Genetic analysis of fertility restoring genes for AL-type male sterility in wheat

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Abstract: In order to screen molecular markers linked to fertility restoring genes and further improve the breeding efficiency of restorer lines, in this study, wheat varieties 18A, 18B and 99AR144-1 were used as experimental materials to establish F₂ fertility-segregating population. Plant quantitative trait “major gene + polygene mixed model” separation analysis method and simple sequence repeat (SSR) molecular markers were adopted for genetic analysis of four generations, including the parents (P₁ and P₂), and hybrid (F₁ and F₂) populations. The results show that AL-type fertility restoring gene is controlled by two pairs of additive-dominant-epistatic genes and additive-dominant polygene; two primers linked to fertility restoring genes were selected by SSR molecular markers, including Xgwm95 on chromosome 2A and Barc61 on chromosome 1B, with the linkage distance of 15.0 cM and 18.0 cM, respectively. Based on verification, these two markers are reliable for distinguishing AL-type wheat sterile lines and restorer lines.

Key words: wheat; cytoplasmic male sterility (CMS); restoring gene; genetic analysis; SSR molecular marker

1 Introduction

Utilization of heterosis is an effective way to improve wheat yield. Compared with two-line hybrid, three-line hybrid have greater application potential due to the low cost of seed production, high purity of hybrid seeds and other advantages. It has been reported that the creation of excellent new restorer sources is the most important issue for the breakthrough of application of three-line hybrids in wheat production.¹⁰⁰

At present, using molecular marker technology is an effective way to improve the efficiency of breeding. Molecular marker-assisted breeding has made relatively great progress in cotton, rice, maize and other crops;¹⁰⁻¹⁴ however, researches of fertility restoring gene markers of cytoplasmic male sterility (CMS) are mostly concentrated in T-type restorer lines. Ma and Sorrells¹⁵ carried out molecular mapping of restoring genes Rf/3 and Rf/4 in T-type restorer line R113 and found the molecular markers closely with them in 1B and 6BS. Guan Rongxia et al.¹⁷ analyzed hybrid F₂ fertility-segregating population of wheat T-type restorer line 2114 and sterile line ND44A by using inter simple sequence repeat (ISSR) markers, and selected two pairs of primers which were linked to restoring gene Rf₆, with the genetic distance of 7.9 cM and 4.9 cM, respectively. Kojima et al.¹⁸ carried out specific requirement fragment length polymorphism (RFLP) marking and positioning of restoring gene Rf/3 located on Triticum timopheevi chromosome by using near-isogenic lines of restoring gene Rf of T-type cytoplasmic male sterile lines, and reported that the genetic distance between Rf/3 in 1BS and the two markers Xcdo388 and Xabc156 was 1.2 cM and 2.6 cM, respectively. Zhang Cui et al.¹⁹ analyzed the F₂ population of T-type...
cytoplasmic male sterile line 75-3369 and restorer line 7269-10 by using simple sequence repeat (SSR) markers, and determined that the restorer line contained two major restoring genes which were linked to primers Xgwm136 and Xgwm550, with the genetic distance of 6.7 cM and 5.1 cM, respectively.

No research has been reported on molecular markers of AL-type fertility restoring genes. AL-type wheat male sterile line was bred by Wang Shijie et al from Henan Institute of Education with plump seeds and high germination rate, which could be maintained by common wheat varieties and was easily adopted to select restoring gene resources. For instance, the wheat male sterile line could be maintained by more than 90% of common wheat varieties and showed 100 % sterile degree and sterile rate of sterile lines bred by continuous backcrossing, and the sterility remained stable under climate conditions in different years. Based on the important application value of AL-type wheat and the excellent application potential of molecular markers for restorer line breeding, it is necessary to carry out researches on molecular mar-kers of AL-type wheat restoring gene.

In this study, by using the quantitative genetic model separation analysis method proposed by Zhang Yuanming et al \(^{[10]}\) and SSR molecular marker technology, genetic analysis and molecular marker investigation of the major restoring genes of AL-type wheat cytoplasmic male sterile line 18A and restorer line 99AR144-1 were carried out, in order to screen the molecular markers linked to fertility restoring genes, which laid application foundation for the molecular marker-assisted breeding of AL-type wheat restoring genes.

