DOI : 10.5958/2277-8934.2024.00010.9 *Vol 31 No 1, p 57-63*

MOLECULAR CHARACTERISATION OF KERATIN-ASSOCIATED PROTEIN-7 (*KRTAP7*) GENE FOR HAIR QUALITY IN INDIAN DROMEDARY CAMEL

Nistha Yadav[1], Urmila Pannu[1], Basanti Jyotsana[2], Ved Prakash[2], Sagar A. Khulape[2], Ajay Kumar[3], Gayatri Gujar[1] and Manju Nehara[1]

[1]College of Veterinary and Animal Science, RAJUVAS, Bikaner, Rajasthan – 334001, India
[2]ICAR-National Research Centre on Camel, Bikaner, Rajasthan – 334001, India
[3]Division of Textile Manufacture and Textile Chemistry, ICAR-CSWRI, Avikanagar, Malpura (Tehsil) Tonk, Rajasthan 304501

ABSTRACT

The keratin-associated proteins (*KRTAPs*) play important role in describing the physical and mechanical properties of the fibre *viz.* fibre thickness and curliness to the hair fibres. In this report, the molecular and functional characterisation of the *KRTAP7* gene in four Indian camel breeds i.e. Bikaneri, Jaisalmeri, Kachchhi and Mewari is described based on a comprehensive analysis of the nucleotide and amino acid sequences. The blood sample was collected from representative animals differing in fibre quality. The *KRTAP7* gene was amplified, sequenced and analysed for genetic characterisation. The coding sequence of the *KRTAP7* gene was of 264bp. The *KRTAP7* gene sequences from all four breeds of camel were identical. No SNPs were noticed in coding (CDS) and non-coding (5′ UTR and 3′ UTR) regions of *KRTAP7* gene. The complete coding sequence (CDS) of the *KRTAP7* gene translated to 87 amino acids (aa) long *KRTAP7* protein. The phylogeny analysis of nucleotide and protein sequence of Indian dromedary *KRTAP7* gene revealed closet relationship with *Camelidae* family. This study provides information about the *KRTAP7* gene in Indian dromedary camel.

Key words: Camel, dromedary, hair fibre, keratin-associated protein-7 (*KRTAP7*) phylogeny

Coat colour and fleece type traits have pleiotropic effect at genetic level and comes under qualitative traits as their expression is dependent on one or several genes with little or no environmental effects. On the other hand, the amount of fibre produced or fineness (diameter) have polygenic effect and come under quantitative traits as determined by several genes with minor effects per gene while major environment effect (Mackay, 2003).

Calderon *et al* (2021) identified set of SNPs located at or nearby candidate genes (*KRT, KRTAP, ASIP, MC1R, TYRP1*) for fibre quality and colour in *Huacaya alpacas* by genotyping by sequencing (GBS). Some keratin (*KRT*) and keratin-associated protein (*KRTAP*) genes are important candidate genes for fleece and fibre quality (Allain and Renieri, 2010). The process of keratinisation is most important among skin adaptations which helps in positive selection mechanism by interaction of fibrous (keratin) and matrix proteins (*KRTAPs*) (Alibardi *et al,* 2009; Rogers *et al,* 2007). Fibre is produced by secondary hair follicles which are composed of hair-keratins and keratin-associated proteins (*KAPs*). These multigene subfamilies encoded KAP proteins have specific in high or ultra-high sulphur (contributed by cysteine) content (HS) and a high glycine-tyrosine (HGT) (Wu *et al,* 2008). Such proteins also define the particular structural and chemical characteristics of the different types of hair, fur, wool and quills in various animals (Fujimoto *et al,* 2014). The discovery and analysis for variation in the quality of hair/fibre revealed over 100 and 88 keratin-associated proteins (*KRTAPs*) which have been identified in various mammalian species and human, respectively (Khan *et al,* 2014; Rogers *et al,* 2008). *KRTAPs* play an important role in describing the physical and mechanical properties of the fibre *viz.* fibre thickness and curliness to the hair fibres by acting as a matrix for cross linking the hair-keratins (Gong *et al,* 2016; Li *et al,* 2019). The different evolution rate is responsible for a high degree of diversification and homogenisation in *KRTAP7* gene family with more than 30 subfamilies. Our study considered molecular characterisation of the *KRTAP7* gene for hair quality traits in Indian dromedary camel.

