



Feb 23, 2019

Working

Species-specific quantitative PCR (qPCR) protocol developed to identify *Haplosporidium pinnae*

Version 1

PLOS One

Montserrat López-Sanmartín¹, Gaetano Catanese², Amalia Grau², Jose María Valencia², Jose Rafa García-March³, José Ignacio Navas¹

¹IFAPA Agua del Pino, ²LIMIA-INAGEA, ³IMEDMAR-UCV

dx.doi.org/10.17504/protocols.io.xe7fjhn



Montserrat López-Sanmartín
IFAPA Agua del Pino



ABSTRACT

The aim of this study has been to develop species-specific quantitative PCR (qPCR) protocol carrying out a fast, specific and effective molecular diagnose of *Haplosporidium pinnae*. In this sense, the detection limit for qPCR was equal to 30 copies of SSU rDNA / ng of DNA using plasmid alone and when 100ng DNA of non-infected oyster were added.

EXTERNAL LINK

<https://doi.org/10.1371/journal.pone.0212028>

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

López-Sanmartín M, Catanese G, Grau A, Valencia JM, García-March JR, Navas JI, 2019. Real-Time PCR based test for the early diagnosis of *Haplosporidium pinnae* affecting fan mussel *Pinna nobilis*. PLOS ONE. Submitted

PROTOCOL STATUS

Working

MATERIALS

NAME ▾

CATALOG # ▾

VENDOR ▾

Water

primers

PowerUp SYBR Green Master Mix

A25741

MATERIALS TEXT

Primers used in qPCR:

Forward HpF3: 5'GCGGGCTTAGTTCAGGGG 3'

Reverse FpR3: 5'ACTTGTCTTCTCTAATAATAAGG3'

- 1 The qPCR assay for *H. pinnae* detection and quantification was carried out in duplicate using the species-specific primer pair (HpF3/HpR3) in a Mx3000P Thermocycler (Agilent).
- 2 Amplification reactions were performed in a total volume of 10 µl comprising:
- 3 2 µl of genomic DNA (100 ng),

- 4 5 µl of PowerUp™ SYBR™ Green Master Mix (Applied Biosystems),
- 5 0.2 µM each specific primer and
- 6 adjusted to 10µl with distilled water.
- 7 Negative control (without DNA or with *H. pinnae* non-infected fan mussel DNA, previously confirmed by qPCR),
- 8 positive controls (samples with positive cPCR amplification for *H. pinnae*) and
- 9 standard curve (plasmid HpF3/HpR3) were included in each qPCR assay.
- 10 After testing various annealing temperature, the final qPCR program was: 1 cycle for 2 min at 50°C; 1 cycle for 2 min at 95°C, 40 cycles of amplification at 95°C for 15 s, 60°C for 18 s and 72°C for 1 min and followed by a dissociation stage for determining the melt curve (Quantitative SYBR Green with dissociation curve).
- 11 Two standard curves were calculated using serial dilutions of the plasmid and plasmid diluted with DNA of fan mussel;
- 12 the efficiency (E) was from the slope of the standard curve following formula [11] $E=10^{-1/\text{slope}-1}$.
- 13 Melting curve was generated with temperatures increments of 0.5°C s⁻¹ starting at 60°C and ending at 95°C in order to ensure that a single PCR product was amplified for the primers.
- 14 Amplification was also confirmed by electrophoresis on 2% agarose gels, in 1% TAE (Tris acetate EDTA buffer), stained with Red Safe (Niton Biotechnology) and scanned in a GelDoc-It Imagen System Ultraviolet Transilluminator (Biolmaging Systems).



This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited