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The qPCR and loop mediated isothermal amplification for rapid detection of *Ustilago tritici*

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Wheat loose smut caused by *Ustilago tritici* a seed-borne disease, is difficult to control due to the expansion of wheat planting area and difficulty of pathogen detection. In this study, real-time fluorescence quantitative PCR (qPCR) and loop-mediated isothermal amplification (LAMP) assays were used to rapidly amplify the DNA of *U. tritici*. Five pairs primers for qPCR and two series primers for LAMP were designed. Firstly, the specificity of primers were carried out by using the DNAs of *U. tritici*, *Fusarium graminearum*, *Blumeria graminis*, *Rhizoctonia cerealis*, *Puccinia striiformis*, *Bipolaris sorokiniana*, and *Alternaria solani* as templates. Then the amplification systems are optimized. Finally, the sensitivity of qPCR and LAMP assays were quantified. The results show that using the primers pairs Y430F/R, Y307F/R, Y755F/R and Y139F/R for qPCR, primers L-139 and L-988 for LAMP assay could be used for *U. tritici* detection. In the sensitivity test, the detection limit of qPCR assay is 10 pg μL^{-1} of genomic DNA, the detection limit of LAMP assay is 100 fg μL^{-1} . We successfully performed qPCR and LAMP assays on two wheat loose smut wheat samples, and confirmed sequenced *U. tritici* infection by subsequently sequencing. This paper established two methods for *U. tritici* detection, which could be used for wheat loose smut diagnose in lab and field.

1 **The qPCR and loop mediated isothermal amplification for rapid detection of *Ustilago tritici***

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17 ABSTRACT

18 Wheat loose smut caused by *Ustilago tritici* a seed-borne disease, is difficult to control due to the expansion of
19 wheat planting area and difficulty of pathogen detection. In this study, real-time fluorescence quantitative PCR
20 (qPCR) and loop-mediated isothermal amplification (LAMP) assays were used to rapidly amplify the DNA of
21 *U. tritici*. Five pairs primers for qPCR and two series primers for LAMP were designed. Firstly, the specificity of
22 primers were carried out by using the DNAs of *U. tritici*, *Fusarium graminearum*, *Blumeria graminis*,
23 *Rhizoctonia cerealis*, *Puccinia striiformis*, *Bipolaris sorokiniana*, and *Alternaria solani* as templates. Then the
24 amplification systems are optimized. Finally, the sensitivity of qPCR and LAMP assays were quantified. The
25 results show that using the primers pairs Y430F/R, Y307F/R, Y755F/R and Y139F/R for qPCR, primers L-139
26 and L-988 for LAMP assay could be used for *U. tritici* detection. In the sensitivity test, the detection limit of
27 qPCR assay is 10 pg μL^{-1} of genomic DNA, the detection limit of LAMP assay is 100 fg μL^{-1} . We successfully
28 performed qPCR and LAMP assays on two wheat loose smut wheat samples, and confirmed sequenced *U.*
29 *tritici* infection by subsequently sequencing. This paper established two methods for *U. tritici* detection, which
30 could be used for wheat loose smut diagnose in lab and field.

31 **Subjects** Molecular biology, Biological detection

32 **Keywords** LAMP, qPCR, *Ustilago tritici*, wheat loose smut

33 INTRODUCTION

34 Wheat is one of the most important food crops in the world, and it is also the staple food for most of the
35 world's population (Garg et al., 2014). Its global planting area is as high as 220 107 600 hectares (Zhao et al.,
36 2018). With the popularization of wheat planting area and the immaturity of seed detection technology, the
37 damage of wheat loose smut has become more serious, and it has gradually become one of the most important
38 diseases in wheat field (Knox & Menzies, 2012).

39 At present, the most effective control method of wheat loose smut disease is seed dressing sterilization
40 before seeding (Singh et al., 2014; Duan et al., 2016). There are no suitable and effective control measures after
41 sowing. The long-term use of chemical agents can easily pollute the environment, endanger the health of
42 humans and livestock, and a large number of single used can easily lead to the emergence of drug resistance
43 (Crane et al., 2013). Therefore, the detection of pathogen *Ustilago tritici* is very necessary. The original
44 detection method of *U. tritici* is serological identification, but it is time-consuming and can only be concluded
45 by professional. Meanwhile, its accuracy and sensitivity are not satisfactory (Walcott, 2003; Munkvold, 2009).
46 Now, the common detection method for wheat loose smut is PCR (Martínez-Espinoza et al., 2003). However,
47 the PCR cannot perform accurate quantitative analysis, and cross-contamination can easily cause false positive
48 (Bretagne, 2003). Quantitative PCR (qPCR) has quickly become a hotspot in scientific research and clinical
49 diagnosis (Kuypers et al., 2006; Yan et al., 2012). At the same time, there are some shortcomings of it, such as
50 the expensive instruments, the need for professional personnel operation, poor practicality. Notomi et al. (2000)
51 invented a novel method for rapid, efficient, and highly specific amplification of target DNA-loop mediated
52 isothermal amplification (LAMP). The principle of the experiment is to design four different primers (F3, B3,
53 FIP, BIP) for six different positions of the target sequence (F3C, F2C, F1C, B1, B2, B3) (Tomita et al., 2008;
54 Notomi et al., 2015), under the action of *Bst* DNA polymerase, the water bath instead of the PCR instrument,
55 the reaction is performed at 60-65 °C for 60-90 min and the target DNA is amplified 10^9 - 10^{10} times (Dhama et
56 al., 2014). Compared to PCR, the LAMP assay shortens the reaction time, eliminates the gel electrophoresis,
57 does not require expensive PCR instruments, and completes the experiment with the *Bst* DNA polymerase and
58 reaction under constant temperature conditions. The reaction results are determined by the color reaction of
59 fluorescent dyes. Currently, the fluorescent dyes are calcein (Rane et al., 2015), PicoGreen (Curtis, Rudolph &
60 Owen, 2008), hydroxy naphthol blue (HNB) (Goto et al., 2010; Mohon et al., 2014), SYBR Green (Balne et al.,