SEND REPRINT REQUEST TO VED PRAKASH email: ved.prakash4@icar.gov.in

The pseudogenisation rate in one or more proteins from the repertoire of the KRTAP genes family are responsible for the diversification patterns in hair fibre in different species such as in sloth (175 KRTAP genes with 141 being intact for long and coarse hair) and dolphin (35 *KRTAPs*). The modification of hair structure and function due to changes in the KRTAP gene repertoire are responsible for surface adaptation in different species such as *alpaca* (fibre), *armadillo* (modified scales), hedgehog (spines) and dolphin (mostly hairless and aquatic). However, the reports on molecular characterisation of the *KRTAP7* gene with respect to the Indian camel is scanty. The present study was therefore, designed with the objective of characterising the *KRTAP7* gene and translated protein in Indian dromedary camel.

Materials and Methods

Sampling structure

The sampling was done under permission of Institutional Ethics Committee. The blood samples were collected from the jugular veins in BD Vacutainer® blood collection tubes from 35 camels of 4 breeds namely Bikaneri (10), Jaisalmeri (9), Kachchhi (6) and Mewari (10). The samples were collected from the institutional camel herd of ICAR-National Research Centre on Camel (NRCC) Bikaner, India. The animals were selected on the basis of hair quality attributes such as fibre diameter and medullation percent. The fibre diameter (µ) from sampled animals was ranging between 21.10-36.56 for Bikaneri, 24.44-73.61 for Jaisalmeri, 26.54-60.83 for Kachchhi and 36.98-62.19 for Mewari breed. The medullation per cent was ranging between 13.33-81.33 for Bikaneri, 32.33-97.00 for Jaisalmeri, 33.00-93.67 for Kachchhi and 39.00-94.00 for Mewari breed in sampled animals.

Molecular characterisation of the KRTAP7 gene

The total DNA was isolated from blood samples using the QIAamp DNA Blood Mini Kit (QIAGEN, Aarhus, Denmark) as per manufacturer's guidelines. The *KRTAP7* gene fragment was amplified from isolated genomic DNA samples using custom designed primers (Forward: **5'**AGGTATCACCCTATCCTGGTGT**3'**; Reverse: **5'**AGTCTGTGGGCTCCT TTGTATG**3'**) using reference genome sequence locus [NC_044511]. The PCR reaction mix (25 µL) for amplification of *KRTAP7* gene fragment was prepared by adding 1 µL of each primer (10 pmol), 2 µL of genomic DNA, 13 µL of Taq PCR Master Mix (Qiagen, USA) and 8 µL of Nuclease free water. The PCR reaction was performed in Veriti® thermocycler (Applied Biosystems, USA) using the time-temperature combination: an initial denaturation at 95° C for 5 min followed by 34 cycles of denaturation (94°C for 1 min), annealing (59.5°C for 45 sec) and extension (72 °C for 1 min) followed by a single cycle of final extension (72°C for 10 min). A single band of 995 bp was observed when the PCR products were checked for amplification by electrophoresis on 1.0% agarose gel (Himedia), in parallel with 100-1500bp NEX-GEN DNA ladder (Puregene, Genetix Biotech Asia Pvt. Ltd.) (Fig 1). The PCR products were purified using Wizard® SV Gel and PCR Clean-Up System kit (Promega Corporation, USA). The bidirectional sequencing of the purified *KRTAP7* amplicons were performed by Sanger's dideoxy chain termination method (Eurofin Genomics, USA). The forward and reverse sequences were manually curated and analysed using Codon Code Aligner Software (Codon Code Corporation, USA). The *KRTAP7* sequences generated for Indian dromedary camel breeds were compared with the reference genome sequence locus [NC_044511] using BLAST software program (http://www. ncbi.nlm.nih.gov/). The pair wise and multiple sequence alignments of identified Indian camel *KRTAP7* gene sequence were done to study the variation and identity with other reported camelid and the sequences of domesticated species using Clustal2.1(https://www.ebi.ac.uk/Tools/msa/clustalo/n) and dismat-EMBOSS (https://www. ebi.ac.uk/Tools/emboss/) software package. The estimation of evolutionary relationship and phylogenetic tree construction (Table 1) between nucleotide sequences and the deduced amino acid sequences of different species and Indian dromedary camel were inferred by Maximum Likelihood bootstrapped method using Molecular Evolutionary Genetics Analysis software (MEGA 11.0) (Tamura *et al,* 2021).

