

## Supplementary material

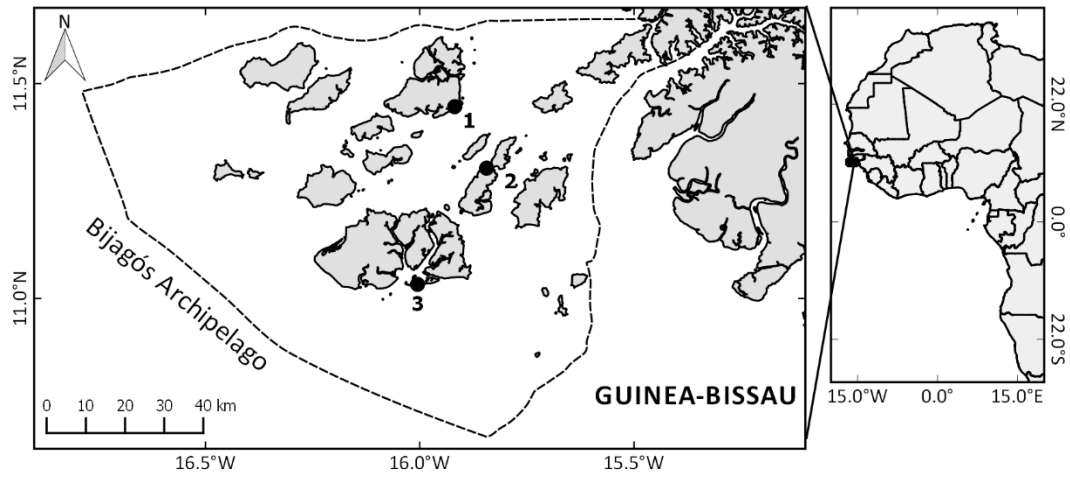


Fig. S1 – Map of the sampling sites in the Bijagós Archipelago (Guinea-Bissau), 1 Formosa, 2 – Bubaque, 3- Orango.

## **Text S1. Supporting Information: Invertebrate processing**

DNA from invertebrates collected in the sampling area was extracted using E.Z.N.A.<sup>®</sup> Tissue DNA Kit - DNA Blood and Tissue Kit (Omega, Bio-Tek) following the manufacturer's protocol and including batches of 23 samples plus a negative control to check for possible contamination. Two DNA elutions of 100 µL were obtained and stored at -20°C until DNA amplification. DNA amplification of the mitochondrial cytochrome c oxidase (COI) gene was performed by amplification of two COI smaller fragments using two primer sets: COI-B2 (BF2: 5'- GCHCCHGAYATRGCHTTYCC -3', BR2: 5'- TCDGGRTGNCCRAARAAYCA-3'; Elbrecht & Leese, 2017;) and COI-LCnew (fwhF1: 5'-YTCHACWAAYCAYAARGAYATYGG-3', C\_R: 5'- GGIGGRTAIACIGTTCAICC-3'; Shokralla et al., 2015; Vamos, Elbrecht, & Leese, 2017). PCR reactions were carried out in a total volume of 10µL comprised 5µL of Qiagen Multiplex PCR Master Mix with 2.5 µL of H<sub>2</sub>O, 0.3µL of each primer 10pM and 2µL of DNA. Cycle conditions for the amplification of the fragment B2 consisted on an initial denaturing step at 95°C for 15min, followed by 40 cycles of denaturing at 95°C for 30s, annealing at 46°C for 60s and extension at 72°C for 45s with a final extension step at 60°C for 10 min. Cycle conditions for the amplification of the fragment LC consisted on an initial denaturing step at 95°C for 15min, followed by 35 cycles of denaturing at 95°C for 30s, annealing at 45°C for 90s and extension at 72°C for 45s with a final extension step at 60°C for 10 min. The successful product amplification was confirmed on a 2% agarose gel the next steps for library preparation followed the manufacturer's protocol for metagenomic sequencing (Illumina) as described above. The library was sequenced using a whole v3 run of a MiSeq desktop sequencer (Illumina; 1000 reads per sample).

