer partial resistance to P. irregulare and P. ultimum var. ultimum (Scott et al. 2019): A major QDRL was identified on Chr. 8 conferring resistance to P. irregulare, P. sylvaticum, and P. torulosum (Clevinger et al. 2021). Another large effect QDRL on Chr. 6 was also identified imparting partial resistance to P. sylvaticum and P. irregulare (Clevinger et al. 2021). All these pleiotropic QDRL as well as the novel ones identified in this study will be of particular importance for breeding partial resistance against different species of Pythium pathogens.

Epistatic interactions have been frequently identified in soybean resistance to diseases such as SCN (Wu et al. 2009), SDS (Zhang et al. 2015; Tan et al. 2018), white mold (Moellers et al. 2017), Phytophthora sojae (Wang et al. 2010) and Ph. sansomeana (Lin et al. 2021). In this study, we identified the epistatic interactions of qPirr16.1 and qPsyl15.1 against P. sylvaticum. Interestingly, the combination of qPirr16.1 and qPsyl15.1 confer partial resistance to three isolates of P. sylvaticum: C-MISO2-2–30, O_14-6, and INSO 1-10c, however, qPirr16.1 significantly reduced the function of qPsyl15.1 to Neso 2–13 and MISO_6-2. It appears that qPirr16.1 is a regulator of qPsyl15.1, but further investigation is needed to unravel the mechanism of this epistatic interaction.

Partial resistance or quantitative resistance has been widely considered race non-specific, while isolate-specific QDRL have also been identified and confirmed (Marcel et al. 2008; Poland et al. 2009; St. Clair 2010; Lee et al. 2014; Mundt 2014; Stasko et al. 2016; Nelson et al. 2018; Karhoff et al. 2019). In the current study, qPirr16.1 conferred significant partial resistance to all four isolates of P. irregulare and therefore appears isolate non-specific against P. irregulare. However, the combination of qPirr16.1 and qPsyl15.1 showed clearly isolate-specific epistatic interactions with different isolates of P. sylvaticum. More interestingly, for some isolates of P. sylvaticum (C-MISO2-2–30, O_14-6, and INSO 1-10c), qPirr16.1 works together with qPsyl15.1 to enhance the resistance, whereas for other isolates, qPirr16.1 appears to suppress the resistance of the other QDRL. Isolate-specific QDRL have also been identified in soybean partial resistance to other diseases such as Ph. sojae and Ph. sansomeana. For instance, a QDRL on soybean Chr. 3 was identified conferring significant resistance to isolate 1.S.1.1 of Ph. sojae, but not to isolate OH30. In the same study, isolate-specific QDRL were identified on soybean chromosomes 6, 9, 13 and 18 that conferred resistance to only one of the two isolates of Ph. sojae (Lee et al. 2014). Lin et al. (2021) identified two isolate-specific QDRL (qPsan5.1 and qPsan16.1) conferring different patterns of resistance against eight isolates of Ph. sansomeana using the same population in this study. Interestingly, qPsan5.1 and qPsan16.1 also showed epistatic interactions to some of the isolates of Ph. sansomeana.

To explain the isolate specificity of minor QDRL, Parlevliet and Zadoks (1977) proposed a ‘minor-gene-for-minor-gene’ (MGFMG) model which suggested that the gene-for-gene interactions for major resistance genes also work for minor QDRL in a similar pattern. While the MGFMG model could explain the interactions of a single gene with the pathogens which could be confirmed in several studies (Marcel et al. 2008), it did not provide an explanation to the epistatic interactions of the QDRL as discovered in the current study and Ph. sansomeana (Lin et al. 2021). As such, we are proposing a ‘epistatic gene-for-gene’ model, where the host genes (either minor or major) with epistatic interactions contributed to the resistance and work together for the interaction with the pathogen in a gene-for-gene manner. This model can explain our observations of the epistatic isolate-specific partial resistance against P. sylvaticum and Ph. sansomeana and may be more universal in host–pathogen interactions than was previously known.