Results and Discussion

Molecular characterisation of KRTAP7 gene

The amplification and sequencing of *KRTAP7* gene was done in Indian dromedary camel breeds. The 995 base pairs long fragment of *KRTAP7* gene was amplified (Fig 1). The sequencing of the PCR products from 35 animals resulted in retrieval of 915 bp long sequence after alignment and editing of the forward and reverse sequences. The 915 bp long sequence covered 264 bp long coding region and 518 bp long non-coding 5′ UTR region and 133 bp long 3′ UTR region. The 264 bp long coding ORF domain

of *KRTAP7* gene translated into 87 amino acids (aa) length protein sequence in Indian dromedary camel breeds.

No SNPs were noticed in coding (CDS) and non-coding (5′ UTR and 3′ UTR) regions of *KRTAP7* gene. In resemblance to our study, no polymorphism in the CDS region of *KRTAP7* gene was observed in bovine species such as Chinese yak breeds and Indonesian zebu cattle (Arlud *et al,* 2017). However, in contrast to present study the identified novel SNPs at different positions of *KRTAP7*-1 were associated with the mechanical strength and shape of hair fibre in llama (c.99C>T, c.185G>A, c.198T>C and c.237C>G) (Daverio *et al,* 2019) and sheep (c.93C>A and c.173G>A) (Liu *et al,* 2014; Gong *et al,* 2012). The genetic variants with AA (n = 169) and AB (n = 51) genotypes were associated with wool production traits such as mean yield (79.9 ± 2.72% and 81.9 ± 3.37%) and mean staple length (MSL: 47.3 ± 0.57 mm and 50.9 ± 0.65 mm), respectively in Pakistani sheep breeds (Ullah *et al,* 2020). The hair characteristics are controlled by vast repertoire of keratin gene family such as 80 *KRTAPs* (25 families) in humans (Gong *et al,* 2012), 29 *KRTAPs* (13 families) in sheep (Li *et al,* 2017), 12 *KRTAPs* (9 families) in goats (Wang *et al,* 2017), 5 keratin (KRT) gene and 4 candidate gene as makers (BMP4, COL1A2, GLI1, SFRP4) in alpaca (Mendoza *et al,* 2020). Monomorphic nature of *KRTAP7* gene in yak and Indian dromedary camel indicates very limited variations, its unique intrinsic structural property (e.g., > 21% high glycine content) and vital functional role in strength and shape of hair fibre. Conclusively, the definite role of *KRTAP7* gene in wool traits *viz.* yield and structural variation was indicated in some mammalian species but not in Indian dromedary.

The CDS region and translated protein sequence for *KRTAP7* were subjected for comparative per cent identity analysis with different mammalian species (Table 2 and 3). The local alignment (NCBI-BLASTN and NCBI-BLASTP), identity matrix and distance matrix of targeted *KRTAP7* proteins indicated 100% identical sequence with the keratin associated protein7-1 gene of *Camelus dromedarius* (reference sequence). The lowest divergence for gene (72.47) and protein (4.60) was noticed with *Camelus bactrianus* and *Vicugna pacos,* respectively. However, *Camelus bactrianus* and *Camelus ferus* also showed 100% identity with each other among all compared sequences. Highest divergence for targeted protein was shown with *Sus scrofa* (79.90) and *Capra hircus* (47.06) while lowest identity was with *Mus musculus* (74.42). The, overall highest divergence for *KRTAP7* proteins (49.41) was noticed between *Mus musculus* and *Capra hircus* (Table 3).

