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Supplemental Lab-Protocol for Barcoding Primers: dEURYT-BRBM2, LCO1490-JJ, LCO1490-JJ2 & LCO1490-JJ3

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Protocol status: Working

We use this protocol and it's working.

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Abstract

As a detailed and extended supplement to Astrin & Stüben, 2008; Astrin et al., 2016; Rulik et al., 2017; Jafari et al., 2023; Jaume-Schinkel et al., 2024.

Guidelines

Follow the general laboratory etiquette. Wear gloves to avoid contamination of the samples. Clean the work bench with 96% EtOH before starting.

Materials

Present protocol is based on Qiagen products:

DNeasy Blood & Tissue Kit: <https://www.qiagen.com/us/products/discovery-and-translational-research/dna-rna-purification/dna-purification/genomic-dna/dneasy-blood-and-tissue-kit?catno=69504>

BioSprint 96 DNA Blood Kit (384): <https://www.qiagen.com/us/products/discovery-and-translational-research/dna-rna-purification/dna-purification/genomic-dna/biosprint-dna-blood-kits?catno=940057>

QIAGEN Multiplex PCR Kit (100): <https://www.qiagen.com/us/products/discovery-and-translational-research/pcr-qpcr-dpcr/pcr-enzymes-and-kits/end-point-pcr/qiagen-multiplex-pcr-kit?catno=206143>

QIAGEN Multiplex PCR *Plus* Kit (100): <https://www.qiagen.com/de-de/products/discovery-and-translational-research/pcr-qpcr-dpcr/pcr-enzymes-and-kits/end-point-pcr/qiagen-multiplex-pcr-plus-kit?catno=206152>

Safety warnings

 None.

Before start

Make sure all chemicals & buffers are prepared and ready to use before starting.

DNA extraction

- 1 Prepare 96 block format or single tube with  20 µL Proteinase K and  180 µL ATL Buffer per well or tube → centrifuge briefly.
- 2 Put a small subsample (leg, piece of tissue ca. 1-2mm) of each sample or whole body of the specimen into the well/tube.
- 3 Sterilize the instruments (forceps, scissors etc.) by flame-scarfing and wiping with ethanol-soaked tissue paper after each sample or use a glass microsphere steriliser like Steri 250.
- 4 Incubate at  56 °C in an thermomixer with gentle shaking overnight (we use constant shaking with  300 rpm) → for more detailed information see:

Citation

Jaume-Schinkel S, Müller B, Avila-Calero S, Kukowka S, Rduch V, Mengual X (2024) . Preserving morphology while extracting DNA: a non-destructive field-to-museum protocol for slide-mounted specimens.

<https://doi.org/10.3897/BDJ.12.e119448>

LINK

- 5 DNA isolation is performed using the magnetic bead-based BioSprint 96 DNA Blood Kit or DNeasy Blood and Tissue Kits (both QIAGEN GmbH - Germany).
- 6 Quantity and quality check of the extracted DNA by e.g. NanoDrop Spectrophotometer, QuantusTM Fluorometer or capillary electrophoresis by Agilent Fragment Analyzer Systems.
- 7 Using DNeasy® Blood & Tissue kit, follow the manuals guidelines:
<https://www.qiagen.com/us/resources/resourcedetail?id=68f29296-5a9f-40fa-8b3d-1c148d0b3030&lang=en>
- 8 Using BioSprint 96 DNA Blood Kit, follow the manuals guidelines:
<https://www.qiagen.com/us/resources/resourcedetail?id=64902c5d-9c3c-4fe3-a3f7-668c4704d9eb&lang=en>



PCR chemicals & conditions

- 9 PCR was done with the QIAGEN Multiplex PCR Kit [Cat. No. 206143] or QIAGEN Multiplex PCR *Plus* Kit [Cat. No. 206152]. Other than the given volume of  50 μL per sample according to the instructions of the manufacturer, here we used a reduced reaction volume of  20 μL per sample:

The master mix for a 96 PCR well plates is composed as follows:  1000 μL Multiplex ,