2 Materials and methods

2.1 Materials

2.1.1 Breeding of wheat sterile line 18A, maintainer line 18B and restorer line 99AR144-1

Wheat sterile line 18A is a stable AL-type wheat cytoplasmic male sterile line bred by continuous backcrossing with 781A (introduced from Henan Institute of Science and Technology) as female parent and common wheat (\(T. aestivum\)) Xindong 18 as male parent.

Restorer line 99AR144-1 is a hybrid bred with the first backcross generation of 781A and 305-2 (an advanced wheat line bred in Wheat Research Center, Institute of Crop Research, Xinjiang Academy of Agricultural Reclamation Science) as female parent (still complete sterile) and 91TR2 (a restorer line introduced from Henan Institute of Science and Technology) as male parent. Individual wheat plants with high pollination and excellent agronomic traits were continuously selected for selfing; test cross of sterile line and F1 was carried out during selfing. Restorer line 99AR144-1 with high restoring force was selected, and single spike method was adopted for breeding and purifying.

2.1.2 Verification materials

The materials used in molecular marker verification experiment were stable sterile lines and restorer lines randomly selected from Wheat Research Center, Institute of Crop Research, Xinjiang Academy of Agricultural Reclamation Science, and the restorer line showed high recovery rate for AL-type sterile lines. Sterile lines were Shi 98-7138A, 503 You A, Xindong 18A, Xindong 20A, Xindong 22A, Jinan 17A, Fengshou A, Lankao 906A, 3235A and 4394A; the restorer lines were 07AR55, 08AR26, 07 AR83, 07AR64 and 07AR60.

2.2 Methods

2.2.1 Survey of seed setting rate

Experimental materials were planted in the experimental field of Institute of Crop Research in Xinjiang Academy of Agricultural Reclamation Science in 2008. A randomized block design was adopted. The plot length was 1.8 m, spacing was 0.2 m, and 20 seeds were artificially sown in each line with two replications. When the small spikelets generated 1.5 cm, the main stem ear was selected, bagged artificially, marked and recorded. After mature, the wheat was harvested for indoor seed determination.

Domestic method: Selfed seed setting rate (%) = Bearing number of base flowers in both sides of effective spikelets/(Effective spikelet number of each spike × 2) × 100 %

2.2.2 Genetic model analysis

Plant quantitative trait "major gene + polygene mixed model" analysis method proposed by Zhang Yuanming et al \(^{[10]}\) was adopted to analyze the fertility of F2 population. There were a total of 24 conjoint analysis genetic models of P1, P2, F1 and F2 populations, which were divided into five types, including one pair of major gene models, two pairs of major gene models, polygene type, one pair of major gene + polygene types, and two pairs of major gene + polygene types. According to maximum likelihood value (MLV) and intertated expectation and conditional maximization (IECM) algorithm, the distribu-
tion parameters of related ingredients in the mixture distribution were estimated. The optimal genetic model was selected based on Akaike’s information criterion (AIC) determination and suitability test, and the effect value, variance and other genetic parameters of major genes and polygene were estimated. 

2.2.3 DNA extraction (phenol-chloroform extraction method)

Wheat genomic DNA was extracted from samples by using modified cetyl trimethyl ammonium bromide (CTAB) method [19]. Leaves of seven-day-old seedling of parental lines and derivatives cultured in petri dishes in the dark were collected and grinded into particles in plastic tubes after being frozen in liquid nitrogen. SSR markers published on GrainDB database which evenly distributed over 21 wheat chromosomes, were applied to investigate polymorphisms among parental lines, AL18A and 99AR144-1.

2.2.4 Detection of polymerase chain reaction (PCR) products

PCR amplification product was detected by using non-denaturing polyacrylamide gel electrophoresis for 80~100 min (dependent on the molecular weight of primers), the gel concentration was 8~10%, gel size was 180 mm × 120 mm × 2 mm, electrophoresis buffer was 0.5 × tris boric acid (TBE), and the constant voltage was 160 V. DYY-12 electrophoresis apparatus (Beijing Liuyi Instrument Factory) was adopted.

The total PCR amplification reaction system was 10 μL, containing 5.11 μL of ddH2O, 1.3 μL of 10× PCR buffer, 0.26 μL of deoxy-ribonucleoside triphosphate (dNTP), 10 mmol/L MgCl2, 0.13 μL of Taq polymerase, 0.6 μL of upper and downstream primers, and 1 μL of DNA template.

