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The complete mitochondrial genome of the American lobster, *Homarus americanus* (Crustacea, Decapoda)

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Abstract
Although relatively a large number of the complete mitochondrial genome sequences have been determined from various decapod species (29 mtDNA sequences reported so far), the information for the infraorder Astacidea (including lobsters, crayfishes, and their relatives) is very limited and represented by only one complete sequence from the Australian freshwater crayfish species *Cherax destructor*. In this study, we determined the complete mitochondrial DNA sequence of *Homarus americanus*, the first representative of the family Nephropidae to be fully characterized. Comparison of the gene arrangement reveals that *H. americanus* mtDNA is identical to those of other pancrustacean species but differs from the other astacidean species (*C. destructor*). Based on these data, it can be assumed that an idiosyncratic gene order discovered in *C. destructor* mtDNA may be secondarily acquired from the ancestral lineage of the Astacidea.

Keywords: *American lobster, Astacidea, complete mitochondrial genome,* Homarus americanus

The American lobster *Homarus americanus* (Decapoda, Astacidea, Nephropidae) is a commercially important species because it is a favored crustacean seafood species worldwide. Although a relatively large number of complete mitochondrial genome sequences have been determined from various decapod species (29 whole mtDNA sequences reported thus far), the information for the infraorder Astacidea (including lobsters, crayfishes, and their relatives) is very limited and represented by only one complete sequence from the Australian freshwater crayfish species *Cherax destructor* (Miller et al. 2004). Interestingly, it has been reported that *C. destructor* showed a very unique gene arrangement, differentiating it from the putative ancestral gene order of Pancrustacea (Crustacea + Hexapoda). It is, therefore, anticipated that additional mitochondrial genomes from unstudied decapod taxa will advance our understanding of the mitochondrial genome diversity and the evolution of the decapods.

A fresh specimen of the American lobster was purchased at the fishery market in Incheon, Korea. The total genomic DNA was extracted using the DNeasy® Blood & Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. The partial sequences of *cox1* and *16S rDNA* were initially determined using previously published primers (Folmer et al. 1994; Crandall and Fitzpatrick 1996). The nucleotide sequences from each of the partial gene fragments were then used for designing *H. americanus*-specific primers for long PCR (Polymerase Chain

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Table I. Mitochondrial genome organisation of *H. americanus*.

Locus	Position		Sequence length		Codons		Intergenic sequence
	Start	End	Nucleotides	Amino acids	Initiation	Termination	
cox1	1	1537	1537	512	ATC	T	
trnL2	1538	1602	65				
cox2	1603	2290	688	229	ATG	T	
trnK	2291	2358	68				
trnD	2359	2423	65				
atp8	2424	2582	159	52	ATG	TAA	
atp6	2576	3249	674	224	ATG	TA	−7
cox3	3250	4041	792	263	ATG	TAA	
trnG	4044	4108	65				2
nad3	4109	4460	352	117	ATT	T	
trnA	4461	4525	65				
trnR	4527	4592	66				1
trnN	4593	4659	67				
trnS1	4660	4727	68				
trnE	4727	4792	66				−1
trnF	4900	4834	67				41
nad5	6626	4901	1726	575	ATT	T	
trnH	6694	6630	65				3
nad4	8034	6695	1340	446	ATG	TA	
nad4L	8330	8028	303	100	ATG	TAA	−7
trnT	8333	8398	66				2
trnP	8463	8399	65				
nad6	8466	8983	518	172	ATC	TA	2
cytb	8984	10,118	1135	378	ATG	T	
trnS2	10,119	10,188	70				
nad1	11,159	10,221	939	312	ATG	TAG	32
trnL1	11,263	11,198	66				38
rrnL	12,603	11,264	1340				
trnV	12,676	12,604	73				
rrnS	13,519	12,677	843				
CR	13,520	15,007	1488				
trnI	15,008	15,071	64				
trnQ	15,141	15,073	69				1
trnM	15,140	15,210	71				−2
nad2	15,211	16,210	1000	333	ATG	T	
trnW	16,211	16,277	67				
trnC	16,370	16,304	67				26
trnY	16,432	16,370	62				−1

Note: The genes that are encoded on the light strand are underlined.

Reaction) amplification. The nucleotide sequencing and gene annotation for the complete mtDNA were carried out by following the methods used by Min and Park (2009). The complete mtDNA sequence of *H. americanus* is 16,432 bp in length (GenBank accession no. HQ402925). Among 37 genes, 14 (eight tRNA genes, four protein-coding genes, and two ribosomal RNA genes) are encoded on the light strand, whereas 13 genes are encoded on the heavy strand (Table I). The A + T content of the entire sequence is 69.5% (34.4% A, 35.1% T, 18.3% C, and 12.1% G). This is considerably higher than that of *C. destructor* (62.4%) but it approximates the average of other decapod species (Liu and Cui 2010). The 22 tRNA genes, ranging from 62 to 73 bp in size, conform to the typical cloverleaf secondary structure. The majority of protein-coding genes (9 of 13 genes) use ATG as a start codon, whereas *cox1* and *nad6* start with ATC, and *nad3* and *nad5* initiate with ATG. It is also important to note that the majority of protein-coding genes (8 of 13 genes) are inferred to terminate with an incomplete stop codon T—(*cox1*, *cox2*, *nad3*, *nad5*, *cob*, and *nad2*) or TA—(*atp6* and *nad4*), whereas the other four end with the complete stop codon TAA (*atp8, cox3*, and *nad4L*) or TAG (*nad1*). Comparison of gene arrangement reveals that *H. americanus* mtDNA is identical to those of other pancrustacean species but differs from the other astacidean species (*C. destructor*). Based on these data, it can be assumed that the idiosyncratic gene order discovered in *C. destructor* mtDNA may have been secondarily acquired from the ancestral lineage of the Astacidea.

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