61 2013; Zhou et al., 2014), etc. SYBR Green I and HNB have the highest detection sensitivity between them,
62 which is 10 times of calcein (Gao et al., 2009). And HNB and SYBR Green I can produce long-term stable
63 color changes and brightness in closed pipes and prevent cross-contamination (Almasi et al., 2013).
64 Meanwhile, its high affinity with double-stranded DNA makes it one of the most commonly used fluorescent
65 dyes. In this study, SYBR Green I was used in both qPCR assay and LAMP assay. However, it can bind to both
66 specific and non-specific products so that the specificity of the primers should be further identified. Therefore,
67 in qPCR assay, an extra melting curves were performed to identify the specificity of the primers. And in LAMP
68 assay, the primers were screened by PCR to determine whether the primers form dimers, and the control
69 bacteria DNA were used to determine the specificity of the primers. The combination of LAMP and fluorescent
70 dyes makes biodetection simpler and more intuitive. At present, LAMP technology and qPCR has been used in
71 many bacteria, fungi, viruses and other aspects detection, such as *Verticillium albo-atrum* (Tian et al., 2016),
72 *Listeria monocytogenes* strains (Wang et al., 2012), parasites (Abdul-Ghani, Al-Mekhlafi & Karanis, 2012),
73 *Candidatus Liberibacter asiaticus* (Rigano et al., 2014), etc. Now there have been reports on the detection of
74 *Rhizoctonia cerealis* (Sun et al., 2015), *Tilletia controversa* Kühn (Nian et al., 2009) by qPCR assays. And the
75 detection of Fusarium head blight (Niessen & Vogel, 2010), wheat stripe rust (Huang et al., 2011) by LAMP
76 assays. However, the detection of wheat loose smut by two methods has not been reported. In this study, we
77 used qPCR and LAMP assays to rapidly detect wheat loose smut.

78

79 **MATERIALS AND METHODS**

80 **Materials**

81 **Bacterial strain.**

82 *Ustilago tritici*, *Fusarium graminearum*, *Blumeria graminis*, *Rhizoctonia cerealis*, *Puccinia striiformis*,
83 *Bipolaris sorokiniana*, *Alternaria solani*.

84 **Culture environment.**

85 The wheat variety used in the experiment is Mingxian169. After germination for 24 h in dark conditions, the
86 seeds were planted in a pot and placed in a light incubator at 22 °C, 12 h days and 18 °C, 12 h night. *U. tritici*
87 were collected from the diseased wheat ears. Wheat powdery mildew were derived from diseased leaves. *F.*
88 *graminearum*, *R. cerealis*, *B. sorokiniana*, *A. solani* were inoculated on the PDA mediums covered with glass
89 paper, and cultured at 25 °C for 7 to 8 days. *P. striiformis* was collected in the experimental field.

90 **Genomic DNA extraction.**

91 DNA was extracted from wheat loose smut by modified CTAB. Briefly, lysis buffer (10 mM Tris-HCl [pH 8.0],
92 100 mM EDTA, 0.5% sodium dodecyl sulfate and 100 µg mL⁻¹ proteinase) was added to the sample, followed
93 by a water bath at 55 °C for 1 h. The DNA was extracted with phenol-chloroform-isoamyl alcohol (25:24:1),
94 precipitated with isopropanol and washed with ethanol (70%). After centrifugation, 30 µL of ddH₂O was added
95 and stored at -20 °C.

96 **Methods**

97 **The qPCR and Lamp primer design.**

98 Primers (Table 1) were designed by Primer Premier 5.0 according to the sequences of *U. tritici*
99 sequences published in NCBI. We selected the AJ236139.1, DQ132988.1 nucleic acid sequence for
100 LAMP assay, and designed primers for AJ236139.1 and DQ132988.1 by Primer Explorer V5
101 (<http://primerexplorer.jp/lampv5e/index.html>) (Table 2). The primers were synthesized by BGI, and
102 dissolved in ddH₂O, stored at -20 °C.

103 **QPCR assays**

104 **Specificity of qPCR assays.**

105 DNA of *U. tritici* are used as template for primers specific detection, the amplification condition is 95 °C for 3
106 min, 95 °C for 30 s, 52 °C for 30 s, 72 °C for 40 s, 34 cycles, 72 °C for 5 min, preservation at 16 °C. The
107 amplification products are detected by 1% agarose gel electrophoresis and then sequenced (Fig. 1). Based on
108 the preliminary screening results, primers are further screened by qPCR using the control strains as templates,
109 and then determined whether the primers were specific by the Ct value reflected with the amplification curves
110 (Fig. 2).

111 **Optimization of qPCR assays.**

112 Appropriate ratios have an impact on the accuracy of the results of qPCR so that system optimization is
113 indispensable for it. System Optimization experiment was performed on the volume of ChamQ™ SYBR qPCR
114 Master Mix with 4 µL, 6 µL, 8 µL, 10 µL, 12 µL, 14 µL and 16 µL volume gradient for qPCR assays (Fig. 3).
115 After demonstrating the optimum system ratio, the temperature was tested. We designed seven temperature
116 gradients, 52 °C, 54 °C, 56 °C, 58 °C, 60 °C, 62 °C, 64 °C (Fig. 4). The melting temperature and gel
117 electrophoresis can be combined to determine the optimum temperature.

118 **QPCR for *U. tritici*.**

119 The reaction system is 20 µL: DNA 1 µL, each of the forward and reverse primer is 1 µL, Master Mix 10 µL,
120 ddH₂O 7 µL. The reaction condition is 94 °C for 3 min, 94 °C for 20 s, 60 °C for 30 s, 40 cycles, 72 °C for 5
121 min. Each template DNA is diluted to 6 concentration gradients, with 3 replicates in each group. Then took the
122 melting curves to verify the specificity of the results (Fig. 5).

123 **Sensitivity detection of qPCR assays.**

124 We used 100 ng µL⁻¹ DNA as the template and diluted to seven concentration gradients. These DNA
125 concentrations are 100 ng µL⁻¹, 10 ng µL⁻¹, 1 ng µL⁻¹, 100 pg µL⁻¹, 10 pg µL⁻¹, 1 pg µL⁻¹, 100 fg µL⁻¹. Then
126 performed qPCR on Y430 with two replicates per concentration (Fig. 6).

127 LAMP assay**128 Specificity of LAMP assays.**

129 Tested whether the primers were normal and whether there was primer-dimer formation by PCR assay. The
130 PCR system is 25 μL : DNA 0.5 μL , dNTPs 1 μL , *Taq* DNA polymerase 1 μL , F3 1 μL , B3 1 μL , MgSO_4 1 μL ,
131 2 x Phanta Max Buffer 12.5 μL , ddH₂O 7 μL , the two sets of primers are F3-1F/B3-1R, F3-2F/B3-2R, and each
132 set of primers had three replicates. The control template is complemented by ddH₂O. Added the fluorescent dye
133 to the amplification results (Fig. 7). And then *F. graminearum*, *B. graminis*, *R. cerealis*, *P. striiformis*, *B.*
134 *sorokiniana*, *A. solani* were used as the controls for LAMP assay (Fig. 8).

