Identification of Black Rot Resistance in a Wild Brassica Species and Its Potential Transferability to Cauliflower

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Received: 20 August 2020; Accepted: 7 September 2020; Published: 16 September 2020

Abstract: Black rot is a destructive disease that affects B. oleracea crops, causing significant losses to growers throughout the world. The purpose of this study was to screen out new sources resistant to Xanthomonas campestris pv. campestris race 4 (Xcc4) in 26 cauliflower and six related wild species, and to assess the inheritance of resistance. The results indicate that most of the tested accessions were susceptible or had intermediate resistance, except the Boc4601 (a cauliflower stable inbred line) and PI435896, UNICT5168, and UNICT5169 (wild accessions). Among them, UNICT5169 (Brassica montana) and PI435896 (Brassica balearica) showed the strongest resistance to Xcc4, with significantly lower disease index (DI), area of the infected part (AIP) and proportion of the infected part to the total leaf area (PTL) values. UNICT 5169 was selected as an Xcc4-resistant parent because of its relatively good cross seed-setting rate with cauliflower cultivars. F1 hybrids were successfully produced between this wild resistant accession (UNICT 5169) and one susceptible cauliflower breeding line (Boc3202-4), indicating the potential transferability of this resistance to cauliflower. The results of the symptoms severity evaluation of the F2 population indicate that Xcc4 resistance in UNICT5169 is a quantitative trait, which guides future resistance gene location and black rot resistance breeding.

Keywords: black rot; Brassica oleracea; resistance; cross-compatibility; genetics

1. Introduction

Cauliflower (Brassica oleracea var. botrytis) is an important vegetable, which is widely grown in China, India, Italy, and other countries located mainly in Asia and Europe [1–3]. Black rot is a destructive disease caused by Xanthomonas campestris pv. campestris (Xcc), which reduces the performance, yield, and quality of B. oleracea crops [4–8]. This pathogen invades host plants through hydathodes or wounds, with rapid multiplication that produces high amounts of extracellular polysaccharides and xanthan, clogging the vascular system and, thereby forming typical “V”-shaped chlorotic lesions along the edges of the leaves [9]. With the enlargement of the lesions, the veins also become black and eventually, the entire plant might wither and die. The pathogen has a strong ability to spread and is difficult to control using standard agronomic practices. Pesticide is ineffective because of the potential hazards of pesticide residue and environmental pollution; therefore, breeding Xcc-resistant varieties is undoubtedly the most effective way to control black rot disease.
The search for sources resistant to Xcc is complicated because of the existence of nine races of this pathogen, among which races one and four are predominant worldwide [10,11]. Previous studies have reported that Brassica B-genomic crops are resistant to race one, such as Brassica nigra (BB), B. juncea (AABB), and B. carinata (BBCC), while A-genome crops are resistant to race four, including B. rapa (AA), B. juncea (AABB) and B. napus (AACC) [12–15]. However, B. oleracea crops with the C genome lack specific resistance to races one and four, whereas some resistance to non-mainstream (two, three, six, and seven) and non-specific races has frequently been found [16–19]. It is difficult to transfer the genes resistant to race one and four that exist in the Brassica A and B genomes to C-genome crops due to interspecific hybridization obstacles, hybrid sterility, etc. [20,21]. Therefore, breeders still seek new resistant sources of B. oleracea to develop black rot-resistant varieties.

The seven cultivated varieties of B. oleracea crops have several wild relatives, such as B. balearica, B. incana, B. insularis, B. macrocarpa, B. montana, and B. villosa. These closely related wild species generally have the same 18 chromosomes as the C-genome crops and present a certain degree of sexual cross-compatibility with the B. oleracea cultivars [22]. Moreover, these wild species possess high resistance to various pests and diseases. B. incana and B. villosa are reported to be resistant to Brevicoryne brassicae, Sclerotinia sclerotiorum and Verticillium longisporum [23–25]. In addition, B. macrocarpa and B. insularis are reported to have high resistance to Leptosphaeria maculans and Pyrenopeziza brassicae, respectively [26–28]. In our study, disease resistance tests were carried out on different cauliflower accessions and wild relatives and a new Xanthomonas campestris pv. campestris race 4- (Xcc4)-resistant source (UNICT 5169, B. montana) was identified from the wild species. F1 hybrids were also successfully produced between this wild resistant accession and one susceptible cauliflower breeding line (Boc3202-4), indicating the potential transferability of this resistance to cauliflower. The symptoms severity evaluation results of the F2 population indicate that Xcc4 resistance in UNICT 5169 (B. montana) is a quantitative trait, which guides future resistance gene location and black rot resistance breeding. Therefore, the present study was framed to identify new black rot resistance source(s) and explore the genetics of resistance in a wild relative of B. oleracea.

