

## RESEARCH NOTE

### Putative sex-linked heteroplasmy in the tellinid bivalve *Limecola balthica* (Linnaeus, 1758)

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Doubly uniparental inheritance (DUI) is a remarkable exception to the maternal inheritance of mitochondria in metazoans. Found in bivalves, DUI is characterized by females transmitting ‘female’ (F) mitochondria that persist in oocytes and in somatic tissues of both sexes, whereas males pass on ‘male’ (M) mitochondria that persist in the male germ line (reviewed by [Zouros, 2013](#)). The evolution and maintenance of this feature remains unclear, especially as its prevalence among bivalve species is still unknown. DUI can be detected by looking for distinct mitochondrial DNA sequences (or mitotypes) in the sperm and somatic tissues of males. Although it has been found in about 40 species ([Dégletagne et al., 2015](#)), authors have pointed out the difficulties of detecting DUI, as the genetic distance between the F and M mitotypes can be very high, reaching 50% amino-acid divergence in some unionoids ([Doucet-Beaupré et al., 2010](#)). Testing for the presence of DUI is therefore of prime interest for understanding how this feature spread within the Bivalvia and how many times it evolved.

We set out to test for the presence of DUI in *Limecola balthica* (Linnaeus, 1758) (previously known as *Macoma balthica*; [Huber, 2015](#)). This marine bivalve is gonochoristic ([Lammens, 1967](#)) and belongs to the family Tellinidae, for which DUI has not been reported to date. The closest relative of *L.*

*balthica* for which DUI has been detected is another tellinoidean, *Donax trunculus* (Theologidis *et al.*, 2008). A nuclear genome scan on *L. balthica* suggested that mito–nuclear genetic incompatibilities may be involved in maintaining barriers to gene flow among European populations, as multiple genes involved in ATP production and transport were detected as  $F_{ST}$  outliers (Pante *et al.*, 2012). If *L. balthica* is characterized by DUI, mito–genetic incompatibilities could be expressed not only between the F mitotype and nuclear genes (in somatic tissues and oocytes in females), but also between the M mitotype and nuclear genes in sperm of interpopulational hybrids. This context makes the search for DUI particularly relevant for this species.

Ten individuals of *L. balthica* were sampled on the sandy mudflat of Aytré, France (46°07'32.51" N, 1°7'42.94" W). This population belongs to the *rubra* lineage, based on mitochondrial and nuclear data (Becquet *et al.*, 2012). Sampling was conducted on 20 April, 2016, when most individuals had fully mature gametes (Saunier, 2015). Gonads were nicked with a clean scalpel and gametes were pipetted out. Individuals were sexed by observing gametes under a light microscope; individuals that could not be unambiguously sexed were left out of the study. Gametes and foot tissue were sampled for one female and four males; gametes from a fifth male were sampled. Total DNA was extracted from  $\leq 15$  mg of tissue (gametes and foot muscle) using the Nucleospin Tissue kit (Machery-Nagel, Düren, Germany) following the manufacturer's protocol. DNA was quantified using a Nanodrop ND-2000 spectrophotometer (Thermo Scientific, Waltham, USA) and gel electrophoresis (1% agarose).

To investigate the presence of sex-linked heteroplasmy, three mitochondrial genes that are evenly spaced on the mitogenome of *L. balthica* were selected: *cox1*, *cox2* and *rnL* (Saunier *et al.*, 2014). DNA amplifications were performed using the Perfect Taq PCR kit (5 Prime; Dominique Dutscher, Brumath, France) with the following conditions: 0.75 unit of Taq, 1X reaction buffer, 200  $\mu$ M of each dNTP, 0.2  $\mu$ M of each primer, 1.5 mM of  $MgCl_2$ , 15-60 ng of template DNA in a total volume of 25  $\mu$ L. Reactions were performed on a SensoQuest (Göttingen, Germany) thermal cycler; thermal profiles

are provided in Table 1. We ran both an extraction blank and PCR negative controls. PCR purification and Sanger sequencing (ABI 3730xl) were done by GATC (Konstanz, Germany).

A first attempt to amplify the mitochondrial *cox1* and *cox2* genes was made using primers specific to *L. balthica* (Table 1). While sharp bands were obtained from ovocytes and foot muscle from both sexes, sperm samples yielded very little to no amplification (example gel in Fig. 1). When sperm PCR was concentrated enough to attempt sequencing, the same haplotype was systematically retrieved from sperm and muscle, for each individual tested (this was true for both *cox1* and *cox2*). The sequences retrieved were blasted (blastn; Zhang *et al.*, 2000) and showed matches of 99–100% with known *cox1* and *cox2* haplotypes (Luttikhuizen *et al.*, 2003; Saunier *et al.*, 2014). We relaxed the PCR conditions by (1) attempting a *cox1* amplification using primers that should amplify broadly among molluscs (Folmer *et al.*, 1994; Table 1) and (2) running a gradient PCR on *cox2*, but the same result was obtained (no sequencing was attempted).