135 Temperature optimization of LAMP assay.

136 In order to determine the accuracy and sensitivity of the results, the system concentration and temperature of
137 LAMP assay were optimized. Here, the concentration we used is already the optimal concentration ratio. The
138 concentration ratio of the inner and outer primers used in this experiment are 8:1, the concentration of FIP and
139 BIP are 1.6 $\mu\text{mol L}^{-1}$, F3 and B3 are 0.2 $\mu\text{mol L}^{-1}$. The concentration of Mg^{2+} referred to the relevant literatures
140 (Kubota et al., 2008; Abdelsalam et al., 2011) is 6 mmol L^{-1} . We designed nine temperature gradients for LAMP
141 assay to determine the optimum temperature based on the final color reaction (Fig. 9).

142 LAMP assays on *Ustilago tritici*.

143 The LAMP reaction system used in the experiment is 25 μL : DNA 1 μL , 10 x *Thermopol* Buffer 2.5 μL ,
144 MgSO_4 2 μL , dNTPs 2 μL , F3 1 μL , B3 1 μL , FIP 1 μL , BIP 1 μL , *Bst* DNA polymerase 1 μL , Betaine 5 μL ,
145 ddH₂O 7.5 μL , and each set of primers is repeated three times. The control template is complemented by ddH₂O
146 (Fig. 10).

147 Sensitivity detection of LAMP assays.

148 We diluted the extracted DNA 10 times and then used it as the template and then diluted the template DNA to 9

149 concentration gradients, and the concentrations are 100 ng μL^{-1} , 10 ng μL^{-1} , 1 ng μL^{-1} , 100 pg μL^{-1} , 10 pg μL^{-1} , 1
150 pg μL^{-1} , 100 fg μL^{-1} , 10 fg μL^{-1} , 1 fg μL^{-1} . Observing the experimental results with naked eyes under natural
151 light, the experimental results can be judged according to the color (Fig. 11).

152

153 RESULTS

154 In qPCR assays, in order to determine whether the designed primers are specific, we performed PCR
155 experiments on the DNA of the *Ustilago tritici* (Fig. 1), and it was very accurate to obtain five sets of sequence
156 bands by primers. Based on the preliminary screening results, primers are further screened by qPCR using the
157 control strains as templates, and then determined whether the primers were specific by the Ct value reflected with
158 the amplification curves (Fig. 2). The results show that Y334 can amplify *Fusarium graminearum* (Fig. 2A)
159 and there for it is not specific for *U. tritici*. The primers Y430, Y307, Y755, Y139 can specifically amplify the
160 target DNA. The four sets of primers were used to detect the *U. tritici*. By optimizing the system, we get the
161 most volume added to ChamQ™ SYBRqPCR Master Mix. The results of gel electrophoresis on the
162 amplification are shown in Fig. 3. When the volume of ChamQ™ SYBRqPCR Master Mix was added to 8-12
163 μL , the amplification results are the best. We took the intermediate value, the optimal volume of ChamQ™
164 SYBR qPCR Master Mix added in qPCR assay was 10 μL . At the same time, in the results of qPCR
165 temperature gradient test on *U. tritici*, the relative fluorescence unit can reach a higher value at 58 °C and 60
166 °C, and the Ct value is about thirty-three, which is in line with our expected results. In gel electrophoresis, the
167 band shown at 58 °C is the brightest. In combination with Fig. 4A and Fig. 4B, we finally chose 58 °C as the
168 temperature set in the final experiment. The amplification curves of the four pairs of primers show that the Ct
169 values ranged from twenty-nine to thirty-five for samples (Fig. 5). It indicated that the four sets of primers
170 could amplify the target DNA under certain concentration conditions. The melting curves corresponding to

171 each primer exhibit a single peak, which further ruled out non-specific amplification. Combining the
172 amplification curves and the melting curves, it can be known that the target DNA can be successfully amplified
173 by using the four pairs of primers designed to quantify the *U. tritici*. Finally, we used 100 ng μL^{-1} DNA as the
174 template and diluted to seven concentration gradients to verify the lowest concentration detectable by qPCR.
175 The results of seven concentrations of fluorescence show (Fig. 6) that the first five concentration gradients had
176 fluorescence signal accumulation so that the lowest DNA concentration detected by qPCR is 10 pg μL^{-1} .

177 In LAMP assays, the results of the PCR system under natural light and gel imager (Fig. 7) indicated that
178 primers designed for LAMP assay can be used for PCR amplification. Then pathogens such as *F. graminearum*
179 and so on (Table 3) as controls to verify the specificity of the primers. In order to determine the specificity of
180 the primers, five other fungal diseases commonly found in wheat were selected as controls. At the same time, a
181 group of non-wheat fungi were selected as controls. L-139 and L-988 were used to perform LAMP assays on
182 seven different bacteria (Fig. 8). The results show that L-139 and L-988 only amplified the DNA sequence of
183 *U. tritici*. As can be seen from Fig. 9, the optimum reaction temperature for LAMP assay is from 62 °C to 64
184 °C. This experiment is taken at 63 °C. In the optimal ratio and temperature, we carried out LAMP test on *U.*
185 *tritici*. Under the gel imaging system (Fig. 10A), the positive samples are white and the negative controls are
186 colorless. Under natural light (Fig. 10B), the three replicates of the two sets of primers show bright green, and
187 the negative controls are light orange. The light orange color of the negative control indicated that no primer-
188 dimer formed and no false positives caused by the external environment. Sensitivity testing of the LAMP test
189 indicates that the DNA concentration of the lowest *U. tritici* detectable by the LAMP assay is 100 fg μL^{-1} . We
190 performed multiple verifications for experimental accuracy in order to test seed carriers and compare the two
191 methods in terms of sensitivity and operation, so we did not distinguish between the different species.

192 Based on the successful amplification of DNA from *U. tritici* by qPCR and LAMP assays, we used Y334
193 to perform qPCR and L-139 and L-988 to perform LAMP assay on diseased seed (Fig. 12). In the qPCR
194 results, the Ct value tends to be flat at twenty-seven, and the melting curve also shows a single peak. Similarly,
195 in the LAMP experiment results, both samples show bright green color, and the expected slow band appeared in
196 agarose gel electrophoresis. Combining the results of the two methods, we conclude that we can use qPCR and
197 LAMP technology to efficiently and sensitively detect *U. tritici*.

198

199 **DISCUSSION**

200 Wheat loose smut is a systemic disease infested flower organ (Ngugi & Scherm, 2006). It currently occurs in
201 all wheat growing area of the world, particularly serious in Canada (Randhawa et al., 2009) and parts of Africa
202 (Zegeye, Dejene & Ayalew, 2015). Due to the expansion of the disease area and the single prevention method
203 that the detection of pathogenic fungi in seeds is particularly important. In this study, both of the qPCR and
204 LAMP assays can specifically, efficiently and accurately amplify the DNA of *Ustilago tritici*.

