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Identification and Transfer of a New Powdery Mildew Resistance Gene *PmCAHM* from Landrace Changanhongmai into Common Wheat

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Abstract: Powdery mildew is a severe wheat disease that causes substantial yield losses in wheat production worldwide. The Chinese wheat landrace Changanhongmai (CAHM) exhibits high resistance to the physiological race E09 of powdery mildew. In this study, we characterized the powdery mildew resistance gene in CAHM, and developed molecular markers for wheat marker-assisted selection. To investigate the genetic characteristics of this resistant gene, we developed F_1 plants, F_2 generation population, and $F_{2:3}$ families by crossing CAHM with SY225 (Shaanyou '225' as susceptible male parent). Genetic analysis demonstrated that all F_1 plants were resistant to the disease, while the ratio of resistant to susceptible plants was 3: 1 in both the F_2 population and $F_{2:3}$ families, indicating that CAHM is inherited in a manner of a single dominant powdery mildew resistance gene, which was tentatively designated as *PmCAHM*. By using bulk segregation analysis, we constructed a genetic map encompassing *Xgwm273*, *Xwmc626*, *Xgwm11*, *Xgwm18*, *Xgdm28*, *Xgpw7812*, *Xgpw5195*, *Xwmc694*, and *PmCAHM*. Among these markers, *Xgpw7812* and *Xgpw5195* are flanking markers that are tightly linked to *PmCAHM* at a genetic distance of 2.5 cM and 8.4 cM, respectively. Furthermore, nullisomic-tetrasomic analysis revealed that *PmCAHM* is located on chromosome 1B. These results indicate that *PmCAHM* differs from the internationally recognized powdery mildew resistance genes in both location and source. In addition, a new germplasm/line NW1748 with stronger powdery mildew resistance and large grains was developed from the cross and backcross populations of Fengyou1718 (FY1718)/CAHM/5/FY 1718. Therefore, *PmCAHM* can serve as a novel powdery mildew resistance source for breeding of wheat by using NW1748 as the donor in the future.

Keywords: common wheat; powdery mildew; molecular marker; genetic population

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1. Introduction

Wheat (*Triticum aestivum* L., $2n = 6x = 42$, AABBDD) is the largest food crop in the world, providing most calories for appropriately 40% of the world's total population [1,2]. Wheat powdery mildew, arising from wheat-specific *Blumeria graminis* f. sp. *tritici* (*Bgt*), is a foliar disease occurring in almost all major wheat-producing areas [3,4]. Development and breeding of wheat varieties with resistance to powdery mildew is the most economical, viable, safe, and effective approach to minimize fungicide use and production loss caused by this disease [3,5,6]. To seek for higher production, the cultivation and management level has been greatly improved in recent years along with improvement of water and fertilizer conditions. Additionally, it is a common practice to use single disease-resistant varieties and the same resistance sources in the main cultivated varieties in various regions,

which tends to increase the risk of loss of resistance. As a result, powdery mildew is becoming increasingly prevalent in many main production areas of wheat worldwide, posing a significant threat to global food security.

Currently, 69 genes associated with powdery mildew resistance have been identified and assigned with official names [7]. However, due to the presence of numerous physiological races, rapid virulence variations, and the emergence of new strains, many of these resistance genes have lost their effectiveness. Additionally, some of the resistance genes are associated with some undesirable traits, making it challenging to utilize them in breeding. As a result, only a very limited number of such resistance genes can be truly employed in practical production. *Pm8*, a gene conferring powdery mildew resistance to wheat and originated from rye 1RS, was extensively utilized between the 1970s and the mid-1980s. However, global loss of resistance gradually occurred due to heavy reliance on a single source of resistance, ultimately leading to a widespread powdery mildew pandemic [8]. The long-term use of single-resistant varieties may lead to the recurrence of powdery mildew pandemics. Currently, the powdery mildew resistance gene *Pm21* stands out as the strongest and most stable gene. Numerous wheat varieties developed by utilizing *Pm21* have been approved and promoted in production [9–12]. However, this wide use of disease-resistant varieties carrying *Pm21* will also pose significant pressure on *Pm21*. Therefore, it is a crucial ongoing task to discover new resistance genes against powdery mildew. Additionally, it is urgent to achieve broad-spectrum resistance with disease-resistance genes and incorporate them into major cultivated varieties.

