Rapid screening mutations of first-line-drug-resistant genes in *Mycobacterium tuberculosis* strains by allele-specific real-time quantitative PCR

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Tuberculosis (TB) is a worldwide health, economic, and social burden, especially in developing countries. Drug-resistant TB (DR-TB) is the most serious type of this burden. Thus, it is necessary to screen drug-resistant mutations by using a simple and rapid detection method. A total of 32 pairs of Allele-specific PCR (AS-PCR) primers were designed to screen mutation and/or wild-type alleles of 16 variations in four first-line drug-resistant genes (*katG*, *rpoB*, *rpsL*, and *embB*) of TB strains. A pair of primers was designed to amplify 16S rRNA gene and to verify successful amplification. Subsequently, we tested the specificity and sensitivity of these AS-PCR primers. The optimized condition of these AS-PCR primers was first confirmed. All mutations could be screened in general AS-PCR, but only 13 of 16 variations were intuitively investigated by using real-time quantitative PCR and AS-PCR primers. The results of specificity assay suggested that the AS-PCR primers with mutation and /or wildtype alleles could successfully amplify the corresponding allele under optimized PCR conditions. The sensitivity of nine pairs of primers was 500 copy numbers, and the other seven pairs of primers could successfully amplify correct fragments with a template comprising 10^3 or 10^4 copy numbers template. An optimized AS-qPCR was established to screen drug-resistant mutations in TB strains with high specificity and sensitivity.

1 **Rapid screening mutations of first-line-drug-resistant genes in *Mycobacterium tuberculosis***

2 **strains by allele-specific real-time quantitative PCR**

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15 **Abstract**

16 Tuberculosis (TB) is a worldwide health, economic, and social burden, especially in developing

17 countries. Drug-resistant TB (DR-TB) is the most serious type of this burden. Thus, it is

18 necessary to screen drug-resistant mutations by using a simple and rapid detection method. A

19 total of 32 pairs of Allele-specific PCR (AS-PCR) primers were designed to screen mutation

20 and/or wild-type alleles of 16 variations in four first-line drug-resistant genes (*katG*, *rpoB*, *rpsL*,

21 and *embB*) of TB strains. A pair of primers was designed to amplify 16S rRNA gene and to

22 verify successful amplification. Subsequently, we tested the specificity and sensitivity of these

23 AS-PCR primers. The optimized condition of these AS-PCR primers was first confirmed. All

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26 assay suggested that the AS-PCR primers with mutation and /or wildtype alleles could

27 successfully amplify the corresponding allele under optimized PCR conditions. The sensitivity of

28 nine pairs of primers was 500 copy numbers, and the other seven pairs of primers could

29 successfully amplify correct fragments with a template comprising 10^3 or 10^4 copy numbers

30 template. An optimized AS-qPCR was established to screen drug-resistant mutations in TB

31 strains with high specificity and sensitivity.

32

33 **Keywords:** AS-qPCR; drug-resistant mutations; TB; specificity and sensitivity

1. **Introduction**

35

36   Tuberculosis (TB) is a disease with high prevalence and mortality rate. It is caused by

37 *Mycobacterium tuberculosis* (*M. tuberculosis*) infection. One-third of the world population is

38 infected with *M. tuberculosis*, and 5% of infected people developed into TB in their lifetime

39 (Comstock et al. 1974; Koul et al. 2011). In 2017, 10.1 million people suffered from TB, among

40 which 1.6 million people died. Though morbidity and mortality of TB gradually decreased with

41 the appearance of anti-TB drugs, the mutation rate of drug-resistant genes in *M. tuberculosis*

42 seemed to increase recently. The cost of TB treatment and research reached 10.4 billion $ in

43 2018. Half of this amount was used to treat drug-resistant TB (DR-TB) patients (WHO 2018).

44   In the middle of 20th century, DR-TB strains were reported for the first time (Crofton &

45 Mitchison 1948). Unfortunately, the researchers did not focus on this phenomena at that time

46 (Zignol et al. 2016). Recently, the number of patients with DR-TB, especially those with

47 multiple drug-resistant TB (MDR-TB), seriously increased. The numbers of patients with MDR-

48 TB reached 160, 684 in 2017. A total of 10, 800 cases of extensive drug-resistant TB (XDR-TB)

49 were reported by 77 countries, and 88% XDR-TB cases were from European and South-East

50 Asia regions (WHO 2018). Due to abuse of antibiotics and environmental disruption, drug-

51 resistant TB strains have turned out to be barriers to tuberculosis treatment.