205 Our ultimate goal is to find a simple and high-speed detection method. Both of the two methods to detect
206 seeds can help to prevent the spread and occurrence of pathogens from the source. By comparing the two
207 methods, it is not difficult to find that the qPCR assay can accurately determine the initial amount and
208 amplification of the template, it can also be used to visually determine whether there was non-specific
209 amplification by melting curve peaks. Combining the amplification curves with melting curves, it was verified
210 that the primers Y430, Y307, Y755, Y139 can specifically, efficiently and accurately detect *U. tritici*. This
211 method avoids the influence of gel electrophoresis and other operations on the result. However, the
212 experimental requirements for personnel operations, equipment, and environment are much high. Therefore, it
213 has been widely used in the analysis of gene expression (Ma et al., 2013), virus detection (Albinana-Gimenez et

214 al., 2009), disease diagnosis (Moreira et al., 2013). Compared with qPCR, the LAMP assay has the advantages
215 of high sensitivity, short reaction time, easy operation, and low equipment requirements (Kiddle et al., 2012).
216 After its combination with fluorescent dyes, the color reaction is more favorable for our observation of the
217 amplification results so that it is widely used in biological disease detection (Jung et al., 2015), medical
218 diagnosis (Hopkins and Bell, 2013), food testing (Sun et al., 2015) and other aspects. Compared with PCR,
219 both the qPCR and LAMP assays can effectively avoid the influence of agarose gel electrophoresis and the
220 minimum detectable concentrations of them are higher than PCR. However, there are still many problems in the
221 basic application of the two methods. For example, the instruments for performing qPCR assays are expensive.
222 The LAMP assay can only detect one disease at a time. The combination of fluorescent dye with dsDNA is not
223 specific so that the LAMP assay has a high false positive rate. And the field situation is complicated, the
224 reaction system and concentration ratio are difficult to optimize, etc.

225 At present, the qPCR and LAMP assays are being improved. On the basis of qPCR, multiplex PCR have
226 emerged to make up for the shortcomings of detecting only one disease at a time. The various conditions of
227 qPCR assay limit its ability to be applied to field-based assays. Accurate analysis of the data and good
228 reproducibility of the experiment make it become the ubiquitous mainstay of molecular biology. With the
229 deepening of molecular biology, fluorescence quantification will become an indispensable part of it. At the
230 same time, the Multiple LAMP assay have also been proposed to accelerate the efficiency of detection (Chen et
231 al., 2016; Lodh et al., 2017). And kits for LAMP assay have been developed (Marti, Stalder & González, 2015),
232 which eliminates system optimization and matching, thus simplifying the procedure. Its advantages make it
233 well suited for use in resource-poor areas. With the advancement of technology and humanity, chemical control
234 will be gradually replaced by early prevention. The LAMP method is a very valuable diagnostic alternative
235 with a potential of being used also in endemic settings. The improvement of LAMP technology will make it

236 more promising in disease prevention and control.

237

238 **Conflicts of interest**

239 Compliance with Ethical Standards: The authors declare no conflicts of interest.

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Figure 1

PCR amplification of template DNA with different primers

M: DNA maker, 1-6 ITS-4/ITS-5, JN367334.1, AF135430.1, JN367307.1, KP256755.1, AJ236139.1.

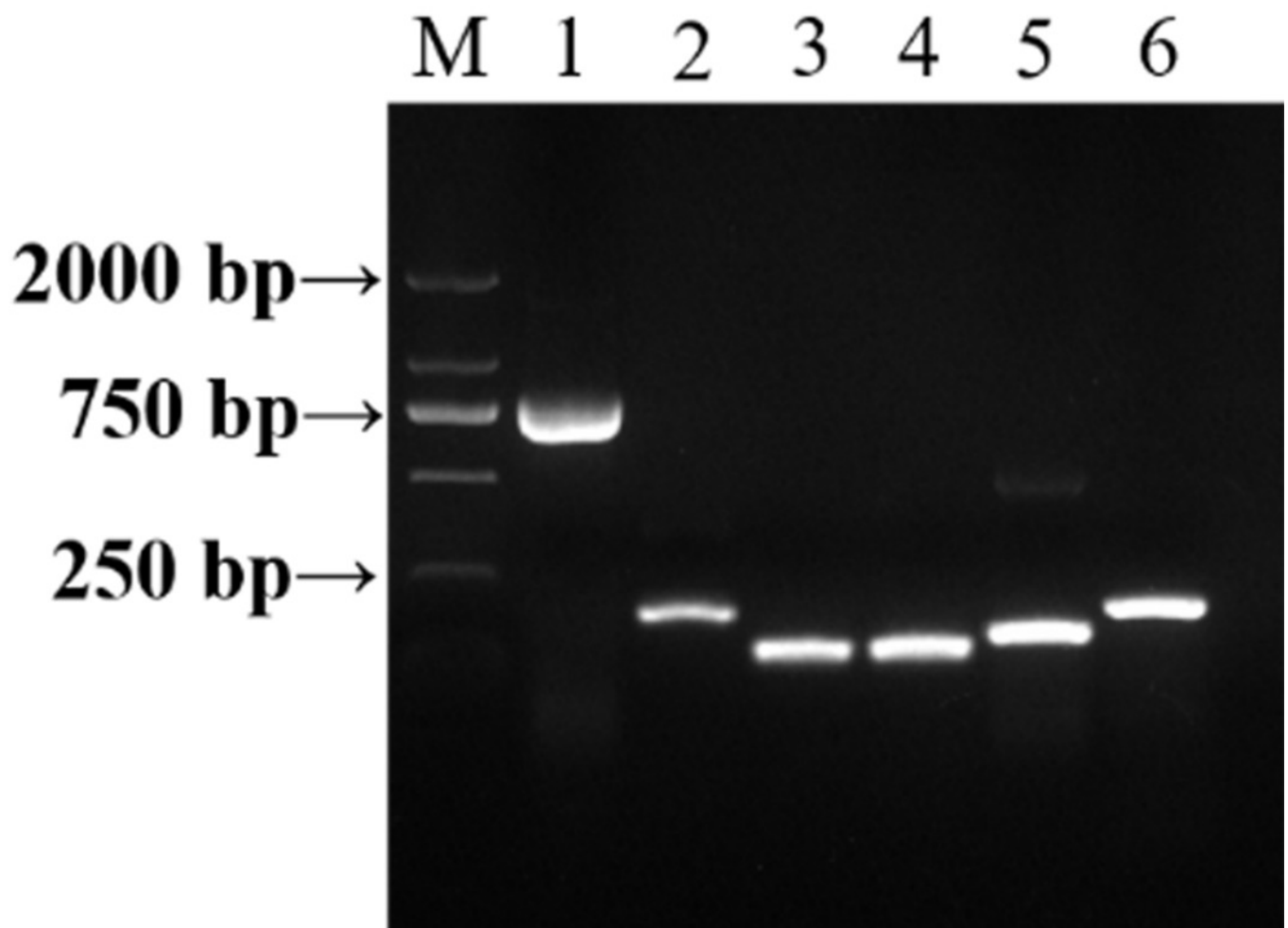


Figure 2(on next page)

Amplification curves of qPCR for control fungi using five sets of primers.

