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Arginine Kinase from the Tardigrade, *Macrobiotus occidentalis*: Molecular Cloning, Phylogenetic Analysis and Enzymatic Properties

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Arginine kinase (AK), which catalyzes the reversible transfer of phosphate from ATP to arginine to yield phosphoarginine and ADP, is widely distributed throughout the invertebrates. We determined the cDNA sequence of AK from the tardigrade (water bear) *Macrobiotus occidentalis*, cloned the sequence into pET30b plasmid, and expressed it in *Escherichia coli* as a 6x His-tag-fused protein. The cDNA is 1377 bp, has an open reading frame of 1080 bp, and has 5'- and 3'-untranslated regions of 116 and 297 bp, respectively. The open reading frame encodes a 359-amino acid protein containing the 12 residues considered necessary for substrate binding in *Limulus* AK. This is the first AK sequence from a tardigrade. From fragmented and non-annotated sequences available from DNA databases, we assembled 46 complete AK sequences: 26 from arthropods (including 19 from Insecta), 11 from nematodes, 4 from mollusks, 2 from cnidarians and 2 from onychophorans. No onychophoran sequences have been reported previously. The phylogenetic trees of 104 AKs indicated clearly that *Macrobiotus* AK (from the phylum Tardigrada) shows close affinity with *Epiperipatus* and *Euperipatoides* AKs (from the phylum Onychophora), and therefore forms a sister group with the arthropod AKs. Recombinant 6x His-tagged *Macrobiotus* AK was successfully expressed as a soluble protein, and the kinetic constants (K_m , K_d , V_{max} and k_{cat}) were determined for the forward reaction. Comparison of these kinetic constants with those of AKs from other sources (arthropods, mollusks and nematodes) indicated that *Macrobiotus* AK is unique in that it has the highest values for k_{cat} and K_d/K_m (indicative of synergistic substrate binding) of all characterized AKs.

Key words: guanidino kinase, phosphagen kinase, arginine kinase, creatine kinase, water bear, *Macrobiotus occidentalis*

INTRODUCTION

Phosphagen (guanidino) kinases catalyze the reversible transfer of the high-energy phosphoryl group of ATP to naturally occurring guanidine compounds. Members of this enzyme family play a key role in animals as ATP-buffering systems in cells that display high and variable rates of ATP turnover. Phosphorylated high-energy guanidines are referred to as phosphagens. In vertebrates, phosphocreatine is the only phosphagen, and the corresponding phosphagen kinase is creatine kinase (CK). In contrast, invertebrates have various phosphagens in addition to phosphocreatine: phosphoglycocyamine (catalyzed by glycocyamine kinase: GK), phosphotaurocyamine (taurocyamine kinase: TK), phosphohypotaurocyamine (hypotaurocyamine kinase: HTK), phospholombricine (lombricine kinase: LK) and phosphoarginine (arginine kinase: AK). Phosphagen kinases are phylogenetically separated into two distinct groups: the AK group, which includes AK and HTK, and the

CK group, which includes CK, GK, LK and TK (Ellington, 2001; Wyss et al., 1992; Schlattner et al., 2005; McLeish and Kenyon, 2005; Ellington and Suzuki, 2006; Uda et al., 2005a). Interestingly, several AKs such as those from the echinoderm *Stichopus* and the annelid *Sabellastarte* are clustered in the CK group, indicating that they have evolved secondarily from CK (Suzuki et al., 1999; Uda and Suzuki, 2007).

Most AKs are monomers of 40 kDa, but in some species they exist as dimers (Seals and Grossman, 1988; Suzuki et al., 1999) or contiguous dimers (two-domain AKs), presumably as a result of gene duplication and subsequent fusion (Suzuki et al., 1997; Suzuki et al., 1998).

Typical AKs are most widely distributed among organisms such as arthropods, mollusks, nematodes, cnidarians, poriferae, protozoans (ciliates and choanoflagellates), and bacteria, indicating their ancient origin (Andrews et al., 2008; Uda et al., 2006). In three major invertebrate groups (arthropods, nematodes, and mollusks), AK is the only phosphagen

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ABBREVIATIONS

AK, arginine kinase; CK, creatine kinase; GK, glycocyamine kinase; GS region, guanidine specificity region; LK, lombricine kinase; TK, taurocyamine kinase; EST, expressed sequence tag.

Table 1. AKs used for the phylogenetic analysis.