We therefore targeted a more conserved mitochondrial gene, *rnL*, with broad-spectrum primers (Palumbi *et al.*, 2002; Table 1); sharp PCR amplifications were obtained from sperm, ovocytes and foot tissues from all individuals of both sexes. Sequences were initially 470 bp long and quality-trimmed to 287 (sperm) and 284 bp (all other sequences). Trimmed sequences from ovocytes, male and female muscle tissues were identical (GenBank acc. no. KX831970) and blasted to known *L. balthica* haplotypes (blastn: 100% query coverage, 99% identity, e-value < 1e-140; best matches: Saunier *et al.*, 2014). The two *rnL* haplotypes (0.7% divergence; GenBank acc. nos KX831969, KX838910) recovered from trimmed sperm sequences blasted to other tellinid bivalves (74-84% query coverage, 81-83% identity, e-value < 1e-40; *Pinguitellina* sp., AB751357; *Tellina staurella*, AB751346; *Moerella rutila*, AB751334; *L. balthica*, KM373201; *Nitidotellina iridella*, AB751340; *Loxoglypta* sp. AB751338, AB751339).

These results taken together (failed amplification for sperm at *cox1* and *cox2* and sex-linked heteroplasmy at *rnL*) suggest that the presence of DUI should be further investigated in *L. balthica*. In the case of *cox1* and *cox2*, we were able to get very faint PCR product for some sperm samples. In the presence of DUI, these products might reflect contamination of sperm samples by somatic cells containing the F mitotype (Venetis *et al.*, 2006), a pattern that was also reported for *D. trunculus* (Theologidis *et al.*, 2008). At *rnL*, the Kimura 2-parameter distance between the ovocyte/muscle haplotype and the sperm strict consensus sequence was 25.7% (alignment in Supplementary Material). This is on par with the F/M mitotype distance observed for *rnL* in *D. trunculus* (Kimura 2-parameter = 36.6%; 68% of our sequenced gene fragment overlaps with that of *D. trunculus*; Theologidis *et al.*, 2008). The male sequences were 3 bp longer than the female ones, a pattern that was also reported in e.g. *Meretrix lamarckii* (Bettinazzi *et al.*, 2016). We thus conclude that DUI is probably present in the Tellinidae, a bivalve family for which DUI had not been detected before.

Future work should now focus on sequencing the full male mitochondrial genome for *L. balthica* in order to measure the overall divergence between male and female mitotypes and evaluate its functional significance.

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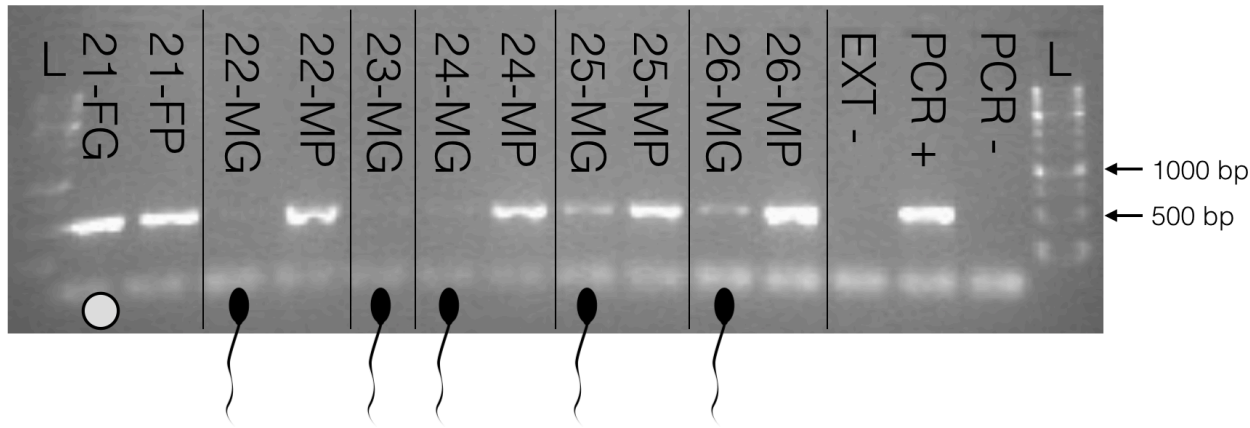
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**Table 1.** Primers used for PCR amplification and thermal profiles.

