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Molecular Characterization of Thyroid Hormone Receptors from the Leopard Gecko, and Their Differential Expression in the Skin

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Thyroid hormones (THs) play crucial roles in various developmental and physiological processes in vertebrates, including squamate reptiles. The effect of THs on shedding frequency is interesting in Squamata, since the effects on lizards are quite the reverse of those in snakes: injection of thyroxine increases shedding frequency in lizards, but decreases it in snakes. However, the mechanism underlying this differential effect remains unclear. To facilitate the investigation of the molecular mechanism of the physiological functions of THs in Squamata, their two specific receptor (TR α and β) cDNAs, which are members of the nuclear hormone receptor superfamily, were cloned from a lizard, the leopard gecko, *Eublepharis macularius*. This is the first molecular cloning of thyroid hormone receptors (TRs) from reptiles. The deduced amino acid sequences showed high identity with those of other species, especially in the C and E/F domains, which are characteristic domains in nuclear hormone receptors. Expression analysis revealed that TRs were widely expressed in many tissues and organs, as in other animals. To analyze their role in the skin, temporal expression analysis was performed by RT-PCR, revealing that the two TRs had opposing expression patterns: TR α was expressed more strongly after than before skin shedding, whereas TR β was expressed more strongly before than after skin shedding. This provides good evidence that THs play important roles in the skin, and that the roles of their two receptor isoforms are distinct from each other.

Key words: thyroid hormone receptor, TR, skin shedding, reptile, Squamata, leopard gecko

INTRODUCTION

The thyroid hormones (THs), thyroxine (T₄) and thyronine (T₃), are pleiotropic factors important for many developmental and physiological processes in vertebrates. There has been a lot of research into the physiological significance of THs in various vertebrates. For example, THs are known to be important for inner ear and retina development, liver metabolism in mice (Flamant and Samarut, 2003), metamorphosis in axolotl and *Xenopus* (Nakajima *et al.*, 2005; Sachs *et al.*, 2000; Safi *et al.*, 2004), and embryogenesis and metamorphosis in many teleost fish (Power *et al.*, 2001).

In reptiles, THs have been suggested to affect tail regeneration (Turner and Tipton, 1971), metabolic rate and metabolic enzyme activity (John-Alder, 1990; John-Alder and Joos, 1991), and shedding frequency (Chiu *et al.*, 1967; Chiu and Lynn, 1970). Above all, their effect on shedding frequency is particularly interesting. In lizards, the injection of thyroxine increases shedding frequency, and thyroidectomy decreases it (Chiu *et al.*, 1967). In contrast, in snakes, the injection of thyroxine decreases the shedding frequency,

and thyroidectomy increases it (Chiu and Lynn, 1970). The mechanisms underlying these completely opposite phenomena have not been clarified, partly due to the lack of investigation of the molecular mechanism of THs in reptiles.

THs can regulate target genes by interacting with thyroid hormone receptors (TRs), which are members of the nuclear receptor superfamily. Two isoforms, TR α and TR β , have been isolated from species of four classes of vertebrate, but not from reptiles (Forrest *et al.*, 1990; Kawakami *et al.*, 2003; Murray *et al.*, 1988; Yaoita *et al.*, 1990). These isoforms share high homology and have similar biochemical properties. However, they have distinct spatial and temporal expression profiles in overlapping patterns, suggesting that two genes mediate both individual and common biological functions.

Unlike other squamate animals, the leopard gecko, *Eublepharis macularius*, is easily maintained and bred in the laboratory. The leopard gecko is therefore expected to become an experimental model. Indeed, several molecular studies of the endocrine system have already been conducted on this species (Endo and Park, 2004; Endo and Park, 2005; Ikemoto and Park, 2003; Ikemoto *et al.*, 2004; Kato *et al.*, 2005; Valleley *et al.*, 2001).

In this study, we cloned TR α and β from the leopard gecko to augment investigations on the molecular mechanisms of the physiological functions of THs in reptiles. In

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addition to identifying two isoforms of TR, we performed phylogenetic and expression analyses. We also demonstrated the differential expression of the TR isoforms, and herein discuss their possible roles in shedding.

MATERIALS AND METHODS

Animals

The leopard geckos (*Eublepharis macularius*) were treated according to the guidelines of the Bioscience Committee at the University of Tokyo. The animals were provided meal worms, crickets, water, and powdered calcium supplement *ad libitum*. Animals were anesthetized with sodium pentobarbital and killed by rapid decapitation, followed by complete bloodletting. Tissues and organs were immediately dissected, frozen in liquid nitrogen, and stored at -80°C until use.