Phylogenetic analysis

Phylogram revealed the dissemblance of *Sus scrofa, Capra hircus, Equus caballus, Mus musculus, Homo sapiens, Vicugna pacos, Bubalus bubalis* and from that of *Camelus dromedarius* during evolution. Phylogenetic relationship among considered nucleotide and amino acid sequences was established to infer the evolutionary history using the Maximum Parsimony method with 500 bootstrapped replicates (Fig 2 and 3). Multiple protein alignments for considered species was shown accordingly in Fig 4.

Table 1. Details of sequences subjected for comparison for *KRTAP7* gene.

S. No.	Species	Reference acc no.	Chr no.	Accession no. (Protein)	Gene (bp)	CDS (bp)	Protein (AA)
1	*Camelus dromedarius*	NC_044511.1	1	KAB1284088.1	732	264	87
2	*Camelus bactrianus*	NW_011514130.1	Un	XP_010954900.1	730	264	87
3	*Camelus ferus*	NC_045696.1	1	EQB78523.1	729	264	87
4	*Vicugna pacos*	NW_021964153.1	1	XP_006216075.1	734	264	87
5	*Homo sapiens*	NC_000021.9	21q22.11	NP_853637.2	721	264	87
6	*Mus musculus*	NC_000082.7	16; 16 C3.3	NP_082047.1	621	264	87
7	*Equus caballus*	NC_009169	26	XP_014591977.1	739	264	87
8	*Sus scrofa*	NC_010455.5	13	XP_003358967.2	597	258	85
9	*Bubalus bubalis*	NC_059157.1	1	XP_006053907.3	740	264	87
10	*Bos taurus*	KJ551549.1	1	AHZ89844.1	285	264	87
11	*Capra hircus*	NC_030808	1	QES86378.1	707	258	85
12	*Ovis aries*	NC_056054	1	QPP12018.1	676	258	85

acc. no.= Accession number; Chr no.= Chromosome number; Un= Unknown; bp=base pairs; CDS= Coding sequence; AA=Amino acids

Table 2. Per cent Identity Matrix of *KRTAP7* gene between Indian dromedary camel and different species subjected for comparison.

S.no.	Accession no.	1	2	3	4	5	6	7	8	9	10	11	12	13
1	Camelus		36.90	97.39	100.00	99.18	99.18	82.35	82.06	83.49	82.04	89.77	79.40	38.41
2	NC_000082.7	74.56		63.13	63.58	63.74	63.74	61.52	66.22	66.16	63.99	76.89	64.57	64.14
3	NW_021964153.1	76.70	76.49		97.26	96.84	96.98	80.70	78.17	80.55	78.88	89.39	77.12	76.28
4	NC_044511.1	76.50	76.01	76.09		99.18	99.18	80.34	78.87	81.32	78.98	89.77	77.41	76.43
5	NW_011514130.1	72.47	71.18	75.48	76.30		100.00	80.34	78.59	80.85	78.79	89.77	77.12	76.43
6	NC_045696.1	75.03	76.81	71.74	72.98	73.94		80.34	78.59	80.83	78.90	89.77	77.12	76.43
7	NC_010455.5	79.90	76.55	72.70	74.37	78.39	74.04		79.05	83.25	83.53	91.09	81.59	80.32
8	NC_000021.9	75.59	43.96	76.42	74.48	69.21	75.45	75.88		82.73	76.40	89.02	75.15	73.95
9	NC_009169.3	75.51	80.03	43.19	78.14	75.89	73.25	72.36	74.48		79.89	90.53	78.77	78.16
10	NC_059157.1	73.92	74.88	72.89	70.08	72.33	75.45	72.19	71.71	62.92		98.11	94.89	93.48
11	KJ551549.1	76.89	73.11	78.79	71.59	73.86	64.02	78.79	76.89	78.41	76.52		96.12	96.12
12	NC_030808.1	77.51	74.24	72.14	78.64	74.82	66.20	71.52	75.53	72.28	76.66	74.62		98.08
13	NC_056054.1	73.52	71.50	76.48	73.22	66.57	75.15	76.38	73.08	72.78	72.78	74.24	74.41	

Above diagonal: Per cent identity; below diagonal: Divergence

NC_000082.7: *Mus musculus;* NW_021964153.1: *Vicugna pacos;* NC_044511.1: *Camelus dromedarius*; NW_011514130.1: *Camelus bactrianus;* NC_045696.1: *Camelus ferus;* NC_010455.5: *Sus scrofa;* NC_000021.9: *Homo sapiens;* NC_009169.3: *Equus caballus;* NC_059157.1: *Bubalus bubalis;* KJ551549.1: *Bos taurus;* NC_030808.1: *Capra hircus;* NC_056054.1: *Ovis aries*.