52   First-line anti-TB drugs, including isoniazid, rifampicin, streptomycin, ethambutol, and

53 pyrazinamide, are still widely used in clinic. Inevitably, drug-resistant genes exist in *M.*

54 *tuberculosis*, thereby allowing it to resist first-line anti-TB drugs. *katG* and *inhA* genes are two

55 common candidate genes in isoniazid (INH) -resistant TB strains. Mutations in other genes, such

56 as *sigI*, *ndh*, and others, also reportedly to lead to INH-resistance in TB (Guo et al. 2006).

57 Similarly, *rpoB*, *embB*, *rpsL*, and *pncA* were major drug-resistant genes for Rifampicin (RIF)-,

58 Ethambutol (EMB)-, Streptomycin (SM)-, and Pyrazinamide (PZA)- resistant TB strains (Lee et

59 al. 2012; Sandy et al. 2002; Zhang & Yew 2009). Although the mutant spectra showed

60 distinction in different countries, there were some hotspot mutations in these candidate genes.

61 The mutation at codon 315 of the *katG* gene was the most popular INH-resistant mutation, and

62 more than 50% of INH-resistant mutations located in this codon (Afanas'ev et al. 2007; Yuan et

63 al. 2012). Most of RIF-resistant mutations located in hotspot region of the *rpoB* gene, but the

64 mutant frequency varied from 75% to 90% in different countries (Franco-Sotomayor et al. 2018;

65 Thirumurugan et al. 2015). Mutations at codon 43 and 88 were two common SM-resistant

66 mutations in the *rpsL* gene, and over 65% SM-resistant TB strains were caused by these two

67 mutations (Tudo et al. 2010; Zhao et al. 2015). About 70% of EMB-resistant TB strains had

68 mutations which located at codon 306, 406, or 497 in the *embB* gene (Brossier et al. 2015). Thus,

69 rapid screening these mutations was necessary.

70   Long-time and inappropriate drug usage could lead to drug-resistance. Thus, rapid and

71 convenient diagnosis of drug-resistant TB patients is necessary for further effective treatment.

72 Based on the drug-resistant mutations (including hotspot and rare mutations) in our previous

73 study (Li et al. 2017), we established an optimized allele-specific real-time quantitative PCR

74 (AS-qPCR) method to screen mutations in drug-resistant TB strains rapidly and with high

75 sensitivity and specificity.

76

77 **2. Materials and Methods**

78 **2.1 *M. tuberculosis* strains collection and DNA extraction**

79   Drug-resistant *M. tuberculosis* strains were collected and cultured in Lowenstein-Jensen (LJ)

80 medium by doctors in Kunming Third People's Hospital. Drug susceptibility testing (DST) was

81 performed by using the following drugs: INH, 0.2 mg/ L; RIF, 40 mg/ L; SM, 4.0 mg/ L; EMB,

82 2.0 mg/ L; and PZA, 100 mg/ L. G^+ Bacteria Genomic DNA Kit (ZOMANBIO, China) was used

83 to extract genomic DNA from *M. tuberculosis* strains according to the manufacturer's

84 instructions. This study was approved by the institutional review board of Kunming University

85 of Science and Technology (Approval No. 2014SK027).

86

87 **2.2 Primer design and AS-PCR optimization**

88   A total of 32 pairs of primers for AS-PCR were designed to screen the 16 variations

89 (including mutation and wild-type alleles), which were located in four genes (*katG*, *embB*, *rpsL*,

90 and *pncA*), by using Oligo Primer Analysis Software v.7 (Table S1). To strengthen the

91 specificity of primers, a non-complementary nucleotide in 3' end of the allele-specific primer

92 was factitiously changed and marked in red in Table S1. One pair of inner control primers (16S

93 915-F/16S 1018-R) was used to control and identify PCR quantification (Table S1).

