

Intraspecies Regulation of Ribonucleolytic Activity[†]

R. Jeremy Johnson[‡], Luke D. Lavis[§], and Ronald T. Raines^{‡,§,*}

Page	Contents
1	Table of Contents
2	FIGURE S-1: Sequence identities for RIs and ribonucleases
3	FIGURE S-2: Multiple sequence alignment of RIs
4	FIGURE S-3: Multiple sequence alignment of ribonucleases
4	Reference

A

Percent Identity	human RI	chimp RI	mouse RI	rat RI	bovine RI	porcine RI	chicken RI
human RI		98	73	75	74	77	49
chimp RI	98		73	75	74	77	49
mouse RI	73	73		90	76	76	48
rat RI	75	75	90		76	76	50
bovine RI	74	74	76	76		84	49
porcine RI	77	77	76	76	84		47
chicken RI	49	49	48	50	49	47	

B

Percent Identity	human RNase	chimp RNase	mouse RNase	rat RNase	bovine RNase	porcine RNase	chicken RNase
human RNase		97	70	65	69	75	30
chimp RNase	97		68	65	69	75	31
mouse RNase	70	68		76	70	74	35
rat RNase	65	65	76		66	66	27
bovine RNase	69	69	70	66		79	28
porcine RNase	75	75	74	66	79		31
chicken RNase	30	31	35	27	28	31	

FIGURE S-1: Percent identity between RIs (A) and ribonucleases (B) in Figure 5. Percent identities were determined by using the default values in the program Clustal W (1).

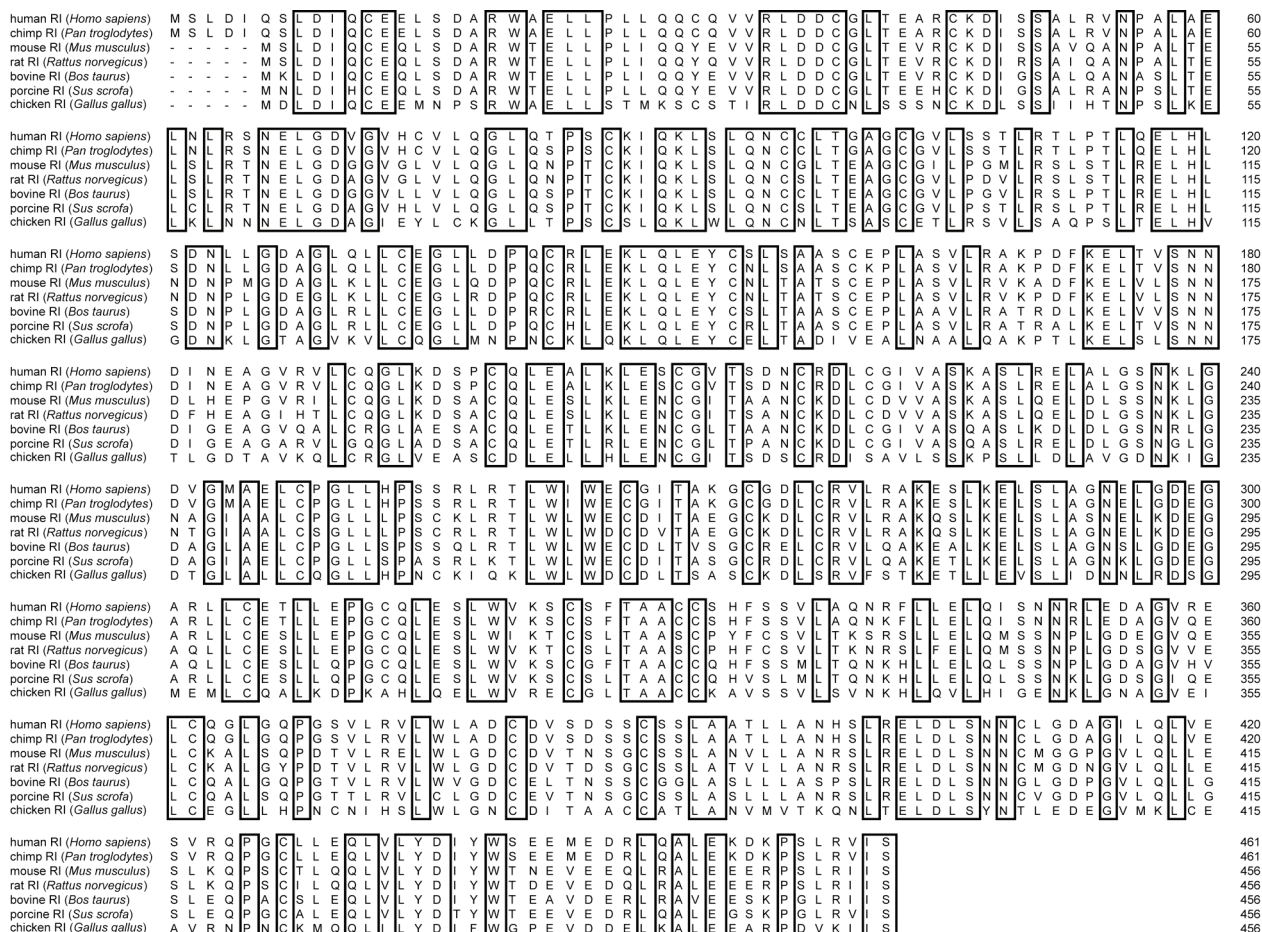


FIGURE S-2: Multiple sequence alignment of RIs used to construct the phylogenetic tree in Figure 5A. Conserved residues are shown as black boxes. Sequence alignments of RI were performed by using the default values in the program Clustal W (1). Accession codes for RI are listed in the experimental procedures.