Table 3. Per cent Identity Matrix of *KRTAP7* protein between Indian dromedary camel and different species subjected for comparison.

S.no.	Accession no.	1	2	3	4	5	6	7	8	9	10	11	12	13
1	NP_082047.1		77.38	76.74	78.57	80.23	79.07	78.57	80.23	72.09	74.42	74.42	75.58	75.58
2	XP_003358967.2	49.41		85.88	86.75	87.06	87.06	86.75	85.88	82.35	84.71	84.71	84.71	84.71
3	XP_014591977.1	27.59	41.18		89.41	89.66	89.66	89.41	89.66	87.36	89.66	89.66	89.66	89.66
4	QES86378.1	49.41	23.53	48.24		96.47	96.47	97.65	88.24	85.88	88.24	88.24	88.24	88.24
5	AHZ89844.1	25.29	38.82	10.34	43.53		97.70	96.47	88.51	86.21	88.51	88.51	88.51	88.51
6	XP_006053907.3	26.44	40.00	10.34	44.71	2.30		96.47	88.51	86.21	88.51	88.51	88.51	88.51
7	QPP12018.1	48.24	23.53	47.06	2.35	42.35	43.53		88.24	85.88	88.24	88.24	88.24	88.24
8	NP_853637.2	24.14	42.35	10.34	47.06	11.49	11.49	45.88		86.21	88.51	88.51	88.51	88.51
9	XP_006216075.1	32.18	42.35	12.64	48.24	13.79	13.79	47.06	13.79		95.40	95.40	93.10	93.10
10	Camelus	29.89	41.18	10.34	47.06	11.49	11.49	45.88	11.49	4.60		100.00	97.70	97.70
11	KAB1284088.1	29.89	41.18	10.34	47.06	11.49	11.49	45.88	11.49	4.60	0.00		97.70	97.70
12	XP_010954900.1	28.74	41.18	10.34	45.88	11.49	11.49	44.71	11.49	6.90	2.30	2.30		100.00
13	EQB78523.1	28.74	41.18	10.34	45.88	11.49	11.49	44.71	11.49	6.90	2.30	2.30	0.00	

Above diagonal: Percent identity; below diagonal: Divergence

NP_082047.1: *Mus musculus;* XP_003358967.2: *Sus scrofa;* XP_014591977.1: *Equus caballus;* QES86378.1: *Capra hircus;* AHZ89844.1: *Bos taurus;* XP_006053907.3: *Bubalus bubalis;* QPP12018.1: *Ovis aries;* NP_853637.2: *Homo sapiens;* XP_006216075.1: *Vicugna pacos;* KAB1284088.1: *Camelus dromedarius*; XP_010954900.1: *Camelus bactrianus;* EQB78523.1: *Camelus ferus.*

The phylogeny tree based on nucleotide and amino acid sequence for the KRTAP7 gene depicted different evolutionary patterns among species considered for evolutionary relationship analysis. Both the phylogeny trees depicted similar relationship patterns between Camelus ferus and Camelus dromedarius in comparison to other Camelidae species. The highest amino acid sequence homology was noticed among the Camelidae family followed by the Homo sapiens, Mus musculus, Sus scrofa, Equus caballus and other species. The nucleotide sequences of Capra hircus were farthest related compared to other bovine (cattle, buffalo) and ovine species. The multiple protein sequence analysis revealed the highest amino acid similarity between camelids and the highest amino acid differences with Mus musculus (Fig 4)