2. Materials and Methods

2.1. Plant Materials

A total of 32 accessions were screened for black rot resistance (Table 1), including 26 cauliflower materials (eight were F1 varieties and the other 18 were the stable breeding lines) and six related wild species (B. balearica, B. incana, B. insularis, B. macrocarpa, B. montana, and B. villosa). Cauliflower varieties were purchased from a Chinese market and the other stable breeding lines were created through microspore culture or self-breeding of the purchased varieties. For the wild species, PI435896 and PI662587 were initially collected from U.S. National Plant Germplasm System (NPGS) in 2017. UNICT4785, UNICT5168, UNICT3512 and UNICT5169 were collected from the University of Catania in Italy in 2015. They showed a relatively consistent phenotype in the year of introduction. After that, we selected the most vigorous plant for each accession to carry out artificial self-pollination. For the black rot resistance test, PI435896 and PI662587 were at F3 generation and UNICT4785, UNICT5168, UNICT3512 and UNICT5169 were at F5 generation.

A total of 20 seeds for each accession were sown in a 72-hole-tray with nursery substrate and then kept in an artificial climate chamber at 24/2 °C day/night and 75–80% humidity. The first three days consisted of dark conditions, followed by a 10/14 h cycle of light and darkness. The light source was a full spectrum of light emitting diode (LED) with an intensity of 12,000 lux. After 35 days, seedlings with 4–5 true leaves were used for inoculation. Two detached leaves per seedling were selected for inoculation. The evaluations were conducted on nine seedlings per accession, with three replicates.
Two small holes were poked near a secondary vein, approximately halfway between the mid-rib and the leaf margin, in the upper third of the leaf. A bacterial suspension (3 \( \mu \text{g} \)) was grown in potato dextrose agar (PDA) medium for 48–72 h at 30 °C. All inoculated leaves were kept in an artificial climate chamber at 29/25 °C day/night and 85–95% humidity.

### 2.2. Inoculation and Disease Resistance Assay

\( Xcc4 \), which was kindly provided by Professor Liu Fan (Beijing Academy of Agriculture and Forestry Sciences, China), was used for the inoculation of all tested accessions. Bacterial cultures were grown in potato dextrose agar (PDA) medium for 48–72 h at 30 °C and then the medium was carefully removed using sterile distilled water. The turbidity of the bacterial suspension was adjusted to an absorbance of 1.4 at 600 nm, corresponding to a concentration of 1.0–3.0 \( \times 10^{9} \) cfu/mL. Seedlings with 4–5 true leaves were used for inoculation. The second and third leaves of the seedlings were cut from the petioles with scissors and placed inside a transparent plastic box. The bottom of the box was covered with two layers of non-woven fabric and 15 mL of sterile water was added. All items used in the experiment, including scissors, non-woven fabrics and boxes, were autoclaved (110 °C, 20 min). Two small holes were poked near a secondary vein, approximately halfway between the mid-rib and the leaf margin, in the upper third of the leaf. A bacterial suspension (3 \( \mu \text{L} \)) was inoculated on each hole. All inoculated leaves were kept in an artificial climate chamber at 29/25 °C day/night and 85–95% humidity.