Some certain species of wheat can serve as crucial gene sources to breed wheat varieties with resistance to powdery mildew and prevent its damage [13,14]. China possesses a wide range of local wheat varieties, and 60% of the materials stored in the national germplasm bank were derived from these varieties. These local varieties represent significant resistance gene resources, including several varieties unique to China, which represent a valuable national asset [15–18]. For example, Huang et al. [19] identified a powdery mildew resistance gene *Pm5E* from the farm variety of Fuzhuang 30 in China. Xue et al. [20] also found a powdery mildew resistance gene *Pm24* from the local variety Ziayacao. Additionally, Ma et al. [21] discovered the wheat variety Yingbo700, which carries the *PmYB* allele in its chromosomal region. These alleles, known for their broad-spectrum resistance, can effectively resist 48 different powdery mildew strains from various regions in China. However, the mining of powdery mildew resistance genes in local wheat varieties is still insufficient to meet the demands in wheat production. The Shaanxi landrace Changanhongmai (CAHM) ($2n = 6x = 42$, AABBDD) demonstrates a high level of resistance to powdery mildew, but it has not been adopted in wheat farms yet, suggesting that it may be a valuable source of disease resistance in the development and breeding of wheat varieties, though its agronomic traits are not particularly outstanding. Particularly, by utilizing molecular marker-assisted selection during empirical breeding, we can identify new disease-resistant germplasm resources and develop new pre-breeding materials. This will allow strategical distribution and accumulation of disease-resistant genes, thereby addressing the issue of single resistance, which will be crucial for ensuring food production security.

This study aims to investigate the resistance of CAHM to the *Bgt* pathotype in Huanghuai area, China. CAHM was used as the female parent and crossed with the common susceptible wheat SY225 to obtain the F_2 segregated population, which was further analyzed with bulk segregation analysis (BSA) coupled with SSR molecular markers and Chinese Spring nulli-tetrasomics. Specifically, the objectives include determination of the inheritance pattern of *PmCAHM*, identification of the associated molecular markers, localization of the chromosomal position of the related locus, and transfer of *PmCAHM* into the common wheat FY1718 through the germplasm that can be directly utilized in wheat breeding. This study holds significant theoretical and practical value by expanding the genetic basis for local wheat disease resistance breeding.

2. Materials and Methods

2.1. Plant Materials

Three materials were selected for the experiment due to their different characters. The common wheat landrace Changanhongmai (CAHM), which originated in Shaanxi, China, was selected as the resistant material considering its immune resistance to powdery mildew. Another cultivar 'Shaanyou 225' (SY225) accession 1993257 (authorized variety from Shaanxi Province in 1993), which has high-quality strong gluten and many excellent traits, was used as the susceptible material due to its susceptibility to powdery mildew. Fengyou1718 (FY1718, authorized variety from Shaanxi Province in 2007) is a widely adaptable cultivar with favorable overall agronomic traits, except for high susceptibility to powdery mildew. In addition, the chromosomal location of the simple sequence repeat (SSR) markers was determined by using Chinese Spring (CS) nulli-tetrasomic lines N1A-T1B, N1B-T1D, N1D-T1A, N2A-T2B, N2B-T2D, N2D-T2A, N3A-T3B, N3B-T3D, N3D-T3A, N4A-T4B, N4B-T4D, N4D-T4A, N5A-T5B, N5B-T5D, N5D-T5A, N6A-T6B, N6B-T6D, N6D-T6A, N7A-T7B, N7B-T7D, and N7D-T7A.

F_1 plants, F_2 populations, and $F_{2:3}$ families constructed by crossing CAHM as the female parent and SY225 as the male parent were used for identification and genetic analysis of powdery mildew resistance genes. The F_2 generation was also employed as a mapping population to construct a genetic linkage map. NW1848 was obtained by hybridizing FY1718/CAHM. We selected plants exhibiting excellent agronomic characteristics and resistance to *Bgt* E09 from NW1848 populations in the field through system breeding. After harvest, the data including the plant height, spike length, spike grain number, and TGW were recorded to select desirable agronomic traits and powdery mildew resistance, which was repeated in the field and greenhouse. After five generations, one morphologically identical line was obtained with excellent agronomic traits and resistance to *Bgt* race E09, which was named as NW1848. All these experimental materials and the *Bgt* isolate E09 were provided by the College of Agronomy, Northwest A&F University and Institute of Crop Germplasm Resources, Shandong Academy of Agricultural Sciences.