Phylum	Class	Order	Genus/Species/Isoform	Accession number/Database ^a	
Alveolata	Oligohymenophorea	Hymenostomatida	<i>Tetrahymena thermophila</i> AK1 <i>Tetrahymena thermophila</i> AK2	EAS01428 EAS01429	
Arthropoda	Arachnida	Arachnida	<i>Aleuroglyphus ovatus</i> AK <i>Loxosceles laeta</i> AK	ABU97463 EY188599	
		Araneae	<i>Aphonopelma</i> sp. AK	Genbank EST : FC823446, FC824317	
	Astigmata		<i>Dermatophagoides farinae</i> AK1 <i>Dermatophagoides farinae</i> AK2	AAP57094 ABU97470	
			<i>Ixodes scapularis</i> AK	Genbank EST : EW821872, EW873512	
			<i>Tetranychus urticae</i> AK	Trace Archive : 2267574886, 2267695435	
	Branchiopoda	Anostraca	<i>Artemia franciscana</i> AK	AAL25092	
		Diplostraca	<i>Daphnia pulex</i> AK	Trace Archive : 895565747, 897280293, 895554084	
	Insecta	Blattaria	<i>Blattella germanica</i> AK	ABC86902	
			<i>Periplaneta americana</i> AK	AAT77152	
		Coleoptera	<i>Tribolium castaneum</i> AK	Trace Archive : 569305708, 580631152	
			<i>Drosophila melanogaster</i> AK	AAN11983	
		Diptera	<i>Anopheles gambiae</i> AK	EAA44056	
			<i>Aedes aegypti</i> AK	ABF18260	
			<i>Ceratitis capitata</i> AK	Genbank EST : FG083307, FG075954	
			<i>Drosophila pseudoobscura</i> AK	Genbank EST : DR124999, DR145664	
			<i>Glossina morsitans</i> AK	Genbank EST : DV618298, FM982907	
			<i>Lutzomyia longipalpis</i> AK	Genbank EST : AM109228, AM109239	
			<i>Phlebotomus papatasi</i> AK	Genbank EST : EY204603, EY214760	
			<i>Cochliomyia hominivorax</i> AK	Genbank EST : FG300496, FG296874	
	<i>Teleopsis dalmanni</i> AK		Genbank EST : GO297058, GO298184		
	<i>Homalodisca vitripennis</i> AK		AAT01074		
	Hemiptera	<i>Oncometopia nigricans</i> AK	AAU95198		
		<i>Nilaparvata lugens</i> AK	Genbank EST : DB840416, DB826716		
		<i>Rhodnius prolixus</i> AK	Genbank EST : EH114777, FG544166		
	Hymenoptera	<i>Solenopsis invicta</i> AK	ACF04198		
		<i>Apis mellifera</i> AK	AAC39040		
	Lepidoptera	<i>Nasonia vitripennis</i> AK	Trace Archive : 1081135584, 1076813375, 1068958665, 1105139233		
<i>Lysiphlebus testaceipes</i> AK		Genbank EST : EH010491, EH015342, EH010390			
<i>Plodia interpunctella</i> AK		CAC85911			
<i>Bombyx mori</i> AK		ABD36282			
<i>Danaus plexippus</i> AK		Genbank EST : EY260080, EY271098			
<i>Spodoptera frugiperda</i> AK		Genbank EST : DV076460, DY898274			
<i>Manduca sexta</i> AK		Genbank EST : BF046795, BE015379, BE015528			
<i>Trichoplusia ni</i> AK		Genbank EST : CF259256, FF370292			
<i>Ostrinia nubilalis</i> AK		Genbank EST : GH997366, GH989259			
<i>Schistocerca americana</i> AK		AAC47830			
Orthoptera	<i>Locusta migratoria</i> AK	ABF68036			
	<i>Gryllus bimaculatus</i> AK	Genbank EST : DC443130, DC446501			
	<i>Pediculus humanus</i> AK	Trace Archive : 1382191351, 1379696849, 1386063845			
	<i>Gammarus pulex</i> AK	Genbank EST : EH275731, EH275602			
	<i>Pachygrapsus marmoratus</i> AK	AAG01175			
	<i>Litopenaeus vannamei</i> AK	ABI98020			
	<i>Fenneropenaeus chinensis</i> AK	AAV83993			
	<i>Neohelice granulata</i> AK	AAF43438			
	<i>Callinectes sapidus</i> AK	AAF43436			
	<i>Marsupenaeus japonicus</i> AK	AAB31477			
	<i>Homarus gammarus</i> AK	CAA48654			
	<i>Procambarus clarkii</i> AK	2020435A			
Malacostraca	Phthiraptera	<i>Limulus polyphemus</i> AK	BAH56609		