### Table 1. Investigation of \( Xanthomonas campestris \) pv. \( campestris \) race 4 (\( Xcc4 \)) Resistance of Different \( B. oleracea \) Accessions.

| No. | Name           | Species       | Type     | DI Score | Resistance | AIP (cm\(^2\)) | PTL (%) |
|-----|----------------|---------------|----------|----------|------------|----------------|---------|
| 1   | SH-80          | Cauliflower   | F\(_1\)  | 33.8 ± 2.2 p | IR         | 1.4 ± 0.2 op   | 14.4 ± 2.5 |
| 2   | SH-88          | Cauliflower   | F\(_1\)  | 45.7 ± 2.8 klm | IR         | 1.8 ± 0.3 n    | 17.9 ± 2.2 |
| 3   | QN-65          | Cauliflower   | F\(_1\)  | 50.6 ± 2.5 hiij | S         | 4.3 ± 0.3 def  | 40.2 ± 2.8 |
| 4   | QN-80          | Cauliflower   | F\(_1\)  | 43.8 ± 2.4 lm | IR         | 2.9 ± 0.2 k    | 28.0 ± 2.0 |
| 5   | QN-90          | Cauliflower   | F\(_1\)  | 37.8 ± 2.3 o  | IR         | 1.6 ± 0.2 no   | 15.9 ± 2.1 |
| 6   | ZS-50          | Cauliflower   | F\(_1\)  | 56.1 ± 1.2 fg  | S         | 4.7 ± 0.2 c    | 46.3 ± 2.1 |
| 7   | ZS-60          | Cauliflower   | F\(_1\)  | 45.7 ± 1.5 klm | IR         | 3.1 ± 0.1 j    | 32.7 ± 1.1 |
| 8   | BY-80          | Cauliflower   | F\(_1\)  | 33.9 ± 2.9 p   | IR         | 1.4 ± 0.1 op   | 14.3 ± 1.4 |
| 9   | Boc3202-4      | Cauliflower   | DH       | 83.2 ± 2.5 a   | HS         | 5.8 ± 0.3 a    | 53.1 ± 2.8 |
| 10  | Boc3226-4A     | Cauliflower   | DH       | 56.9 ± 2.3 fg  | S         | 4.5 ± 0.3 cd   | 46.1 ± 3.0 |
| 11  | Boc3206-1      | Cauliflower   | DH       | 41.7 ± 2.2 mn  | IR         | 2.2 ± 0.3 m    | 21.2 ± 2.9 |
| 12  | Boc3206-4      | Cauliflower   | DH       | 58.5 ± 3.1 ef  | S         | 4.2 ± 0.4 efg  | 45.3 ± 4.4 |
| 13  | Boc3225-21     | Cauliflower   | DH       | 39.3 ± 1.8 no  | IR         | 1.7 ± 0.1 n    | 17.2 ± 1.1 |
| 14  | Boc3201-1      | Cauliflower   | DH       | 47.2 ± 3.2 jkl | IR         | 3.4 ± 0.3 ij   | 24.9 ± 2.3 |
| 15  | Boc3005-1      | Cauliflower   | DH       | 43.7 ± 2.4 lm  | IR         | 2.6 ± 0.2 l    | 28.4 ± 2.2 |
| 16  | Boc3228-4      | Cauliflower   | DH       | 76.4 ± 3.1 b   | HS         | 5.3 ± 0.4 b    | 52.8 ± 4.1 |
| 17  | Boc3203-4      | Cauliflower   | DH       | 54.3 ± 4.1 gh  | S         | 3.9 ± 0.4 h    | 42.1 ± 4.4 |
| 18  | Boc4259        | Cauliflower   | SI       | 65.5 ± 3.1 c   | S         | 4.6 ± 0.3 cd   | 44.5 ± 2.9 |
| 19  | Boc4258        | Cauliflower   | SI       | 64.3±2.6 cd    | S         | 4.5 ± 0.3 cde  | 42.2 ± 2.8 |
| 20  | Boc4222-3      | Cauliflower   | SI       | 61.4 ± 3.3 de  | S         | 5.0 ± 0.3 b    | 51.4 ± 2.9 |
| 21  | Boc4229        | Cauliflower   | SI       | 56.8 ± 1.9 fg  | S         | 4.4 ± 0.2 cdef | 45.2±2.1 |
| 22  | Boc4710-1      | Cauliflower   | SI       | 53.8 ± 2.3 gh  | S         | 4.3 ± 0.2 def  | 43.3 ± 1.9 |
| 23  | Boc4601        | Cauliflower   | SI       | 22.9 ± 1.3 q   | R         | 1.0 ± 0.1 q    | 12.2 ± 1.2 |
| 24  | Boc4604        | Cauliflower   | SI       | 65.3 ± 1.3 cd  | S         | 5.2 ± 0.2 b    | 51.1 ± 2.2 |
| 25  | Boc4605        | Cauliflower   | SI       | 51.6 ± 3.0 hi  | S         | 3.9 ± 0.4 gh   | 39.9 ± 3.0 |
| 26  | Boc4251        | Cauliflower   | SI       | 48.8 ± 2.5 ijk | IR         | 3.5 ± 0.3 i    | 35.8 ± 2.7 |
| 27  | PI435896       | Brassica balearica | WD | 11.2 ± 0.6 r | R | 0.5 ± 0.08 r | 4.6 ± 0.9 |
| 28  | PI662587       | Brassica insularis | WD | 38.8 ± 2.6 no | IR | 1.7 ± 0.2 n | 18.6 ± 2.3 |
| 29  | UNICIT4785     | Brassica macrocarp | WD | 42.4 ± 1.8 mn | IR | 4.2 ± 0.2 fg | 42.9 ± 2.1 |
| 30  | UNICIT5168     | Brassica villosa | WD | 26.0 ± 1.7 q  | R | 1.2 ± 0.1 pq | 11.3 ± 1.1 |
| 31  | UNICIT3512     | Brassica incana | WD | 63.7 ± 2.4 cd | S | 5.2 ± 0.3 b | 44.5 ± 2.6 |
| 32  | UNICIT5169     | Brassica montana | WD | 7.8 ± 0.5 r  | HR | 0.3 ± 0.06 r | 2.9 ± 1.2 |

