



Protocol for amplification of three DNA regions from Nephila clavipes (Araneae: Araneidae). Version 2

Luiz Filipe Bartoleti

Abstract

Protocol for amplification of the mitochondrial gene "Citocrome Oxidase I" and the nuclear genes "subunit a from the Histone 3" and "Internal Transcribed Spacer 2" from *Nephila clavipes* (Araneae: Araneidae).

Citation: Luiz Filipe Bartoleti Protocol for amplification of three DNA regions from Nephila clavipes (Araneae:

Araneidae).. protocols.io

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

Published: 06 Nov 2017

Guidelines

Mitochondrial gene Citochrome Oxidase I (COI)

Primers: LCO1490 and HCO2198

Reference: Folmer, O., Black, M., Hoeh, W., Lutz, R., Vrijenhoek, R. (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, **3**(5), 294–299.

PCR Reaction: 1μ L of template DNA, 1U of Taq DNA Polymerase (Thermo-Fisher), 2.5μ L of 10X KCl Buffer (Thermo-Fisher), 2.8μ L of 25mM MgCl₂ (Thermo-Fisher), 1μ L of 10mM dNTP mix (GE Healthcare), 0.5μ L of each forward and reverse primer 10μ M, and ddH_2O to the volume of 25μ L.

PCR cycling: a denaturation step of 3 min at 94° C, 30 cycles of a denaturation step at 94° C for 45s, an annealing step at 51° C for 45s and an extension step at 72° C for 2 min, and a final extension step at 72° C for 3 min.

Nuclear gene for the subunit a of the Histone 3 (H3a)

Primers: H3aF2 and H3aR2

Reference: Colgan, D.J., McLauchlan, A., Wilson, G.D.F. *et al.* (1998) Histone H3 and U2 snRNA DNA sequences and arthropod molecular evolution. *Australian Journal of Zoology*, **46**, 419–437.

PCR Reaction: 1μ L of template DNA, 1U of Taq DNA Polymerase (Thermo-Fisher), 2.5μ L of 10X KCl Buffer (Thermo-Fisher), 2.3μ L of 25mM MgCl₂ (Thermo-Fisher), 0.5μ L of 10mM dNTP mix (GE Healthcare), 0.5μ L of each forward and reverse primer 10μ M, and ddH_2O to the volume of 25μ L.

PCR cycling: a denaturation step of 3-4 min at 94° C, 30 cycles of a denaturation step at 94° C for 45s, an annealing step at 46° C for 1 min and an extension step at 72° C for 1 min, and a final extension step at 72° C for 10 min.

Nuclear intron internal transcribed spacer 2 (ITS2)

Primers: 5.8S and ITS4

Reference: White, T.J., Bruns, T., Lee, S., Taylor, J. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, et al., eds. PCR Protocols: A Guide to Methods and Applications. New York: Academic Press, 315–322.

PCR Reaction: 1μ L of template DNA, 1U of Taq DNA Polymerase (Thermo-Fisher), 2.5μ L of 10X KCl Buffer (Thermo-Fisher), 3.5μ L of 25mM MgCl₂ (Thermo-Fisher), 0.5μ L of 10mM dNTP mix (GE Healthcare), 0.4μ L of each forward and reverse primer 10μ M, and ddH_2O to the volume of 25μ L.

PCR cycling: a denaturation step of 4 min at 95° C, 30 cycles of a denaturation step at 95° C for 45s, an annealing step at 61° C for 45s and an extension step at 72° C for 2 min, and a final extension step at 72° C for 10 min.

Protocol