**Table S1.** Species-specific blocking primers design for COI Leray fragment.

<b>Host Species</b>	<b>Blocking Primer Sequence</b>
Common Sandpiper <i>Actitis hypoleucos</i>	AGT ATA TCC CCC TCT TGC TGG TAA CCT AGC CCA T [SpC3]
Ruddy Turnstone <i>Arenaria interpres</i>	TGT ATA CCC ACC CCT TGC TGG TAA CCT AGC CCA T [SpC3]
Sanderling <i>Calidris Alba</i>	AGT ATA TCC TCC ACT TGC TGG TAA CCT AGC CCA T [SpC3]
Dunlin <i>Calidris alpina</i>	AGT ATA TCC TCC ACT TGC TGG CAA CTT AGC CCA T [SpC3]
Red Knot <i>Calidris canutus</i>	AGT ATA CCC CCC ACT CGC TGG TAA CCT AGC CCA T [SpC3]
Curlew Sandpiper <i>Calidris ferruginea</i>	AGT ATA CCC CCC ACT CGC CGG TAA CCT AGC CCA T [SpC3]
Kentish Plover <i>Charadrius alexandrinus</i>	CGT ATA CCC GCC TCT GGC CGG TAA TCT AGC CCA C [SpC3]
Common Ringed Plover <i>Charadrius hiaticula</i>	CGT CTA CCC ACC CCT AGC TGG CAA CCT AGC ACA T [SpC3]
White-Fronted Plover <i>Charadrius marginatus</i>	CGT ATA CCC GCC CCT AGC CGG TAA TCT AGC CCA C [SpC3]
Eurasian Oystercatcher <i>Haematopus ostralegus</i>	CGT ATA CCC CCC TCT AGC TGG CAA CCT CGC CCA T [SpC3]
Bar-tailed Godwit <i>Limosa lapponica</i>	AGT TTA TCC TCC TCT CGC TGG TAA CCT TGC CCA C [SpC3]
Whimbrel <i>Numenius phaeopus</i>	CGT ATA TCC CCC TCT CGC TGG CAA CCT AGC CCA C [SpC3]
Grey Plover <i>Pluvialis squatarola</i>	TGT ATA CCC TCC CCT AGC TGG CAA CCT AGC TCA C [SpC3]
Common Greenshank <i>Tringa nebularia</i>	AGT ATA TCC TCC TCT CGC TGG TAA TCT AGC CCA T [SpC3]
Common Redshank <i>Tringa totanus</i>	AGT ATA TCC TCC TCT CGC CGG TAA CCT AGC CCA T [SpC3]

**Table S2.** Frequency of occurrence (FO) of all prey items identified in the droppings of shorebirds species from the Bijagós Archipelago, Guinea-Bissau (samples sizes are indicated). NID - not identified.

Phylum •Class ••Order •••Family ••••Species	<i>Actitis hypoleucos</i> N=4	<i>Arenaria interpres</i> N=3	<i>Calidris alba</i> N=26	<i>Calidris alpina</i> N=6	<i>Calidris canutus</i> N=30	<i>Calidris ferruginea</i> N=21	<i>Charadrius alexandrinus</i> N=9	<i>Charadrius hiaticula</i> N=29	<i>Charadrius marginatus</i> N=7	<i>Haematopus ostralegus</i> N=8	<i>Limosa lapponica</i> N=22	<i>Numenius phaeopus</i> N=28	<i>Pluvialis squatarola</i> N=10	<i>Tringa nebularia</i> N=4	<i>Tringa totanus</i> N=8
<b>Annelida</b>															
•Polychaeta	0.5	0.3	0.6	0.8	0.1	0.8	0.3	0.9	0.3	0	0.4	0.04	0.7	0	0.4
••Eunicida	0	0	0	0	0	0.07	0.08	0.2	0	0	0.1	0	0.5	0	0
•••Eunicidae	0	0	0	0	0	0	0	0.03	0	0	0	0	0.1	0	0
•••• <i>Marphysa</i> sp.	0	0	0	0	0	0	0	0.03	0	0	0	0	0.1	0	0
•••Lumbrineridae	0	0	0	0	0	0	0.08	0.07	0	0	0.1	0	0.2	0	0
•••Onuphidae	0	0	0	0	0	0	0	0.03	0	0	0	0	0.3	0	0
•••• <i>Diopatra neapolitana</i>	0	0	0	0	0	0	0	0.03	0	0	0	0	0.3	0	0
••Phyllodocida	0	0	0.15	0.33	0	0.39	0	0.62	0	0	0.22	0	0.4	0	0.13
•••Glyceridae	0	0	0.04	0	0	0.21	0	0.24	0	0	0.22	0	0.2	0	0.13
•••• <i>Glycera</i> sp.	0	0	0.04	0	0	0.21	0	0.24	0	0	0.22	0	0.2	0	0.13
•••Nereididae	0	0	0.12	0.33	0	0.18	0	0.59	0	0	0	0	0.1	0	0
••••Nereis	0	0	0.12	0.33	0	0.18	0	0.59	0	0	0	0	0.1	0	0
••Polychaeta_Maldanidae	0	0.33	0.04	0	0	0.21	0.17	0.03	0.14	0	0.04	0	0	0	0.13
•••Maldanidae	0	0.33	0.04	0	0	0.21	0.17	0.03	0.14	0	0.04	0	0	0	0.13
•••• <i>Petaloproctus terricolus</i>	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0
••Polychaeta_Orbiniidae	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0
•••Orbiniidae	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0
Spionida	0	0	0	0	0	0.11	0	0	0	0	0	0	0	0	0
••Spionidae	0	0	0	0	0	0.11	0	0	0	0	0	0	0	0	0
•••• <i>Dipolydora</i> sp.	0	0	0	0	0	0.11	0	0	0	0	0	0	0	0	0