RNA preparation and cDNA synthesis

Total RNA was extracted using ISOGEN (NIPPON GENE, Tokyo, Japan). The cDNAs used as templates for RT-PCR were synthesized from 3 μg of denatured total RNA using 5 μM oligo(dT) primer and 100 units of M-MLV Reverse Transcriptase (Promega, Madison, WI) in a 20 μl reaction volume with incubation at 42°C for 1.5 h. The cDNA used for rapid amplification of cDNA ends (RACE) was synthesized from 3 μg of total RNA using a SMART RACE cDNA Amplification Kit (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions.

Molecular cloning of TR cDNAs by RT-PCR and RACE

RT-PCR was carried out to obtain partial TR cDNAs from skin cDNA using degenerate primers (Table 1). All of the following PCR amplifications were performed in 20 μl reaction volumes containing

each primer at 1 μM , 0.25 unit of TaKaRa Ex Taq (TaKaRa, Shiga, Japan), each dNTP at 250 μM , and Ex Taq Buffer (TaKaRa). The PCR product was separated by electrophoresis, extracted using a QIAquick Gel Extraction Kit (QIAGEN K.K., Tokyo, Japan) and directly sequenced. After determination of the partial sequence, RACE was carried out to determine the complete sequence of TR cDNAs. PCR and nested PCR were performed with gene-specific primers (Table 1) in combination with Universal Primer A Mix (Clontech) or Nested Universal Primer A (Clontech). The amplified products were sequenced as described above. This procedure was repeated independently at least twice to avoid PCR amplification errors.

Comparison of the amino acid sequences of various TRs

CLUSTAL X software (version 1.81) (Thompson *et al.*, 1997) was used with default settings to align the deduced amino acid sequences of the TRs of the leopard gecko and other species.

Amino acid identities were calculated for the C domain, E/F domain, and entire ORF.

Molecular phylogenetic analysis

The nucleotide sequences of the entire ORFs of the TRs from the leopard gecko and from several species representing all other vertebrate classes were aligned using CLUSTAL X with default settings. The alignment of the nucleotide sequences was used to generate a phylogenetic tree, using the neighbor-joining method (Saitou and Nei, 1987). Bootstrap values were calculated with 1000 replications to estimate the robustness of internal nodes. The GenBank accession numbers of TRs used in the phylogenetic analysis are as follows: *Homo sapiens* (human) TR α , **M24748**; *Homo sapiens* TR β , **X04707**; *Mus musculus* (mouse) TR α , **MMCERBA1**; *Mus musculus* TR β , **S62756**; *Gallus gallus* (chicken) TR α , **Y00987**; *Gal-*

Table 1. Oligonucleotide primers used for RACE, RT-PCR, and sequencing.

Name	Nucleotide sequence	Usage	
TR α	SE01 GCCGCTCGAGGATCCCATTTCCTG	Seqencing	
	SE02 ACCCGNAAYCAGTGYCAGYTS	Degenerate PCR	
	SE03 ATGCTGAAATCTCTTCAGCATCGG	Seqencing	
	SE04 CCTCAGACCCGAGTGGGCTGATCTGC	3' -RACE	
	SE05 CCGACCTGCGCATGATTGGGGCTTGC	Seqencing	
	SE06 CCCCACCTCATCACCTCGGACACAAC	Seqencing	
	AS01 TTSGGCCAGAAGTGVGGAAT	Degenerate PCR	
	AS02 CTTTGTCCCATCGGGCATGGAGG	Seqencing	
	AS03 GCCGTCGGCTCTGGCCGATGCTGAAG	5' -RACE	
	AS04 CCTCTTTGCGCCGCTCTCTCGGTTT	5' -RACE	
	AS05 TTTACGTTTCCCATCCGGCCACCGG	Seqencing	
	AS06 GTGTCCCAACCCCTATCACCAACGC	Seqencing	
	TR β	SE01 GGGTCACACTACTCCTGTCTCCAG	Seqencing
		SE02 CVMGNAAYCARTGYCARGAA	Degenerate PCR
		SE03 AGAGCTGCAGAAGACAATTGGGATA	3' -RACE
		SE04 TGGACAAGCACCAATAGTAAATGCC	Seqencing
SE05 TGGGGAGATGGCAGTGACAAGGGGCC		3' -RACE	
SE06 GCCCAACAGAACTCTTTCCCCCTTTG		Seqencing	
SE07 GTTCTTGAAGTCTTTGAGGATTAA		Seqencing	
SE08 CAATGCGGGTACTTGTGACAATTGC		Seqencing	
AS01 RTCYTCRAASACYTCYARGA		Degenerate PCR	
AS02 TTKGGCCARAARTGYGYMAC		Degenerate PCR	
AS03 CTTTCCCGCCTTCTGGGGCATTTA		5' -RACE	
AS04 GTCTTCTTCTGCAGCTTCCCGACG		5' -RACE	
AS05 GTAACGGGTATGTACCCTGACATGC		Seqencing	
AS06 GTATTCTCAACGTCAAACCTTTTCCA		Seqencing	

Abbreviations for degenerate nucleotides: K, G or T; M, A or C; R, A or G; S, C or T; V, A or G; Y, C or T. N represents all four nucleotides.