94   PCR was performed in 20 μL reaction volume and involved 30 ng of genomic DNA, 10 μL

95   2×TSINGKE^{TM} Master Mix (including 1 U DNA polymerase,1.5 mM MgCl$_2$, 50 mM KCl,

96   and 100 mM dNTP) (TSINGKE, China) or ChamQ^{TM} SYBR qPCR Master Mix (Vazyme,

97   China), and 0.5 μM each primer (including AS-PCR primers and internal control primers). After

98   optimization, we used the following PCR condition: one cycle of 95 ^{o}C for 3 min; 35 cycles of

99   95 ^{o}C for 30 s, optimized temperature for 30 s (Table S1), 72 ^{o}C for 10 s; and one extension

100 cycle of 72 ^{o}C for 5min.

101

102 **2.3 Plasmids construction**

103   Five pairs of primers (Table S2) were designed to amplify fragments containing all

104 mutations. PCR amplification products were ligated into the pClone 007 Blunt Simple Vector by

105 using pClone 007 Vector Kit (TSINGKE, China). All constructed plasmids were identified to

106 carry the specific mutation or wildtype allele by sequencing. Plasmid extraction small Kit

107 (TIANGEN, China) was used to purify the plasmids.

108

109 **2.4 Specificity and sensitivity tests**

110   We amplified 14 wildtype TB samples (identified by sequencing) and all templets of each

111 mutation to test the specificity of AS-PCR by using both wildtype and mutation primers. If there

112 was only one sample with a certain mutation, we duplicated the AS-PCR by using the same

113 mutation sample. The sensitivity results were determined based on the appearance and intensity

114 of the products on the agarose gel. Moreover, wildtype AS-PCR primers were also used to

115   amplify plasmids with corresponding mutations. After qualifying the plasmids, we diluted

116   plasmids to 10^4, 10^3, and 5×10^2 copy numbers to achieve a sensitive assay.

117

118   **2.5 AS real-time quantitative PCR**

119   According to the results of optimized AS-PCR, we performed AS real-time quantitative

120   PCR (AS-qPCR) assays, in order to directly detect the products and determine the mutation or

121   wild type allele. PCR was performed in 20 μL reaction volume and involved 30 ng of genomic

122   DNA, ChamQTM SYBR qPCR Master Mix (Vazyme, China), and 0.3 μM each primer

123   (including mutation and wild type AS-PCR primers of each allele) on Takara Thermal Cycler

124   Dice Real Time System TP800 (TaKaRa, Japan).

125

126   **3.   Results**

127   A total of 16 point mutations in four first-line drug-resistant genes were used to establish

128   AS-PCR detecting method, which were identified in 57 drug-resistant *M. tuberculosis* strains by

129   sequencing in our previous study (Li et al. 2017). After optimizing the conditions of PCR with

130   these primers, we obtained concordant results by sequencing, i.e. the correct bands were

131   successfully amplified by using mutant AS-PCR primers and mutation template but not wild-

132   type samples, and vice versa (Fig. 1). The specificity test results suggested all primers in this

133   study could identify the mutation or wildtype alleles with high fidelity (Fig. S1). As shown in

134   Figure 2, a 206 bp fragment could be amplified by using samples with wild-type *rpsL* gene and

135   primers *RpsL* 128A-F/*RpsL* 128-R (the primer for wild-type allele A at amino acid codon 128).

136   However, this amplicon did not exist when samples with *rpsL* 128G were used. On the contrary,

137   the primers *RpsL* 128G-F/*RpsL* 128-R (for mutant allele G) could amplify a 206 bp fragment

138   when the samples carried the mutation allele 128G in the *rpsL* gene. The presentation of the 104

139   bp inner control fragment suggested a successful amplification.

140   Plasmids with mutation and wildtype alleles were constructed to evaluate the sensitivity of

141   AS-PCR primers. As shown in Figure 3, the sensitivity of primers for amino acid codon 128 in

142   the *rpsL* gene was estimated by using a plasmid with 10^4, 10^3, and 5×10^2 copy numbers. When

143   the copy number of the plasmids was 5×10^2, we could visualize a faint band. However, the bands

144   were obvious and clear when we increased the plasmids to 10^3 or 10^4 copy numbers. The

145   sensitivity of all 32 pairs of primers were tested, and half of these primers could amplify an

146   observable band when the plasmid copy number was 5×10^2 (Fig. S2). However, the others

147   needed more copy numbers (10^3 or 10^4, Fig. S2 and Table S1).