**Table S2** (continued)

••Terebellida	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0
Polychaeta NID	0.5	0	0.38	0.5	0.1	0.18	0.08	0.28	0.14	0	0.04	0.04	0.1	0	0.13
<b>Arthropoda</b>															
•Arachnida	0	0	0.04	0	0	0	0	0.03	0	0	0	0	0	0	0
••Araneae	0	0	0.04	0	0	0	0	0.03	0	0	0	0	0	0	0
•••Lycosidae	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
•••Salticidae	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0
•Hexanauplia	0	0	0.08	0	0	0.04	0	0	0	0	0.09	0	0	0	0
••Calanoida	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0	0
Hexanauplia NID	0	0	0.08	0	0	0	0	0	0	0	0.09	0	0	0	0
•Insecta	0.25	0	0.15	0	0.03	0.07	0.08	0.24	0.71	0.13	0.17	0.04	0.4	0.5	0
••Coleoptera	0	0	0	0	0.03	0	0	0.1	0.43	0.13	0.09	0	0.1	0	0
•••Dermestidae	0	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0
•••Tenebrionidae	0	0	0	0	0	0	0	0.03	0	0	0.04	0	0	0	0
••Dermaptera	0	0	0	0	0	0	0	0	0.29	0	0	0	0.1	0	0
•••Labiduridae	0	0	0	0	0	0	0	0	0.29	0	0	0	0	0	0
•••• <i>Labidura riparia</i>	0	0	0	0	0	0	0	0	0.29	0	0	0	0	0	0
••Diptera	0	0	0.04	0	0	0.07	0	0	0	0	0	0	0	0.25	0
••Hemiptera	0	0	0.12	0	0	0	0	0	0	0	0	0	0.1	0	0
•••Cicadellidae	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0
•••Delphacidae	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0
••Hymenoptera	0	0	0	0	0	0	0	0	0.43	0	0.04	0.04	0	0	0
•••Formicidae	0	0	0	0	0	0	0	0	0.43	0	0	0.04	0	0	0
•••Ichneumonoidea	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0
•••• <i>Stilbops</i> sp.	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0
••Lepidoptera	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0
••Odonata	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
•••Libellulidae	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
•••• <i>Orthetrum chrysis</i>	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0

Table S2 (continued)