Note: Accessions 1–8 are cauliflower varieties that are popular in different regions of China. Accessions 27–32 are \( B. oleracea \)-related wild species. \( F_1, F_2 \) variety; DH, doubled haploid; SI, stable inbred line; WD, wild species. HR, high resistance, \( DI \leq 10; R \), resistant, \( 10 < DI \leq 50; IR \), intermediate resistance, \( 30 < DI \leq 50; S \), susceptible, \( 50 < DI \leq 70; HS \), highly susceptible, \( 70 < DI \leq 100 \). SD, disease index; AIP, the area of the infected part; PTL, the proportion of the infected part relative to the total leaf area.

The values in the columns with the same letters are not statistically different with Duncan’s multiple range test at \( p \leq 0.05 \).

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humidity under a 10/14 h light/dark cycle. The light source was a full spectrum of LED with an intensity of 12,000 lux. The symptoms severity of infected leaves was investigated 10 days after inoculation.

Two methods were used to evaluate the severity of symptoms. One was the traditional grading method with a six-point scale from 0 to 9 based on the relative lesion size and severity (0 = no symptoms; 1 = slight necrosis or chlorosis surrounding the inoculated points; 3 = small V-shaped lesion covering 3–10% of leaf area; 5 = spreading V-shaped lesions covering 10–30% of leaf area; 7 = large V-shaped lesions covering 30–50% of leaf area; 9 = severely infected lesions covering 50%–100% of entire leaf area) [12]. The disease index (DI) was calculated as follows: \( \Sigma (si \times ni) \times 100/9 N \) (si, the incidence level; ni, the number of leaves with the corresponding incidence level; N, the total number of leaves investigated. The DI value was divided into five levels: high resistance (HR), DI ≤ 10; resistance (R), 10 < DI ≤ 30; intermediate resistance (IR) 30 < DI ≤ 50; susceptibility (S), 50 < DI ≤ 70; high susceptibility (HS), 70 < DI ≤ 100 [12].

The other method used to evaluate the severity of symptoms was based on the plant phenotype measurement system (PPMS, PlantExplorer Spectral HS, Netherlands). \( Fv/Fm \) is an important chlorophyll fluorescence parameter and indicator of the photochemical efficiency of photosystem II, which was used to evaluate the degree of leaf disease after infection by the black rot pathogen. Ten days after inoculation, all tested leaves were photographed by the PPMS and the \( Fv/Fm \) value of each leaf was calculated by its own PhenoVation Analysis software. The \( Fv/Fm \) score of the outermost part of the chlorotic area was considered the critical value, and for most infected leaves, the value was approximately 0.4. Therefore, leaves with an \( Fv/Fm \) value less than 0.4 were considered to be infected, and those with an \( Fv/Fm \) value higher than 0.4 were considered to be normal. The area of the infected part (AIP) spreading from the inoculated site and its proportion to the total leaf area (PTL) were used to evaluate the severity of infected leaves.