This maiden report describes the molecular characterisation of the *KRTAP7* gene and protein in four Indian dromedary camel breeds differing in

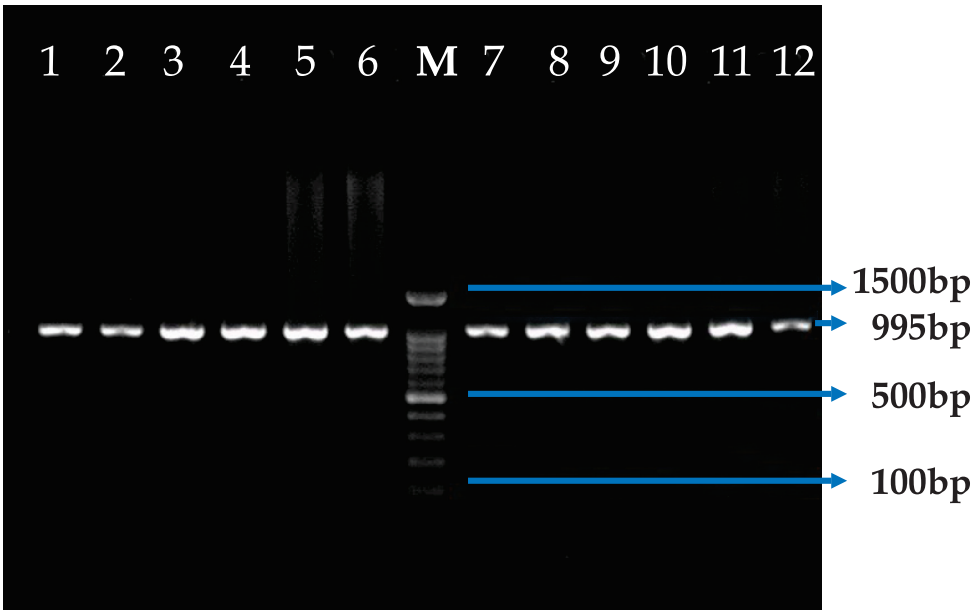
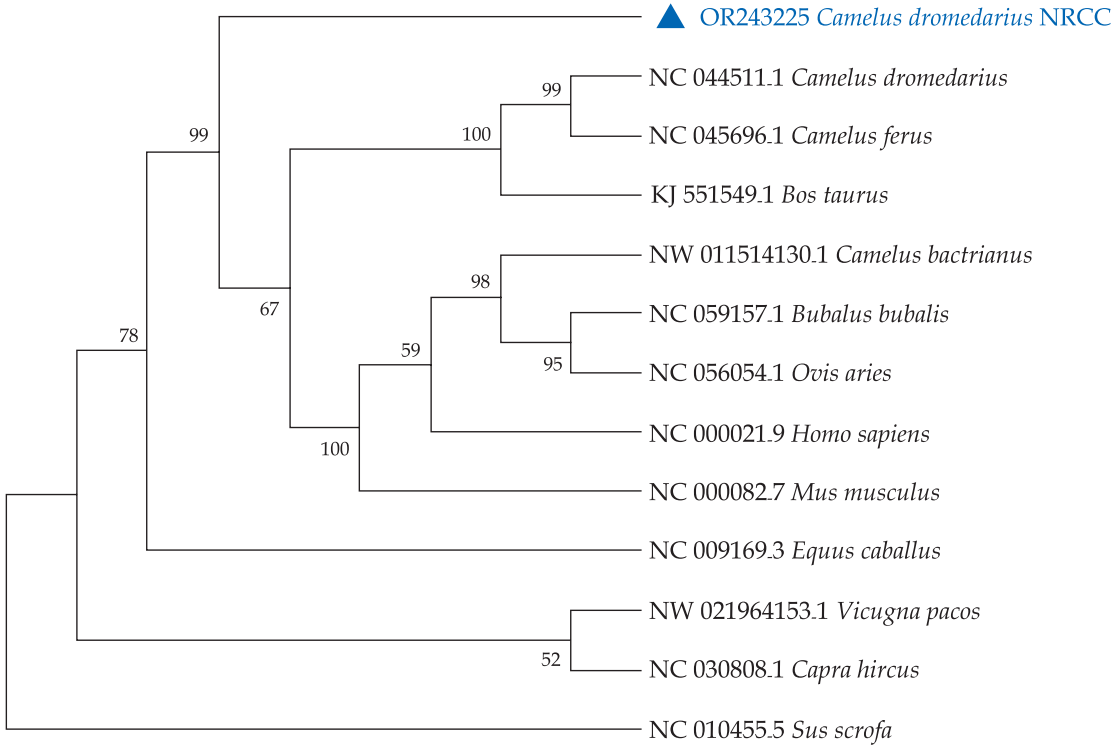