148   To directly and rapidly investigate the testing results of AS-PCR, we combined AS-PCR

149   primers and real-time quantitative PCR for subsequent observation. By observing the melt-curve

150   of these products, we determined whether mutations existed. We firstly defined the baseline at

151   100 relative fluorescence units (RFU)/min as the detecting level. According to this standard, we

152   tested all 16 mutations by using AS-qPCR. However, only 13 mutations were rapidly and

153   directly genotyped (Fig. S3). As shown in Figure 4, we could rapidly identify the allele at 128

154   nucleotide in the *rpsL* gene. By using the optimized AS-qPCR, we rapidly distinguished the

155   mutation and/or wild-type allele in one PCR reaction with two pairs of primers.

156

157   **4. Discussion**

158   China is among the top 22 countries with the highest burden of TB and with the second

159   highest burden of DR-TB. About 120,000 persons developed into TB in China each year (Du et

160   al. 2017; Zhao et al. 2012). Many factors could lead to DR-TB, such as contaminative

161   environment, drug abuse, long-time therapy, and host genetic factors. Some TB strains might

162   change to drug-resistance or solo DR-TB might develop to XDR-TB after the long-term

163   treatment of TB patients. Thus, it was important and necessary to rapidly diagnose DR-TB,

164   especially for first-line DR-TB. Point mutations of drug-resistant genes were common reasons

165   for the development of first-line DR-TB strains. Mutations in the *katG* and/or *inhA* gene were the

166   two main causes of INH-resistant TB. About 51% and 10% isoniazid-resistant TB strains were

167   caused by mutations in the *katG* and *inhA* genes, respectively (Guo et al. 2006). Mutations in the

168   *rpoB* gene, *rpsL* gene, *embB gene*, and *pncA* gene were the main factors for RIF- resistant, SM-

169   resistant, EMB- resistant, and PZA- resistant TB strains, respectively (Brossier et al. 2015;

170   Scorpio & Zhang 1996; Stoffels et al. 2012; Villellas et al. 2013). Furthermore, some hotspot

171   mutations still exist in these drug-resistant genes (Banerjee et al. 1994; Dalla Costa et al. 2009;

172   Lee et al. 2012; Seifert et al. 2015; Waagmeester et al. 2005). Most commercialized detecting

173   kits for DR-TB strains only contained hotspot mutations. Hence, some rare mutations might be

174   missed. In our previous study, we identified some mutations in these genes of Yunnan DR-TB

175   strains, and some of them were hotspot mutations and others were rare mutations (Li et al. 2017).

176   Because no hotspot mutation has been found in the *pncA* gene, eighteen mutations of the other

177   four genes (including *katG*, *rpoB*, *rpsL*, and *embB* genes) were used as candidate mutations in

178   this study. Unfortunately, two mutations, including G1388T (at codon 463) in the *katG* gene and

179   A1490G (at codon 497) in the *embB* gene, could not genotyped by using AS-PCR. Thus, it

180   seemed that not all drug- resistant mutations could be well detected by using AS-PCR.

181   DST is the classic method and the "gold standard" for the evaluation of drug-resistant TB

182   strains (Ahmad & Mokaddas 2009). Until now, DST is still widely used in laboratory and

183   hospital, but methods to screen mutations of drug-resistant genes were speedily developed after

184   invention of PCR. Multi-fluorescence real-time quantitative PCR is one of the most common

185   methods to detect RIF- and INH-resistant *M. tuberculosis* (Peng et al. 2016). Other technologies,

186   such as whole-genome sequencing (WGS) (Pankhurst et al. 2016), high-resolution melt (HRM),

187   PCR-single strand conformation polymorphism (PCR-SSCP), and oligonucleotide microarrays

188   (Caoili et al. 2006; Herrmann et al. 2006; Pietzka et al. 2009; Traore et al. 2006), have also been

189   widely used to screen the mutations of candidate genes in DR-TB strains. However, these

190   technologies have their advantages and shortcomings. For example, high quality and various

191   mutation type could be detected by using WGS, but the expensive equipment and reagent limited

192   its usage.

