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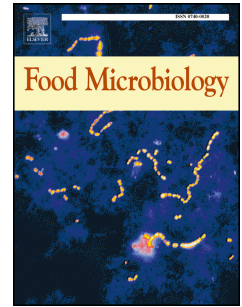
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Yiheng Shi, Zishan Tan, Di Wu, Yongning Wu, Guoliang Li



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1 *Pyrococcus furiosus* Argonaute based *Alicyclobacillus acidoterrestris* detection in fruit juice

2 Yiheng Shi^a, Zishan Tan^a, Di Wu^b, Yongning Wu^{a,c}, Guoliang Li^{a*}

3 ^a School of Food Science and Engineering, Shaanxi University of Science and Technology, Xi'an

4 710021, China

5 ^b Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast, 19

6 Chlorine Gardens, Belfast, BT9 5DL, United Kingdom

7 ^c NHC Key Laboratory of Food Safety Risk Assessment, Food Safety Research Unit (2019RU014)

8 of Chinese Academy of Medical Science, China National Center for Food Safety Risk Assessment,

9 Beijing 100021, China

10 ***CORRESPONDING AUTHOR:**

11 E-mail: 61254368@163.com

12 **Abstract:** *Alicyclobacillus acidoterrestris* is the major threat to fruit juice for its off-odor producing
13 characteristic. In this study, *Pyrococcus furiosus* Argonaute (*PfAgo*), a novel endonuclease with
14 precise DNA cleavage activity, was used for *A. acidoterrestris* detection, termed as PAD. The
15 partially amplified 16S rRNA gene of *A. acidoterrestris* can be cleaved by *PfAgo* activated by a
16 short 5'-phosphorylated single strand DNA, producing a new guide DNA (gDNA). Then, *PfAgo*
17 was activated by the new gDNA to cut a molecular beacon (MB) with fluorophore-quencher reporter,
18 resulting in the recovery of fluorescence. The fluorescent intensity is positively related with the
19 concentration of *A. acidoterrestris*. The PAD assay showed excellent specificity and sensitivity as
20 low as 10^1 CFU/mL, which can be a powerful tool for on-site detection of *A. acidoterrestris* in fruit
21 juice industry in the future, reducing the economic loss.

22 **Keywords:** *Alicyclobacillus acidoterrestris*, *Pyrococcus furiosus* Argonaute, nucleic acid detection,
23 fluorescence, fruit juice

24 Introduction

25 *Alicyclobacillus acidoterrestris* is an acidophilic, thermophilic, spore-producing, rod-shaped
26 bacterium, which has been identified as the main contamination in commercial fruit juice (Neggazi
27 et al., 2023). The spore is highly resistance to heat, which survive pasteurization and subsequently
28 germinate in juice matrix (Wahia et al., 2021). Moreover, *A. acidoterrestris* have wide soluble solid
29 content growth range of 5.4-16.2 °Brix, allowing it to persist and metabolize in a diversity of
30 juice(Splittstoesser et al., 1994). The main metabolic characteristic of *A. acidoterrestris* is to utilize
31 the juice components to produce 2-methoxyphenol and halophenols, resulting in “medical, phenolic
32 and antiseptic” off-flavor in fruit juices (Pornpukdeewattana et al., 2020). As *A. acidoterrestris* is
33 more resistant to heat than pectin methylsterase, a pasteurization indicator, therefore, *A.*
34 *acidoterrestris* has been suggested as reference microorganism to design pasteurization process and
35 to determine the quality of fruit juice. However, in most cases, the identification of juice spoilage
36 caused by *A. acidoterrestris* remain challenge, since it is not related to gas production or acidity and
37 turbidity alteration (Wahia et al., 2022). And observable minimal sediment and perceptible off-odor
38 only appear when the contamination level of *A. acidoterrestris* in fruit juice reach the critical
39 concentration of 10^5 CFU/mL (Cai, Yuan, et al., 2015). Therefore, necessary means should be
40 developed to efficiently detect *A. acidoterrestris* in fruit juice to reduce spoilage-related economic
41 loss.