(A): primers Y334. (B): primers Y430. (C): primers Y307. (D): primers Y755. (E): primers Y139.

Color 1: *Ustilago tritici*. Color 2: *Fusarium graminearum*. Color 2-7: *Fusarium graminearum*, *Blumeria graminis*, *Rhizoctonia cerealis*, *Puccinia striiformis*, *Bipolaris sorokiniana*, *Alternaria solani*. Color 3-7: *Blumeria graminis*, *Rhizoctonia cerealis*, *Puccinia striiformis*, *Bipolaris sorokiniana*, *Alternaria solani*.

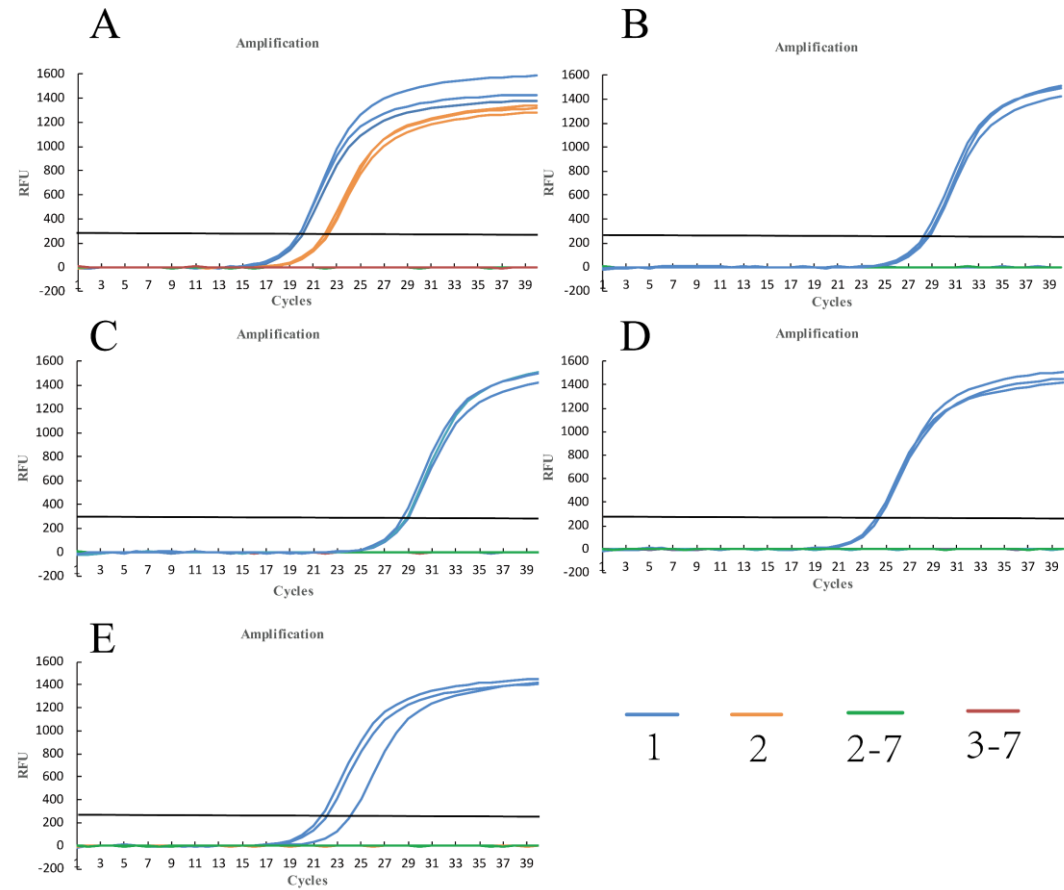


Figure 3

Volume Optimization of qPCR for ChamQ™ SYBR qPCR Master Mix.

qPCR Master Mix. M: Maker, 1-7: 4 μ L, 6 μ L, 8 μ L, 10 μ L, 12 μ L, 14 μ L, 16 μ L.

