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Mitochondrial genome of the Peruvian scallop *Argopecten purpuratus* (Bivalvia: Pectinidae)

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31 **Abstract**

32 The mitochondrial genome of the Peruvian scallop *Argopecten purpuratus* was
33 determined. The length of the mitochondrial coding region is 15,608 bp. A typical
34 bivalve mitochondrial composition was detected with 12 protein-coding genes,
35 two ribosomal RNA genes, and 21 transfer RNA genes, with the absence of the
36 *atp8* gene. Fifty percent of the protein-coding genes use typical ATG start codon,
37 whereas five genes utilize ATA as their start codon. Only one gene was found to
38 utilize TTG as its start codon. The *A. purpuratus* mitogenome shows a significant
39 similarity to that of *A. irradians irradians*, in length as well as in gene
40 composition.

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The Peruvian scallop, *Argopecten purpuratus* (Pteriomorpha, Pectinidae), is naturally distributed along the Southern Pacific Coast, being the second most commercially important mollusk species in Peru. Surprisingly, few molecular studies have been carried out in this species and some nuclear and mitochondrial markers have been developed (Mandiola-Quillongo et al., 2012; Marín et al., 2012, 2013). In spite of the high economic value and unique mitogenome features (e.g. high gene rearrangement) that make Pectinidae species ideal subjects for taxonomic and evolutionary studies, to date only five scallop mitogenomes have been determined. In this study, the complete mitochondrial coding region of *A. purpuratus* was sequenced by primer walking strategy.

The length of the nearly complete *A. purpuratus* mitogenome is 15,608 bp (GenBank access: KF601246). The largest non-coding region of the *A. purpuratus* mitogenome is located between the genes *trnG2* and *nad2*. This region is characterized for the presence of tandems AT repeats and homopolymer runs, which affect the sequence process by polymerase slippage. Different strategies were applied to overcome sequence drop-off and double peaks after homopolymer regions. However, we could not sequence a partial fragment of the control region.

The structure and organization of *A. purpuratus* mitogenome showed characteristics of a typical marine bivalve mitogenome: 12 protein-coding genes (*atp6*, *cox1-3*, *cob*, *nad1-6*, *nad4L*), two ribosomal RNA genes, and 21 transfer RNAs (Table 1). As in most marine bivalves the *atp8* gene is missing. All identified genes are encoded in the same strand. The A + T content was 56.2%

(A= 19.8%, T= 36.4%, G= 28.4% and C= 15.4%). As in other marine bivalves, *A. purpuratus* mitogenome showed different alternate start codons. The most common eukaryotic genome start codon ATG was found in 50% of all protein-coding genes (*nad1*, *cox1*, *nad6*, *cox2*, *nad4L*, *nad4*), whereas five genes (*nad2*, *nad5*, *atp6*, *cox3*, *nad3*) utilize ATA as their start codon. Only the gene *cob* was found to utilize TTG as its start codon. Eleven of the open reading frames in *A. purpuratus* mitogenome end with a TAG stop codon. The remaining gene *nad4* ends with a TAA stop codon. No incomplete (T-, TA-) stop codons were found. In *A. purpuratus*, the length of the 12S rRNA and 16S rRNA genes were 903 and 1317 bp and A + T content of 55.4% and 58.2%, respectively. The 12S rRNA gene is located between *trnK* and *trnQ* genes, and the 16S rRNA gene between *trnR* and *cox1* genes. The mitogenome of *A. purpuratus* encodes a total of 21 tRNA genes, ranging from 62 (*trnF*) to 71 nucleotides (*trnI*). *A. purpuratus* appeared approximately 6 million years ago in the south Pacific Ocean and became separated from the Atlantic stock with the closure of the Central American seaway. On the other hand, *A. irradians* split off around 1.5 million years ago during the Pleistocene (Waller, 1969). Thus, relatively low divergence time estimation between *Argopecten* species (4.5-5 million years) may be reflected in their low levels (genetic distance 0.18) of mitogenome differentiation.

99 **Declaration of interest**

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Table 1. Annotation of the mitochondrial genome of *Argopecten purpuratus*.

Gene	Location	Size (bp)	Start codon	Stop codon	Intergenic nucleotides
<i>nad2</i>	1-993	993	ATA	TAG	
<i>trnD</i>	996-1059	64			2
<i>trnI</i>	1061-1131	71			1
<i>trnH</i>	1133-1195	63			1
<i>trnW</i>	1199-1266	68			3
<i>trnP</i>	1266-1328	63			-1
<i>nad5</i>	1368-3050	1683	ATA	TAG	39
<i>atp6</i>	3174-3809	636	ATA	TAG	123
<i>trnC</i>	3809-3871	63			-1
<i>trnY</i>	3876-3939	64			4
<i>trnT</i>	3939-4005	67			-1
<i>trnA</i>	4006-4068	63			0
<i>trnL1</i>	4067-4131	65			-2
<i>trnM</i>	4131-4198	67			-1
<i>trnG1</i>	4202-4266	65			3
<i>trnK</i>	4265-4329	65			-2
<i>rrnS</i>	4332-5234	903			2
<i>trnQ</i>	5237-5302	66			2
<i>trnV</i>	5308-5340	63			5
<i>nad1</i>	5492-6319	828	ATG	TAG	151
<i>trnR</i>	6349-6416	68			29
<i>rrnL</i>	6448-7764	1317			31
<i>cox1</i>	7765-9366	1602	ATG	TAG	0
<i>trnF</i>	9367-9428	62			0
<i>trnE</i>	9500-9563	64			71
<i>nad6</i>	9725-10252	528	ATG	TAG	161
<i>trnL2</i>	10252-10315	64			-1
<i>cob</i>	10317-11474	1158	TTG	TAG	1
<i>cox2</i>	11598-12173	576	ATG	TAG	123
<i>nad4L</i>	12174-12506	333	ATG	TAG	0
<i>cox3</i>	12503-13330	828	ATA	TAA	-4
<i>nad3</i>	13343-13690	348	ATA	TAG	12
<i>trnN</i>	13758-13821	64			67
<i>nad4</i>	13862-15139	1278	ATG	TAA	40
<i>trnG2</i>	15512-15577	66			372