2.2. Evaluation of Powdery Mildew Resistance

The powdery mildew resistance of the target materials was identified in the artificial climate incubator at the seedling stage. The materials were planted in white rectangular trays of 42 × 31 × 7 cm, respectively. CAHM, CS, and F_1 plants were planted in three rows with 10 plants in each row. In total, 176 F_2 plants were cultivated in the remaining space. From each $F_{2:3}$ family, fifteen plants were selected for genotype identification of the parental F_2 plants. It is worth noting that SY225 serves as both a parent and a susceptible control. According to the research method of Zhao et al. [22], the susceptible variety SY225 was inoculated with *Bgt* race E09 after obtaining conidia at the two-leaf stage. After two weeks, when the plant showed obvious symptoms, the resistance of the target material to powdery mildew was evaluated. The infection level was described as 0–4, with 4, 3, 2, 1, and 0 indicating high sensitivity, moderate sensitivity, moderate resistance, and high resistance, and immunity, respectively [5]. In addition, the resistance of the NW1848 line and its parents (CAHM and FY1718) at the booting and filling stages to powdery mildew was evaluated [5]. They were grown at the Northwest A&F University, Yanglin, China.

2.3. Molecular Marker and Nulli-Tetrasomic Analysis

Fresh leaves were carefully selected and placed in numbered 2 mL centrifuge tubes. The tubes were then subjected to freeze-drying using a vacuum freeze-dryer. The freeze-dried leaves were stored for future use. DNA extraction from the leaves was conducted following the procedure described by Huang et al. [23]. Among the F_2 generation isolation populations, we used the BSA method to randomly select 10 individual plants with extreme disease resistance based on the disease resistance identification results, and mixed their DNA in equal amounts to create a disease-resistant pool. We also randomly selected 10 extremely susceptible individual plants and mixed their DNA in equal amounts to construct a

susceptible pool [24]. We selected 766 pairs of SSR primers currently distributed in the chromosome groups A, B, and D in the laboratory to conduct polymorphism screening between parents and offspring. The finally selected SSR primers were used for PCR amplification verification of the DNA of all F_2 individual plants, and linkage analysis of disease resistance genes was performed and analyzed statistically. Then, nullisomic–tetrasomic analysis was performed using markers on both sides of the linkage map, ultimately determining the gene location on the chromosome in common wheat.

2.4. Genetic Mapping and Data Analysis

The specific location on the chromosome where the linked marker is located was checked in the Cereal Genetics website (https://graingenes.org/cgi-bin/GG3/browse.cgi) to clarify the location of the powdery mildew resistance gene. Joinmap4.0 [25] software was used to calculate the genetic distance, and the amplification results of all individual plants of the F_2 population marked by SSR primers were input into an Excel table for statistics and analysis. We defined the CAHM-specific genotype as "a", the genotype of SY225 as "b", and then the heterozygous genotype as "h". There were always some individuals with missing data, which needed to be represented by "-". A Chi-squared test was used to evaluate the goodness of fit of observed and expected segregation ratios of the powdery mildew reaction and molecular markers. Linkages between markers and the resistance gene were established using JoinMap 4.0. A genetic map was created using Mapdraw V2.1 [12]. For the agronomic trait test, statistical analysis of ten plants harvested from the target materials was used to calculate the average data for plant height, spike length, spike grain number, and thousand grain weight (TGW).

3. Results

3.1. Genetic Analysis of Powdery Mildew Resistance Gene in Changanhongmai

We first determined the disease resistance of parents and their hybrid progenies to powdery mildew. The results are shown in Table 1. CAHM showed immunity, while SY225 showed high sensitivity to the disease. All the F_1 plants exhibited immunity. In the F_2 generation population, among the 176 identified individual plants, 122 plants displayed resistance while 54 plants were susceptible to the disease. Among 176 F_2 plants, the segregation ratio of resistant to susceptible plants was 122:54 plants, which approximates to a 3:1 ratio ($\chi^2_{3:1} = 2.73$, $p = 0.9$). The reactions of the 176 $F_{2:3}$ families could be categorized into 47 homozygous resistant, 75 segregating, and 54 homozygous susceptible types, respectively, which agrees with a ratio of 1:2:1 ($\chi^2$3:1 = 4.40, df = 2, $p = 0.96$) (Table 1). Therefore, the resistance of CAHM to isolate E09 followed the principle of dominant inheritance of a single gene, and the resistance was likely governed by a pair of dominant genes, which was tentatively designated as *PmCAHM*.

Table 1. Resistance response of Changanhongmai and its genetic populations to powdery mildew.

Materials	Observed Plant Number			Expected Ratio	χ^2 Value	*p*-Value
	Resistant	Segregating	Susceptible			
CAHM	10					
SY225			10			
F_1	10					
F_2	122		54	3:1	2.73	0.90
$F_{2:3}$	47	75	54	1:2:1	4.4	0.96

Note: $\chi^2(0.05,1) = 3.84$; $\chi^2(0.05,2) = 5.99$.