		<i>Homo sapiens</i> MCK ^b	AAO15713		
	Amphipoda	<i>Anthopleura japonica</i> 2DAK	AAO15713		
		<i>Aiptasia pallida</i> AK	AAO15713		
		<i>Eurydice pulchra</i> AK	AAO15713		
		<i>Carinus maenas</i> AK	Genbank EST : FE756031, FE750140		
		<i>Limulus polyphemus</i> AK	AAD48470		
		<i>Homo sapiens</i> MCK ^b	Genbank EST : CO869027, CO868808, CO868911		
		<i>Anthopleura japonica</i> 2DAK	P51541		
		<i>Aiptasia pallida</i> AK	AAA96609		
		<i>Acropora millepora</i> 2DAK	O15992		
		<i>Scapharca broughtonii</i> AK	Genbank EST : GH579704, GH574852, GH575418		
Chordata	Mammalia	<i>Homo sapiens</i> MCK ^b	Genbank EST : DY586394, EZ016454, EH038119, EH037125		
		<i>Homo sapiens</i> MCK ^b	BAD11949		
	Cnidaria	Anthozoa	<i>Anthopleura japonica</i> 2DAK	BAD11950	
			<i>Aiptasia pallida</i> AK	BAA95594	
	Mollusca	Bivalvia	<i>Scapharca broughtonii</i> AK	BAA95609	
			<i>Crassostrea gigas</i> AK	BAA95610	
		Cephalopoda	Nautilida	<i>Nautilus pompilius</i> AK	BAB41095
			Octopoda	<i>Octopus vulgaris</i> AK	BAB41096
		Gastropoda	Teuthida	<i>Septoteuthis lessoniana</i> AK	P51544
			Aplysiomorpha	<i>Aplysia kurodai</i> AK	BAA22870
		Dacrydophora	<i>Cellana grata</i> AK	BAA22871	
			<i>Haliotis madaka</i> AK	Genbank EST : DW282592, DW279554	
Polyplacophora		Neoloricata	<i>Batillius cornutus</i> AK	Genbank EST : DB918583, DB916072, DB919901	
		Cephalopoda	<i>Liolophura japonica</i> AK	Trace Archive : 1161815795, 1809265942, 1182066208, 1162368191	
Nematoda		Gastropoda	<i>Euprymna scolopes</i> AK	Genbank EST : ES491406, FC856201	
			<i>Idiosepius paradoxus</i> AK	Trace Archive : 1724989270, 1724991545	
	Anaspidea	<i>Aplysia californica</i> AK	ABK76312		
		<i>Biomphalaria glabrata</i> AK	Trace Archive : 989893386, 987437388, 760524991		
	Basommatophora	<i>Trichinella spiralis</i> AK	Genbank EST : FG097924, BI500767, AI988904		
		<i>Toxocara canis</i> AK	AAO21426		
	Adenophorea	<i>Pristionchus pacificus</i> AK1	CAB00062		
		<i>Pristionchus pacificus</i> AK2	CAB05517		
	Chromadorea	<i>Caenorhabditis elegans</i> AK1	CAE00062		
		<i>Caenorhabditis elegans</i> AK2	CAE00062		
	Onychophora	Ascariida	<i>Caenorhabditis elegans</i> AK3	CAE00062	
			<i>Caenorhabditis elegans</i> MiAK	AAK21503	
Diplogasterida		<i>Heterorhabditis bacteriophora</i> AK	Trace Archive : 1877615891, 1949656867		
		<i>Haemonchus contortus</i> AK	Genbank EST : CB015139, BM139164		
Rhabditida		<i>Strongyloides ratti</i> AK1	Genbank EST : BI073820, FC816131, FC816421		
		<i>Strongyloides ratti</i> AK2	Genbank EST : FC812688, FC818348, BI742298		
Tylenchida		<i>Heterodera glycines</i> AK1	AAO49799		
		<i>Heterodera glycines</i> AK2	AAP41028		
Enoplea		<i>Globodera rostochiensis</i> AK	Genbank EST : BM355956, BM354963		
		<i>Meloidogyne hapla</i> AK	Genbank EST : CA997516, CA997485		
Secernentea		<i>Xiphinema index</i> AK	Genbank EST : CV568581, CV509691, CV581377		
		<i>Dictyocaulus viviparus</i> AK	Genbank EST : EV853193, EV851844		
Onychophora	<i>Epiperipatus</i> sp. AK	Genbank EST : AM499754, AM500583			
	<i>Euperipatoides kanangrensis</i> AK	Trace Archive : 1987166188, 1987167250			
Platyhelminthes	Trematoda	Plagiorchiida	<i>Paragonimus westermani</i> TK ^c	ACT37385	
Sipuncula	Sipunculidea	Sipunculida	<i>Siphonosoma cumanense</i> HTK ^c	BAE16970	