42 Plate counting method are traditionally internationally acceptable approach in juice industry for the
43 detection of *A. acidoterrestris* (Henczka et al., 2013). Although it is economical and accurate, the
44 time-consuming and labor-intensive features have limited its widespread application. Therefore,
45 some novel methods have emerged to enhance efficiency of the identification of *A. acidoterrestris*

46 (Sourri et al., 2022). Indirect methods including GC-MS (Huang et al., 2015) and electronic nose
47 (Wahia et al., 2020) can rapidly confirm the contamination of *A. acidoterrestris* in juice by
48 monitoring the levels of off-flavors. However, the relevance between cell number of *A.*
49 *acidoterrestris* and concentration of off-flavors are ambiguous, resulting in the reduced accuracy of
50 these approaches. In order to improve the specificity, enzyme-linked immunosorbent assay (ELISA)
51 was proposed for the detection of *A. acidoterrestris*(Li et al., 2014; Li et al., 2013; Shi et al., 2021).
52 Owing to the selective recognition of antibody to surface protein or whole cell, the cross-reaction
53 with non-target was significantly eliminated. However, the limit of detection (LOD) of ELISA could
54 not reach a relatively low level. In contrast, nucleic acid-based detection method such as polymerase
55 chain reaction (PCR) and real-time PCR showed excellent sensitivity as low as several cells benefit
56 for the powerful amplification effect(Li et al., 2021; Wang, Yue, et al., 2021). However, the reliance
57 on professional equipment and the lack of endpoint detection have restricted their flexibility in
58 application. To further broad their applicability especially in on-site test, amplification assays
59 combined with programmable nuclease such as CRISPR (clustered regularly interspaced short
60 palindromic repeats) associated proteins (Cas) have been developed(Chen et al., 2022; Márquez-
61 Costa et al., 2023; Wang et al., 2019). Owing to the specific recognition and cleavage feature of
62 CRISPR/Cas system, these assays showed enhanced specificity and sensitivity. And the detection
63 result can be recognized by portable ultraviolet (UV) lamp, smart phone or test strip(Song et al.,
64 2022; Zhou et al., 2022).

65 The *Pyrococcus furiosus* Argonaute (*PfAgo*) is a novel endonuclease which can perform single-
66 strand DNA (ssDNA) cleavage activated by a small 5'-phosphorylated ssDNA as guide DNA
67 (gDNA)(Swarts et al., 2015). The activated *PfAgo* can precisely cleave the phosphodiester bond

68 between the 10th and 11th nucleotide of target DNA counting from 5'-end of gDNA(Enghiad and
69 Zhao, 2017). In most cases, the gDNA must be strictly complementary to the target DNA, endowing
70 *PfAgo* with highly specificity to identify single base mutation(Zhao et al., 2022). Compared with
71 Cas nucleases, the activity of *PfAgo* do not rely on the protospacer-adjacent motif (PAM) and the
72 *PfAgo* can be guided by DNA rather than RNA. Therefore, the application of *PfAgo* is more flexible
73 and more suitable for multiple targets detection(Ye et al., 2022). Even so, only a few studies explored
74 the potential of *PfAgo* in the DNA-based target detection(He et al., 2021; Li et al., 2023; Wang,
75 Yang, et al., 2021; Wang, He, et al., 2021; Yang et al., 2023).

76 In this work, we developed a *PfAgo* based *A. acidoterrestris* detection (PAD) method. In this assay,
77 only one gDNA was used to trigger the stepwise cleavage activity of *PfAgo* where a new gDNA
78 could be generated from the former gDNA guided cleavage process, which in turn, guided a new
79 round of cleavage. Finally, a reporter strand with fluorophore and quencher was cut off, leading to
80 the recovery of fluorescence and the fluorescence intensity is positively correlated to the
81 concentration of *A. acidoterrestris* (Figure 1). The PAD is sensitive and specific, which showed
82 excellent applicability in fruit juice.