2.3. Cross-Compatibility Survey and \( F_1 \) Production

\( F_1 \) hybrids were obtained by artificial pollination between one wild accession with high resistance to \( Xcc \) race 4 (UNICT5169, male parent) and a cauliflower breeding line that showed high susceptibility (Boc3202-4, female parent). In the flowering period of the maternal line, three plants with strong growth and high-quality inflorescences were selected. A total of three inflorescences were selected from each plant, and six to ten flower buds that were going to open were preserved for each inflorescence and the rest were removed. The stamens of Boc3202-4 were removed with pointed tweezers after wiping with 75% alcohol, and then the pollen of UNICT5169 was pollinated on the stigmas. The number of seeds harvested from each pod was recorded. The cross-affinity index (CI) was calculated by the following formula: CI = total number of hybrid seeds/total number of cross-pollinated buds.

2.4. \( F_1 \) Hybrid Identification

The morphology of the \( F_1 \) hybrids and their parental lines including growth vigor, crown width and leaf profile, was evaluated under greenhouse conditions. Total genomic DNA was isolated from leaf tissue collected in bulk from tested plants using the traditional cetyltrimethylammonium bromide (CTAB) method [29]. Two specific simple sequence repeat (SSR) primer combinations were selected for their clear distinct polymorphic banding patterns between the parents (Table S1) [30].

PCR amplification was performed following Zhao et al. [30]. The PCR products were electrophoresed in 6% polyacrylamide denatured gels, ran at 100 W for 2 h, and the banding patterns were visualized using silver staining as described by Panaud et al. [31]. The gel was photographed after being dried at room temperature.

2.5. Inoculation of Parents and \( F_1 \), and \( F_2 \) Generations

The cultivation procedures and inoculation methods were followed as described above. The parental plants and \( F_1 \) hybrids (nine plants per accession) were tested together with \( F_2 \) plants. For 103 \( F_2 \) generation plants, the inoculation tests of the detached leaves were performed twice.
The first time was at the seedling stage with 4–5 true leaves, and two true leaves were detached for inoculation. The second time was 15 days later and two new true leaves from the same plant were cut and inoculated.

2.6. Data Analysis

Statistical analyses such as Pearson’s simple correlation and analysis of variance (one-way ANOVA and Duncan’s multiple range test) were performed using SPSS Statistics software, version 21.

3. Results

3.1. Investigation of Resistance to Xcc race 4 in Cauliflower and Related Wild Accessions

Three days after inoculation, chlorosis began to appear at the inoculated sites of leaves in vitro. As time progressed, typical V-shaped chlorosis extending inward from the inoculation site was observed accompanied by the browning of the leaf vein. Ten days after inoculation, the severity of symptoms among the tested accessions was significant, signaling that it was an appropriate time to perform the investigation.

3.1.1. Investigation Based on the Traditional Grading Method

We evaluated all inoculated leaves by a six-point scale from 0 to 9 based on the relative lesion size and severity (Figure 1). The results indicate that most of the tested accessions were susceptible or had intermediate resistance, whereas few of them showed resistance to Xcc4 (Table 1). Among the F₁ varieties, six ones had intermediate resistance, with DI scores from 33.8 to 45.7, whereas the other two varieties were susceptible, with DI scores of 50.6 (QN-65) and 56.1 (ZS-50). Among the cauliflower pure breeding lines, the average DI score reached 55.1 with a range from 22.9 (Boc4601) to 83.2 (Boc3202-4). Boc4601 is a late-maturing line with a growth period of more than 100 days and was defined as resistant as its DI value is less than 30. There were five lines with a DI score of 30–50, i.e., intermediate resistance. The majority of the cauliflower breeding lines (10/18) showed susceptibility, with a DI value from 51.6 to 65.5. The DI values of the remaining two lines were 76.4 (Boc3228-4) and 83.2 (Boc3202-4) and these lines were classified as highly susceptible. The wild accessions showed significant differences in Xcc4 resistance. UNICT3512 had the highest DI score of 63.7 and was considered susceptible. Two accessions were classified as intermediate resistance (PI435896 and UNICT4785) and resistant (PI435896 and UNICT5168) according to their DI scores. UNICT5169 had the lowest DI value (7.8) and was the only material identified as highly resistant. However, according to the statistical analysis, there was no significant difference (p ≤ 0.05) in the DI value between UNICT5169 and PI435896, indicating that their resistance level was similar.