^aFor sequences obtained from GenBank, accession numbers are shown. For the assembled sequences in this study, the database name used and accession numbers are shown.

^b*Homo sapiens* MCK is used as an outgroup.

^cRecent phylogenetic analyses of *Paragonimus* TK and *Siphonosoma* HTK indicate that they evolved from AK genes (Uda et al., 2005; Jarilla et al., 2009).

*The 46 newly assembled sequences.

tion. The Maximum-Likelihood (ML) analysis with the approximate likelihood-ratio test for branches (aLRT; Anisimova and Gascuel, 2006) was performed in the program PhyML v3.0 (Guindon and Gascuel, 2003) using the LG amino acid replacement matrix.

RESULTS AND DISCUSSION

cDNA for AK from *Macrobiotus occidentalis* was amplified by PCR and cloned into the plasmids pGEM-T Easy and pET30b. Fig. 1 shows the nucleotide and derived amino acid sequences of *Macrobiotus* AK. The nucleotide sequence consists of 1377 bp, with an open reading frame (ORF) of 1080 bp, and 5'- and 3'-untranslated regions of 116 and 297 bp, respectively. The sequence was deposited into the DDBJ database (accession number: AB537977). This is the first reported AK sequence from a tardigrade.

The ORF codes were consistent with a protein of 359 amino acid residues, with a calculated molecular mass of 40,060 Da and an estimated pI of 6.81. When the amino acid sequence was compared with *Limulus* AK, for which the crystal structure has been determined (Zhou et al., 1998), it was found that *Macrobiotus* AK completely conserved all key residues believed necessary for AK function (underlined in Fig. 1). Conserved residues include seven that interact with the substrate arginine in *Limulus* AK (S63, G64, V65, Y68, E228, C274 and E317) and five residues that interact with the substrate ADP (R127, R129, R232, R283 and R312). The results show that *Macrobiotus* AK and *Limulus* AK may have very similar substrate recognition systems.

At present, at least 60 complete sequences of invertebrate AKs have been deposited in protein or DNA databases. We also know that many EST or genomic DNA databases contain fragmented and non-annotated AK sequences. We performed a comprehensive search for AK fragments across multiple databases using known AK

sequences as references, and assembled the fragments into complete cDNA sequences. As a result, we obtained 46 complete AK sequences: 26 from arthropods (including 19 from Insecta (Coleoptera: *Tribolium castaneum*, Diptera: *Ceratitis capitata*, *Drosophila pseudoobscura*, *Glossina morsitans*, *Lutzomyia longipalpis*, *Phlebotomus papatasi*, *Cochliomyia hominivorax*, *Teleopsis dalmanni*, Hemiptera: *Nilaparvata lugens*, *Rhodnius prolixus*, Hymenoptera: *Nasonia vitripennis*, *Lysiphlebus testaceipes*, Lepidoptera: *Danaus plexippus*, *Spodoptera frugiperda*, *Manduca sexta*, *Trichoplusia ni*, *Ostrinia nubilalis*, Orthoptera: *Gryllus bimaculatus*, Phthiraptera: *Pediculus humanus*)), three from cnidarians, four from mollusks, 11 from nematodes and two from onychophorans (see Table 1). These onychophoran AK sequences are the first to be reported for that taxon.

The amino acid sequences of 104 invertebrate AKs, including *Macrobiotus* AK, the 46 AKs obtained by our in silico analyses (Table 1), and *Paragonimus* TK and *Siphonosoma* HTK (both of which evolved from AK genes; Uda et al., 2005; Jarilla et al., 2009), were aligned using the ClustalW program (data not shown). The sequence of *Macrobiotus* AK showed the highest identity (75%) with AK from the onychophorans *Epiperipatus* and *Euperipatoides*, 62–74% with arthropod AKs, 59–65% with nematode AKs, and 49–55% with mollusk AKs.

A phylogenetic tree was constructed from the above alignments using the ML (Fig. 2) and NJ (data not shown) methods. The two trees show similar topology, and the protostome AK sequences are separated into two distinct groups: lophotrochozoans (mollusks, platyhelminths and sipunculids) and ecdysozoans (arthropods, nematodes, onychophorans and tardigrades). Recent molecular phylogenetic studies suggest three possibilities for the phylogeny of ecdysozoans: (a) Tardigrada and Onychophora are included within Arthropoda (Colgan et al., 2008), (b) Tardigrada has