 200 μL Q-Solution ,

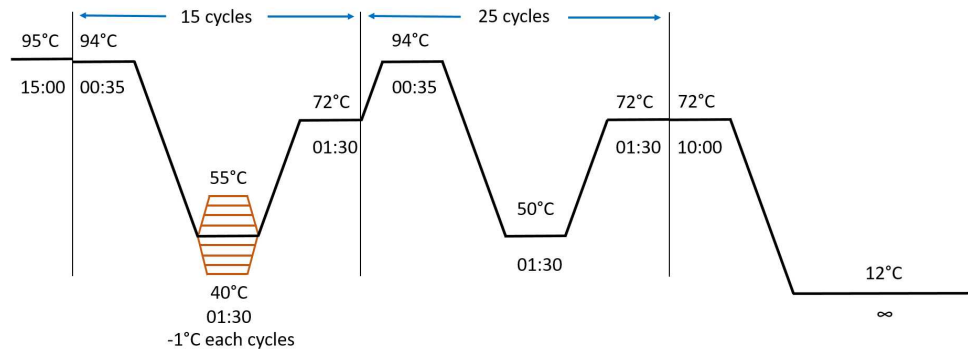
 440 μL RNase-free water ,

 80 μL forward primer (10 pmol/ μL) and  80 μL reverse primer (10 pmol/ μL) .

Each well/tube is filled with  18 μL PCR Mastermix and  2 μL DNA .

- 10 PCR: Initial  00:15:00 at  95 °C , followed by  94 °C denaturation for  00:00:35 ,  55 °C annealing for  00:01:30 and  72 °C elongation for  00:01:30 . Denaturation, annealing and elongation are repeated 15 times, but the annealing temperature is decreased by  1 °C in each cycle. After reaching an annealing temperature of  40 °C , there is no further reduction in temperature. Denaturation, annealing and elongation are repeated 25 times as described above, with a constant annealing temperature of  50 °C . A final elongation at  72 °C for  00:10:00 terminates the PCR and it is then cooled to  12 °C permanently. 28m 35s

Touchdown PCR conditions according to GBOL and GBOL III: Dark Taxa



Conditions for touchdown PCR with forward primers dEURYT-BRBM2, LCO1490-JJ, LCO1490-JJ2 and LCO1490-JJ3 according to GBOL and GBOL III: Dark Taxa

11 Verification of the PCR products by gel electrophoresis.





Protocol references

Citation

Jonas J. Astrin and Peter E. Stüben (2008)

. Phylogeny in cryptic weevils: molecules, morphology and new genera of western Palaearctic Cryptorhynchinae (Coleoptera : Curculionidae).
Invertebrate Systematics.

<https://doi.org/10.1071/IS07057>

LINK

Citation

Astrin JJ, Höfer H, Spelda J, Holstein J, Bayer S, Hendrich L, Huber BA, Kielhorn KH, Krammer HJ, Lemke M, Monje JC, Morinière J, Rulik B, Petersen M, Janssen H, Muster C
(2016). Towards a DNA Barcode Reference Database for Spiders and Harvestmen of Germany.

<https://doi.org/10.1371/journal.pone.0162624>

LINK

Citation

Björn Rulik, Jonas Eberle, Laura von der Mark, Jana Thormann, Manfred Jung, Frank Köhler, Wolfgang Apfel, Andreas Weigel, Andreas Kopetz, Jonas Köhler, Frank Fritzlar, Matthias Hartmann, Karl Hadulla, Joachim Schmidt, Thomas Hören, Detlef Krebs, Florian Theves, Ute Eulitz, André Skale, Dirk Rohwedder, Andreas Kleeberg, Jonas J. Astrin, Matthias F. Geiger, J. Wolfgang Wägele, Peter Grobe, Dirk Ahrens
(2017). Using taxonomic consistency with semi-automated data pre-processing for high quality DNA barcodes.
Methods in Ecology and Evolution.

<https://doi.org/10.1111/2041-210X.12824>

LINK



Citation

Jafari S, Müller B, Rulik B, Rduch V, S Peters R (2023)

. Another crack in the Dark Taxa wall: a custom DNA barcoding protocol for the species-rich and common Eurytomidae (Hymenoptera, Chalcidoidea).

<https://doi.org/10.3897/BDJ.11.e101998>

LINK

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. Preserving morphology while extracting DNA: a non-destructive field-to-museum protocol for slide-mounted specimens.

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Citations

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Astrin JJ, Höfer H, Spelda J, Holstein J, Bayer S, Hendrich L, Huber BA, Kielhorn KH, Krammer HJ, Lemke M, Monje JC, Morinière J, Rulik B, Petersen M, Janssen H, Muster C. Towards a DNA Barcode Reference Database for Spiders and Harvestmen of Germany.

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Step 4

Jaume-Schinkel S, Müller B, Avila-Calero S, Kukowka S, Rduch V, Mengual X. Preserving morphology while extracting DNA: a non-destructive field-to-museum protocol for slide-mounted specimens.

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