671

Peptides (Epigenetic Regulators) in the Structure of Rodents with a Long and Short Lifespan V. Kh. Khavinson^{1,3}, D. Yu. Kormilets², and A. T. Mar'yanovich³

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We have discovered motives of short-chain epigenetically active peptides in some proteins of long-lived African mole rat *Heterocephalus glaber*. These epigenetic regulators are located in the protein structure between lysine and arginine residues, thus facilitating their release in limited proteolysis. Some of these epigenetic regulators are not found in the proteins of short-lived species — Norway rat *Rattus norvegicus* and house mouse *Mus musculus*.

Key Words: aging; peptides; epigenetic regulation

Short peptides (peptide epigenetic regulators, PER, PEGRs) promoting recovery of damaged tissues, including those impaired as a result of aging, are created at St. Petersburg Institute of Bioregulation and Gerontology [2,5-7].

African rodent, naked mole-rat *Heterocephalus* glaber, attracts attention of gerontologists because of its longevity, uncommon for its order: its maximum documented lifespan is more than 30 years [8] — 10-fold longer than in species evolutionally close to it — Norway rat (*Rattus norvegicus*) and house mouse (*Mus musculus*). Naked mole-rat is resistant to cancer [3]. The first observations of malignant tumors in two males aged 20 and 22 years have just been presented [4].

Among other explanations of *H. glaber* longevity is a special stability of its proteins [9], implying effective mechanisms of repair of damaged molecules [10]. The naked mole-rat genome has been described and the primary structure of all its proteins is available.

The aim of our study is to clear out whether the protein structure of the long lived rodent has motives corresponding to peptides (PER) and whether these motives structurally differ from those of related short lived species.

MATERIALS AND METHODS

The most probable sites of enzymatic cleavage, as a result of which a regulatory peptide is "cut" from the precursor protein molecule, are combinations of the main amino acids Lys-Arg (KR), Arg-Arg (RR), Arg-Lys (RK), and Lys-Lys (KK) [1]. Using specially designed AMS14-003 software, we carried out search for PER in easily released forms K—PER—K, K— PER—R, R—PER—K, and R—PER—R in the primary structure of all proteins of *H. glaber*, *R. norvegicus*, and *M. musculus* included in the MEDLINE data base (in the form of FASTA — text format for presentation of protein sequences in a single letter code).

RESULTS

We have found the target motives in 17 proteins of *H. glaber* and compared the fragments containing them with those in *R. norvegicus* and *M. musculus* proteins (Table 1).

Bronchogen-containing *H. glaber* protein, classified up to the present time as uncharacterized protein, is 85% homologous (according to our data) to a fragment of human Nck-associated protein 5-like protein (Table 2), which fact suggests calling the naked mole-rat protein "human Nck-associated protein 5-like protein homolog" or human NAP5-LPH (Nck — non-catalytic region of tyrosine kinase adaptor protein).

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TABLE 1. Short Peptides (PER) Present in Easily Released Form in the Structure of Long Lived *H. glaber* Rodent and Short Lived *R. norvegicus* and *M. musculus* Rodents

Peptides	Proteins						
Epitalon	yon Willebrand factor A domain-containing protein 3B (vWA3B)						
	SRYADGLFPOFHR AEDG RVYNLTANSELIY						
	SRYADGLFPRFYT AEDG RLYNLTAKSELIY						
	SRYADGLFPQIYT AEDG RLYNLTAKTELIC						
	Tubulin-specific chaperone A						
	MK AEDG KNYAIKKQAEILQESQTMIPDCQR						
	MK AEDG ENYAIKKOAEILOESRMMIPDCOR						
	MK AEDG ENYAIKKQAEILQESRMMIPDCQR						
Bronhogen	Fascin (Protein Phf14 in rat)						
	MDEVEWMHRHPK AEDL RIGLISWAGTYLTF						
	MAEVDWIHRHPK AEAL RVGLISWAGTYLTF						
	MAEVDWIHRHPK AEDL RVGLISWAGTYLTF						
	Transcription factor AP-4						
	EGIGSPDIWEDE KAEDLR REMIELRQQLDK						
	EGIGSPDIWEDEKAEDLRREMIELRQQLDK						
	EGIGSPDIWEDEKAEDLRREMIELRQQLDK						
	Uncharacterized protein (human Nck-associated protein 5-like						
	protein homolog)						
	EPESLNISKLMAKAEDLRRALEEEKAYLSR						
	EAESLNISKLMAK AEDL RRALEEEKAYLSR						
	EAESLNISKLMAKAEDLRRALEEEKAYLSR						
	1,25-dihydroxyvitamin D $_3$ 24-hydroxylase, mitochondrial						
	EIQSVLPENQMPR AEDL KKMPYLKACLKES						
	No proteins close by structure were found in data base for rat and mouse						
	EIQSVLPDNQTPRAEDVRNMPYLKACLKES						
	Leucine-rich repeat serine/threonine-protein kinase 1 (LRRK1)						
	KGSRSVAKNGVIR AEDL RMLLVGTGFTKQT						
	KGSRSVAKNGVIR AEDL RMLLVGTGFTQQT						
	KGSRSVAKNGVIQ AEDL RMLLVGTGFTQQT						

Table 1 continued.