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1 gaaaggactggaagaagcogagacatttatttgcactcttggttttttcagtcgcaaaacgactatcagccgcccctttttgtcgtttctt 90
91 cttcttttggtaatacgcaggttttgcattgggcccctgttggatcagcgtcagaaaattctccgaggctcctggcattcttgcgaaggagaccaaa 180
1 M A A V D H A Q K I S E A P G I L Q G D Q K 22
181 AGGGACACTCCCTGCTCAAGAAATACCTGTGCGAAAGATGTCGCGAAAAGTTGAAGAAGCACAACCTGGCATGGGTGCCAGCCTTTGGG 270
23 G H S L L L K K Y L S K D V A E K L K N D K T G M G A S L L W D 52
271 ACTGCATCCAGTCTGGTGTGGCCAATCTGGACAGCGGTGTGGCATCTACGCCCTGATGCGGAATCCTACACCAAATCTCGGATGTCT 360
53 C I Q S G V A N L D S G V G I Y A P D A E S Y T K F S D V F 82
361 TCTATCCCATCATCCAGGATACCACATTTGGATTGCGACTGAAGCTGGAGCCAAACCCACCGGCTGACTTCGGTCTGGACAACTCA 450
83 Y P I I Q D Y H I G F D L K A G A K H P P A D F G L D K L N 112
451 ATTTCCCAATCCGACCCGACTGGCGAATACATATTTGCGACTCGCGTCCGATGGTTCGCTCGCTGGCTGGATATCCGTTCAACCCCG 540
113 F P N P D P T G E Y I I S T R V R C G R S L A G Y P F N P L 142
541 TCTTAAACGAACAGCAATATAAAGAAATGGAAGAGAAAGTGAAGAGCGCACTCACTGGATTGACCGGAGAACTAGCCGGCACTTACTACC 630
143 L N E Q Q Y K E M E E K V K S A L T G L T G E L A G T Y Y P 172
631 CACTTACCGCATGGACAAGGCCACCCAAAACCACTCATCGAGGACATTTCTTGTTCAGGAGGGAGATCGTTCTTGAAGCTGCCA 720
173 L T G M D K A T Q N Q L I E D H F L F K E G D R F L Q A A N 202
Phos.con
721 ACGTAGCCGTTTCTGGCCACTGGTCTGGAATCTTCCACAACAAGGACAAGACTTTCCTGGTCTGGGTCAACGAGGAGGACCATCTCC 810
203 A S R F W P T G R G I F H N K D K T F L V W V N E E D H L R 232
kuma AK R2
811 GCATCATCAGCATGCAAAAGGGCGCGATTGTTGGCAGTCTTCAAGCCTCTGATTGAGGGTGTGAAACAAATCGAGGCGCAAACTGCCCT 900
233 I I S M Q K G G D L L A V F K R L I E G V K Q I E A K L P F 262
kuma AK R1
901 TCTCCCGTGTGACCCGCTGGGTTATTGACTTTCTGCCCGACCAACCTGGGCACCACCATCCGCGCCAGTGTGCATATCAAGCTACCCA 990
263 S R D D R L G Y L T F C P T N L G T T I R A S V H I K L P K 292
991 AGATCAGCAAAACCTCGACGAGTTCCACAAGATTGCCGCTAAATATAACCTCCAAGTTCGTGGTACATCTGGAGAACACTCAGAATCCA 1080
293 I S K N L D E F H K I A A K Y N L Q V R G T S G E H S E S I 322
1081 TCGCGGAGTTTACGACGCTCCCAACAAGCGTCGCATGGGTCTGACCGAATACGATGCCGTCAGGAAATGTACGCGGTATTGTCGAAT 1170
323 G G V Y D V S N K R R M G L T E Y D A V K E M Y D G I V E L 352
1171 TGATCAAGCTGGAGAAAGCTTCTGAgctctggattttgtgcaaatgattgtctgagactcctctactagcgaacaccttggcggctgcaa 1260
353 I K L E K A S * 359
1261 tgcctgacctgacctgctttttctttgaccacctgctgctagaatgcaattggccgagaacgaacgaactttaaattgttcogggagaat 1350
1351 tttgacctataaaqcaactaqaacgccc 1377

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Fig. 1. Nucleotide and derived amino acid sequence of cDNA of *Macrobiotus* AK. Primers used to amplify the cDNA are shown by arrows. The key residues interacting with the substrates, arginine and ADP, are underlined.