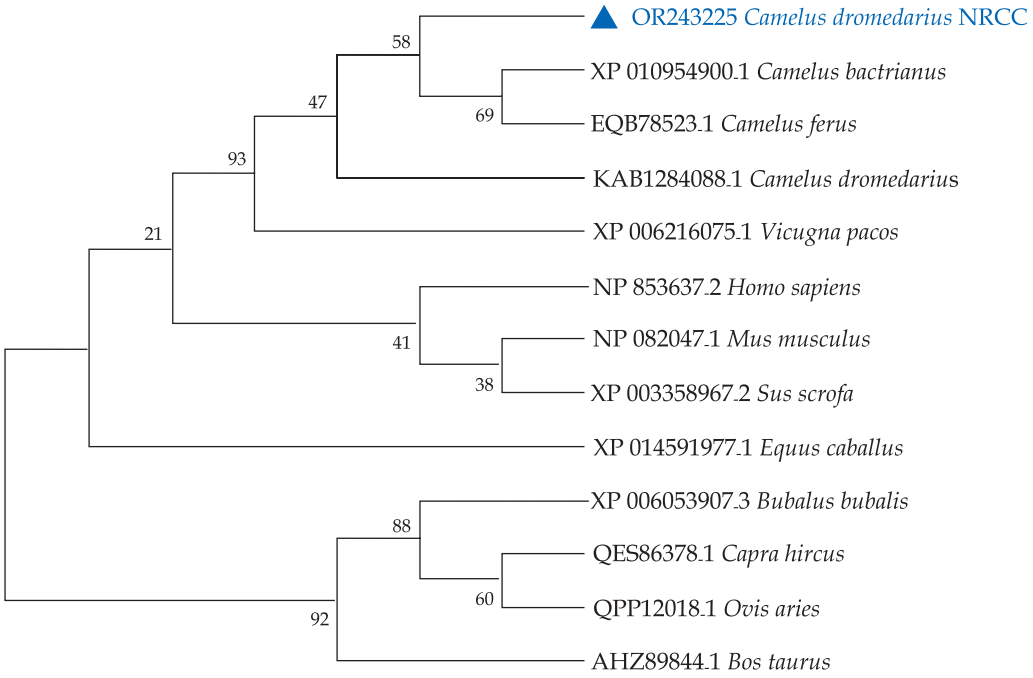
Fig 1. Agarose gel electrophoresis for amplification of the KRTAP7 gene in Indian camel breeds: - Lane 1-3: Mewari; Lane 4-6: Kachchhi; Lane M: 100-1500bp NEX-GEN DNA ladder; Lane 7-9: Bikaneri; Lane 10-12: Jaisalmeri



▲: Indicate considered sequences of India dromedary camel; N.B. in right represent the accession number and scientific name of representative mammalian species.

Fig 2. Phylogeny tree for Coding Sequences of the *KRTAP7* gene depicting evolutionary relationship between Indian camel and other mammalian species.

hair quality attributes. In our study, the identical consensus nucleotide sequence for the *KRTAP7* gene in four Indian camel breeds indicated the monomorphic nature of the gene. This monomorphic nature was present in high and low values of fibre diameter and medullation per cent. In addition,



▲: Indicate considered sequences of India dromedary camel; N.B. in right represent the accession number and scientific name of representative mammalian species.

Fig 3. Phylogenetic analysis for the KRTAP7 amino acid sequence depicting evolutionary relationship between Indian camel and other mammalian species.