A

CGCGAGAGGAGCGAAGAAGCCGCGCGGAAAGCCGCGCGTCGAGGATCCCAATTTCGGTGTTTGCCCCAGAATGTTGATGTTCCAC -165
 CAACGCTGAGGAGCGCGATGCGGATTCGCTCTAGCTCTGGTAACGCCCCCTCCCTCCCAAATTCGAACCTGCATCTGCTGGCGG -75
 GCCACGGAGAGTCGCCTCTGGGGCGGAGCCACCTCGTCTCTCTTCTGGTCTGGATGGAATTCGCGTGA -1

ATGGAACAGAAAGCCAGCAGCGTGGATGCTGTCCAGAGCCAGAGGACACCCCGTGGCCGATGGGAAACGTAAAGAAAAAGCAGCCAA 90
 M E Q K P S T V E C L S E P E D T R W P D G K R K R K S S Q 30

TGTTTCGGTGA AAAAGCAGTATGTCCAGGTACATCCCTAGCTACTTGGACAAAGATGAACAGTGTGTTGATGTGGAGACAAAGCCACAGGG 180
 C S V K S S M S G Y I P S Y L D K D E Q C V V C G D K A T G 60

TACCCTACCGATGCATCACCTGGAGAGGCTCAAGGGCTTTTCCGACGGACCATCCAGAAGAACCTGCACCCACATACCTCTGCAAG 270
 Y H Y R C I T C E G C K G F F R R T I Q K N L H P T Y S C K 90

TACGATGGTTCCTCGCTCATCGACAAGATCACCCGCAACAGTCCAGCTTTGTCGATTCAAGAAGTGCATTGCCGTTGGCATGGCCATG 360
 Y D G S C V I D K I T R N Q C Q L C R F K K C I A V G M A M 120

GACTTGGTGTGGATGACTCCAAGAGGTTAGCCAAAGCGAACTGATCGAAGAGAACCGAGAGAGGCGGCAAAAGAGGAGATGCTGAAA 450
 D L V L D D S K R V A K R K L I E E N R E R R R K K E E M L K 150

TCTCTTCAGCATCGGCGAGCCGACGGCGGAGGATGGGAATGATCCACATTCGCCACAGAGGCACCCGAGTACGAATGCCCAAGGC 540
 S L Q H R P E P T A E E W E L I H I A T E A H R S T N A Q G 180

AGCCACTGAAAACAGAAAGCGAAATTTTCGCTGAAGACATCGGTCACTCAACATGGCCCTCCATGCCCGATGGGCAAAAGTAGACTTG 630
 S H W K Q K R K F L P E D I G Q S P M A S M P D G D K V D L 210

GAGCATTTCAGCGAGTTTACGAAGATCATCAACCCCTGCCATCACTCGTGTGGTGGACTTTGCCAAAACCTGCCCATGTTTCAGAGCTG 720
 E A F S E P T K I I T P A I T R V V D F A K K L P M F S E L 240

CCTTGTGAGGACAGATCATCTGTGAAGGGCTGCTGCATGGAGATCATGTCACCTGCGGGCAGCTGTGCGCTACGACCTGAAAGCGAG 810
 P C E D Q I I L L K G C C M E I M S L R A A V R Y D P E S E 270

ACATGACGCTGAGTGGCAAAATGGCTGTCAAGCGGAAACAGCTGAAGAACGGTGGTCTGGCGTGGTTCGGATGCCATCTTTCAGCTG 900
 T L T L S G E M A V K R E Q L K N G G L G V V S D A I F D L 300

GGCAAGTCCCTCTCGCTTCAACCTGACGACACAGAAGTGGCCCTGCTCCAGGCTGTGCTACTCATGCTCAGACCGCAGTGGCTG 990
 G K S L S A F N L D D T E V A L L Q A V L L M S S D R S G L 330

ATCTGGCTGCAAGATGAAAATGCCAAGAGACTACCTGTTGGCTTTGAACACTACATCAACTATCGAAAACACAACTTCCCCAC 1080
 I C V D K I E K C Q E T Y L L A F E H Y I N Y R K H N I P H 360