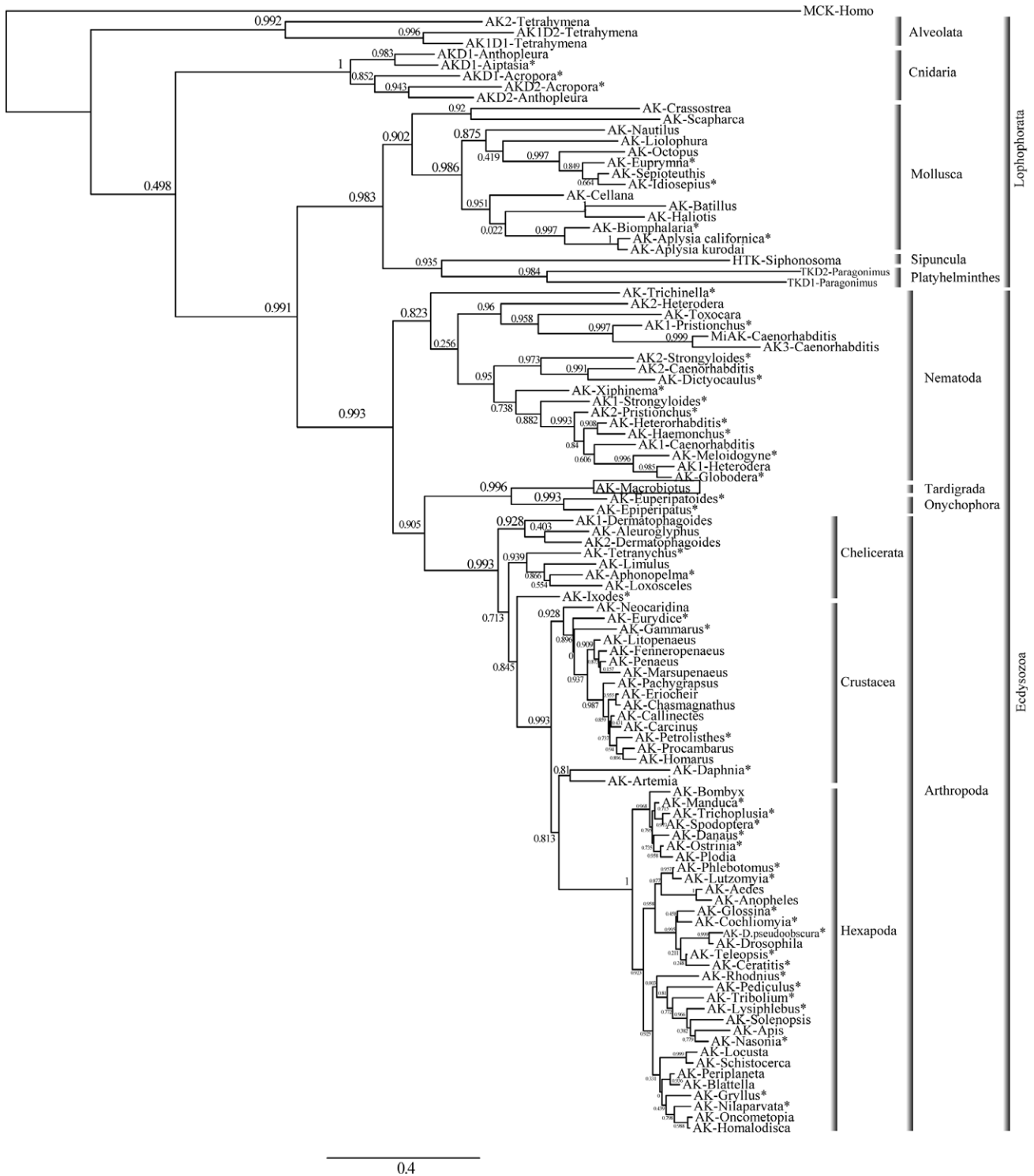


Fig. 2. Maximum-likelihood (ML) tree for amino acid sequences of invertebrate AKs. The tree was constructed using the PhyML program. The approximate likelihood-ratio test (aLRT) values are shown at the branching points. *Homo* muscle-type creatine kinase was used as an out-group. Accession numbers of the sequences are listed in Table 1. *Macrobiotus* AK is boxed, and the 46 newly assembled sequences are marked by asterisks.

close affinity with Onychophora, and they form a sister group with Arthropoda (Mallatt and Giribet, 2006), and (c) Onychophora has close affinity with Arthropoda, and they form a sister group with Tardigrada (Dunn et al., 2008). Our

phylogenetic tree (Fig. 2) indicates that AK from the tardigrade *Macrobiotus* has very close affinity with onychophoran AKs, and forms a sister group with the arthropod AKs. Thus, our analyses support possibility (b), which was originally deduced

from 28S and 18S rRNA analyses using the ML method (Mallatt and Giribet, 2006; Mallatt et al., 2004).