PCR amplification started with initial denaturation at 95 °C for 3 min, followed by 40 cycles of denaturation at 95 °C for 1 min, annealing at 56 °C for 1 min, and extension at 72 °C for 2 min. The amplification was completed by holding the reaction mixture at 72 °C for 10 min to allow complete extension of PCR products. PCR products were stored at 4 °C.

2.2.5 Construction of genetic linkage map

Based on bulked segregant analysis (BSA) [12], 10 highly fertile lines were selected to construct fertile pool F, and 10 completely sterile lines were selected to construct sterile pool S, in order to mark polymorphism screening. Polymorphic markers were selected from highly fertile and completely sterile pools which had consistent differences with fertile parents and sterile parents. F2 population was amplified, and the band forms of various F2 individuals were recorded. Joinmap3.0 mapping software was adopted for genetic linkage analysis of experimental data, and the minimum limit of detection (LOD) was set as 3.0. According to the calculated "LOD groupings (tree), " create groups for mapping " in "population" menu was run. Calculate map was adopted for mapping in the created groups, to obtain the linkage genetic distance.

3 Results and analysis

3.1 Genetic analysis

3.1.1 Genetic characteristics of AL-type wheat CMS fertility restoring genes

AL-type wheat cytoplasmic male sterile line AL18A and restorer line 99AR144-1 were hybridized, to construct 502 F1 segregating plants, which were bagged before blossom pollination for selfing, and the seed setting rate of individual plants was counted. The survey results were shown in Table 1. Fertility heredity was preliminarily analyzed by using chi-square (χ2) test, to divide separation zones based on F1 segregation, thus investigating whether it is consistent with Mendelian ratio to determine the number of genes. Sterile and fertile plants were distinguished using 0 as the boundary for fertility statistics and analysis. Suitability test was carried out for investigating the fertility segregation ratio, \( \chi^2 = \sum | \text{Actual number} - \text{Expected number} | - 0.5^2/\text{Expected number} \). There were 475 fertile plants and 37 sterile plants in F1 population. According to the result of chi-square test (χ2 = 0.89 < χ20.01, 1 = 3.84), the number of fertile and sterile individual plants was consistent with the theoretical separation ratio of 15:1.

3.1.2 Conjoint genetic models of four generations

By using plant quantitative trait "major gene + polygene mixed model" analysis method proposed by Zhang Yuanming et al. [18], conjoint analysis of four constructed generations AL18A (P1), 99AR144-1 (P2), F1, and F2 was conducted. Results showed that (Table 2), among the 24 genetic models, three genetic models showed the minimum AIC value including E-1 (mixed genetic model of two pairs of additive-dominant-epistatic major genes + additive-dominant polygene), E-0 (mixed genetic model of two pairs of additive-dominant-epistatic major genes + additive-dominant-epistatic polygene) and B-1 (genetic model
of two pairs of additive-dominant-epistatic major genes). Therefore these three models might be more suitable and were selected as alternative models. Suitability test \((U_1^2, U_2^2, U_3^2, nW^2, D_3)\) was conducted with the above three alternative models B-1, E-0 and E-1, and the model with relatively less plants reaching significant levels of statistics was selected as the optimal model \([13]\).

### Table 1 Investigation of plant fertility of different parents

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Total plants</th>
<th>Fertile plants</th>
<th>Sterile plants</th>
<th>Domestic method (DM) %</th>
<th>Seed setting rate of the bagged panicles</th>
<th>Seed setting rate of the open panicles</th>
</tr>
</thead>
<tbody>
<tr>
<td>AL18A</td>
<td>50</td>
<td>0</td>
<td>50</td>
<td></td>
<td>0</td>
<td>39.57±33.81</td>
</tr>
<tr>
<td>AL18B</td>
<td>103</td>
<td>103</td>
<td>0</td>
<td>90.13±8.57</td>
<td>92.18±2.63</td>
<td></td>
</tr>
<tr>
<td>99AR144-1</td>
<td>48</td>
<td>48</td>
<td>0</td>
<td>92.19±2.73</td>
<td>92.56±5.15</td>
<td></td>
</tr>
<tr>
<td>(AL18A×99AR144-1)F&lt;sub&gt;1&lt;/sub&gt;</td>
<td>124</td>
<td>124</td>
<td>0</td>
<td>85.16±7.98</td>
<td>88.37±4.52</td>
<td></td>
</tr>
<tr>
<td>(AL18A×99AR144-1)F&lt;sub&gt;I&lt;/sub&gt;</td>
<td>502</td>
<td>475</td>
<td>37</td>
<td>64.89±26.76</td>
<td>82.44±5.8</td>
<td></td>
</tr>
<tr>
<td>F&lt;sub&gt;i&lt;/sub&gt; coefficient of variability, CV (%)</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>41.24</td>
<td>7.04</td>
<td></td>
</tr>
</tbody>
</table>