Peptides	Proteins				
	Dynein heavy chain 2, axonemal				
	YEIPHYVVNVAG <u>RAEDLR</u> ILRENLLLVARD				
	FETPHYVMNVADRAEDLRILRENLLLVARD				
	FETPHYVMNVAERAEDLRILRENLLLVARD				
Testagen	General transcription factor IIF (TFIIF) subunit 2				
	ANHQYNIEYERKKKEDGKRARADKQHVLDM				
	ANHQYNIEYERKKKEDGKRARADKQHVLDM				
	ANHQYNIEYERKKKEDGKRARADKQHVLDM				
Serrate RNA effector molecule-like protein, или Serrate RNA effector					
	molecule homolog, или Arsenite-resistance protein 2 (SRRT, ARS2)				
	gdgerkagdkdd <u>kkedgk</u> qaendgsnddkt				
	gdgerkvndkde <u>kkedgk</u> qaendssnddkt				
	GEGERKANDKDEKKEDGKQAENDSSNDDKT				
	Lipoxygenase-like protein domain-containing protein 1,				
	or Lipoxygenase homology domains 1 (LOXHD1)				
	EFLFLCGRWLSLK KEDG RLERLFYEKEYTG				
	EFLFLCGRWLSL <u>KKEDGR</u> LERLFYEKEYTG				
	EFLFLCGRWLSLK KEDG RLERLFYEKEYTG				
	Patatin-like phospholipase domain-containing protein 7 (PNPLA7),				
	или NTE-related esterase (NRE)				
	YIVLSGRLRSVIR KEDG KKRLVGEYGLRDL				
	YIVLSGRLRSVIR K D DG KKRLAGEYGRGDL				
	YIVLSGRLRSVIR K D DG KKRLAGEYGRGDL				
Livagen	Prostaglandin reductase 1 (PGR1), или leukotriene B4 dehydrogenase				
	GGRERRGQEEEEK KEDA KKEKGRSLMMVRA				
	No proteins close by structure were found in data base for rat and mouse				
	Short stature homeobox protein 2, или homeobox protein Og12X,				
	или paired-related homeobox protein SHOT				
	PRLTEVSPELKDRKEDAKGMEDEGQTKIKQ				
	PRLTEVSPELKDRKEDAKGMEDEGQTKIKQ				
	PRLTEVSPELKDRKDDAKGMEDEGQTKIKQ				

Table 1 continued.

Peptides	Proteins					
Cardiogen	Dehydrogenase/reductase SDR family member 4 (DHRS4)					
	GLSVTGTVCHVGK AEDR KQLVATAVKLHGG					
	GLSVTGVVCHVGKAEDREKLVNMALKLHQG					
	GLSVTGIVCHVGK AEDR EKLITTALKRHRG					
	Eukaryotic translation initiation factor 3 subunit A (EIF3A)					
	LRSERDEVSSWRR AEDR KDDRAEERDPPRR					
	LRSEREEASSWRRTDDRKDDRTEERDPPRR					
	LRSEREEASSWRRTDDRKDDRTEERDPPRR					
Prostamax	MAP7 domain-containing protein 2 (in rat – Brain-enriched E-MAP-115-					
	like protein, in mouse MAP7 domain-containing protein 2 isoform 2)					
	KRTRKSDVSPEVK KEDP KVEIQPVVCVENK					
	KRTRKSDASLEVK KEDP KVEIQPLPDVENK					
	KRTRKSDASLEVK KEDP KVELQPPPDVENK					

Note. Primary structures: upper lines: *H. glaber*, middle lines: *R. norvegicus*, lower lines: *M. musculus*. Coincidence of the rat and mouse amino acid residues with those of naked mole-rat is shown with a gray color. Motives corresponding to PER are shown with bold letters, the adjacent lysine (K) and arginine (R) residues are underlined. Primary structures of tubulin-specific chaperone A and prostaglandin reductase-1 are presented completely, other proteins presented as fragments (*n*=30) including the target short peptides.