Recombinant 6x His-tagged *Macrobiotus* AK was successfully expressed as a soluble protein, and purified by affinity chromatography. Fig. 3 shows the result of SDS-

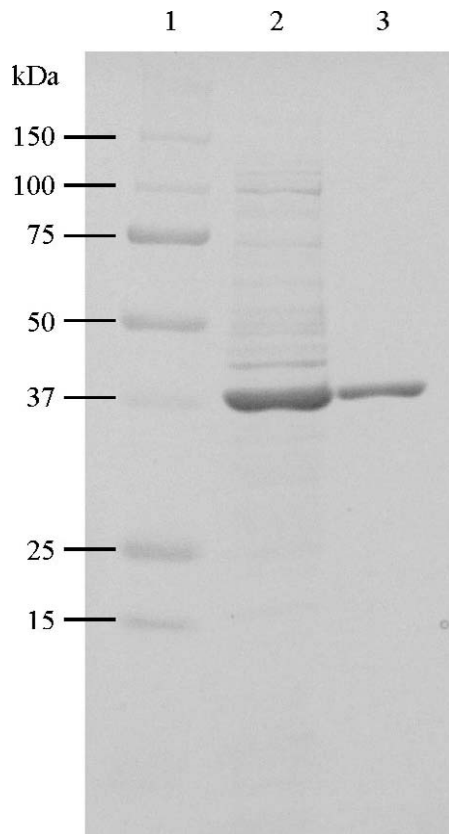


Fig. 3. SDS-PAGE of His-tagged *Macrobiotus* AK. Lane 1, marker proteins (Precision Plus Protein Standards, Bio Rad). Lane 2, soluble proteins from the *E. coli* crude extract. Lane 3, His-tagged *Macrobiotus* AK enzyme purified by affinity chromatography.

PAGE of the purified recombinant enzyme. The recombinant enzyme gave a major single band with a molecular mass of 40 kDa (lane 3), suggesting that the enzyme is sufficiently pure to allow determination of its kinetic constants.

The kinetic constants for *Macrobiotus* AK were obtained using software written by R. Viola (Enzyme Kinetics Programs, ver. 2.0); the results are summarized in Table 2. The kinetic constants were compared with those of AKs from other sources: the arthropods *Locusta* (Wu et al., 2007; Li et al., 2006), *Neocaridina* (Iwanami et al., 2009), *Cissites* (Tanaka et al., 2007), and *Periplaneta* (Brown and Grossman, 2004), the nematode *Toxocara* (Wickramasinghe et al., 2007), the mollusks *Nautilus* (Uda and Suzuki, 2004; Matsumoto and Suzuki, unpublished data), *Scapharca* (Takeuchi et al., 2004), *Octopus* (Takeuchi et al., 2004), and *Crassostrea* (Fujimoto et al., 2005), and the sea anemone *Anthopleura* (Tada et al., 2008; Tada et al., 2010) (Table 2).

The values for K_m^{arg} (0.68 mM) and K_m^{ATP} (0.86 mM) from *Macrobiotus* AK are in the range found for other AKs: 0.12–1.44 mM for K_m^{arg} and 0.14–2.17 mM for K_m^{ATP} .

The K_d/K_m and k_{cat} values for *Macrobiotus* AK appear to be unique. In many phosphagen kinase reactions, two substrates, arginine (or phosphoarginine) and MgATP (or MgADP) in AK reaction, typically exhibit synergistic binding to AK. That is, binding of the first substrate facilitates binding of the second substrate. In terms of kinetic constants, this means that K_d , the dissociation constant in the absence of the second substrate, is higher than K_m ($K_d/K_m > 1$). This synergism may be associated with substrate-induced conformational changes within the tertiary complex. In previous works, we showed that the amino acid residues at positions 62 and 193 (positions relative to *Limulus* AK), which are conserved in normal AKs, including *Macrobiotus* AK, as Asp and Arg, respectively, form a hydrogen bond in the transition state analogue complex in *Limulus* AK (Zhou et al., 1998) and are key residues for synergism (Suzuki et al., 2000; Takeuchi et al., 2004; Fujimoto et al., 2005). Interestingly, *Macrobiotus* AK exhibits higher synergism in substrate binding ($K_d/K_m = 5.78$) than do other AKs ($K_d/K_m = 0.9$ –3.99; Table 2). In addition, the k_{cat} value (291 s^{-1}) of *Macrobiotus*

Table 2. Comparison of kinetic constants of invertebrate AKs at 25°C for the forward reaction (phosphagen synthesis).