The flanking markers of qPirr16.1 delimited a genomic region of 107 kb based on Williams82 reference genome (Gmax2.0). A total of seven genes were predicted in this region (www.soybase.org) (Table S4)
infection (Lu et al. 2003; Gorovits et al. 2013; Jiang et al. 2014), and therefore may be considered candidate genes.

LRR-RLK proteins has been shown to play a central role in defense pathways against the infection of plant pathogens (Afzal et al. 2008; Liu et al. 2011; Yeh et al. 2016; and Liu et al. 2017), and heat shock protein play important roles in plant disease resistance and virus infection (Lu et al. 2003; Gorovits et al. 2013; Jiang et al. 2014), and therefore may be considered candidate genes.

E13390 and E13901 are both recently improved soybean lines for high yielding and other desirable agronomic traits adaptive to the environments of central and southern Michigan, U.S. To initiate the integration of the desirable QDRL into new soybean varieties, the flanking markers of the three QDRL (qPirr16.1, qPsyl15.1, and qPsyl18.1) identified in this study, as well as the two QDRL (qPsan5.1 and qPsan16.1) for partial resistance to Ph. sansomeana (Lin et al. 2021) were used to identify superior progeny lines containing all the desirable alleles of the five QDRL. A total of three F6:7 lines were identified including 150020–167, 150029–192, and 150029–217 and the latter two, 150029–192 and 150029–217 were used as breeding parents (21P059 and 21P060, respectively) in 2021. Marker-assisted selection will be performed to select superior progenies containing the QDRL. Seed increase was also performed for the two lines which will be used for advanced yield trials next year.

**Supplementary Information** The online version contains supplementary material available at https://doi.org/10.1007/s00122-022-04201-0.

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**Author contributions statement** DW and FL designed the research. FL, WL, AGM, NZ, JJ, SC, SHW, and CG carried out the experiments. FL, WL, and XH analyzed the data. FL developed the draft manuscript. DW and MIC supervised the manuscript. All authors revised the manuscript and contributed to the final manuscript.

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**Data availability** The genotype and phenotype data generated for mapping QDRL is available in ‘Supplementary Data’. The data for RHS group (qPirr16.1) and RR/RS/SR/SS group (qPirr16.1/qPsyl15.1) are available in supplementary ‘Table S1’ and ‘Table S2’, respectively; Marker-assisted resistance spectrum analysis (MARS) data are available in supplementary ‘Table S3’. Additional information is available upon request.

**Declarations**

**Conflict of interest** The authors declare that there is no conflict of interest.

**References**

Afzal AJ, Wood AJ, Lightfoot DA (2008) Plant receptor-like serine threonine kinases: roles in signaling and plant defense. Mol Plant Microbe Interact 21(5):507–517

Alejandro Rojas J, Jacobs JL, Napieralski S, Karaj B, Bradley CA, Chase T, Esker PD, Giesler LJ, Jardine DJ, Malvick DK, Markell SG (2017) Oomycete species associated with soybean seedlings in north america—part I: Identification and pathogenicity characterization. Phytopathology 107(3):280–292

Allen TW, Bradley CA, Sisson AJ (2017) Soybean yield loss estimates due to diseases in the United States and Ontario, Canada, from 2010 to 2014. Plant Health Prog 18(1):19–27

Araf RA, Kamel SM, Abd-Elsalam KA (2020) The genus pythium: genomics and breeding for resistance pythium diagnosis, diseases and management. CRC Press, Boca Raton, Florida

Bates GD, Rothrock CS, Rupe JC (2008) Resistance of the soybean cultivar archer to pythium damping-off and root rot caused by several pythium spp. Plant Dis 92(5):763–766

Broders KD, Lipps PE, Paul PA, Dorrance AE (2007) Characterization of pythium spp. associated with corn and soybean seed and seedling disease in ohio. Plant Dis 91(6):727–735

Churchill GA, Doerge RW (1994) Empirical threshold values for quantitative trait mapping.. Genetics 138(3):963–971. https://doi.org/10.1093/genetics/138.3.963