3.2. Linkage Analysis of SSR Polymorphic Markers

The genomic DNA of CAHM and SY225 were amplified by 766 pairs of SSR primers distributed on 42 wheat chromosomes in the laboratory, and 85 pairs of primers showed polymorphic differences between CAHM and SY225. These primers were further amplified and screened between the resistant pool and the sensitive pool, and eight pairs of

SSR markers, including *Xgpw7812*, *Xgwm273*, *Xwmc626*, *Xgwm11*, *Xgwm1818*, *Xgdm2828*, *Xwmc694*, and *Xgpw5195*, were obtained. The query results on the Graingenes website for basic information of the eight pairs of SSR tags are listed in Table 2. The screened molecular markers which are closely associated with the disease-resistance gene *PmCAHM* are of great significance to future wheat breeding [26,27].

Table 2. Eight pairs of SSR primers with differences in polymorphism.

Marker	Forward-Primer (5′-3′)	Reverse-Primer (5′-3′)	Tm °C/t (h)
Xgpw7812	ACTGTCCTCGATTGTGTGTCC	CTTTATCAGGCATGGAACTGC	60
Xgwm273	ATTGGACGGACAGATGCTTT	AGCAGTGAGGAAGGGGATC	60
Xwmc626	AGCCCATAAACATCCAACACGG	AGGTGGGCTTGGTTACGCTCTC	60
Xgwm11	GGATAGTCAGACAATTCTTGTG	GTGAATTGTGTCTTGTATGCTTCC	62
Xgwm1818	TGGCGCCATGATTGCATTATCTTC	GGTTGCTGAAGAACCTTATTTAGG	62
Xgdm2828	ATCTGACTTCATGGTTTATAT	TCAAGAATGAAGACATAGTT	62
Xwmc694	ATTTGCCCTTGTGAGCCGTT	GACCTGGGTGGGACCCATTA	58
Xgpw5195	CGACTCTCGCTTCAGCTTG	GGTTCTTCACGCCATTGATT	60

Furthermore, we used the eight pairs of SSR primers to amplify the DNA of 176 plants in the F_2 population of CAHM/SY225. As a result, these SSR primers could amplify specific bands in the F_2 plants (Figure 1). It could be inferred that *Xgpw7812*, *Xgwm273*, *Xwmc626*, *Xgwm11*, *Xgwm1818*, *Xgdm2828*, *Xwmc694*, and *Xgpw5195* are associated with the gene tentatively named as *PmCAHM*.