83 **2. Materials and methods**

84 **2.1 Bacterial strains and Chemicals**

85 *A. acidoterrestris* (ATCC 49025) and other bacterial strains used in the experiment were purchased
86 from American Type Culture Collection (ATCC, US) previously and stored in our laboratory. All
87 the oligonucleotides and molecular beacon (MB) used in this experiment (Table 1) were synthesized
88 by Sangon Biotech Co. Ltd. (China). The plasmid pET-23a containing *PfAgo* gene (pET-23a-*PfAgo*)
89 was kindly provided by Dr. Wang Fei (Hubei University, China). The T4 Polynucleotide Kinase was

90 purchase from New England Biolabs (US). The TIANamp Bacterial DNA Kit was purchased from
91 Tiangen Biotech Co. Ltd., (China). The juice samples were collected from the local market.

92 **2.2 Expression and purification of *PfAgo***

93 The plasmid pET-23a-*PfAgo* was first transformed into *Escherichia coli* BL21 (DE3) pLysS and
94 cultured at 37 °C overnight. Then the culture was inoculated in LB medium containing 100 µg/ml
95 ampicillin and 50 µg/ml chloramphenicol and cultured at 37 °C. When the OD_{600nm} reached 0.6-0.8,
96 isopropyl β-d-thiogalactopyranoside (IPTG) was added to a final concentration of 1 mM, followed
97 by incubated at 18 °C for 17 h to induce the over-expression of *PfAgo*. The cell was harvested and
98 resuspended in lysis buffer (50 mM NaH₂PO₄, 300 mM NaCl, 10 mM imidazole, pH=8.0), followed
99 by lysed by ultrasonic disruptor. Cell lysates were centrifuged at 12000×g for 15 min to collect
100 supernatants. After treatment with heating at 75 °C for 30 min, the *PfAgo* in the supernatants were
101 purified with Ni-NTA resin affinity purification column following manual's instruction (Figure S1).
102 The protein sample was concentrated using dialysis bag and resuspended in storage buffer (50 mM
103 NaH₂PO₄, 300 mM NaCl, 0.5 mM MnCl₂, 15% (v/v) glycerol, pH 8.0) and stored at -80 °C for
104 further use.

105 **2.3 Genomic DNA extraction and DNA amplification**

106 The genomic DNA of *A. acidoterrestris* was extracted with the TIANamp Bacterial DNA Kit
107 according to the instruction. The PCR mixture in a final volume of 20 µL containing 2 µL of the
108 extracted genomic DNA, 2 µL of primers (10 µM for forward primer and reverse primer), 10 µL
109 2×Taq premix and 6 µL sterilized water was prepared. The PCR reaction was performed as follow:
110 initial denaturation at 94 °C for 4 min, 30 thermo-cycles of denaturing at 94 °C for 30 s, annealing
111 at 60 °C for 30 s and extending at 72 °C for 30 s, then keeping at 72°C for 10 min. The products

112 were stored at -20 °C for further use.

113 **2.4 *PfAgo* based for *A. acidoterrestris* detection**

114 The gDNA was first phosphorylated by T4 polynucleotide kinase before use. The PCR products (5
115 μL) was mixed with 1.5 μM *PfAgo*, 0.5 μM gDNA, 2 μM MB and nuclease-free water to a final
116 volume of 20 μL . The mixture was then kept at 95°C for 30 min and the fluorescence intensity was
117 recorded.

118 **3. Results and discussion**

119 **3.1 Principle of PAD**

120 In the PAD system, the 16S rRNA gene of *A. acidoterrestris* was selected as the detection target.
121 The amplification zone is located in the 89-169 site of the 16S rRNA gene, which have been proved
122 with high specificity in the detection of *A. acidoterrestris* in previous study (Wang et al., 2014). In
123 the presence of *A. acidoterrestris* in the sample, this representative region of 16S rRNA gene can be
124 exponentially amplified. The resultant fragment is specifically recognized by *PfAgo* guided by the
125 designed gDNA, which is strictly complementary to the special region (112-129 site of the 16S
126 rRNA gene) of one strand of the amplicon. Subsequently, the cleavage activity of *PfAgo* is triggered,
127 resulting in the breakage of the strand at the specific site. Moreover, this process generated a new
128 5'-phosphorylated ssDNA because of the hydrolysis of phosphodiester bond, which can serve as a
129 new gDNA to guide *PfAgo* for another round of cleavage. The target of the second round of cleavage
130 can be the designed MB or the other strand of the amplicon. In the first case, the MB forms hairpin
131 structure to make FAM fluorophore at one end of MB proximity to BHQ1 quencher at another end
132 of MB. And the sequence of MB loop is designed to be complementary to the new gDNA. Therefore,
133 the MB could be cleaved by *PfAgo* guided by the new gDNA, bringing FAM away from BHQ1,

134 leading to the recovery of fluorescence. In the second case, owing to the complementary of two
135 strands of the amplicon, the new gDNA can guide *PfAgo* to cut the other strand. Therefore, the PCR
136 amplicon is divided into two pieces finally.