Clair DA (2010) Quantitative disease resistance and quantitative resistance loci in breeding. Annu Rev Phytopathol 48:247–268
Clevenger EM, Biyashev R, Lerch-Olson E, Yu H, Quigley C, Song Q, Dorrance AE, Robertson AE, Saghai Maroof MA (2021) Identification of quantitative disease resistance loci toward four Pythium species in soybean. Front Plant Sci. https://doi.org/10.3389/fpls.2021.644746

Dorrance AE, Berry SA, Lipps PE (2004) Characterization of Pythium spp. from three Ohio fields for pathogenicity on corn and soybean and metalaxyl sensitivity. Plant Health Prog 5(1):10

Dorrance AE, Berry SA, Anderson TR, Meharg C (2008) Isolation, storage, pathotype characterization, and evaluation of resistance for Phytophthora sojae in soybean. Plant Health Prog 9(1):35

Ellis ML, McHale LK, Paul PA, Martin SK, Dorrance AE (2013) Soybean germplasm resistant to Pythium irregularum and molecular mapping of resistance quantitative trait loci derived from the soybean accession PI 424354. Crop Sci 53(3):1008–1021

Gorovits R, Moshe A, Ghanim M, Czosnek H (2013) Recruitment of the plant host heat shock protein 70 by tomato yellow leaf curl virus protein is required for virus infection. PLoS One 8(7):e70280

Griffin GJ (1990) Importance of pythium ultimum in a disease syndrome of cv. Essex soybean. Can J Plant Pathol 12(2):135–140

Hartman GL, Rupe JC, Sikora EJ, Domier LL, Davis JA, Steffel KL (eds) (2015) Compendium of soybean diseases and pests. American Phytopathological Society, St. Paul, MN

Huzar-Novakowski J, Dorrance AE (2018) Genetic diversity and population structure of pythium irregularum from soybean and corn production fields in Ohio. Plant Dis 102(10):1989–2000

Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA, Blair JE, Cai L, de Cock AW, Dissanayake AJ, Glockling SL, Goonasekara ID, Gorczak M (2014) One stop shop: backbones trees for important phytopathogenic genera: I. (2014). Fungal Divers 67(1):21–125

Jiang S, Lu Y, Li K, Lin L, Zheng H, Yan F, Chen J (2014) Heat shock protein 70 is necessary for rice stripe virus infection in plants. Mol Plant Pathol 15(9):907–917

Karhoff S, Lee S, Mian MR, Ralston TL, Niblack TL, Dorrance AE, McHale LK (2019) Phenotypic characterization of a major quantitative disease resistance locus for partial resistance to phytophthora sojae. Crop Sci 59(3):968–980

Klepado M, Balk CS, Vuong TD, Dorrance AE, Nguyen HT (2019) Molecular characterization of genomic regions for resistance to Pythium ultimum var. ultimum in the soybean cultivar Magellan. Theor Appl Genet 132(2):405–417

Lee S, Mian MAR, Sneller CH, Wang H, Dorrance AE, McHale LK (2014) Joint linkage QTL analyses for partial resistance to Phytophthora sojae in soybean using six nested inbred populations with heterogeneous conditions. Theor Appl Genet 127(2):429–444. https://doi.org/10.1007/s00122-013-2229-z

Lerch-Olson ER, Dorrance AE, Robertson AE (2020) Resistance of the SoyNAM parents to seed and root rot caused by four pythium species. Plant Dis 104:2489–2497

Li N, Zhou Q, Chang K-F, Haitian Yu, Hwang S-F, Conner RL, Strelkov SE, McLaren DL, Turnbull GD (2019) Occurrence, pathogenicity and species identification of pythium causing root rot of soybean in alberta and manitoba, canada. Crop Prot 118:36–43

Lin F, Wani SH, Collins PJ, Wen Z, Gu C, Chilvers MI, Wang D (2018) Mapping quantitative trait loci for tolerance to pythium irregularum in soybean (Glycine max L.). G3 Genes Genome Genet 8(10):3155–3161

