

MITOGENOME ANNOUNCEMENT

**The complete mitogenome of the invasive spiny-cheek crayfish
Orconectes limosus (Rafinesque, 1817) (Crustacea: Decapoda:
Cambaridae)**

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Abstract

The invasive freshwater crayfish *Orconectes limosus* mitogenome was recovered by genome skimming. The mitogenome is 16,223 base pairs in length consisting of 13 protein-coding genes, 2 ribosomal subunit genes, 22 transfer RNAs, and a non-coding AT-rich region. The *O. limosus* mitogenome has an AT bias of 71.37% and base composition of 39.8% for T, 10.3% for C, 31.5% for A, and 18.4% for G. The mitogene order is identical to two other genera of northern hemisphere crayfish that have been sequenced for this organelle.

Keywords

Astacidea, mitochondria, molecular resources

History

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Due to their economic importance and popularity as ornamental species and as fish bait, freshwater crayfish are frequently translocated, within and between countries, continents and hemispheres (Austin, 1985; Holdich et al., 2009; Huner, 1994; Ngyuen, 2005; Saoud et al., 2013). A number of species have been successful in establishing viable long-term feral populations outside their natural distributions and are frequently considered as undesirable alien species (Holdich et al., 2009;

Saoud et al., 2013). The introduction of North American crayfish species to Europe has had an especially negative impact through the introduction of the crayfish plague pathogen to which the native crayfish have little or no resistance. The North American crayfish, *Orconectes limosus* is thought to be the first species to have been introduced to Europe well over 100 years ago and is now recorded to be present in more than 20 countries (Holdich et al., 2009). Based on the sequencing of COI gene,

Table 1. Annotation of the complete mitochondrial genome of *Orconectes limosus*.

Gene	Strand	Position	Length (bp)	Inter-genic_nucleotides (bp)	Start codon	Start codon	Anticodon
cox1	+	1–1536	1536	1	ACG	TAA	
trnL2(taa)	+	1538–1600	63	1			UAA
cox2	+	1601–2335	735	0	GTG	TAG	
trnK(ttt)	+	2289–2352	64	–47			UUU
trnD(gtc)	+	2355–2422	68	2			GUC
atp8	+	2423–2581	159	0	ATG	TAG	
atp6	+	2575–3249	675	–7	ATG	TAA	
cox3	+	3249–4037	789	–1	ATG	TAA	
trnG(tcc)	+	4036–4097	62	–2			UCC
nad3	+	4098–4451	354	0	ATT	TAG	
trnA(tgc)	+	4450–4509	60	–2			UGC
trnR(tcg)	+	4510–4570	61	0			UCG
trnE(ttc)	+	4571–4631	61	0			UUC
putative control region	+	4632–6094	1463	0			
trnQ(ttg)	–	6095–6164	70	0			UUG
trnS1(tct)	–	6181–6247	67	16			UCU

(continued)

Table 1. Continued.

Gene	Strand	Position	Length (bp)	Inter-genic_nucleotides (bp)	Start codon	Start codon	Anticodon
trnN(gtt)	–	6248–6311	64	0			GUU
rrnS	+	6378–7169	792	66			
trnV(tac)	+	7170–7239	70	0			UAC
rrnL	+	7240–8505	1266	0			
trnL1(tag)	+	8506–8568	63	0			UAG
nad1	+	8593–9534	942	24	ATG	TAA	
trnP(tgg)	+	9542–9605	64	7			UGG
trnS2(tga)	–	9609–9672	64	3			UGA
cob	–	9656–10,807	1152	–17	ATG	TAA	
nad6	–	10,807–11,322	516	–1	ATT	TAA	
trnT(tgt)	–	11,340–11,402	63	17			UGU
nad4l	+	11,405–11,698	294	2	ATG	TAA	
nad4	+	11,695–13,041	1347	–4	ATA	TAA	
trnH(gtg)	+	13,041–13,104	64	–1			GUG
nad5	+	13,105–14,838	1734	0	ATG	TAA	
trnF(gaa)	+	14,838–14,901	64	–1			GAA
trnI(gat)	+	14,904–14,966	63	2			GAU
trnM(cat)	+	14,968–15,036	69	1			CAU
nad2	+	15,037–16,029	993	0	GTG	TAA	
trnW(tca)	+	16,028–16,094	67	–2			UCA
trnC(gca)	–	16,094–16,157	64	–1			GCA
trnY(gta)	–	16,158–16,222	65	0			GUA

Filipova et al. (2011) reported extremely low level of haplotype diversity consistent with one single introduction into Europe. In addition to its status as an invasive species, *O. limosus* is of interest due to its capacity to reproduce sexually or parthenogenetically, which is considered to be unique in the Decapoda (Buřič et al., 2011). We recover the complete mitogenome sequence for *O. limosus*, making it the first mitogenome for species of the genus *Orconectes* and the third for genera of the Cambaridae.

The *O. limosus* sample was obtained from a translocated population inhabiting Vonne (Long.0°04'51 E; Lat. 46°27'41 N), Loire hydrographic basin, Poitou-Charentes region, France. Mitogenome sequencing, assembly and annotation were performed as previously described (Gan et al., 2014) with a slight modification, e.g. IDBA-UD (Peng et al., 2012) was used to assemble the mitogenome.

The *O. limosus* mitogenome is 16,223 bp in length (GenBank accession number: KP205431) and contains the typical 37 mitochondrial genes and an AT-rich non-coding region of 1463 bp (Table 1). The base composition is 31.5% A, 39.8% T, 18.4% G and 10.3% C and the mitogene order is the same distinctive arrangement found for *Procambarus clarkii*, *Procambarus fallax* and *Cambaroides similis* (Kim et al., 2012; Shen et al., 2013). Our sample of *O. limosus* is identical to another sample sequenced from Europe for a 16S rRNA gene fragment (Klobučar et al., 2013) and almost identical (488 of 489 bp) for the same gene region for a sample (isolate M2O12) from its native range (Mathews et al., 2008). Given the close genetic relationships among a number of *Orconectes* species and the occurrence of cryptic species and lineages in several other species (Buhay & Crandall, 2008; Filipová et al., 2010; Mathews et al., 2008), it will be useful to sequence the mitogenomes of additional species of *Orconectes*. Furthermore, given there are over 400 species of recognized cambarids, divided among 12 extant genera (De Grave et al., 2009), it will be of interest to study whole mitogenome sequences across this group of freshwater crayfishes for more detailed phylogenetic and molecular taxonomic studies.

Declaration of interest

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