137 **3.2 Feasibility and optimization of PAD**

138 The feasibility of the proposed PAD assay for the detection of *A. acidoterrestris* was verified firstly.
139 As shown in Figure 2A and 2B, in the presence of gDNA and *PfAgo*, the fluorescence intensity of
140 the system changed significantly and strong fluorescence can be observed under UV light. While in
141 the absence of gDNA, there was no obvious fluorescent signal showed and the system remained
142 non-luminance, which means *PfAgo* cannot be activated without gDNA. In the meantime, as shown
143 in Figure 2C, the amplicon was split into two pieces when the gDNA and *PfAgo* co-existed in the
144 system simultaneously. While in other cases, the amplicons remained intact. These phenomena
145 proved the second scenario described in the principle of PAD. All the results demonstrated the
146 developed assay was feasible for *A. acidoterrestris* detection.

147 To achieve the best performance of PAD, the parameters which influence the detection system were
148 optimized. As shown in Figure 3A, when the concentration of gDNA was 0.5 μM , the fluorescence
149 intensity of the system reached highest. While when the concentration of gDNA was lower or higher
150 than 0.5 μM , the fluorescence intensity reduced. Similarly, the fluorescence intensity enhanced with
151 the concentration of *PfAgo* increased, reaching plateau at the *PfAgo* concentration of 1.5 μM (Figure
152 3B). Then, the fluorescence intensity decreased slightly when the concentration of *PfAgo* exceed
153 1.5 μM . These phenomena indicated that the ratio of *PfAgo* to gDNA should be kept in a reasonable
154 range so that *PfAgo* can be activated maximumly(Xun et al., 2021). Therefore, 0.5 μM and 1.5 μM
155 were chosen as the optimal concentration of gDNA and *PfAgo* in this work, respectively. Next, the

156 concentration of MB was optimized. As shown in Figure 3C, the fluorescence intensity reached
157 maximum when the concentration of MB was 2 μ M. And the fluorescence intensity could keep in
158 relative high level at the concentrations above 2 μ M but with some fluctuations. To reduce cost, 2
159 μ M was selected as the best MB concentration for PAD assay. Under these optimal reaction
160 conditions, the fluorescence signal of the detection system response upon time was tested. As shown
161 in Figure 3D, the fluorescence intensity increased rapidly within the first 30 min and reached
162 equilibrium gradually in the 30-50 min time frame. Therefore, 30 min was determined to be the
163 most suitable reaction time for PAD.

164 3.3 Performance of PAD

165 To verify the specificity of PAD method, different bacteria including other species of
166 *Alicyclobacillus* genus and common foodborne pathogens were tested. As shown in Figure 4A, there
167 was a clear difference in fluorescence intensity between positive and negative samples where
168 fluorescent signal was only appeared in the presence of *A. acidoterrestris*. Thus, it can be concluded
169 the developed PAD method has an excellent specificity which can distinguish not only distinct
170 bacterial genera, but also different species of *Alicyclobacillus* genus. This superior specificity can
171 be attributed to two reasons. One reason is that the amplified region is highly variable among
172 *Alicyclobacillus* genus and the designed primers can only amplify the region in the genome of *A.*
173 *acidoterrestris*(Wang et al., 2014). The other reason is that the designed gDNA is strictly
174 complementary to one strand of amplicons where a single nucleotide mismatch between gDNA and
175 complementary sequence could reduce the cleavage activity of *PfAgo* (Xun et al., 2021). Therefore,
176 the negative samples could not be detected by the PAD method.