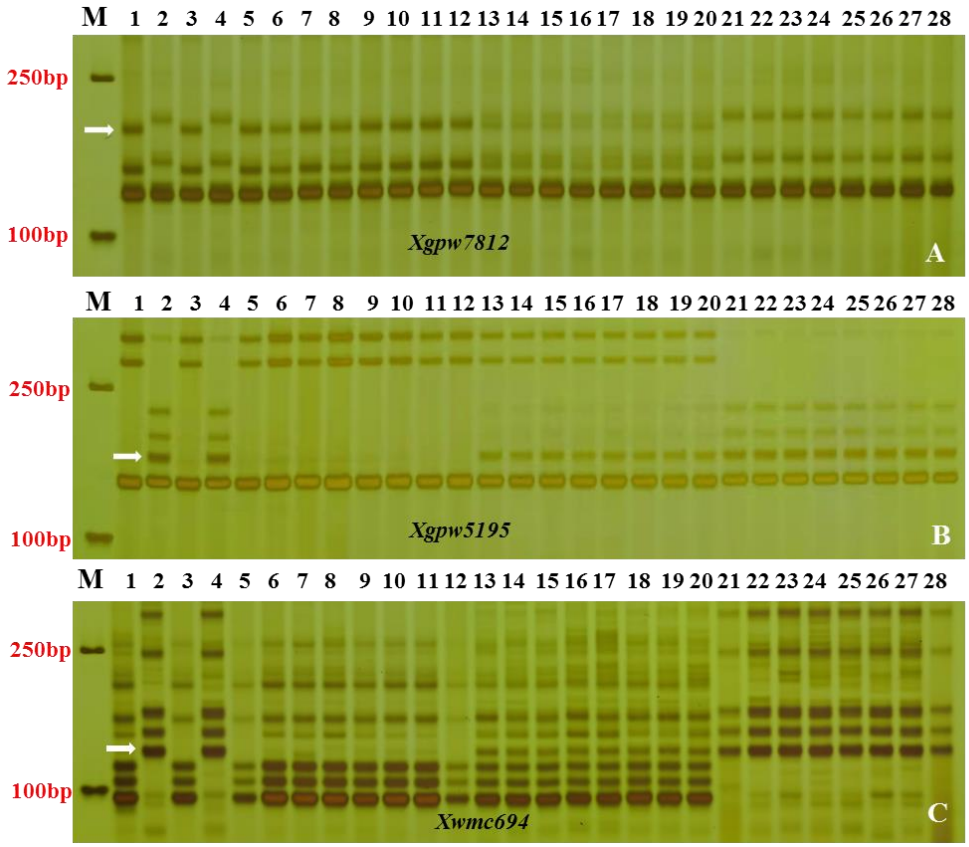

Figure 1. Amplification results of some individual plants in the F_2 population by SSR primers *Xgpw519*, *Xgpw7812*, and *Xwmc694* (**A**–**C**). (M) DL2000; (1) Changanhongmai; (2) SY225; (3) resistance pool; (4) susceptible pool; (5–12) resistant plants; (13–20); (21–28) susceptible plants. The arrow refers to the specific band.

3.3. Chromosomal Mapping and Genetic Linkage Map Construction

Additionally, a comparison between the bands of CS, CAHM, and CS nulli-tetrasomic lines revealed a significant absence of the chromosome 1B-specific bands in CS nulli-tetrasomic lines N1B-T1D, as indicated by the red arrow in Figure 2. The information of the eight pairs of SSR markers was queried in the Graingenes website, and the results also showed that these markers had loci on chromosome 1BS. Hence, nulli-tetrasomic and SSR analysis further revealed that *PmCAHM* was located on chromosome 1BS. The genetic distance was calculated by Joinmap4.0 software and the genetic linkage map was drawn by MapDraw v2.1. As shown in Figure 3, *PmCAHM* was located between the linkage markers *Xgpw7812* and *Xgpw5195*, and the genetic distance was 2.5 cM and 8.4 cM, respectively (Figure 3).