Lin F, Wani SH, Collins PJ, Wen Z, Li W, Zhang N, McCoy AG, Bi Y, Tan R, Zhang S, Gu C (2020) QTL mapping and GWAS for identification of loci conferring partial resistance to pythium sylvaticum in soybean (Glycine max (L.) Merr.). Mol Breed 40:1–1

Lin F, Li W, McCoy AG, Gao X, Collins PJ, Zhang N, Wen Z, Cao S, Wani SH, Gu C, Chilvers MI, Wang D (2021) Molecular mapping of quantitative disease resistance loci for soybean partial resistance to Phytophthora sojae. Theor Appl Genet 134(7):1977–1987. https://doi.org/10.1007/s00122-021-03799-x

Lin F et al (2022) Breeding for disease resistance in soybean: a global perspective. Theor Appl Genet. https://doi.org/10.1007/s00122-022-04101-3

Liu PL, Du L, Huang Y, Gao SM, Yu M (2017) Origin and diversification of leucine-rich repeat receptor-like protein kinase (LRR-RLK) genes in plants. BMC Evol Biol 17(1):47

Lu R, Malcuit I, Moffett P, Ruiz MT, Peart J, Wu AJ, Rathjen JP, Bendahmane A, Day L, Baulcombe DC (2003) High throughput virus-induced gene silencing implicates heat shock protein 90 in plant virus disease resistance. EMBO J 22(21):5690–5699

Marcel TC, Gorguet B, Ta MT, Kohutova Z, Vels A, Niks RE (2008) Isolate specificity of quantitative trait loci for partial resistance of barley to Puccinia hordei confirmed in mapping populations and near-isogenic lines. New Phytol. https://doi.org/10.1111/j.1469-8137.2007.02298.x

Mayeda A, Krainer AR (1992) Regulation of alternative pre-mRNA splicing by hnRNPA1 and splicing factor SF2. Cell 68(2):365–375

Moellers TC, Singh A, Zhang J, Brungardt J, Kabbage M, Mueller DS, Grau CR, Ranjan A, Smith DL, Chowda-Reddy RV, Singh AK (2017) Main and epistatic loci studies in soybean for sclerotinia sclerotiorum resistance reveal multiple modes of resistance in multi-environments. Sci Rep 7(1):1–3

Molin M, Akusjärvi G (2000) Overexpression of essential splicing factor ASF/SF2 blocks the temporal shift in adenovirus pre-mRNA splicing and reduces virus progeny formation. J Virol 74(19):9002–9009

Mundt CC (2014) Durable resistance: a key to sustainable management of pathogens and pests. Infect Genet Evol 1(27):446–455

Navarro A, Krystel A (2019) “Oomycete Community diversity and pathogenicity associated with soybean in Ohio.” PhD diss, The Ohio State University

Nelson R, Wiesner-Hanks T, Wisser R, Balint-Kurti P (2018) Navigating complexity to breed disease-resistant crops. Nat Rev Genet 19(1):21

Noel ZA (2019) Effect of soybean seed treatments on oomycete evolution and diversity for improved seedling disease management. Michigan State University, Michigan

Oojen JW (2006) JoinMap 4: software for the calculation of genetic linkage maps in experimental populations. Kyazma B.V., Wageningen

Parlevliet JE, Zadoks JC (1977) The integrated concept of disease resistance: a new view including horizontal and vertical resistance in plants. Euphytica 26:5–21

Poland JA, Balint-Kurti PJ, Wisser RJ, Pratt RC, Nelson RJ (2009) Shades of gray: the world of quantitative disease resistance. Trends in Plant Science 14(1):21–29. https://doi.org/10.1016/j.tplants.2008.10.006

Radmer L, Anderson G, Malvick DM, Kurle JE, Rendahl A, Mallik MT, Poland JA, Balint-Kurti PJ, Wisser RJ, Pratt RC, Nelson RJ (2009) Homology tagSNP based linkage maps in experimental populations. Kyazma B.V., Wageningen