### Table 2 Values of the maximum likelihood function and AIC values obtained by using IECM algorithm

<table>
<thead>
<tr>
<th>Model</th>
<th>MLV</th>
<th>AIC</th>
<th>Model</th>
<th>MLV</th>
<th>AIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>A-1</td>
<td>12.750</td>
<td>717</td>
<td>D-0</td>
<td>31.095</td>
<td>661</td>
</tr>
<tr>
<td>A-2</td>
<td>−46.814</td>
<td>262</td>
<td>D-1</td>
<td>12.975</td>
<td>680</td>
</tr>
<tr>
<td>A-3</td>
<td>−44.004</td>
<td>074</td>
<td>D-2</td>
<td>−36.139</td>
<td>557</td>
</tr>
<tr>
<td>A-4</td>
<td>−65.190</td>
<td>163</td>
<td>D-3</td>
<td>12.975</td>
<td>683</td>
</tr>
<tr>
<td>B-1</td>
<td>56.411</td>
<td>392</td>
<td>D-4</td>
<td>−36.138</td>
<td>779</td>
</tr>
<tr>
<td>B-2</td>
<td>12.888</td>
<td>06</td>
<td>E-0</td>
<td>47.379</td>
<td>391</td>
</tr>
<tr>
<td>B-3</td>
<td>−45.105</td>
<td>278</td>
<td>E-1</td>
<td>58.027</td>
<td>176</td>
</tr>
<tr>
<td>B-4</td>
<td>−45.103</td>
<td>809</td>
<td>E-2</td>
<td>12.974</td>
<td>786</td>
</tr>
<tr>
<td>B-5</td>
<td>12.673</td>
<td>772</td>
<td>E-3</td>
<td>−36.149</td>
<td>216</td>
</tr>
<tr>
<td>B-6</td>
<td>0.165</td>
<td>223</td>
<td>E-4</td>
<td>−36.148</td>
<td>422</td>
</tr>
<tr>
<td>C-0</td>
<td>−27.882</td>
<td>412</td>
<td>E-5</td>
<td>11.906</td>
<td>598</td>
</tr>
<tr>
<td></td>
<td>67.764</td>
<td>824</td>
<td></td>
<td></td>
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</table>

According to the results (Table 3), the minimum number of significant deviation in E-0 and E-1 was both 4. To be specific, AIC value of E-1 model was minimum; therefore E-1 was the optimal model, indicating that the heredity of fertility restoring genes for AL-type CMS in wheat was consistent with E-1 model and was controlled by two pairs of additive-dominant-epistatic major genes + additive-dominant poly-gene, which was consistent with the results proposed by Cui Fengjian et al \([13]\).

### 3.2 Construction of genetic linkage map

#### 3.2.1 SSR molecular marker screening and genetic linkage analysis of AL-type wheat fertility restoring genes

In this study, SSR primer sequence information provided by Röder et al \([14]\) and Song et al \([15, 16]\) was used, 1 465 pairs of primers distributed on 21 chromosomes of wheat were selected using AL18A and 99AR144-1 as the template, and 149 pairs of polymorphic primers were obtained from fertile and sterile parents by PCR amplification. Polymorphism screening of the above 149 pairs of SSR primers between highly fertile pool and completely sterile pool was carried out, and results showed that three pairs of primers showed the same and stable polymorphism between two pools and two parents, including Xgwm95, Barc10 located on chromosome 2A, and Barc61 located on chromosome 1B.

Xgwm95, Barc10 and Barc61 were adopted for amplification of F<sub>2</sub> populations and the band forms of various F<sub>2</sub> individuals were recorded (Fig.1 and Fig.2). Based on PCR amplification and genetic linkage analysis with Joinmap3.0 mapping software, analysis results showed that Barc10 was not linked to...
AL-type fertility restoring gene, the genetic distance between Xgwm95 and AL-type fertility restoring gene was 15.0 cM (Fig.3), and that between Barc61 and AL-type fertility restoring gene was 18.0 cM (Fig.4).