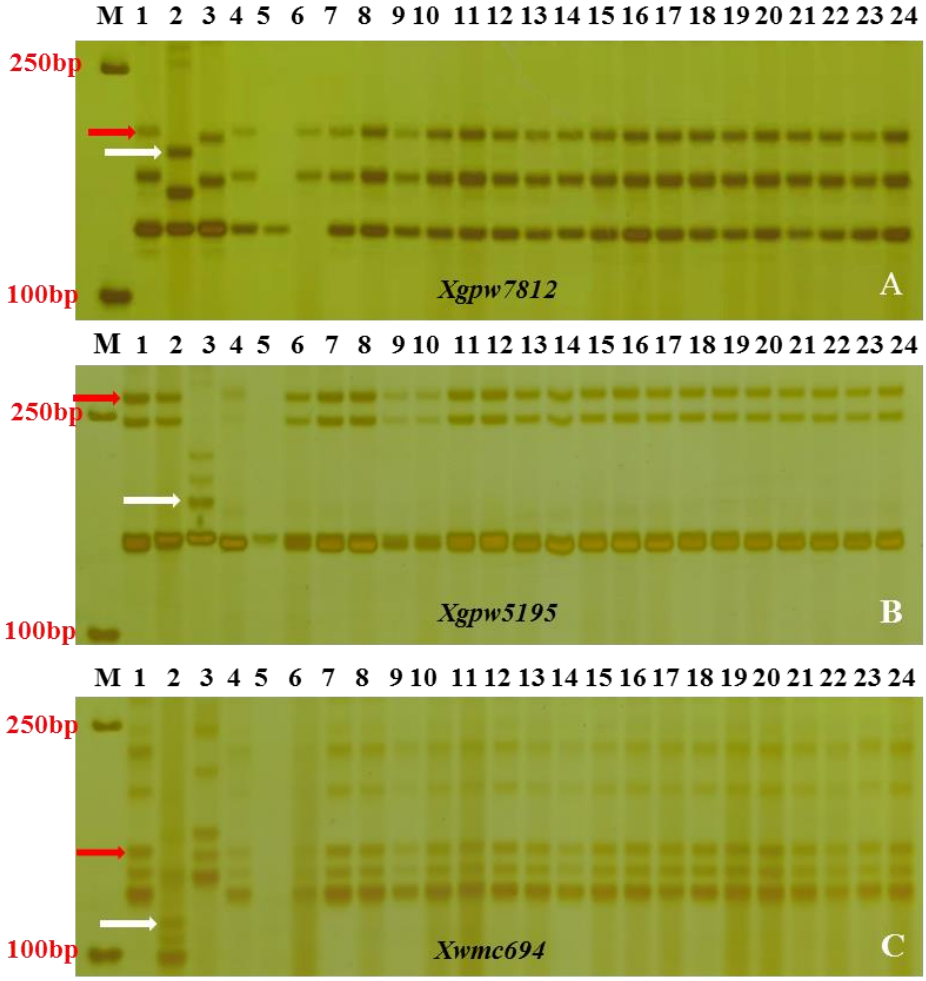

Figure 2. Nullisomic-tetrasomic analysis of Changanhongmai. The white arrows indicate bands specific for CAHM. The red arrows indicate bands specific for CS and the nullisomic-tetrasomic lines. (M) DL2000; (1) CS; (2) CAHM; (3) SY225; (4) CSN1AT1B; (5) CSN1BT1D; (6) CSN1DT1A; (7) CSN2AT2B; (8) CSN2BT2D; (9) CSN2DT2A; (10) CSN3AT3B; (11) CSN3BT3D; (12) CSN3DT3A; (13) CSN4AT4B; (14) CSN4BT4D; (15) CSN4DT4A; (16) CSN5AT5B; (17) CSN5BT5D; (18) CSN5DT5A; (19) CSN6AT6B; (20) CSN6BT6D; (21) CSN6DT6A; (22) CSN7AT7B; (23) CSN7BT7D; (24) CSN7DT7A. (**A**) *Xgpw7812*; (**B**) *Xgpw5195*; (**C**) *Xwmc694*.

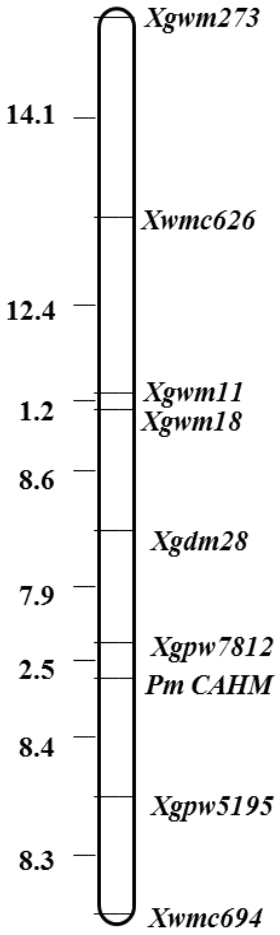

Figure 3. Genetic linkage map of *PmCAHM* and SSR markers on chromosome 1BS.

3.4. Breeding with PmCAHM

To investigate the application of CAHM in wheat improvement, we introduced its disease-resistance gene into the highly adaptable cultivar FY1718, resulting in the development of a new stable line, NW1848. The line was then verified by the amplification of specific markers (Figure 4b). According to the evaluation results of powdery mildew resistance, the recurrent parent FY1718 showed susceptibility to *Bgt* races, but NW1848 exhibited high resistance (Figure 4c). Hence, the *Pm* locus of CAHM had been successfully transferred into FY1718. These findings also confirm that this Pm locus has important contributions to powdery mildew resistance. We then investigated the agronomic traits of NW1848 and its recurrent parent (CAHM and FY1718) during the growing season. The biomorphology of NW1848 was similar to that of FY1718, with abundant tillers and vigorous growth. Moreover, NW1848 had a significantly longer average main spike length than CAHM (Figure 4a,d, Table 3).

Table 3. Biological traits of germplasms with the transfer of *PmCAHM* to common wheat.

Materials	TGW (g)	Plant Height (cm)	Spike Length (cm)	Spike Grain Number	Infection Type
Changanhongmai	45.0	120	8.5	42	0
FY1718	44.5	80	9.0	46	4
NW1748	45.9	95	9.2	46	0–1

Note: The data of biological traits are all averages.