Source	Enzyme state	Reference	K_m^{arg} (mM)	K_d^{arg} (mM)	K_m^{ATP} (mM)	K_d^{ATP} (mM)	k_{cat} (1/s)	K_d/K_m
Tardigrada								
<i>Macrobiotus</i>	His-tag	This work	0.683 ± 0.15	3.95 ± 0.70	0.858 ± 0.119	4.96 ± 1.16	291 ± 27	5.78
Arthropoda								
<i>Locusta</i>	Native	Li et al. (2006)	0.94		1.29		163	
	no tag	Wu et al. (2007)	0.951 ± 0.08	2.67 ± 0.22	1.27 ± 0.23	3.56 ± 0.32	159 ± 6.2	3.2
<i>Neocaridina</i>	His-tag	Iwanami et al. (2009)	0.376 ± 0.039	0.466 ± 0.078	0.989 ± 0.064	1.23 ± 0.23	200 ± 5.2	1.24
<i>Cissites</i>	MBP-tag	Tanaka et al. (2007)	1.01 ± 0.07	0.99 ± 0.03	0.95 ± 0.16	0.92 ± 0.16	2.02 ± 0.05	0.99
<i>Periplaneta</i>	Native	Brown and Grossman (2004)	0.49	0.45	0.14	0.17	1.30	0.92
Nematoda								
<i>Toxocara</i>	MBP-tag	Wickramasinghe et al. (2007)	0.12 ± 0.003	0.23 ± 0.03	0.30 ± 0.04	0.60 ± 0.07	29.2 ± 0.19	1.96
Mollusca								
<i>Nautilus</i>	MBP-tag	Uda and Suzuki (2004)	0.67 ± 0.11	2.26 ± 0.07	1.40 ± 0.11	4.72 ± 0.36	2.51 ± 0.16	3.37
	His-tag	Matsumoto and Suzuki (unpublished data)	0.56 ± 0.01				33.0 ± 0.60	
<i>Crassostrea</i>	MBP-tag	Fujimoto et al. (2005)	0.35 ± 0.01	0.82 ± 0.37	0.97 ± 0.25	2.26 ± 0.59	79.7 ± 3.44	2.34
<i>Scapharca</i>	MBP-tag	Takeuchi et al. (2004)	1.44 ± 0.28	2.57 ± 0.29	0.65 ± 0.15	1.16 ± 0.25	72.1 ± 7.5	1.78
<i>Octopus</i>	MBP-tag	Takeuchi et al. (2004)	0.95 ± 0.033	3.78 ± 0.05	0.75 ± 0.121	4.72 ± 0.36	29.4 ± 0.72	3.99
Cnidaria								
<i>Anthopleura</i>	MBP-tag	Tada et al. (2008)	0.25 ± 0.04	0.33 ± 0.07	2.17 ± 0.20	2.83 ± 0.83	129 ± 5.26	1.32
	His-tag	Tada and Suzuki (2010)	0.28 ± 0.05	0.30 ± 0.08	1.52 ± 0.16	1.61 ± 0.55	678 ± 33	1.07

AK is also higher than other AKs (1.3–200 s⁻¹; Table 2), except for that (678 s⁻¹) of *Anthopleura* His-tagged AK, which exhibits an unusual two-domain structure (Tada and Suzuki, 2010). These results indicate that *Macrobiotus* AK is distinguished from other AKs by its high k_{cat} and K_d/K_m values.

We determined preliminary temperature/activity profiles at pH 8.0 for His-tagged recombinant *Macrobiotus* AK and *Nautilus* AK, a well-characterized AK (Fig. 4). Comparison of the profiles indicates that the optimum temperature of *Macrobiotus* AK appears to be shifted about 10°C to the high temperature region, and maintains higher activity over 35°C, compared with *Nautilus* AK.

These characteristics of *Macrobiotus* AK (high k_{cat} and K_d/K_m values, and differences in temperature-dependent activity) may be related to the survival of *Macrobiotus occidentalis* under extreme conditions.

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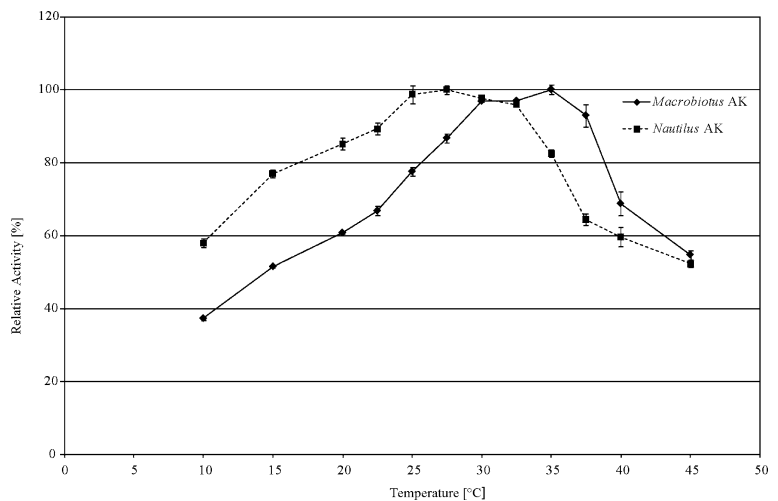


Fig. 4. Temperature/activity profiles of *Macrobiotus* AK and *Nautilus* AK. Profiles represent activity relative to each maximum activity. Activities at pH 8.0 were measured between 10 and 45°C under substrate concentrations of 9.52 mM arginine and 4.76 mM ATP, using His-tagged recombinant enzymes.

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