Table 3 Suitability test of B-1, E-0 and E-1 model

<table>
<thead>
<tr>
<th>Model</th>
<th>Generation</th>
<th>U_1</th>
<th>U_2</th>
<th>U_3</th>
<th>nW</th>
<th>D_1</th>
</tr>
</thead>
<tbody>
<tr>
<td>B-1</td>
<td>P_1</td>
<td>2.056(0.151 6)</td>
<td>1.108(0.292 4)</td>
<td>1.803(0.179 3)</td>
<td>0.427 (6 &gt; 0.05)</td>
<td>0.339 (6 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_2</td>
<td>0.722(0.395 5)</td>
<td>0.030(0.863 2)</td>
<td>6.768(0.009 3)</td>
<td>0.380 (5 &lt; 0.05)</td>
<td>0.196 (8 &gt; 0.05)</td>
</tr>
<tr>
<td>E(E-0)</td>
<td>P_3</td>
<td>1.725(0.189 1)</td>
<td>0.011(0.917 2)</td>
<td>21.813(0.000 0)</td>
<td>0.534 (2 &lt; 0.05)</td>
<td>0.387 (2 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_4</td>
<td>0.003(0.955 3)</td>
<td>0.014(0.906 9)</td>
<td>0.065(0.802 2)</td>
<td>0.112 (2 &lt; 0.05)</td>
<td>0.040 (8 &gt; 0.05)</td>
</tr>
<tr>
<td>E-1</td>
<td>P_5</td>
<td>0.024(0.877 9)</td>
<td>0.192(0.661 1)</td>
<td>5.517(0.018 8)</td>
<td>0.250 (6 &lt; 0.05)</td>
<td>0.273 (3 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_6</td>
<td>0.052(0.819 9)</td>
<td>0.320(0.571 8)</td>
<td>9.878(0.001 7)</td>
<td>0.367 (6 &lt; 0.05)</td>
<td>0.179 (2 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_7</td>
<td>1.255(0.262 6)</td>
<td>0.000(0.996 0)</td>
<td>18.654(0.000 0)</td>
<td>0.446 (1 &lt; 0.05)</td>
<td>0.346 (3 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_8</td>
<td>0.045(0.832 1)</td>
<td>0.191(0.661 7)</td>
<td>0.863(0.352 9)</td>
<td>0.162 (0 &lt; 0.05)</td>
<td>0.043 (5 &lt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_9</td>
<td>0.079(0.778 1)</td>
<td>0.097(0.755 2)</td>
<td>5.473(0.019 3)</td>
<td>0.261 (6 &lt; 0.05)</td>
<td>0.266 (0 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_10</td>
<td>0.145(0.702 9)</td>
<td>0.179(0.672 5)</td>
<td>10.037(0.001 5)</td>
<td>0.391 (1 &lt; 0.05)</td>
<td>0.184 (1 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_11</td>
<td>1.255(0.288 9)</td>
<td>0.001(0.976 9)</td>
<td>17.833(0.000 0)</td>
<td>0.422 (2 &lt; 0.05)</td>
<td>0.336 (0 &gt; 0.05)</td>
</tr>
<tr>
<td></td>
<td>P_12</td>
<td>0.022(0.880 9)</td>
<td>0.144(0.704 1)</td>
<td>0.881(0.348 0)</td>
<td>0.171 (0 &gt; 0.05)</td>
<td>0.044 (0 &gt; 0.05)</td>
</tr>
</tbody>
</table>

Note: '—significant difference at P < 0.05

Fig.1 PCR amplification results by SSR primer Xgwm95 between parents and F_1 populations
Note: M—marker; AR—restorer line of 99AR144-1; A—sterile line of AL18A; 1—9—F_1 populations of AL18A×99AR144-1 (1 and 7 are not sterile band forms; 2, 4, 8 and 9 are fertile band forms; 3, 5 and 6 are hybrid fertile band forms)

Fig.2 PCR amplification results by SSR primer Barc61 between parents and F_1 populations
Note: AR—restorer line; A—sterile line; 1—14—F_1 populations