TTCTGGCCAAAGCTTCTCATGAAGTGAACGACTGCGCATGATGGGGCTTGCACGCGAGTGCCTTCTGCAATGAAGGTGGAATGC 1170
 F W P K L L M K V T D L R M I G A C H A S R P L H M K V E C 390

CCACAGAGCTTCCCCCACTCTTCTCGAAGTCTTCAGGATCAGGAAGTCTAG 1227
 P T E L F P P L F L E V F E D Q E V * 408

GGTGGGGGGAGGGGGGGGAGAGGGTGGCATGGGAAATGGGGAGGAGGAGGATGGGATGACTGTTGGCCCA 1317
 CGAAGCCCCCCTCATCCTCGGACACACAGATTTTCATTTTTTGGTCTGTTTGGTGTTCATTTTCTTTAATTTTGGTT 1407
 TGTTTTCTAAATATGCAAGTCAAGTCAAGTCCACAGAAAGGGGAGGTGAGGCGTGGTGATAGGGGTTGGGACAC 1490

B

AACCGGTCACACTACTCTGCTCCAGTGAAGGTAGGCATCAAGTAATACTGGTGA AAAAGAGGAATGAGAAATGACTACTTTTTGT -15
 TAATTTCCAGCAGC -1

ATGTCAGGGTACATACCCAGTTACTTAGACAAAGGACGAGCTATGTTGTTGTTGGTACAAAGCCACTGGGTATCACTATCGCTGTATC 90
 M S G Y I P S Y L D K D E L C V V C G D K A T G Y H Y R C I 30

ACTTGTGAAGGTGCAAGGATTTTTTCGAAGAACTATTCAGAAAACTTCCACCAACCTACTCTGTAATATGAAGAAAATGTGTG 180
 T C E G C K G F F R R T I Q K N L H P T Y S C K Y E G K C V 60

ATAGACAAAGTCAAGAAACCAATGCCAGGAATGCTGCTTCAAGAAATGCATTTATGTTGGCATGGCAACAGATTTGGTGTGGATGAC 270
 I D K V T R N Q C Q E C R F K K C I Y V G M A T D L V L D D 90

AGCAAGCGATTAGCAAAAAGAACTAATAGAGAAAATCGAGAGAAGAGACGTCGGGAAGAGCTGCAGAAAGCAATGGGATAAAAACCT 360
 S K R L A K R K L I E E N R E K R R R E E L Q K T I G I K P 120

GAGCCACAGATGAAGAGTGGGAGCTTATCAAAAATGTTACTGAAGCACATGTAGTACCAATGCACAAGGAAGCCATGGAAACAAAA 450
 E P T D E E W E L I K I V T E A H V A T N A Q G S H W K Q K 150

AGGAAATTTCTGCCAGAGATATGGACAAAGCACTAATAGTAAATGCCCAAGGCGGAAAGTGAATTTAGAAGCCTTCAGCCAGTTT 540
 R K F L P E D I G Q A P I V N A P E G G K V D L E A F S Q F 180

ACAAAATATCACACAGCAATCACAGAGTGGTGGATTTGCCAAAAGTTGCCTATGTTCTGTGAGCTGCCATGTGAAGACCAGATA 630
 T K I I T P A I T R V V D F A K K L P M F C E L P C E D Q I 210

ATCCTTCTGAAGGTGCTGCATGGAGATCATGCTCCAGAGCAGTTCGCTATGATCCGAGAGCGAGACATTAACGTTAAATGGG 720
 I L L K G C C M E I M S L R A A V R Y D P E S E T L T L N G 240

GAGATGGCAGTGACAAGGGCCAACTGAAGAACGGGGTCTTGGTGTAGTATCTGATGCCATTTTTCGACCTGGGATGTCATCTTCATCA 810
 E M A V T R G Q L K N G G L G V V S D A I F D L G M S L S 270

TTCAAGCTGCATGACAGGAGTGTCTTCTCAGGCTGTTCTGCTGATGCTTCCAGATCGCCAGGCTTGTGAGTGTGAGAGGATA 900
 F N L D D T E V A L L Q A V L L M S S D R P G L V S V E R I 300

GAAAATGTCAGGAGATTTCTCTGCGATTGCAACACTACATTAATTCGGAAGCACCACATTCACACTTTTGGCAAAACTGCTG 990
 E K C Q E S F L L A F E H Y I N Y R K H H I A H F W P K L L 330

ATGAAAGTACAGGATCTCGAATGATCGCGCTGCCACGCTAGCCGCTTCTGCAATGAAGTGGAAATGCCAAGCAAGCACTTTCC 1080
 M K V T D L R M I G A C H A S R P L H M K V E C P T E L F P 360