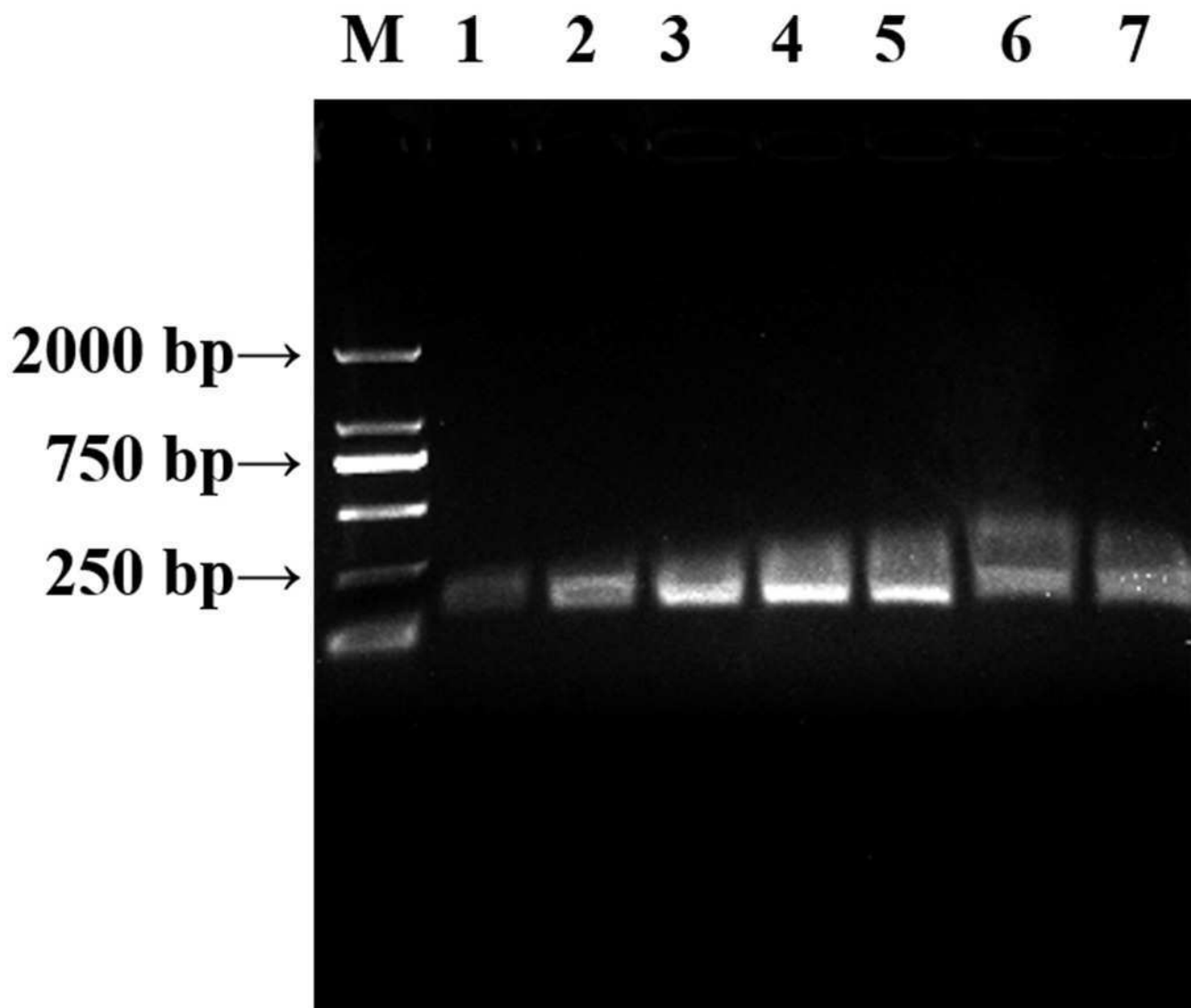


Figure 4(on next page)

Temperature optimization of qPCR.

(A). Amplification curves of qPCR for *Ustilago tritici* under temperature gradients. 1-7: 52 °C, 54 °C, 56 °C, 58 °C, 60 °C, 62 °C, 64 °C. (B). Gel electrophoresis of qPCR on *Ustilago tritici* under temperature gradients M: Marker, 1-7: 52 °C, 54 °C, 56 °C, 58 °C, 60 °C, 62 °C, 64 °C.

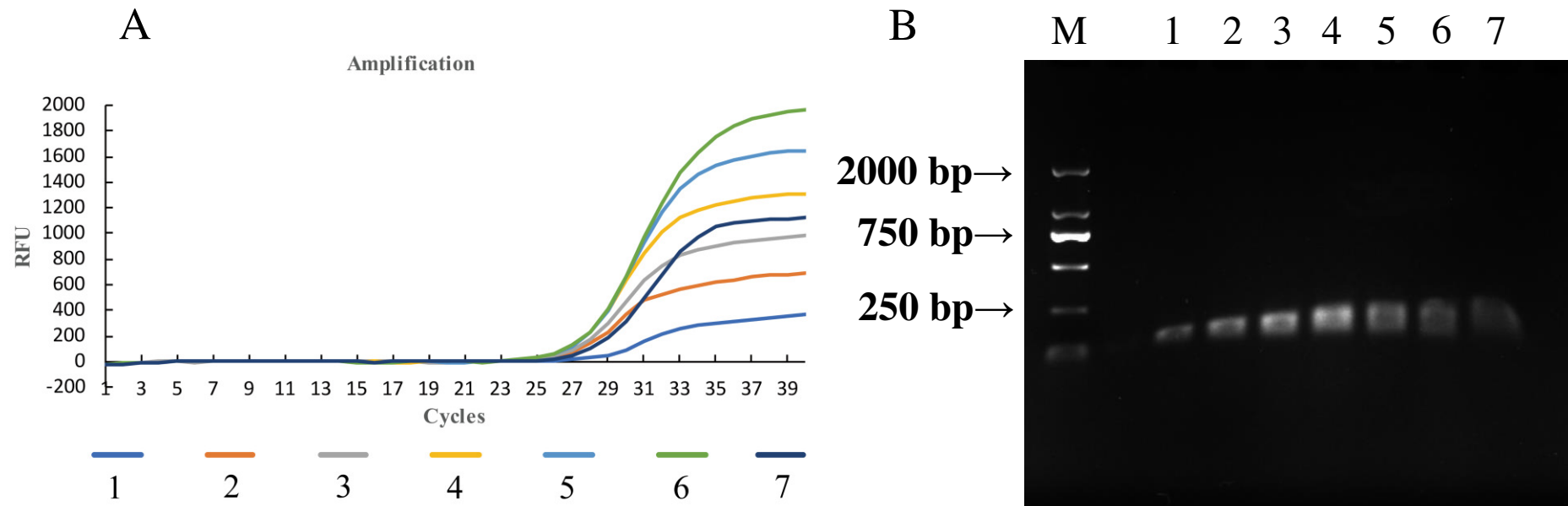


Figure 5(on next page)

qPCR for *Ustilago tritici*.

The amplification curves of qPCR for AJ236139.1(A), KP256755.1(C), JN367307.1(E), AF135430.1(G). The melting curves of qPCR for AJ236139.1(B), KP256755.1(D), JN367307.1(F) and AF135430.1(H).