193   Since AS-PCR was first reported in 1989 (Newton et al. 1989), it has been widely used to

194   screen single nucleotide polymorphisms (SNPs) and mutations. Although AS-PCR is considered

195 as low specificity and sensitivity (Sharma et al. 2016), Onseedaeng *et al.* identified mutations of

196 the *gyrA* and *parC* gene in *Escherichia coli* (*E. coli*) with high sensitivity and specificity by

197 using AS-PCR (Onseedaeng & Ratthawongjirakul 2016). Due to its simple operation, low cost,

198 and relatively high specificity and sensitivity, we successfully used AS-PCR to screen 16

199 mutations in four first-line DR-genes. After optimizing reaction conditions, we successfully

200 amplified the corresponding bands by using AS-PCR primers with high specificity. Most of these

201 primers detected the corresponding mutations when the DNA template reached 500 copy

202 numbers. All these results suggested that optimized AS-qPCR could be used to screen mutations

203 of drug-resistant genes in TB strains with higher specificity and sensitivity. A limitation of

204 current study was the number of drug-resistant mutations in this study was small size. One

205 reason was that no more TB-strains with other drug-resistant mutations were obtained in this

206 experiment; another reason was several drug-resistant mutations could not be well genotyped by

207 using AS-PCR or AS-qPCR method. In further study, we should collect more drug-resistant TB

208 strains from various regions and further optimize AS-PCR condition for rapid screening.

209

210 **5. Conclusion**

211   In summary, we established an optimized AS-qPCR method to screen mutations in four

212 first-line drug-resistant genes of *M. tuberculosis* with relatively high specificity and sensitivity.

213 This AS-qPCR could be widely used in the future to rapidly screen mutations in drug-resistant

214 TB strains.

215

Supplementary Files

Table S1. Information of AS-PCR primers.

Table S2. Information for primers used to construct plasmids.

Figure S1. Electrophoresis map of specific tests.

Figure S2. Electrophoresis map of sensitivity tests.

Figure S3. Melt curves map of real-time quantitative PCR.

222

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225

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Figure 1

Figure 1. Detection of 16 mutations in four first-line drug-resistance genes by using AS-PCR.

M means DNA marker DL2000; m and w mean the AS-PCR primers were used to screen mutation and wildtype alleles, respectively. NC means negative control.
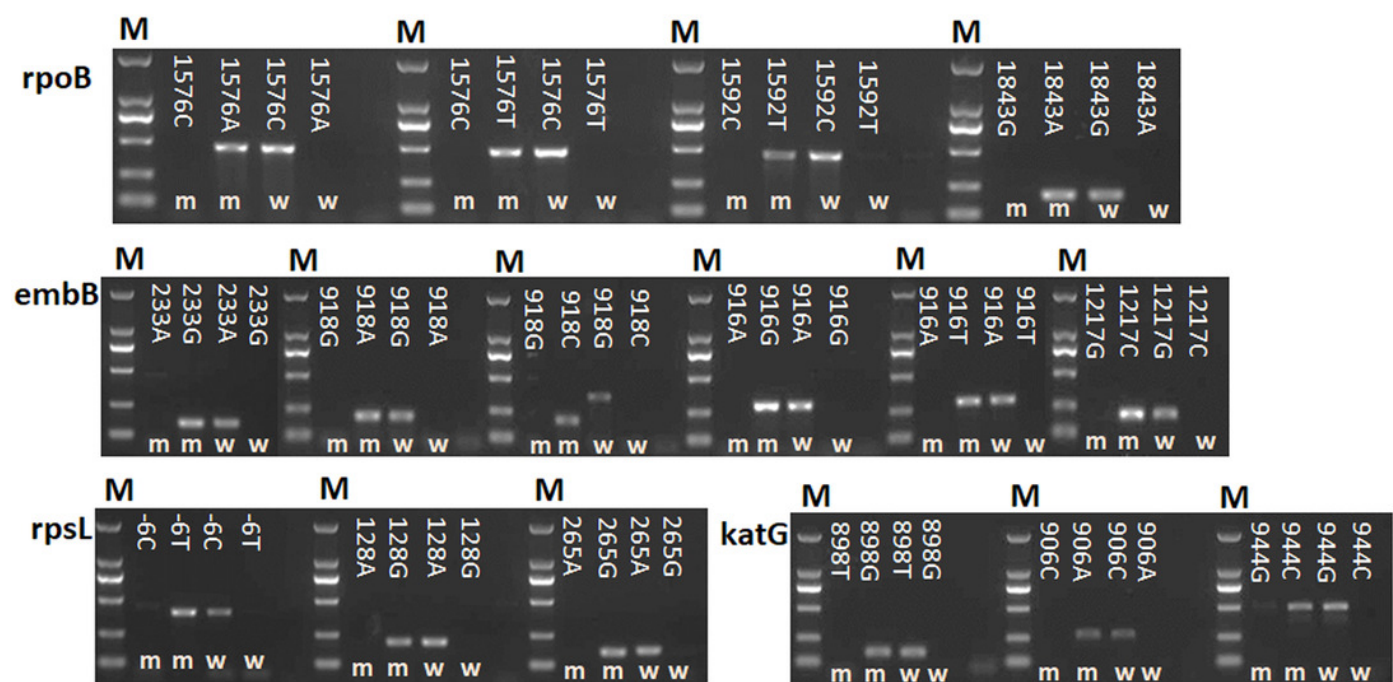
Figure 2