**Orthoptera	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0
***Acrididae	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
***Gryllidae	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0
**** <i>Gryllus bimaculatus</i>	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0
***Tetrigidae	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
***Tettigoniidae	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
**Psocoptera	0.25	0	0.04	0	0	0	0.08	0	0	0	0	0	0	0	0
***Liposcelididae	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**** <i>Liposcelis bostrychophila</i>	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0
***Psyllipsocidae	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0
**** <i>Dorypteryx domestica</i>	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0
Insecta NID	0	0	0	0	0	0	0	0.07	0	0	0	0	0.1	0.25	0
•Malacostraca	0.75	0.67	0.92	0.67	0.23	0.75	1	0.9	0.57	0.63	0.83	0.96	1	1	1
**Amphipoda	0	0	0.65	0.67	0.03	0.04	0	0.52	0	0	0	0.04	0.1	0	0
***Ampithoidae	0	0	0.08	0.17	0	0	0	0.03	0	0	0	0	0	0	0
**** <i>Cymadusa</i> sp.	0	0	0.08	0.17	0	0	0	0.03	0	0	0	0	0	0	0
***Caprellidae	0	0	0	0	0	0.04	0	0	0	0	0	0.04	0	0	0
**** <i>Caprella scaura</i>	0	0	0	0	0	0.04	0	0	0	0	0	0.04	0	0	0
***Corophiidae	0	0	0.58	0.67	0.03	0	0	0.38	0	0	0	0	0.1	0	0
**Cumacea	0	0	0	0	0	0	0	0.03	0	0	0	0.04	0.1	0	0
**Decapoda	0.75	0.67	0.69	0.33	0.17	0.71	1	0.72	0.57	0.63	0.83	0.96	1	1	1
***Alpheidae	0	0	0	0	0	0.04	0	0.34	0	0	0	0	0	0	0
**** <i>Alpheus</i> sp.	0	0	0	0	0	0.04	0	0.28	0	0	0	0	0	0	0
**** <i>Alpheus buckupi</i>	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0
***Crangonidae	0	0	0.08	0	0	0.04	0	0	0	0	0	0.04	0	0	0
***Grapsidae	0	0	0	0	0.03	0.07	0.08	0.1	0	0	0.09	0.11	0	0	0
**** <i>Geograpsus</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0	0
**** <i>Goniopsis pelii</i>	0	0	0	0	0.03	0.07	0.08	0.07	0	0	0.09	0.04	0	0	0
**** <i>Pachygrapsus gracilis</i>	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0

**Table S2** (continued)

***Ocypodidae	0.5	0.67	0.38	0.17	0.03	0.57	1	0.55	0.57	0.63	0.57	0.82	0.8	0	0.5
*** <i>Afruca tangeri</i>	0.5	0.67	0.38	0.17	0.03	0.57	1	0.55	0.57	0.63	0.57	0.82	0.8	0	0.5
***Panopeidae	0	0	0.04	0	0.03	0	0.08	0.07	0	0	0.09	0.07	0.1	0.25	0.5
*** <i>Panopeus</i> sp.	0	0	0	0	0.03	0	0.08	0.03	0	0	0.04	0.04	0	0.25	0
*** <i>Panopeus africanus</i>	0	0	0.04	0	0	0	0	0.03	0	0	0.04	0.04	0.1	0	0.5
***Penaeidae	0	0.33	0.35	0.17	0.13	0.18	0.08	0.24	0	0	0.09	0.07	0.1	0.75	0.88
*** <i>Penaeus</i> sp.	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0
*** <i>Penaeus kerathurus</i>	0	0.33	0.35	0.17	0.13	0.18	0.08	0.17	0	0	0.09	0.07	0.1	0.75	0.88
Portunidae	0.25	0.33	0.19	0	0.03	0.14	0	0.48	0.14	0	0.13	0.07	0.1	0.25	0.13
*** <i>Callinectes</i> sp.	0.25	0.33	0.19	0	0.03	0.14	0	0.48	0.14	0	0.13	0.04	0.1	0	0.13
*** <i>Callinectes pallidus</i>	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0.25	0
***Sesarmidae	0.25	0	0	0	0	0	0.08	0.03	0	0	0.09	0.18	0.1	0	0
*** <i>Armases elegans</i>	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0
*** <i>Metagrapsus curvatus</i>	0	0	0	0	0	0	0.08	0.03	0	0	0.09	0.11	0.1	0	0
*** <i>Perisesarma huzardi</i>	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0	0
***Upogebiidae	0.25	0	0.04	0	0	0.04	0	0	0	0	0.09	0.04	0	0.25	0
***Varunidae	0	0	0.08	0	0.03	0.39	0	0	0	0	0.39	0.18	0.1	0.25	0.13
*** <i>Asthenognathus atlanticus</i>	0	0	0.08	0	0.03	0.39	0	0	0	0	0.39	0.18	0.1	0.25	0.13
**Isopoda	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0.25	0
***Cymothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0
**Stomatopoda	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0
***Squillidae	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0
*** <i>Squilla cadenati</i>	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0
Malacostraca NID	0	0	0	0	0.03	0.04	0	0.03	0	0	0	0	0	0	0
•Ostracoda	0	0	0	0	0.03	0.04	0	0.07	0	0	0	0	0.1	0	0
Arthropoda NID	0	0.33	0.04	0	0	0.04	0	0	0	0	0	0	0	0	0
<b>Chordata</b>															
•Actinopterygii	0	0	0	0.17	0.03	0.18	0	0.76	0	0	0	0.07	0	1	0.5
**Cichliformes	0	0	0	0.17	0	0.07	0	0.21	0	0	0	0	0	0	0