CCTTGTCTTGGAGTCTTTGAGGATTA 1110
 F L F L E V F E D * 369

AAAGGCTGGAGTGGTCTCAGAATTCATAGCACTACTGGGTGTCATTTTCATTCATTCGCTAAATCCTTTTTTCTTTGTCATCTC 1200
 ATTTTGTCCACCTGTTTTTATTTGGGGGATTTTATTTTTAATAGCATGAATGAATGATGCTTCAATGCGGGTACTGTGACA 1290
 ATTGCAATTAATTTTTGTTGCTGTTTTTCTCCTCAGTCTTGGTGTGAATCCTTGGAAAAGTTGACGTTGAGAAATCAAAAC 1377

Fig. 1. Nucleotide and deduced amino acid sequence of the cDNA encoding (A) TR α and (B) TR β of the leopard gecko. Nucleotides (upper row) are numbered from 5' to 3', beginning with the initiator codon (ATG) in the coding region. Amino acid residues (lower row) are numbered beginning with the first Met residue in the ORF. The C and E/F domains are indicated by solid and dashed underlining, respectively. The D domain is between these two domains.

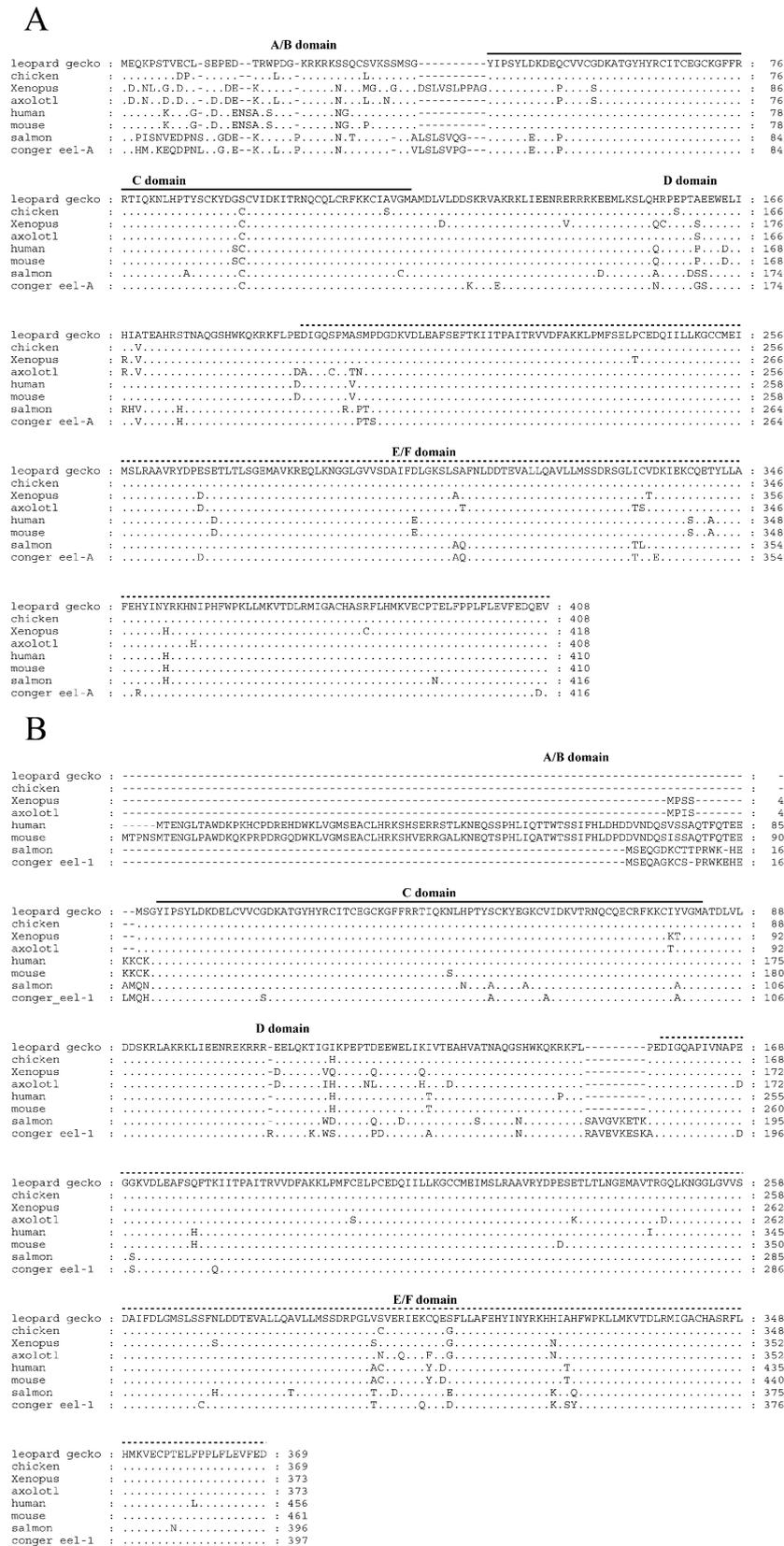


Fig. 2. Alignment of the predicted amino acid sequence of (A) TR α and (B) TR β of the leopard gecko with homologs from other species. Dots indicate identity of amino acids with those of the TRs of the leopard gecko. Dashes indicate gaps inserted during alignment. The domains are indicated.

lus gallus TR β , **X17504**; *Xenopus laevis* (African clawed frog) TR α , **M35344**; *Xenopus laevis* TR β , **M35361**; *Ambystoma mexicanum* (axolotl) TR α , **AY174871**; *Ambystoma mexicanum* TR β , **AY174872**; *Salmo salar* (salmon) TR α , **AF146775**; *Salmo salar* TR β , **AF302251**; *Conger myriaster* (conger eel) TR α , **AB183396**; *Conger myriaster* TR β 1, **AB183394**.

Expression analysis of TRs

To identify the target organs of THs, the spatial expression pattern of the TRs was examined by RT-PCR. Twenty-five nanograms of cDNA from the whole brain, heart, liver, small intestine, large intestine, testis, ovary, and thymus, and 5 ng from the pituitary, were amplified using primers specific for TRs. The primer sets used were TR α