Figure 2. Specificity of AS-PCR primers for A128G in the *rpsL* gene.

(A) PCR were performed by using fourteen DNA templates with allele A and wildtype AS-PCR primers. (**B**) PCR were performed by using fourteen DNA templates with allele A and mutation AS-PCR primers. (**C**) PCR were performed by using eight DNA templates with allele G and mutation AS-PCR primers. (**D**) PCR were performed by using eight DNA templates with allele G and wildtype AS-PCR primers. Fragments at 206 bp mean the specific product by AS-PCR primers; fragments at 104 bp mean the inner control product by inner primers; NC means negative control.

A M   NC

250 bp →
100 bp →

← 206 bp
← 104 bp

B M   NC

250 bp →
100 bp →

← 104 bp

C M   NC

250 bp →
100 bp →

← 206 bp
← 104 bp

D M   NC

250 bp →
100 bp →

← 104 bp
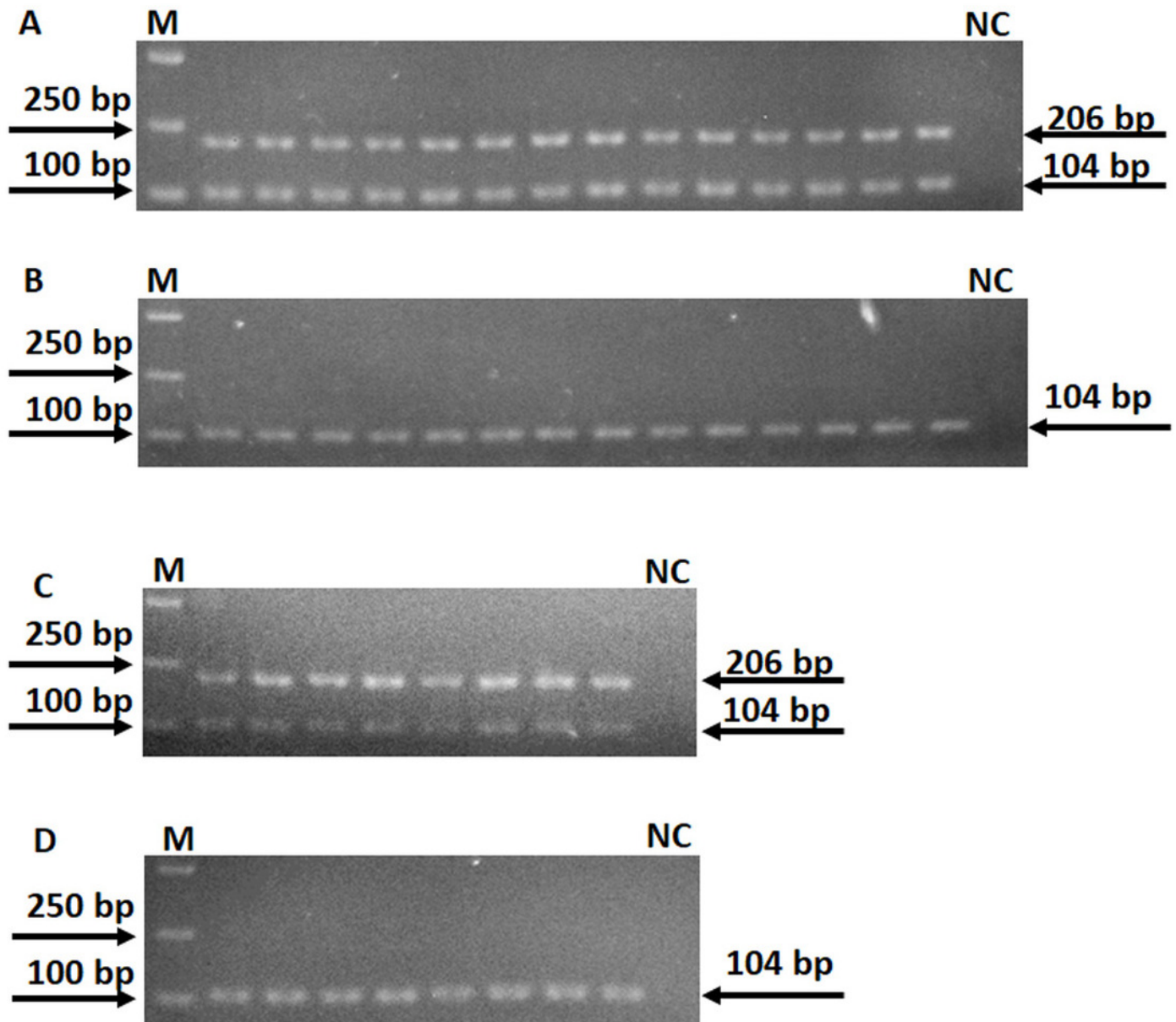
Figure 3

Figure 3. Sensitivity of AS-PCR primers for A128G in the *rpsL* gene.

M means DNA marker DL2000; m and w mean the AS-PCR primers were used to screen mutation and wildtype alleles, respectively.
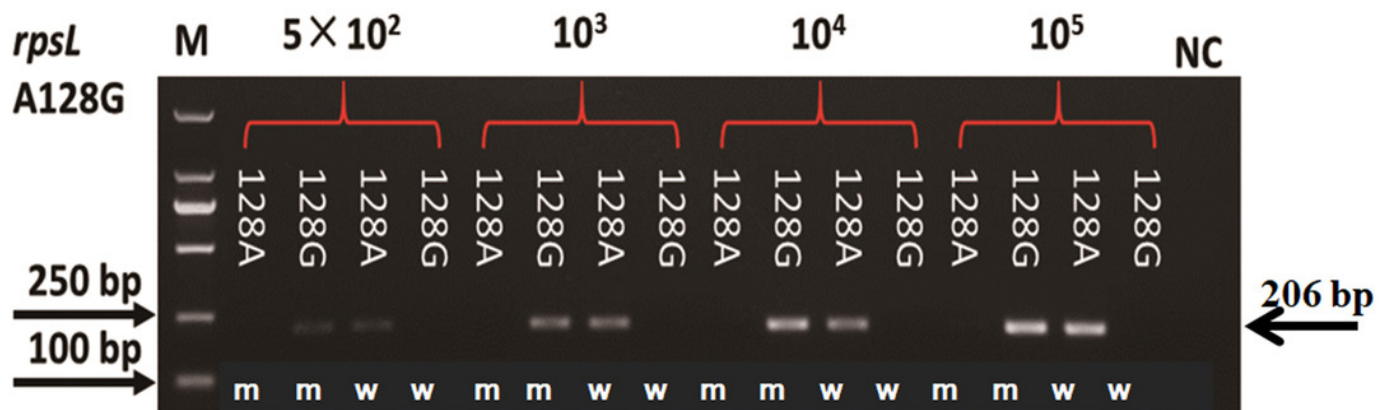
Figure 4

Figure 4. Detecting allele type of A128G in the *rpsL* genes by using AS-PCR primers and real-time quantitative PCR.

(**A**) Melt curves of product by using DNA template with allele A. (**B**) Melt curves of product by using DNA template with allele G.