**Table S2** (continued)

•••Cichlidae	0	0	0	0.17	0	0.07	0	0.21	0	0	0	0	0	0	0
••• <i>Coptodon</i> sp.	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0
••• <i>Hemichromis</i> sp.	0	0	0	0	0	0	0	0.17	0	0	0	0	0	0	0
••• <i>Sarotherodon melanotheron</i>	0	0	0	0.17	0	0.07	0	0.17	0	0	0	0	0	0	0
••Clupeiformes	0	0	0	0	0	0.04	0	0.03	0	0	0	0	0	0	0
•••Clupeidae	0	0	0	0	0	0.04	0	0.03	0	0	0	0	0	0	0
••• <i>Sardina pilchardus</i>	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
••• <i>Sardinella maderensis</i>	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0	0
••Gobiiformes	0	0	0	0	0.03	0.11	0	0.69	0	0	0	0	0	0.75	0.25
•••Gobiidae	0	0	0	0	0.03	0.11	0	0.69	0	0	0	0	0	0.5	0.13
••• <i>Periophthalmus barbarus</i>	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0
••• <i>Porogobius schlegelii</i>	0	0	0	0	0.03	0.07	0	0.59	0	0	0	0	0	0.25	0
••Mugiliformes	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0.13
•••Mugilidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0.13
••• <i>Chelon dumerili</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0.13
••• <i>Liza grandisquamis</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0
Perciformes	0	0	0	0	0	0.07	0	0	0	0	0	0.04	0	0.5	0.13
Gerreidae	0	0	0	0	0	0.07	0	0	0	0	0	0.04	0	0	0
Haemulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0.13
••• <i>Pomadasys</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13
••• <i>Pomadasys rogerii</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0
•Pleuronectiformes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.13
••Spariformes	0	0	0	0	0	0.04	0	0.03	0	0	0	0	0	0	0
•••Sparidae	0	0	0	0	0	0.04	0	0.03	0	0	0	0	0	0	0
••• <i>Pagellus acarne</i>	0	0	0	0	0	0.04	0	0.03	0	0	0	0	0	0	0
Actinopterygii NID	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0.25	0
<b>Cnidaria</b>															
•Hydrozoa	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0
••Siphonophorae	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0



**Table S2** (continued)

•••Agalmatidae	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0
••• <i>Nanomia bijuga</i>	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0
<b>Gastrotricha</b>															
•Gastrotricha_class not assigned	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0	0
••Chaetonotida	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0	0
<b>Hemichordata</b>															
•Enteropneusta	0	0	0	0	0	0	0.08	0	0	0	0	0	0	0	0
<b>Mollusca</b>															
•Bivalvia	0.25	0.33	0.27	0.5	0.97	0.57	0	0.28	0.14	0.13	0.35	0.14	0.6	0	0.13
••Arcoida	0	0	0	0	0.33	0	0	0	0	0.13	0.04	0	0	0	0
•••Arcidae	0	0	0	0	0.33	0	0	0	0	0.13	0.04	0	0	0	0
•••• <i>Senilia senilis</i>	0	0	0	0	0.33	0	0	0	0	0.13	0.04	0	0	0	0
••Cardiida	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0
•••Solecurtidae	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0
•••• <i>Tagelus adansonii</i>	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0
••Lucinida	0	0	0	0	0.1	0.07	0	0	0	0	0	0	0	0	0
••Venerida	0.25	0	0.08	0.33	0.87	0.36	0	0.1	0	0	0.13	0.04	0.1	0	0
•••Veneridae	0.25	0	0.08	0.33	0.87	0.32	0	0.1	0	0	0.13	0.04	0.1	0	0
•••• <i>Pelecycora isocardia</i>	0.25	0	0.08	0.33	0.87	0.32	0	0.1	0	0	0.13	0.04	0.1	0	0
Bivalvia NID	0	0.33	0.23	0.33	0.2	0.18	0	0.17	0.14	0	0.17	0.14	0.5	0	0.13
•Gastropoda	0	0.33	0.38	0.33	0.73	0.21	0.08	0.14	0	0.13	0.13	0.14	0.7	0.25	0.13
••Caenogastropoda	0	0	0	0	0.03	0	0	0.03	0	0	0.04	0	0	0	0
•••Skenidae	0	0	0	0	0.03	0	0	0.03	0	0	0.04	0	0	0	0
••Cephalaspidea	0	0	0	0	0.23	0.04	0	0	0	0	0	0	0.6	0.25	0
•••Haminoeidae	0	0	0	0	0.23	0.04	0	0	0	0	0	0	0.6	0.25	0
•••• <i>Haminoea</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0
••••• <i>Haminoea antillarum</i>	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0
••••• <i>Haminoea orbignyana</i>	0	0	0	0	0.23	0	0	0	0	0	0	0	0.5	0.25	0
••Littorinimorpha	0	0.33	0.38	0.33	0.63	0.18	0.08	0.1	0	0.13	0.09	0.14	0.2	0	0.13