Figure 1. Grading evaluation of infected leaves according to a six-point scale from zero to nine based on the relative lesion size and severity. (Upper row, photos under ordinary brightfield lighting; bottom row, photos analyzed by the plant phenotype measurement system (PPMS).
3.1.2. Investigation Based on the PPMS

The definitions of the tested materials based on AIP or PTL values were generally consistent with the results of the above-mentioned DI survey (Table 1). The DI value was positively correlated with AIP and PTL at the 0.01 level, and the correlation coefficients were 0.93 and 0.91, respectively (Table 2). The accessions with high DI scores generally had high AIP and PTL values. HR and R accessions had AIP values less than 1.2 cm² and PTL scores lower than 12.2%. The AIP values of IR accessions ranged from 1.4 to 3.5 cm², and the PTL scores ranged from 14.3% to 35.8%. For S and HS accessions, the ranges of the AIP and PTL values were 3.9–5.8 cm² and 39.9–53.1%, respectively. In addition, the wild accession UNICT4785 had a DI score of 42.4 and was classified as IR level, but it had high AIP and PTL values of 4.2 cm² and 42.9%, respectively. Based on the Fv/Fm threshold of 0.4, parts of the UNICT4785 leaves that were slightly distal from inoculated points were infected and injured by Xcc4, but no visible symptoms of chlorosis or wilting were observed. However, these injured parts of the leaves could be identified by the PPMS, and their area was also calculated (Figure 2). For UNICT5169 and PI435896, there was no significant difference (p ≤ 0.05) in their AIP values.

Table 2. Correlation Analysis of Important Data Sets based on the Pearson’s Coefficient.

|          | DI   | AIP  | PTL  | I1-DI | I2-DI | I2-AIP |
|----------|------|------|------|-------|-------|--------|
| DI       | /    | 0.93 ** | 0.91 ** | /     | /     | /      |
| AIP      | 0.93 ** | / | 0.98 ** | /     | /     | /      |
| PTL      | 0.91 ** | 0.98 ** | /     | /     | /     | /      |
| I1-DI    | /    | /    | 0.97 ** | /     | /     | /      |
| I2-AIP   | /    | /    | /    | 0.98 ** | /     | /      |

Note: DI, disease index; AIP, area of the infected part; PTL, proportion of the infected part relative to the total leaf area; DI, AIP, and PTL, three sets of data obtained from the investigation of leaf disease severity of the 32 accessions. I1-DI and I2-DI, DI value of inoculation 1 and 2 on F₂ plants; I1-AIP and I2-AIP, AIP value of inoculation 1 and 2 on F₂ plants. **, significantly different at p ≤ 0.01.

Figure 2. The severity of symptoms on leaves of different accessions 10 days after inoculation with the Xcc4 bacterial suspension. (upper row, photos under ordinary brightfield lighting; bottom row, photos analyzed by the PPMS).

3.2. Cross-Compatibility Survey and F₁ production

UNICT5169 and PI435896 are wild relatives of Brassica oleracea, and these accessions showed high resistance to Xcc4 among the tested materials. However, the self-compatibility of PI435896...
Figure 3. The process of artificial pollination between Boc3202-4 (HS, cauliflower, female parent) and UNICT5169 (HR, B. montana, male parent), and F1 hybrid production. (a) Artificial stamens removal of Boc3202-4 buds. (b) Pistils of Boc3202-4 after the removal of stamens and petals. (c) UNICT5169 pollen was used for pollination of Boc3202-4 stigmas. (d) Developmental status of seed pods 15 days after cross-pollination. (e,f) Developmental status of seed pods 35 days after cross-pollination.