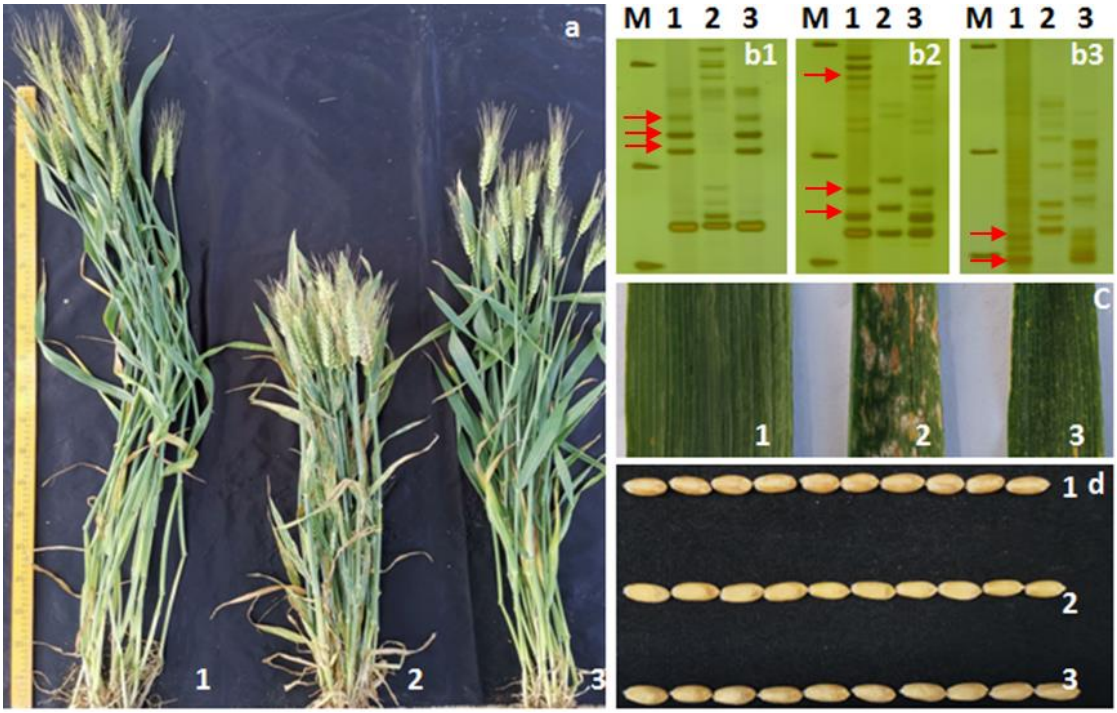

Figure 4. Evaluation of agronomic traits and powdery mildew resistance as well as molecular marker analysis. (**a**) Plants; (**b1**–**b3**) SSR marker amplification; (**c**) resistance reactions; (**d**) grain length. (1) CAHM; (2) FY1718; (3) NW1848. SSR marker (**b1**) *Xgpw5195*; (**b2**) *Xgpw7812*; (**b3**) *Xwmc694*. The red arrows indicate CAHM-specific bands.

4. Discussion

Since the discovery of the first gene that confers powdery mildew resistance gene to wheat, researchers have identified and mapped over 130 powdery mildew resistance genes in both wheat and related species. Currently, there are 69 officially named powdery mildew resistance genes (*Pm1*–*Pm69*), which are distributed across different chromosome loci [7]. *Pm* genes are present in different species and genera, including primary, secondary, and tertiary gene banks. In wheat, disease resistance genes of many ancestral and related species have been introduced, such as *Triticum Urartu*, the A genome donor [28]; *Ae. Speltoides*, the B genome donor [29]; and *Ae. Tauschii*, the D genome donor [30]. To date, a total of 31 *Pm* genes have been found in 22 loci of common wheat and local varieties, suggesting the possible presence of many more unknown *Pm* genes in common wheat and local varieties that remain to be discovered [26]. China has abundant wheat landraces, and the desirable traits can be readily transferred from landraces to some elite common wheat cultivars. So far, five genes that confer powdery mildew resistance have been identified in Chinese wheat landraces, including *Pm63* (PI628024) [31], *Pm61* (Xuxusanyuehuang) [15], *Pm59* (PI181356) [27], *Pm47* (Hongyanglazi) [26], *Pm24* (Chiyacao/Baihulu) [32,33], *Pm11* (Chinese spring) [34], *Pm5e* (Fuzhuang 30) [35,36], and *Pm2c* (Laomai) [37], which were mapped on chromosomal arms of 2BL, 4AL, 7Al, 7BS, 1DS, 6BS, 7BL, and 5DS, respectively. It has been reported that chromosome 1B contains three powdery mildew resistance genes, namely *Pm28*, *Pm32*, and *Pm39*, and their specific locations are chromosomal arms of 1B, T1BL.1SS, and 1BL, respectively [38–40]. The *Pm28* gene of Meri was mapped to chromosome 1B by Peusha et al. [41] through monosomic analysis, and *Pm32* was identified by Hsam et al. [37] through multiple identification of wheat-*Ae. parvum* translocation line L501. It was found that the resistance gene was located on 1BL.1SS. On the other hand, *Pm39* is a *Lr46/Yr29* locus on chromosome 1BL in the RIL population constructed by Saar and Avocet, which is officially named as *Pm39* [32]. In this study, we used the F_2 population to map *PmCAHM* on the chromosome 1BS. We then compared the gene loci and gene origin

with those officially named genes and found that *PmCAHM* is a new powdery mildew resistance gene due to its different chromosomal location on chromosome 1BS.