**Table S2** (continued)

•••Assimineidae	0	0.33	0.31	0.33	0.53	0.14	0.08	0.03	0	0	0.09	0.07	0.1	0	0	
•••Assimineae	0	0.33	0.23	0.33	0.53	0.14	0.08	0	0	0	0.09	0.07	0.1	0	0	
•••Hydrobiidae	0	0	0.12	0.17	0.5	0.07	0	0.1	0	0.13	0	0.07	0.2	0	0.13	
••Trochida	0	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0	
••Trochidae	0	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0	
••• <i>Gibbula</i> sp.	0	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0	
Gastropoda NID	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0	
<b>Nemertea</b>																
•Pilidiophora	0	0	0.04	0	0	0	0	0.03	0	0	0	0	0.1	0	0	
••Heteronemertea	0	0	0.04	0	0	0	0	0.03	0	0	0	0	0.1	0	0	
<b>Porifera</b>																
•Demospongiae	0	0.33	0.04	0.17	0.03	0.07	0	0.03	0	0	0	0	0	0	0	
<b>Sipuncula</b>																
•Sipunculidea	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0	

**Table S3.** Binomial generalized linear model outputs testing performance of each method for prey identification (16S, COI, molecular, i.e., the two primers combined and morphology), using sample as random factor, from droppings of shorebirds from the Bijagós Archipelago, Guinea-Bissau (prey to the order taxonomic level; N=182). SE – Standard Error.

Variable	Estimate	SE	t-value	p-value
Intercept	-0.199	0.149	-1.33	0.183
COI	0.331	0.210	1.57	0.116
molecular	1.862	0.251	7.40	<0.001
morphology	-0.248	0.213	-1.17	0.243

**Table S4.** Pairwise comparison of the estimated marginal means obtained from the generalized linear model (Table S3). SE – Standard Error.

Contrast	Estimate	SE	t ratio	p-value
16S - COI	-0.331	0.210	-1.57	0.395
16S - molecular	-1.862	0.251	-7.40	<0.001
16S - morphology	0.248	0.213	1.17	0.648
COI - molecular	-1.531	0.251	-6.10	<0.001
COI - morphology	0.579	0.213	2.72	0.033
molecular - morphology	2.110	0.253	8.33	<0.001

**Table S5.** Generalized linear model outputs testing performance of each method for prey identification (16S, COI, molecular, i.e., the two primers combined and morphology), using sample as random factor, from droppings of shorebirds from the Bijagós Archipelago, Guinea-Bissau (prey to the family taxonomic level; N=181). SE – Standard Error.

Variable	Estimate	SE	t-value	p-value
Intercept	-0.1439	0.149	-0.97	0.334
COI	-0.1567	0.212	-0.74	0.459
molecular	2.071	0.268	7.72	<0.001
morphology	-1.783	0.268	-6.64	<0.001

**Table S6.** Pairwise comparison of the estimated marginal means obtained from the generalized linear model (Table S5). SE – Standard Error.

Contrast	Estimate	SE	t ratio	p-value
16S - COI	0.157	0.212	0.74	0.881
16S - molecular	-2.071	0.268	-7.71	<0.001
16S - morphology	1.783	0.268	6.64	<0.001
COI - molecular	-2.228	0.269	-8.28	<0.001
COI - morphology	1.627	0.269	6.04	<0.001
molecular - morphology	3.854	0.316	12.21	<0.001

## References

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