177 The sensitivity of the PAD method was determined using a serial concentration of *A. acidoterrestris*

178 with 10^6 - 10^0 CFU/mL. As shown in Figure 4B, the fluorescence intensity was still high at the
179 bacterial concentration of 10^1 CFU/mL. But there was no significant difference in fluorescence
180 intensity between 10^0 CFU/mL of *A. acidoterrestris* and the control group. Therefore, the limit of
181 detection (LOD) of PAD was determined to be 10^1 CFU/mL. The sensitivity of PAD is better than
182 most of the currently available nucleic acid-based detection assays such as PCR, real-time PCR,
183 LAMP (loop-mediated isothermal amplification) and SPIA (single primer isothermal amplification)
184 (Table 2). This excellent sensitivity also can be ascribed to two reasons. One reason is that the PCR
185 procedure could effectively amplify low DNA concentration to detectable level. The second reason
186 is the powerful target recognition and cleavage capacity of *PfAgo* which could detect DNA as low
187 as femtomolar level (Xun et al., 2021). Therefore, the two-stage amplification greatly enhanced the
188 detection sensitivity of PAD assay. Moreover, the delivered results of PAD assay can be simply
189 detected by portable ultraviolet lamp, which do not need agarose gel electrophoresis, gel imaging
190 system or real-time PCR instrument. Therefore, compared with PCR and real-time PCR (Table 2),
191 the result analysis of PAD is cheaper and more convenient. And compared with the isothermal
192 amplification methods such as LAMP and SPIA, the design of primers and gDNA of PAD system
193 is simpler. In addition, the PAD assay has strong anti-interference ability owing to the precise nucleic
194 acid recognition and cleavage capacity of *PfAgo* that the false-positive and high background value
195 scenario often present in the above-mentioned isothermal amplification methods can be effectively
196 avoided. In a word, the proposed PAD assay is simpler, more sensitive and accurate than the listed
197 assays in Table 2.

198 **3.4 Application of PAD in juice samples**

199 To verify the application capacity of PAD in real food samples, fruit juices such as apple juice,

200 orange juice and kiwi juice were first artificially contaminated by *A. acidoterrestris*. Sample 1-4, 6-
201 9, 11-14 represent different juices contaminated with *A. acidoterrestris* in the level of 10^2 - 10^5
202 CFU/mL, respectively. And sample 5, 10, 15 represent un-contaminated juices. Then these samples
203 were detected using the developed sensing system. As shown in Figure 5 A, all positive samples can
204 be recognized by PAD with obvious fluorescence intensity difference compared to the negative
205 samples. The results were consistent with the PCR detection that a clear band with the length of 81
206 bp can be seen in all positive samples and no band was showed in negative samples (Figure 5B).
207 The results highlighted the potential of PAD assay in the detection of real samples.

208 **4. Conclusion**

209 Here, a novel method named PAD was proposed for the detection of *A. acidoterrestris*. This method
210 took advantage of the powerful stepwise cleavage ability of *PfAgo* which could be activated and
211 guided as long as 5'-phosphorylated ssDNA existed in the system and the cleavage process could
212 continuously proceed until the final target is depleted. Therefore, only one guide input could induce
213 the output of obvious fluorescence signal in PAD. Compared with CRISPR/Cas based detection
214 methods, PAD uses DNA as guide which is more stable and cheaper than RNA. The method can
215 detect *A. acidoterrestris* as low as 10^1 CFU/mL without cross-reaction with non-targets. The high
216 sensitivity and specificity endow PAD with great potential in real sample application. However, the
217 requirement of PCR amplification is the main drawback of PAD which restrict its application in on-
218 site detection. The future work will focus on the integration of isothermal amplification techniques
219 to overcome the disadvantage and develop convenient on-site detection system. All in all, this work
220 provides a novel proof-of-concept that all nucleic acid containing creatures such as virus, pathogens
221 and cancer cells can be identified based on this principle.