human (<i>Homo sapiens</i>)	K E S R A K K F Q R Q H M D . S D S S P S S S S T Y C N Q M M R R R R N M - T Q G L C K P V N T F V H E E P L V D V Q N V C	58
chimp (<i>Pan troglodytes</i>)	K E S R A K K F F Q R Q H V M D . S D S S P S S S S T Y C N Q M M R R R R N M - T Q G R C K P V N T F V H E E P L V D V Q N V C	58
mouse (<i>Mus musculus</i>)	R E S A A Q K F F Q R Q H M D . P D G S S I N S P T Y C N Q M M K R R R D M - T N G S C K P V N T F V H E E P L A D V Q A V C	58
rat (<i>Rattus norvegicus</i>)	R E S S A D K F F K R Q H M D . T E G P S K S S P T Y C N Q M M K R R Q G M - T K G S C K P V N T F V H E E P L E D V Q A I C	58
bovine (<i>Bos taurus</i>)	K E T A A A K F F E R Q H M D . S S T S A A S S S N Y C N Q M M K S R N L - T K D R C K P V N T F V H E S L A D V Q A V C	58
porcine (<i>Sus scrofa</i>)	K E S P A K K F F Q R Q H M D . P D S S S S S S S N Y C N L M M S R R R N M - T Q G R C K P V N T F V H E S L A D V Q A V C	58
chicken (<i>Gallus gallus</i>)	- V P T Y Q D F L R T H V D F P K T S F P N I A A Y C N V M M V R R R G I N V H G R C K S L N T F V H T D P R N L N T L C	59
human (<i>Homo sapiens</i>)	F Q E K V T C K N G Q G N C Y K S N S S M H I T D C R L T N G S S R Y P N C A Y R T S P K E R H I I V A C E G S P Y V P V	118
chimp (<i>Pan troglodytes</i>)	F Q E K V T C K N G Q G N C Y K S N S S M R I T D C R L T N G S S R Y P N C A Y R T S P K E R H I I V A C E G S P Y V P V	118
mouse (<i>Mus musculus</i>)	S Q E N V T C K N R K S N C Y K S S S A L H I T D C H L K G N S K Y P N C D Y K T T Q Y Q K H I I V A C E G N P Y V P V	118
rat (<i>Rattus norvegicus</i>)	S Q G Q V T C K N G R N N C H K S S S T L R I T D C R L K G S S K Y P N C D Y T T T D S Q K H I I V A C E G N P Y V P V	118
bovine (<i>Bos taurus</i>)	S Q K N V A C K N G Q T N C Y Q S Y S T M S I T D C R E T G S S K Y P N C A Y K T T Q A N K H I I V A C E G N P Y V P V	118
porcine (<i>Sus scrofa</i>)	S Q I N V N C K N G Q T N C Y Q S N S T M H I T D C R E T G S S K Y P N C A Y K A S Q E Q K H I I V A C E G N P P V P V	118
chicken (<i>Gallus gallus</i>)	I N Q - - - - P N R A L R T T Q Q L P V T D C K L I R S - - H P T C S Y T G N Q F N H R V R V G C W G - - L P V	109
human (<i>Homo sapiens</i>)	H F D A S V E D S T	128
chimp (<i>Pan troglodytes</i>)	H F D A S V E D S T	128
mouse (<i>Mus musculus</i>)	H F D A T V - - -	124
rat (<i>Rattus norvegicus</i>)	H F D A S V - - -	124
bovine (<i>Bos taurus</i>)	H F D A S V - - -	124
porcine (<i>Sus scrofa</i>)	H F D A S V - - -	124
chicken (<i>Gallus gallus</i>)	H L D G T F P - - -	116

FIGURE S-3: Multiple sequence alignment of ribonucleases used to construct the phylogenetic tree in Figure 5B. The sequences of bovine seminal ribonuclease and bovine brain ribonuclease are not shown for clarity. Conserved residues are shown as black boxes. Sequence alignments of ribonucleases were performed by using the default values in the program Clustal W (1). Accession codes for ribonucleases are listed in the experimental procedures.

REFERENCE

- Chenna, R., Sugawara, H., Koike, T., Lopez, R., Gibson, T. J., Higgins, D. G., and Thompson, J. D. (2003) Multiple sequence alignment with the Clustal series of programs. *Nucleic Acids Res.* 31, 3497-3500.