3.3. F1 Hybrid Identification

F1 hybrid authenticity was identified using phenotype and SSR molecular markers. The leaf morphology was intermediate between those of the parents, including leaf shape, color, and edge notch. However, F1 plants did not have cauliflower-type curds. They were tall and had strong growth potential, and the overall phenotype tended to resemble that of the paternal wild species (Figure 4). Two pairs of SSR primers were screened out, because clear and stable polymorphic bands were amplified in the parents. The results show that all 119 F1 plants contained specific bands of their parents, indicating that they were true hybrids (Figure 4).

Figure 4. Identification of F1 hybrids based on morphology and SSR molecular markers. (a) Plant morphology at the seedling stage. (b) Basal leaves of parental lines and the F1 hybrid. (c) SSR analysis of parental lines and the F1 hybrids: one and two, specific band for Boc3202-4; three and four, specific band for UNICT5169; 5–12, F1 hybrids containing the bands from the parents.
3.4. Inoculation of Parents, F₁ and F₂ Generations

The average DI value of the F₁ hybrids was 39.4 and the AIP score was 1.9 cm², i.e., slightly lower than the mid-parent value of 44.4 and 2.9 cm², respectively, indicating that the Xcc4 resistance of UNICT5169 is not completely dominant relative to the susceptible character (Table 3). Two F₁ plants were randomly selected, and an F₂ population was obtained by artificial self-pollination. The self-fertility of the F₁ hybrids was normal, and most pods contained more than five seeds. To better investigate the genomics of resistance, 103 F₂ plants were used to investigate their reaction to Xcc4. The inoculation tests of the detached leaves from F₂ plants were performed twice and there was a significant positive correlation ($p \leq 0.01$) between the two inoculations (Table 2).

### Table 3. Investigation of Xcc4 Resistance of Parents and F₁ Hybrids.

| Accessions | Type       | DI   | AIP  |
|------------|------------|------|------|
| Boc3202-4  | female parent | 80.8 a | 5.6 a |
| UNICT5169  | male parent  | 8.1 d  | 0.3 d |
| Mid-parent value | /     | 44.4 b | 2.9 b |
| F₁        | F₁ hybrids  | 39.4 c | 1.9 c |

Note: DI, disease index; AIP, the area of the infected part. The values in the columns with the same letters are not statistically different with Duncan’s multiple range test at $p \leq 0.05$.

The results indicate that the DI and AIP scores of the F₂ plants were continuously distributed, and there were numerous variations. Moreover, a few F₂ plants showed transgressive inheritance and had higher resistance than UNICT5169. The distribution density of F₂ plants showed a slight right-skewed distribution with a main peak, indicating that the Xcc4 resistance of UNICT5169 was a quantitative trait, and there might be a major gene control (Figure 5).

![Figure 5](image_url)

**Figure 5.** Investigation of symptoms severity to Xcc4 in the F₂ population from Boc3202-4 (♀) and UNICT5169 (♂). (a) Resistance/sensitivity of F₁ hybrids and their parents to Xcc4 (S, Boc3202-4. R, UNICT5169). (b) Resistance investigation of the F₂ plants. Frequency distribution of Xcc4 resistance in the F₂ population based on artificial grading (c) and PPMS (d).

4. Discussion

Screening out materials resistant to black rot is required for the location and cloning of resistance genes, which is also the basis for resistance transfer and breeding new varieties of cauliflower resistant to black rot. The genes resistant to Xcc4 mainly exist in *Brassica* A-genome crops, such as Chinese cabbage (*Brassica rapa*, 2n = 2x = 20) [14,32] and rape (*Brassica napus*, AACC; 2n = 4x = 38) [33]. However, due to the problems of interspecific hybridization and the sterility of hybrids, it is difficult to transfer the Xcc4-resistance genes from A-genome crops to *Brassica oleracea* crops. Although some genotypes
of *B. oleracea* have been identified as having *Xcc*-resistance [14,17,34], the breeding application of these resistant accessions has had limited success. In the present study, several accessions with good *Xcc*-4-resistance were identified among the wild species, which could be crossed with cauliflower to obtain hybrid seeds without using costly methods such as embryo rescue or protoplast fusion. This discovery is very valuable because resistance to race four is very rare among C-genome crops. The identified wild accessions with high *Xcc*-4-resistance can be directly utilized in sexual hybridization for the transformation of resistance to cauliflower and other *B. oleracea* crops.