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225 **Declaration of interest**

226 The authors declare that they have no conflicts of interest in relation to this study.

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341 Figure legends

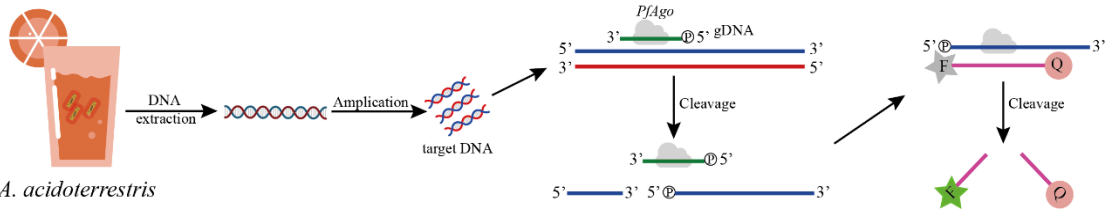
342 Figure 1. Schematic illustration of PAD.

343 Figure 2. Feasibility of PAD. (A) Fluorescent spectra of different sample. (B) Fluorescent image of
344 different sample under 365 nm UV lamp. (C) Gel image of different sample. “+” represents in the
345 presence of *PfAgo* or gDNA. “-” represents in the absence of *PfAgo* or gDNA.

346 Figure 3. (A) Optimization of gDNA concentration in the PAD system. (B) Optimization of *PfAgo*
347 concentration in the PAD system. (C) Optimization of MB concentration in the PAD system. (D)
348 Optimization of reaction time in the PAD system.

349 Figure 4. (A) Specificity of PAD. (B) Sensitivity of PAD.

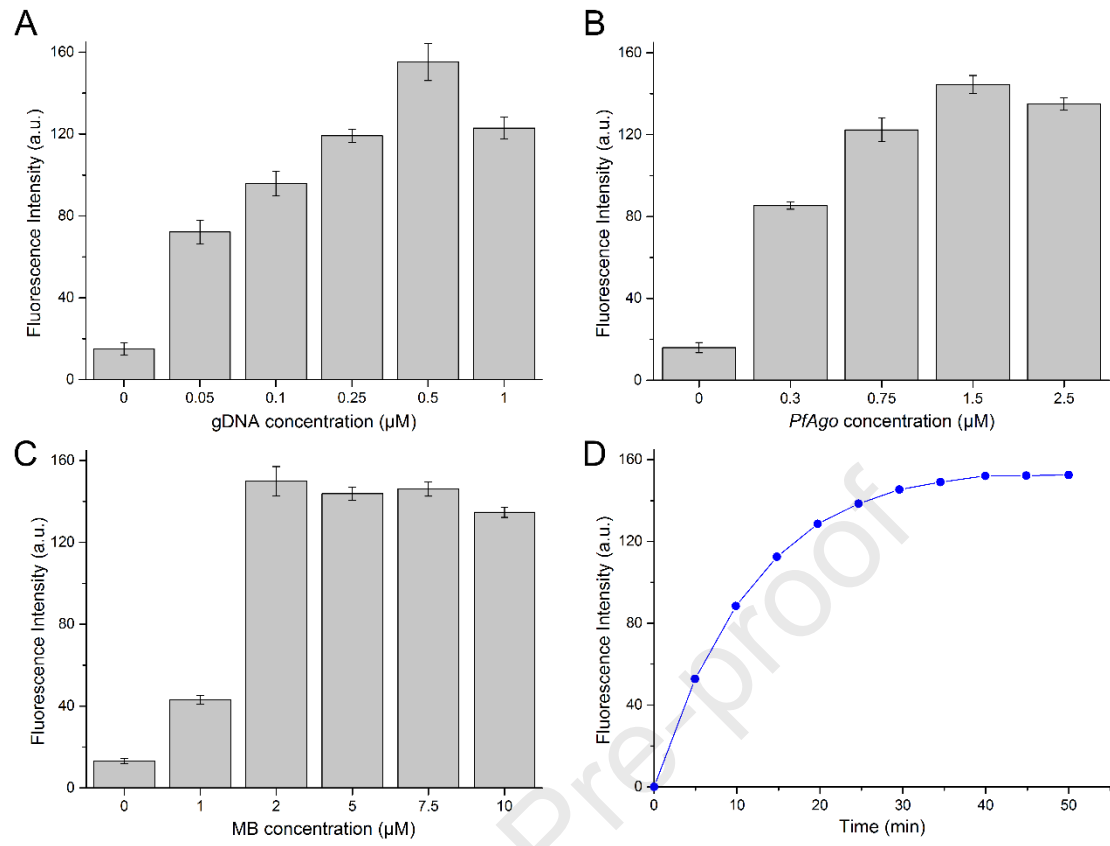
350 Figure 5. (A) Detection of *A. acidoterrestris* in fruit juice samples using PAD assay. (B) Gel image
351 of fruit juice samples tested by PCR assay. Sample 1-4, 6-9, 11-14 represent different juices
352 contaminated with *A. acidoterrestris* in the level of 10^2 - 10^5 CFU/mL, respectively. Sample 5, 10,
353 15 represent un-contaminated juices.