TABLE 2. H. glaber Uncharacterized Protein (Fragment, n=1003)

XSSGPNCAPGSSSSSSDEAGDPNEAPSPDTLLGALARRQLNLGQLLEDTESYLQAFLAGAAG PLNGDHPGPGQSSSPDQAPPQLSKSKGLPKSAWGGGTPEAHRPGFGATSEGQGPLPFLSMFMG AGDAPLGSRPGHPHSSSQVKSKLQIGPPSPGEAQGPLLPSPARGLKFLKLPPTSEKSPSPGGP QLSPQLPRNSRIPCRNSGSDGSPSPLLARRGLGGGELSPEGAQGLPTSPSPCYTTPDSTQLRP PQSALSTTLSPGPVVSPCYENILDLSRSTFRGPSPEPPPSPLQVPTYPQLTLEVPQAPEVLRS PGVPPSPCLPESYPYGSPQEKSLDKAGSESPHPGRRTPGNSSKKPSQGSGRRPGDPGSTPLRD RLAALGKLKTGPEGALGSEKNGVPARPGTEKTRGPGKSGESAGDMVPSIHRPLEQLEAKGGIR GAVALGTNSLKQQEPGLMGDPGARVYSSHSMGARVDLEPVSPRSCLTKVELAKSRLAGALCPQ VPRTPAKVPTSAPSLGKPNKSPHSSPTKLPSKSPTKVVPRPGAPLVTKESPKPDKGKGPPWAD CGSTTAQSTPLVPGPTDPSQGPEGLAPHSAIEEKVMKGIEENVLRLQGQERAPGAEVKHRNTS SIASWFGLKKSKLPALNRRTEATKNKEGAGGGSPLRREVKMEARKLEAESLNISKLMAKAEDL RRALEEEKAYLSSRARPRPGGPAPGPNTGLGOVOGOLAGMYOGADTFMOOLLNRVDGKELPSK SWREPKPEYGDFQPVSSDPKSPWPACGPRNGLVGPLQGCGKPPGKPSSEPGRREEMPSEDSLA EPVPTSHFTACGSLTRTLDSGIGTFPPPDHGSSGTPSKNLPKTKPPRLDPPPGVPPARPPPLT KVPRRAHTLEREVPGIEELLVSGRHPSMPAFPALLPAAPGHRGHETCPDDPCEDPGPTPPVQL AKNWTFPNTRAAGSSSDPLMCPPRQLEGLPRTPMVRIAAEERERTREQEGVMWGDQFLQ

Note. Gray background shows amino acid residues common for this protein in naked mole-rat and human NAP5-LPH. Motives corresponding to PER are shown with bold letters, the adjacent lysine (K) and arginine (R) residues are underlined.

TABLE 3. Coincid	ence/Noncoincidence	of Short Peptide	e (PER) Struc	ctures in Protei	ns of Rodents	s with a Long	(H. glaber)
and Short Lifespar	n (R. norvegicus, M. n	usculus)					

Coinciding structures	Protein	PER in proteins		
PER and terminal Arg/Lys	Fascin	Lys-Bronhogen-Arg (KAEDLR)		
	Transcription factor AP-4	Lys-Bronhogen-Arg (KAEDLR)		
	Uncharacterized protein (human Nck-associated protein 5-like protein homolog)	Lys-Bronhogen-Arg (KAEDLR)		
	General transcription factor IIF (TFIIF) subunit 2	Lys-Testagen-Lys (KKEDGK)		
	Serrate RNA effector molecule-like protein, or Serrate RNA effector molecule homolog or Arsenite-resistance protein 2 (SRRT, ARS2)	Lys-Testagen-Lys (KKEDGK)		
	Lipoxygenase-like protein domain-containing protein 1, or Lipoxygenase homology domains 1 (LOXHD1)	Lys-Testagen-Lys (KKEDGK)		
	MAP7 domain-containing protein 2	Lys-Prostamax-Lys (KKEDPK)		
Only PER	von Willebrand factor A domain-containing protein 3B (vWA3B)	Epitalon (AEDG)		
	Tubulin-specific chaperone A			
	Epitalon (AEDG)			
	Dehydrogenase/reductase SDR family member 4 (DHRS4)	Cardiogen (AEDR)		
3 of 4 PER amino acids	Eukaryotic translation initiation factor 3 subunit A (EIF3A)	Cardiogen (XEDR)		
	Patatin-like phospholipase domain-containing protein 7 (PNPLA7), or NTE-related esterase (NRE)	Testagen (KXDG)		

Table 3 presents data on the structural similarity of PER in long lived and short lived rodent species.

The motives corresponding to PER are found in the rodent protein composition, including the regions adjacent to lysine and arginine residues facilitating peptide release as whole molecules during partial proteolysis. The structure of the above motives in the molecules of some proteins of long lived *H. glaber* species differs significantly from that in short lived *R. norvegicus* and *M. musculus*: in eukaryotic translation initiation factor 3; in patatin-like phospholipase domain-containing protein 7, and in dehydrogenase/ reductase SDR family member 4 Differences in the structure of von Willebrandt factor and tubulin-specific chaperone A are less significant.

Short peptides, identical to PER, are present in the protein structure of *H. glaber*. These short peptides are located between lysine and arginine residues, which facilitates significantly the release of these peptides in limited proteolysis. Some of these peptides, found in the naked mole-rat proteins, are not found in the proteins of short lived species Norway rat and house

mouse. The structure and function of these proteins deserve special attention in further studies of the longevity phenomenon.

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676

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