The leaves infected with *Xcc* showed V-shaped lesions, but they were irregular, and it was difficult to calculate their area. The traditional method to evaluate the phenotype of infected leaves by a DI based on artificial grading is easily affected by sensory factors, which may lead to deviations in experimental results [19]. In this study, PPMS technology was used to assess the symptom severity of leaves inoculated with black rot pathogen. The diseased leaves with chlorotic or yellow lesions consistently exhibited a sharp decrease in the chlorophyll content and photosynthetic efficiency. *Fv/Fm* is an important chlorophyll fluorescence parameter that can reflect the photochemical efficiency of photosystem II. Therefore, the *Fv/Fm* value can be used to evaluate the degree of leaf disease after being infected by black rot pathogen. The results of this study show that the disease spot area calculated by the *Fv/Fm* value of 0.4 was consistent with the traditional DI evaluation, which can reflect the disease grade of leaves. In this way, it is possible to carry out high-throughput and accurate quantitative analysis of susceptible leaves using the PPMS technology. AIP and PTL are two important indexes to measure the disease severity of leaves infected with black rot pathogen. The present results indicate that the consistency of the two sets of data was quite high, so only one index needs to be used. In addition, PPMS technology can detect non-visible damage that occurs after *Xcc*4 bacterial infection, thereby improving the accuracy of phenotypic investigation.

Previous research on the heredity laws of resistance to black rot in *B. oleracea* crops indicated that the different resistant accessions of inter- or intra-species had different inheritance patterns. One major recessive gene and two modifiers were reported to control resistance in the cabbage variety 'Early Fuji' [35]. With respect to the cauliflower accessions SN455 (no race information) and BR-161 (*Xcc* race one), a single dominant gene controls their resistance [36,37]. Vicente et al. [12] reported a single dominant locus governed resistance to *Xcc* race three in cabbage breeding lines BOH85c and PI436606. In this study, based on a combination of the *F1* and *F2* phenotypic values, the resistance to *Xcc*-4 in UNICT5169 is a quantitative trait that might be controlled by a major gene accompanied by multiple genetic modifications. However, a larger number of plants of the *F2* population and multiple types of segregation populations, such as BC, are needed to accurately assess the inheritance of *Xcc*-4 resistance.

5. Conclusions

In this study, *Xanthomonas campestris pv. campestris* race 4 resistance tests were carried out on different cauliflower accessions and wild relatives. Two methods of traditional DI classification and PPMS technology were used to evaluate the severity of symptoms. A new *Xcc*-4-resistant source (UNICT 5169, *B. montana*) was identified and successfully hybridized with one susceptible cauliflower breeding line (Boc3202-4) to obtain *F1* hybrids, indicating the potential transferability of this resistance to cauliflower. The results of the symptoms severity evaluation of the *F2* population indicate that *Xcc*-4 resistance in UNICT5169 is a quantitative trait, which guides future resistance gene location and black rot resistance breeding.

**Supplementary Materials:** The following are available online at [http://www.mdpi.com/2073-4395/10/9/1400/s1](http://www.mdpi.com/2073-4395/10/9/1400/s1), Table S1: Two selected SSR primers with polymorphic parental bands.

**Author Contributions:** Conceptualization, X.-G.S. and H.-H.G.; methodology, Z.-Q.Z. and Y.-S.S.; software, X.-G.S. and Y.-S.S.; validation, J.-S.W. and H.-F.Y.; formal analysis, X.-G.S. and F.B.; investigation, J.-S.W.; resources, H.-H.G. and F.B.; data curation, X.-G.S.; writing—original draft preparation, X.-G.S.; writing—review and editing, H.-H.G. and F.B.; visualization, X.-G.S. and H.-F.Y.; funding acquisition, H.-H.G. All authors have read and agreed to the published version of the manuscript.
Acknowledgments: We are grateful to Liu Fan of Beijing Academy of Agriculture and Forestry Sciences, China for financial support through projects (2017YFD0101805, 2017YFE0114500), Science and Technology Department of Zhejiang Province (LGN18C150010, 2016C20251-5-4), and Zhejiang Academy of Agricultural Sciences (A1).

Conflicts of Interest: The authors declared no conflict of interest.

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