SE03 and TR α AS02 for TR α , and TR β SE03 and TR β AS03 for TR β (Table 1). The PCR products were visualized by electrophoresis on a 1.2% TAE agarose gel and stained with ethidium bromide. Each DNA fragment was extracted from the gel and directly sequenced to confirm its identity.

Temporal expression analysis of TRs in skin

Total RNA was extracted from the skin of three animals within 24 hours before or after shedding. cDNA from the skin (7.5 ng) was amplified using the specific primers described above. The PCR conditions were as follows: 94°C for 3 min; 30 cycles of 94°C for 40 s, 64°C for 25 s, and 72°C for 30 s; and 72°C for 2 min. The PCR products were analyzed by electrophoresis on a 1.2% TAE agarose gel.

RESULTS

Molecular cloning of TR cDNAs from the leopard gecko

Full-length TR cDNAs were isolated from the skin of the leopard gecko by RT-PCR and RACE. TR α cDNA comprised 1,744 bp, which included a 5'-UTR of 254 bp, an ORF of 1,227 bp encoding 408 amino acid residues, and a 3'-UTR of 263 bp. TR β cDNA comprised 1,481 bp, including a 5'-UTR of 104 bp, an ORF of 1,110 bp encoding 369 amino acid residues, and a 3'-UTR of 267 bp. The domains are indicated in Fig. 1. Sequences of full-length cDNAs were deposited in GenBank (Accession Nos. **AB204861** and **AB204862**).

Comparison of the amino acid sequences of various TRs

Alignments of the predicted amino acid sequence of leopard gecko TRs (lgTRs) with those of other species are shown in Fig. 2. Across the entire ORF, the lgTRs showed very high identity (87–96% for TR α and 77–98% for TR β) with their homologs from other species. When the specific domains were considered, stronger conservation was observed in the C domain (91–97% between lgTR α and its vertebrate homologs; 95–99% for TR β) and in the E/F domain (94–95% between lgTR α and its vertebrate homologs; 92–99% for TR β).