Roth MG, Webster RW, Mueller DS, Chilvers MI, Faske TR, Mathew FM, Bradley CA, Damicone JP, Kabbage M, Smith DL (2020) Integrated management of important soybean pathogens of the united states in changing climate. J Int Pest Manag 11(1):17

Scott K, Balk C, Veney D, McHale LK, Dorrance AE (2019) Quantitative disease resistance loci towards Phytophthora sojae and Phytophthora megasperma. Theor Appl Genet 137(7):1777–1787. https://doi.org/10.1007/s00122-019-02852-y

Shades of gray: the world of quantitative disease resistance. EMBO J 19(19):9002–9009
three species of Pythium in six soybean nested association mapping populations. Crop Sci 59(2):605–623
Song Q, Hyten DL, Jia G, Quigley CV, Fickus EW, Nelson RL, Cregan PB, Zhang T (2013) Development and evaluation of SoySNP50K a high-density genotyping array for soybean. PLoS ONE 8(1):e54985. https://doi.org/10.1371/journal.pone.0054985
Stasko AK, Wickramasinghe D, Nauth BJ, Acharya B, Ellis ML, Taylor CG, McHale LK, Dorrance AE (2016) High-Density Mapping of Resistance QTL Toward Phytophthora sojae, Pythium irregulare, and Fusarium graminearum in the Same Soybean Population. Crop Sci 56(5):2476–2492
Tan R, Serven B, Collins PF, Zhang Z, Wen Z, Boyse JF, Gu C, Chivers ML, Diers BW, Wang D (2018) QTL mapping and epistatic interaction analysis of field resistance to sudden death syndrome (Fusarium virguliforme) in soybean. Theor Appl Genet 131(8):1729–1740
Van Ooijen JW (2006) JoinMap® 4, software for the calculation of genetic linkage maps in experimental populations. Kyazma BV, Wageningen 33:101371
Wang Z, Dai L, Jiang Z, Peng W, Zhang L, Wang G, Xie D (2005) GmCOI1, a soybean F-box protein gene, shows ability to mediate jasmonate-regulated plant defense and fertility in Arabidopsis. Mol Plant Microbe Interact 18(12):1285–1295
Wang H, Waller L, Tripathy S, Martin SK, Zhou L, Krampis K, Tucker DM, Mao Y, Hoeschele I, Saghai-Maroof MA, Tyler BM (2010) Analysis of genes underlying soybean quantitative trait loci conferring partial resistance to Phytophthora sojae. Plant Genome. https://doi.org/10.3835/plantgenome2009.12.0029
Wang S, Basten CI, and Zeng Z-B (2012) Windows QTL Cartographer 2.5. Department of Statistics, North Carolina State University, Raleigh, NC
Wu X, Blake S, Sleper DA, Shannon JG, Cregan P, Nguyen HT (2009) QTL, additive and epistatic effects for SCN resistance in PI 437654. Theor Appl Genet 118(6):1093–1105
Wu W, Ogawa F, Ochiai M, Yamada K, Fukui H (2020) Common strategies to control pythium disease. Rev. Agricultural Sci 8:58–69
Yeh YH, Panzeri D, Kadota Y, Huang YC, Huang PY, Tao CN, Roux M, Chien HC, Chin TC, Chu PW, Zipfel C (2016) The Arabidopsis maelectin-like/LRR-RLK IOS1 is critical for BAK1-dependent and BAK1-independent pattern-triggered immunity. Plant Cell 28(7):1701–1721
Zhang BQ, Chen WD, Yang XB (1998) Occurrence of Pythium species in long-term maize and soybean monoculture and maize/soybean rotation. Mycol Res 102(12):1450–1452
Zhang J, Singh A, Mueller DS, Singh AK (2015) Genome-wide association and epistasis studies unravel the genetic architecture of sudden death syndrome resistance in soybean. Plant J 84(6):1124–1136
Zitnick-Anderson KK, Nelson Jr BD (2015) Identification and pathogenicity of Pythium on soybean in North Dakota. Plant Dis 99(1):31–38

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