3.2.2 Reliability verification of markers Xgwm95 and Barc61
Xgwm95 and Barc61 were respectively adopted for verification of experimental materials. The results showed that amplification of sterile lines using Xgwm95 showed no fertile target band Xgwm95. Specific marker linked to fertility restoring gene was only amplified from restorer line 07AR64, indicating that restorer lines 99AR144-1 and 07AR64 might have the same fertility restoring gene on chromosome 2A, while 07AR55, 08AR26, 07AR83 and 07AR60 had no fertility restoring gene linked to Xgwm95. Amplification of sterile lines using Barc61 showed sterile band forms except Lankao 906A. Specific marker linked to fertility restoring gene was amplified from all the restorer lines except 07AR60, indicating that restorer lines 07AR55, 08AR26, 07AR83 and 07AR64 contained fertility restoring gene linked to Barc61, while no fertility restoring gene linked to

Fig.3 Genetic linkage map of Xgwm95 linked to restoring gene in AL-type wheat

Fig.4 Genetic linkage map of Barc61 linked to restoring gene in AL-type wheat
Barc61 was found in 07AR60. Markers Xgwm95 and Barc61 were adopted to distinguish AL-type wheat sterile lines and fertile lines, and showed reliable results (Fig.5 and Fig.6).

![Fig.5 Reliability verification of SSR primer Xgwm95](image)

**Note:** Marker 1—D2000 ladder; 1—Shi 98-7138A; 2—503 You A; 3—Xindong 20A; 4—Jinan 17A; 5—Xindong 22A; 6—Xindong 18A; 7—Fengshou A; 8—Lanka 906A; 9—3235A; 10—4394A; 11～15 stable restorer lines 11.07AR55, 12.08AR26, 13.07AR83, 14.07AR64 and 15.07AR60. The same number as below represents the same cultivars

![Fig.6 Reliability verification of SSR primer Barc61](image)

**Note:** AR—99AR144-1; A—AL18A

4 Conclusions

Fertility traits of AL18A×99AR144-1 combination are controlled by two pairs of additive-dominant-epistatic major genes + additive-dominant polygene. In China, many researches have been carried out on the fertility genetic law of CMS in other wheat varieties. Li Hongxia et al [17] reported that the fertility of glutinous wheat cytoplasmic male sterile lines was controlled by one pair of major restoring genes and several pairs of minor genes. Lu Liangfeng et al [18] reported that the restore of K-CMS in wheat was controlled by three pairs of major restoring genes. Guan Rongxia et al [7] reported that the restore of T-CMS in wheat was controlled by one pair of major restoring genes. These results are different from the fertility restoring gene of AL-type sterile system in this study. It can be seen that the genetic traits of fertility restoring genes for different types of male sterility in wheat vary. Therefore, during the application of hybrid breeding, different types of sterile systems should be selected based on different purposes.

There are two SSR molecular markers linked to two pairs of major restoring genes of AL-type wheat sterile lines, including Xgwm95 on chromosome 2A and Barc61 on chromosome 1B, with the linkage distance of 15.0 cM and 18.0 cM, respectively. In this study, among the five stable restorer lines for restoring AL-type sterile lines, only one material (07AR64) can amplify target band using primer Xgwm95, which might be due to that only 07AR64 contains the restoring gene linked to Xgwm95 of AL-type restorer lines. Based on verification test with 10 stable sterile lines, one material (Lanka 906A) can amplify target fertile band using primer Barc61.

Liu Baoshen et al [19] conducted SSR analysis of K-type restorer lines and found that the genetic distance between fertility restoring gene of restorer line LK783 and SSR markers Xgwm11, Xgwm118 and Xgwm 273 was (6.54±4.37) cM, and that between fertility restoring gene of LK783 and SSR marker Xgwm264a was (5.71±4.10) cM. By using nullisomic-tetrasomic lines and double-end system, these four SSR loci were located on 1BS, and the relative location of the restoring gene on 1BS was different from the locus of rvl gene [20], indicating that it was another restoring gene on 1BS for K-type sterile lines. In previous experiments, T-type restorer lines can be used to restore AL-type sterile lines, indicating that AL-type sterile lines have at least one pair of restoring genes with the same or similar function as T-type restorer lines. However, the results of this study reveal that the AL-type wheat restoring gene linked to Barc61 is not located on the same locus as T-type restoring gene [21]. In conclusion, chromosome 1BS contains many cytoplasmic types of restoring genes, which indicates that restoring genes might be distributed in clusters. Therefore, carrying out intensive study on fertility restoring genes for CMS in wheat may provide useful inspiration from the perspective of origin.

References


Author
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