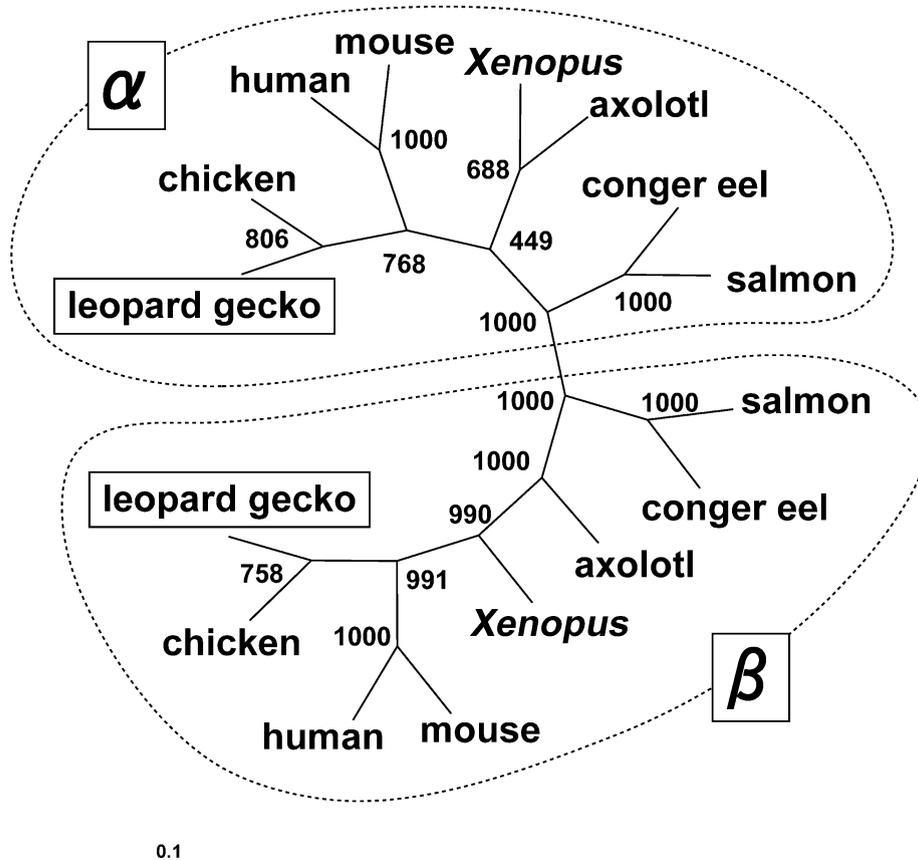


Fig. 3. Unrooted neighbor-joining phylogenetic tree of the TRs. The tree was constructed from the nucleotide sequences of the entire ORFs. Bootstrap values of 1000 resamplings are indicated for all nodes on the tree. The scale bar beneath the tree corresponds to the estimated evolutionary distance unit. Species names and GenBank accession numbers are given in Materials and Methods.

Molecular phylogenetic analysis

A phylogenetic tree of the TRs was constructed using the entire ORF nucleotide sequences of selected species representing all classes of vertebrate (Fig. 3). The TRs formed two groups, TR α and TR β , in accordance with these two isoforms being derived from distinct genes. As expected, both the leopard gecko TRs clustered with their chicken homologs.

Expression analysis

As expected, a wide TR distribution was observed. RT-PCR products of the expected size were obtained from all tissues and organs examined (Fig. 4). The authenticity of the RT-PCR products was confirmed by direct sequencing. A control without RT was also used for 40 or 45 cycles of PCR, and no signal was detected (data not shown).

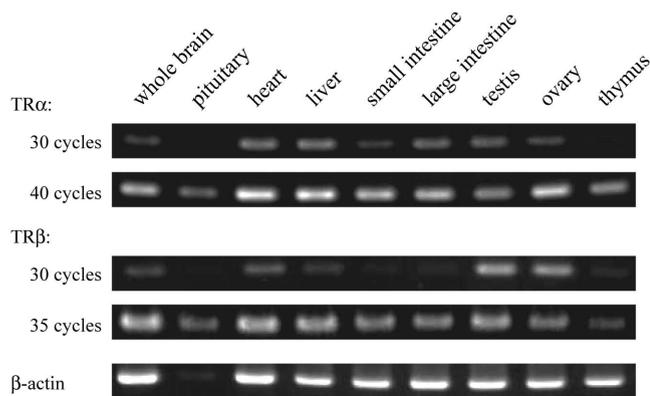


Fig. 4. Expression of the TR mRNAs in the leopard gecko. Five nanograms of cDNA from the pituitary, and 25 ng of cDNA from the whole brain, heart, liver, small intestine, large intestine, testis, ovary, and thymus, were subjected to PCR for TRs and β -actin of the leopard gecko.

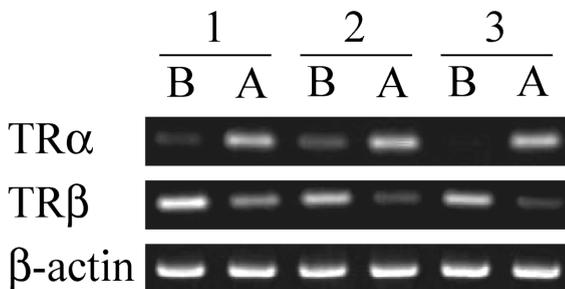


Fig. 5. Expression of TR mRNAs in the skin of the leopard gecko. The samples subjected to RT-PCR were taken from three animals before (indicated by "B") or after (indicated by "A") skin shedding. RT-PCR products beneath each horizontal bar were from mRNA taken from the skin of the same animal.