Full exploration and utilization of beneficial genetic resources in wheat local varieties and farm-grown varieties are of great significance for modern wheat disease-resistant breeding and genetic improvement. However, in actual wheat breeding, the utilization efficiency of local varieties is very low due to their inferior agronomic traits (such as low grain yield, lodging), long breeding time, and difficulty in breaking the genetic balance of unfavorable genes [40–43]. Most studies of powdery mildew resistance in local varieties are based on gene localization [44,45]. *Pm5e*, *Pm24*, *Pm47*, and *Pm61* are exclusively present in some specific Chinese wheat landraces. For example, *Pm24* is the only powdery mildew resistance locus known to be located on chromosome 1DS. *Xgwm789*/*Xgwm603* and *Xbarc229* are the markers flanking *Pm24a* at a distance of 2.4 and 3.6 cM, respectively, while *Pm24a* was also approximate to *Xgwm337* and co-segregated with *Xgwm1291*. Additionally, the genetic map of *Pm24b* was also constructed by the flanked markers *Xgwm337* and *Xbarc229* with genetic distances of 3.7 and 1.0 cM. Notably, Xue et al. tested the reactions of Pm24b to 23*Bgt* isolates and showed that Baihulu was clearly distinguishable from Chiyacao and varieties or lines possessing documented *Pm* genes. Allelism analysis indicated that *mlbhl* is a new gene, and was designated as *Pm24b*. Xiao et al. used SSR markers closely linked to the resistance gene for chromosome physical mapping, resulting in the mapping of *Pm47* in the 7BS-1-0.27-1.00 region at the end of the short arm of chromosome7B from Hongyanglazi [26]. Through molecular marker analysis, *Pm61* was localized on chromosome arm 4AL in a 0.46-cM genetic interval from Xuxusanyuehuang, and *Pm61* was assigned to a 1.3-Mb physical interval in the chromosome 4AL genomic sequence of Chinese Spring by physical mapping of the closest flanking markers *Xgwm160* and *Xicsx79* [15]. *Pm59* [27] and *Pm63* [31] can be exclusively found in some specific abroad wheat landraces. *Pm59* was characterized as a novel powdery mildew resistance gene in Afghanistan wheat landrace PI 181356, which was mapped to an interval between sequence tag site (STS) markers *Xmag1759* and *Xmag1714* with genetic distances of 0.4 cM distal to *Xmag1759* and 5.7 cM proximal to *Xmag1714* in the distal bin 7AL 0.99–1.00 of the long arm. *Pm59* confers resistance to *Bgt* isolates from the state of Montana and the Great Plains. *Pm63* was identified from the Iranian wheat landrace PI 628024 and mapped to the terminal region (710.3–723.4 Mb) of the long arm of chromosome 2B in Chinese Spring reference sequence. According to Bin mapping, *Pm63* was assigned to the terminal bin 2BL6-0.89-1.0, which is 1.1 cM proximal to STS marker *Xbcd135-2* and 0.6 cM distal to SSR marker *Xstars419*. Allelism tests have demonstrated the great application potential of *Pm63* to enhance powdery mildew resistance in the Great Plains, western, and southeastern regions of the USA. So far, the most successful transfer of landrace genes into common wheat is *PmXNM* [46], which was originated from the Chinese wheat landrace Xiaonanmai and located to a 300.7-kb interval with enrichment of resistance genes. Molecular mapping and bulked segregant analysis delimited *PmXNM* to the distalterminal region of chromosome 4AL, which is flanked by *caps213923* and *kasp511718* markers and comprises nine high-confidence genes according to the reference genome sequence of CS. There are seven candidate gene-specific markers proven to be effective for marker-assisted introgression of *PmXNM* into modern elite cultivars Bainong 207 and development of breeder-friendly molecular markers for its better utilization in wheat breeding.

Therefore, on the basis of genetic analysis, we transferred *PmCAHM* to common wheat FY1718 by molecular marker-assisted selection. The new germplasm line NW1848 showed elimination of the disadvantages of local varieties, and exhibited excellent characteristics of large grains, low plant height, and powdery mildew resistance. Hence, it can be used as a parent to breed new wheat varieties, and also help to greatly enrich and better utilize the wheat gene bank.

5. Conclusions

Our results indicate that CAHM harbors a pair of dominant powdery mildew resistance genes, which were tentatively designated as *PmCAHM*. Molecular marker and nullisomic–tetrasomic analysis demonstrated that *PmCAHM* is located on chromosome 1BS. We then constructed a genetic linkage map for *PmCAHM*. Among the analyzed markers, *Xgpw7812* and *Xgpw5195* were identified as the closest to each other and located on opposite sides of the gene. We compared these gene loci and gene origin with officially named genes. *PmCAHM* was identified as a newly discovered powdery mildew resistance gene located on chromosome 1BS. Identification of *PmCAHM* and transferring it to wheat cultivars by breeding may generate novel powdery mildew-resistant wheat varieties for commercial cultivation.

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