354 *A. acidoterrestris*

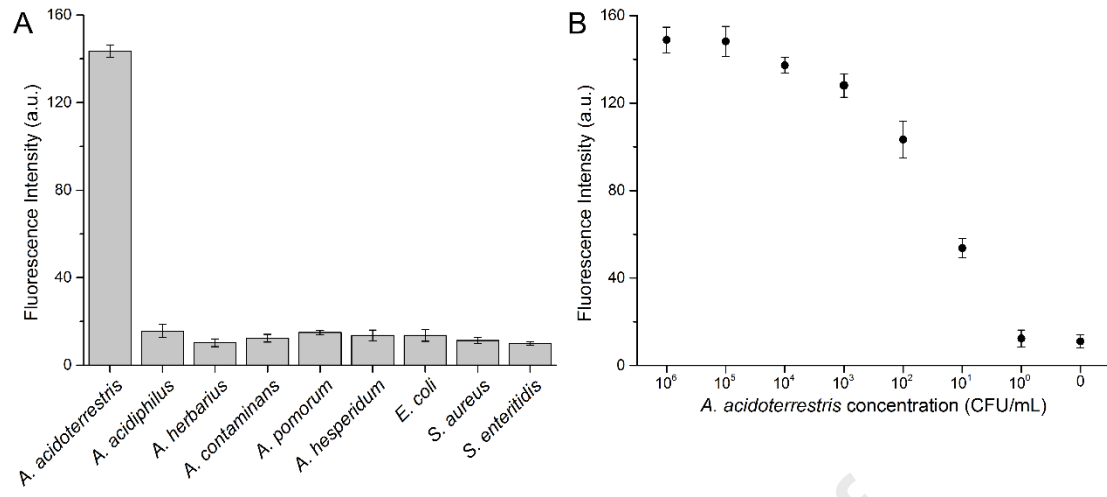
355 Figure 1.