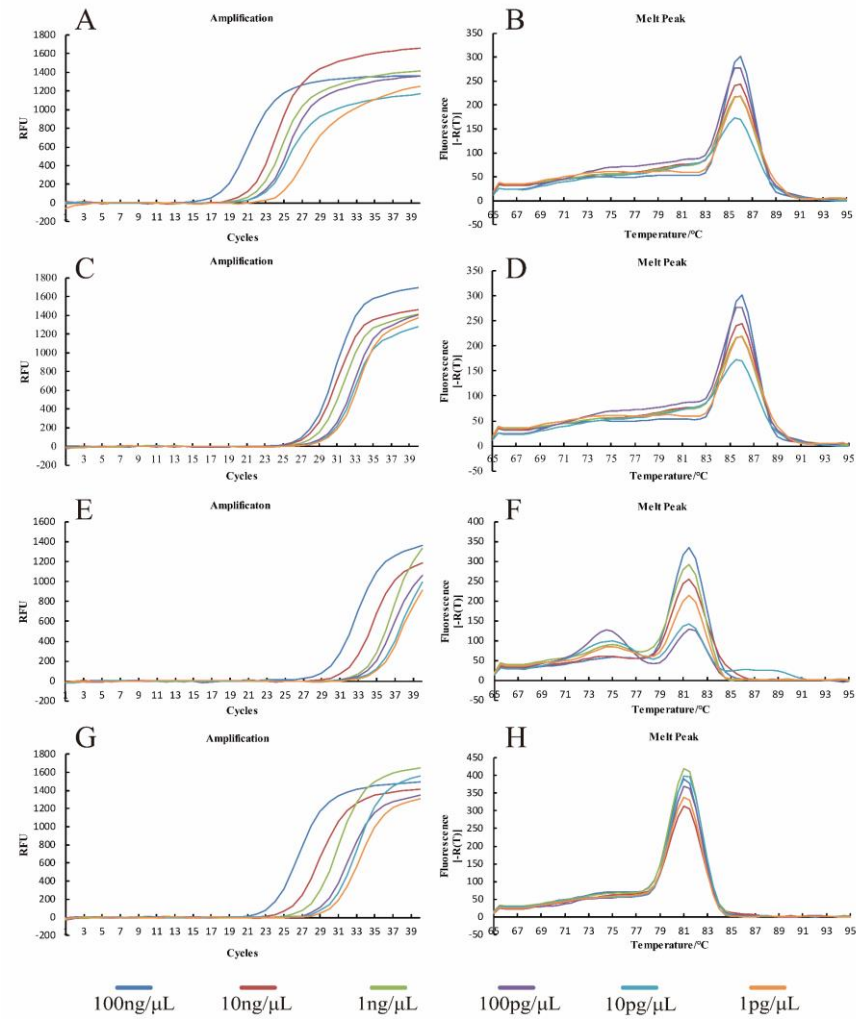


Figure 6 (on next page)

Sensitivity detection of qPCR assays by primer Y430.

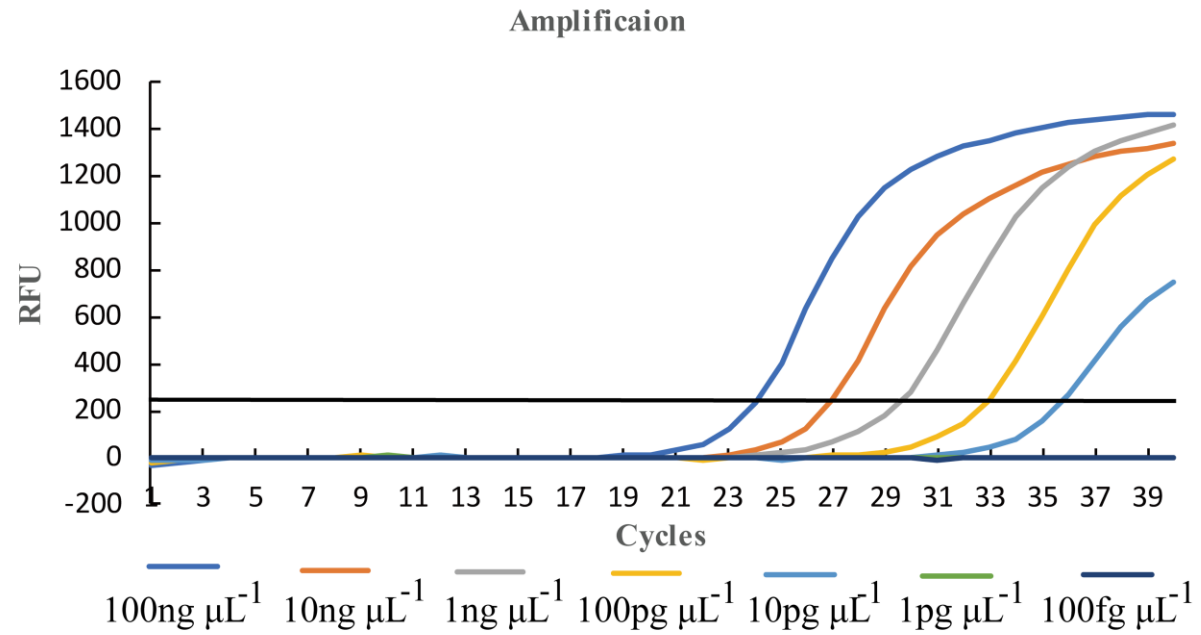


Figure 7

The results of PCR.

(A). Observing the amplification results in the gel imaging system. (B). Observing the amplification results by the naked eye. 1-3: L-139. 4-6: L-988. 7: Negative control.

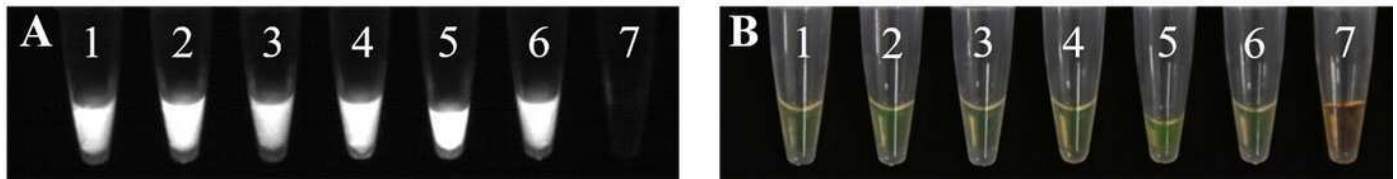


Figure 8

Specific detection of LAMP assays.

1-7: The results of LAMP assay with L-139. DNA from 1-7: *Ustilago tritici*, *Fusarium graminearum*, *Blumeria graminis*, *Rhizoctonia cerealis*, *Puccinia striiformis*, *Bipolaris sorokiniana*, *Alternaria solani*. 8-14: The results of LAMP assay with L-988. DNA from 8-14: *Ustilago tritici*, *Fusarium graminearum*, *Blumeria graminis*, *Rhizoctonia cerealis*, *Puccinia striiformis*, *Bipolaris sorokiniana*, *Alternaria solani*.