Temporal expression analysis in skin

The expression of the TRs in the skin was investigated by RT-PCR. TR α was expressed more strongly in the skin after shedding than before. In contrast, TR β was expressed more strongly before shedding than after.

DISCUSSION

The THs are pleiotropic factors important for many func-

tions in vertebrates. In reptiles, THs are suggested to affect tail regeneration, metabolic rate, metabolic enzyme activity, and shedding frequency. To augment the investigation of the molecular mechanism of THs in reptiles, we characterized their receptors at the molecular level.

In this study, we cloned two isoforms of TR from the leopard gecko, *Eublepharis macularius*. This is the first molecular identification of full-length TRs from reptiles. The deduced amino acid sequences of the cDNAs demonstrated the classic modular structure of members of the nuclear receptor superfamily, and exhibited high identity with their homologs in other species. The highest identities were shown with their chicken homologs (96 and 98%). There are eleven conserved Cys residues in the C domain of TR α . Although the seventh Cys in IgTR α , which does not contribute to the formation of a disulfide bond or zinc finger (Zhao *et al.*, 1998), is substituted by Ser, other Cys residues are completely conserved in all TR α s. It is therefore conceivable that cloned IgTR α does not lose the ability to bind DNA by this substitution. In the future, ligand binding studies will be helpful. In the phylogenetic tree, TRs formed groups, TR α and TR β . Both IgTRs clustered with their chicken counterparts, as expected.

mRNA expression of the IgTRs was detected in all the tissues and organs examined, indicating that thyroid hormones are pleiotropic factors important for many functions in the leopard gecko as well as other animals. In lizards, it has been reported that THs can regulate cardiac function (Venditti *et al.*, 1996), enzyme activity in the liver (John-Alder, 1990), and testis activity (Cardone *et al.*, 2000; Plowman and Lynn, 1973). It is therefore conceivable that TRs mediate such effects in these organs. In other species, the expression of TRs has been also demonstrated in various tissues, but significant isoform-specific functions are poorly understood. For instance, although the expression of TRs in the adult brain has been demonstrated in mammals, their specific roles have not yet been clarified (Schwartz *et al.*, 1992). It is known that THs can regulate steroidogenesis; however, although the expression of TRs in the human ovary has been confirmed, their specific roles remain unknown (Zhang *et al.*, 1997). There is less information for the testis, and the type of TR expressed there remains controversial (Maran, 2003).

THs are known to regulate the shedding frequency in Squamata. Intriguingly, the effect of thyroxine appears to be reversed between lizards and snakes. To obtain a better understanding of the potential role of THs in skin shedding, we analyzed the temporal expression of TRs in the skin. The expression of TR α was stronger after skin shedding than before, whereas the result was the opposite for TR β . Although Chiu *et al.* (1967) have discussed the indirect effect of THs on shedding frequency, our results strongly suggest that THs can directly affect the skin, and that the two isoforms of TR play distinct roles in skin shedding.

The shedding cycle can be divided into two phases: resting and proliferation. As the skin is in the resting phase after shedding (Maderson and Licht, 1967), our result suggests that TR α plays a role in the resting phase, such as maintaining this condition so as not to enter the proliferation phase. Furthermore, we suspect that TR β mediates the effect of THs in the proliferation phase, since TR β was

strongly expressed in the skin before shedding. It is conceivable that the condition of the skin taken before shedding in this experiment was at around the last stage of the proliferation phase (Maderson and Licht, 1967). This is supported by an *in vitro* study demonstrating that the epidermis can differentiate by itself but cannot shed (Flexman *et al.*, 1968). This indicates that the capacity for the complex changing pattern of cell differentiation is intrinsic to the epidermis, but that shedding is not. Extrinsic factor(s) is/are necessary for shedding, and THs may be one such factor. It has also been reported that THs have no effect on the skin in the proliferation phase, either directly or indirectly, as even thyroidectomized animals shed (Chiu *et al.*, 1967). This discrepancy may be because it is always difficult to completely remove the thyroid surgically (Chiu *et al.*, 1967). The interpretation of the physiological significance of up- or down-regulation of mRNA expression of TRs needs further study, such as *in situ* hybridization to analyze where and when during the shedding cycle TRs are expressed. The differential expression of TR isoforms has also been reported for other species, such as frogs during development (Sachs *et al.*, 2000). Although both isoforms appear to be involved in regulating metamorphosis, their functional differences are not yet clear.

In this report, we characterized leopard gecko TRs and demonstrated the possibility of their direct involvement in skin shedding. These results will facilitate investigation of the physiological significance of THs and of the molecular mechanisms by which they regulate shedding frequency in Squamata.

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