Gene	Primer name	Sequence (5' - 3')	Tm (°C)	Cycle	Size (bp)	Reference
<i>cox1</i>	1 CO1F	TTAGTGACTTCACACGGTTTGC	55.6	1-2: 93:30,57:30,72:40	437	Luttikhuizen <i>et al.</i> (2003)
	2 CO1R	AGTACAGGTATAGCAACCACCAG	56.1			Luttikhuizen <i>et al.</i> (2003)
	3 LCO1490-F	GGTCAACAAATCATAAAGATATTGC	51.0	3-4: 93:30,45:30,72:30	580	Folmer <i>et al.</i> (1994)
	4 HCO2198-R	TAAACTTCAGGGTGACCAAAAAATCA	55.3			Folmer <i>et al.</i> (1994)
<i>cox2</i>	5 CO2F	GGTTGTGCTAGTGGTTTGGG	59.4	5-6: 93:30,57:30,72:40	516	This study
	6 CO2R	AAACTGCCCATACCGGAAGC	59.4			This study
<i>rnL</i>	7 16Sar-L	CGCCTGTTTATCAAAAACAT	49.2	7-8: 93:30,43:30,72:30	515	Palumbi <i>et al.</i> (2002)
	8 16Sbr-H	CCGGTCTGAACTCAGATCACGT	58.6			Palumbi <i>et al.</i> (2002)

Size: PCR fragment size calculated based on sequence from the full *cox1*, *cox2* and *rnL* genes (complete genome from individual A6, KM373201; Saunier *et al.*, 2014). Cycle: thermal profiles (temperature in °C: time in s; 30-32 cycles) following an initial denaturation step at 93 °C for 3 min and preceding a final elongation step at 72 °C for 5 min.

**Figure 1.** Example of PCR results on mitochondrial DNA amplification from gamete and foot tissue of *Limecola balthica*. Gel electrophoresis (1% agarose) for the *cox2* gene. Specimens are labeled as follows: individual number followed by a dash, followed by the sex of the individual (M, male; F, female) and the tissue type (G, gamete; P, foot tissue); L, 1kb DNA ladder; EXT, the PCR amplification of extraction negative control; PCR + and –, PCR positive and negative controls, respectively.





159 **Supplementary Material.**

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161 Alignment of *rnL* sequences retrieved from sperm (24-MG) and from foot tissue (24-MP) from  
162 a single individual of *Limecola balthica*, showing the extent of intra-individual sequence  
163 divergence. Indels are symbolized with semi-colons. Sequence differences (point mutations  
164 or indels) are symbolized with filled circles. The coordinates on the *rnL* gene precede the  
165 sequences; this number corresponds to the position on the gene based on the reference  
166 genome A6 from foot muscle (GenBank Acc. KM373201). The raw chromatograms are  
167 presented for the 1104-1113 portion of the alignment (black box). Alignment was performed  
168 in Sequencher v. 5.4.1.

169

24-MG #941 accccatcgagcttggttacttatactatTTTTTA:tatg  
 24-MP accctgttgagcttggt:aaggctagt:tctcttagaatt  
 . . . . .

24-MG #981 tgag:gatgttttgtcggggctgataggga:gggaaagaa  
 24-MP agagctatgtttgttcggggctga:agggaaggagataa  
 . . . . .

24-MG #1021 tgcctcctttgttaata:tgaagatccggcattaggccga  
 24-MP tgccttctatgtta:tagaaaagatcc::aatttgattga  
 . . . . .

24-MG #1061 ttggaagaagatagttaccgtggggataacagcgcaat:g  
 24-MP ttgggtggaagatagttaccacagggataacagcgcaatca  
 . . . . .

24-MG #1101 ttccattaagcacatatttgagggggcggttgcgacctc  
 24-MP ttctgat:aaggccatatttaaggagtggtttgcgacctc  
 . . . . .

24-MG #1141 gatggtgaatcaggattatctattaggtgcagcagcttag  
 24-MP gatggtgaatcaaaatt:tctactaggtgtagcagcttag  
 . . . . .

24-MG #1181 taagtgggactgttcgtcctttgaaatcctacgtgatctg  
 24-MP taagtgggactgttcgtcctttaaaattttacgtgatctg  
 . . . . .

24-MG #1221 agttcagaccgg  
 24-MP agttcagaccgg