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358

359 Figure 3.



360

361 Figure 4.

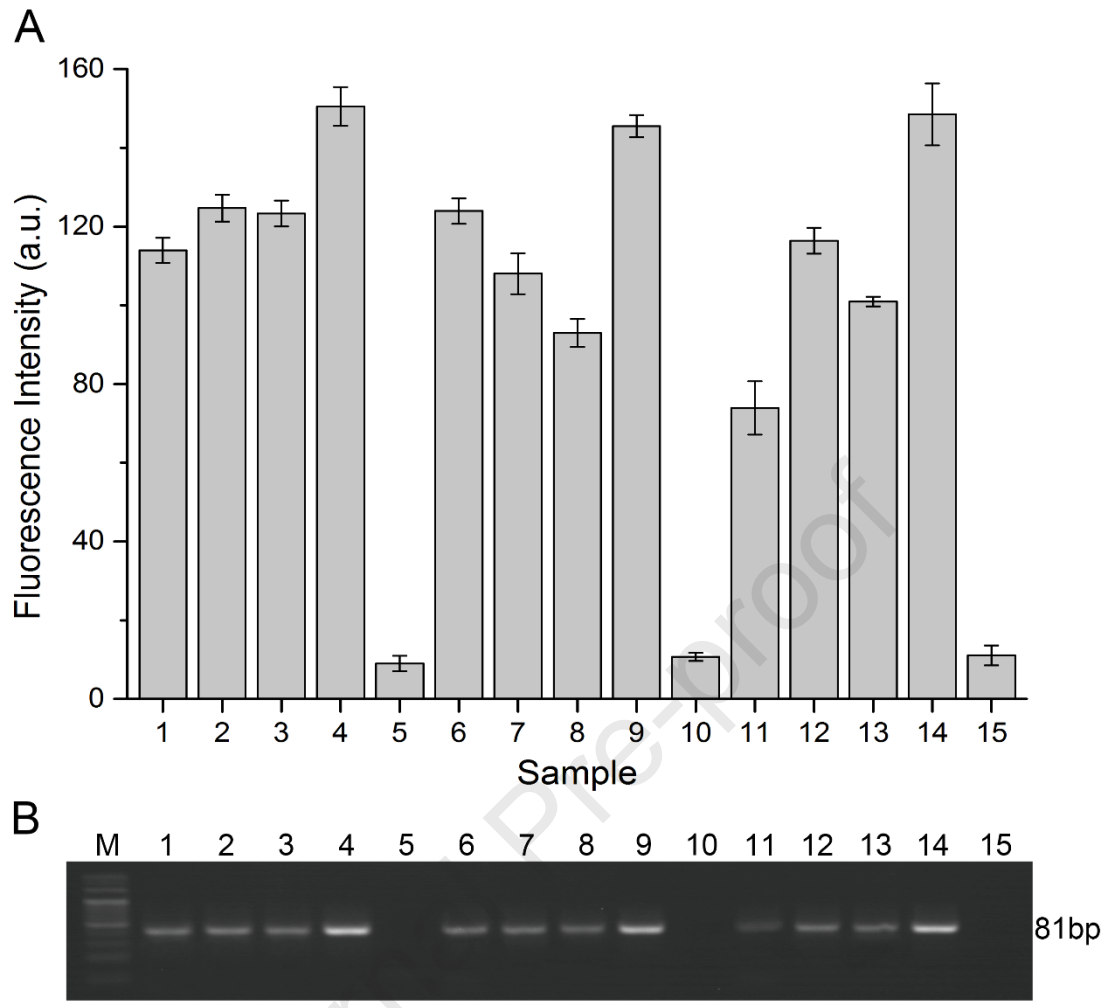


Figure 5.

364 Table 1. oligonucleotide sequences

Type	Description	Sequence (5'-3')
Primers	16S rRNA-Forward	TGAGTAACACGTGGGCAATCTG
	16S rRNA-Reverse	CTACCCGTGTATTATCCGGCAT
gDNA	guide DNA of <i>PfAgo</i>	CTACCCGTGTATTATCCGGCAT
Molecular beacon	MB	FAM-cgcaccCAATCTGCCTTTCAGACTggtgcg-BHQ1

365

366 Table 2. Comparison of different nucleic acid detection method for *A. acidoterrestris*

Method	LOD (CFU/mL)	Specificity	Reference
Quantitative PCR	2.6×10^2	Yes	(Li et al., 2021)
Real-time PCR	<10	No	(Luo et al., 2004)
	<100	No	(Connor et al., 2005)
IMS ^a real-time PCR	<10	Yes	(Wang et al., 2014)
	2.8×10^1	No	(Cai, Wang, et al., 2015)
Asymmetric nested RT-PCR ^b coupled with electrochemical detection	2	Not report	(Barrios Eguiluz et al., 2009)
Random genomic DNA Microarray	2×10^3	No	(Jang et al., 2011)
LAMP ^c	2.25×10^1	Yes	(Chen et al., 2011)
SRCA ^d	4.5	Yes	(Yuan et al., 2020)
SPIA ^e	4.8	Yes	(Yang et al., 2017)
PAD	10^1	Yes	This work

367 ^a Immunomagnetic separation.368 ^b Reverse transcription PCR.369 ^c Loop-mediated isothermal amplification.370 ^d Saltatory rolling circle amplification.371 ^e Single primer isothermal amplification.

- A novel nucleic acid detection method based on argonaute for *A. acidoterrestris* was developed.
- The assay showed excellent specificity and sensitivity with a limit of detection of 10^1 CFU/mL.
- The assay exhibited good performance in real sample analysis.

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Declaration of interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

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