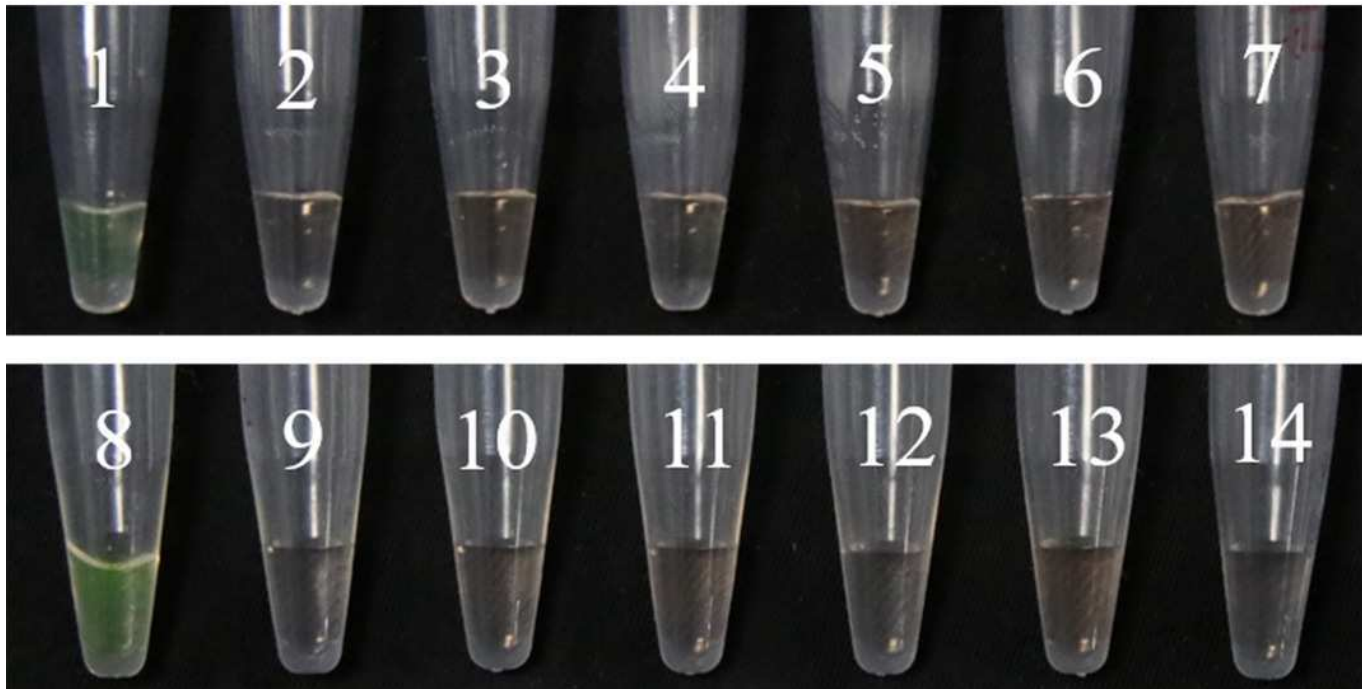


Figure 9

Temperature optimization of LAMP assay.

1-9: 58 °C, 59 °C, 60 °C, 61 °C, 62 °C, 63 °C, 64 °C, 65 °C, 66 °C.

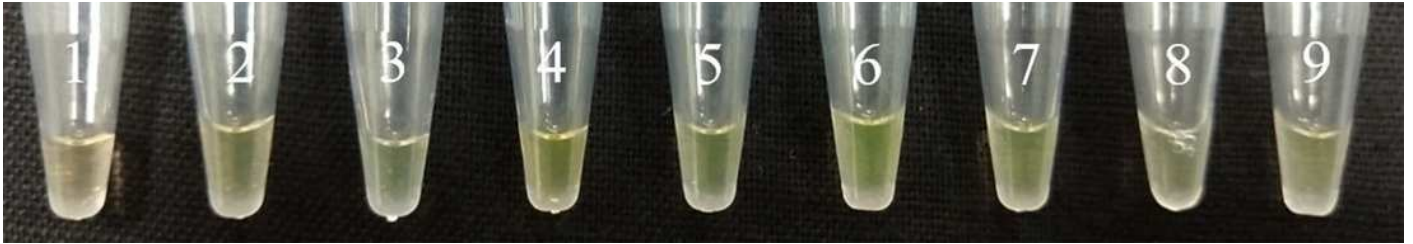


Figure 10

The results of LAMP assay.

(A). Observing the amplification results in the gel imaging system. (B). Observing the amplification results of the LAMP assays by the naked eye. 1-3: L-139. 4-6: L-988. 7: Negative control.

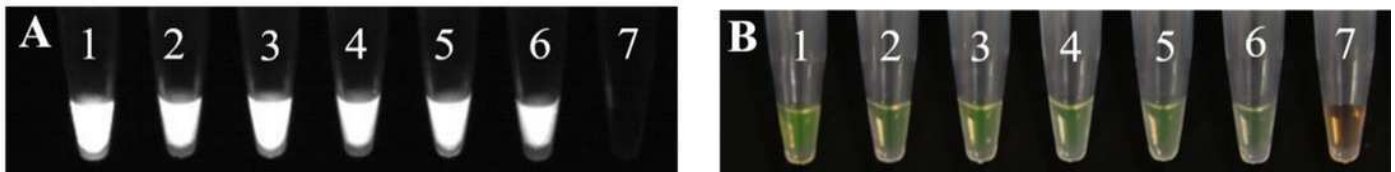


Figure 11

Sensitivity detection of LAMP assays.

DNA concentration from 1-9: 100 ng uL-1, 10 ng uL-1, 1 ng uL-1, 100 pg uL-1, 10 pg uL-1, 1 pg uL-1, 100 fg uL-1, 10 fg uL-1, 1 fg uL-1.

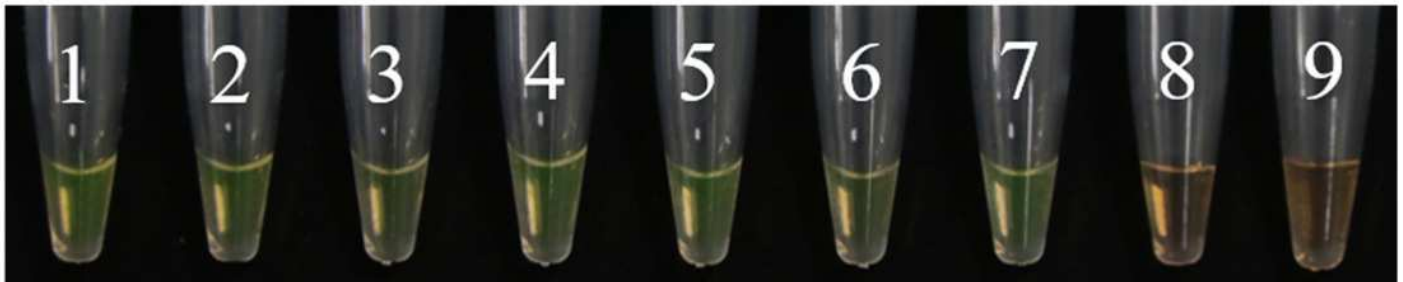


Figure 12(on next page)

Detection of diseased seed in the field by qPCR and LAMP assays.

(A). Amplification curves of qPCR for detection of wheat loose smut in field. (B). Melting curves of qPCR for detection of wheat loose smut in field. (C). LAMP detection of wheat loose smut in the field under natural light. Tube 1-2: The results of LAMP assay with L-139. Tube 3-4: The results of LAMP assay with L-988. (D). Detection by agarose electrophoresis after LAMP assay. Strip 1-2: The results of LAMP assay with L-139. Strip 3-4: The results of LAMP assay with L-988.