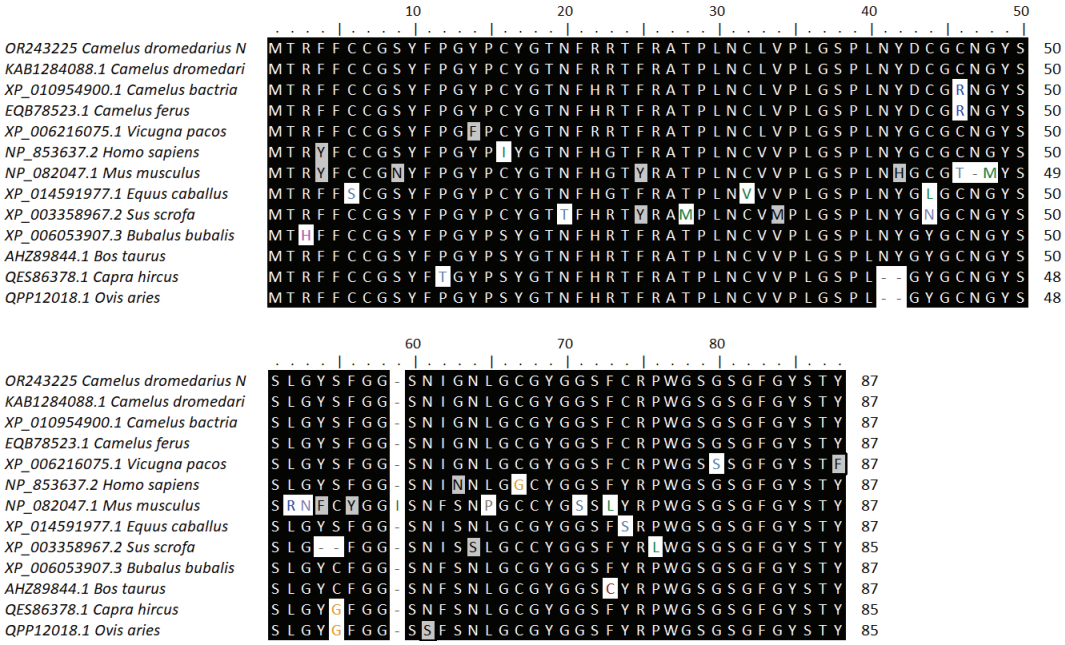


Fig 4. Multiple protein sequence alignment for *KRTAP7* protein with different species

considering other associated gene(s) may establish the genetic association of hair fibre traits.

Acknowledgements

The authors thank the Director, ICAR-NRCC, Bikaner for providing all the necessary support for the present study. The financial support for the first author by CVAS, Bikaner, Rajasthan, India with an Institutional fellowship during the work is thankfully acknowledged.

Conflict of Interest

No any conflict of interest.

References

Alibardi L, Dalla Valle L, Nardi A and Toni M. Evolution of hard proteins in the sauropsid integument in relation to the cornification of skin derivatives in amniotes. Journal of Anatomy. 2009; 214(4):560-586.

Allain D and Renieri C. Genetics of fibre production and fleece characteristics in small ruminants, Angora rabbit and south American camelids. Animal. 2010; 4(9):1472-1481.

Arlud S, He N, Sari EM, Ma ZJ, Zhang H, An TW and Han JL. Highly conserved keratin-associated protein 7-1 gene in Yak, Taurine and Zebu Cattle. Folia Biologica (00155500). 2017; 63(4).

Calderon M, More MJ, Gutierrez GA and Ponce de León FA. Development of a 76k Alpaca (*Vicugna pacos*) single nucleotide polymorphisms (SNPs) microarray. Genes. 2021; 12:291.

Daverio MS, Anello M, Ersinger VA, Alvarez S, Frank E, Vidal-Rioja L and Di Rocco F. Identification of llama *KRTAP7*-1 and KRTAP8-1 fibre genes and polymorphism screening. Small Ruminant Research. 2019; 175:149-154.

Fujimoto S, Takase T, Kadono N, Maekubo K and Hirai Y. KRTAP11-1, a hair keratin-associated protein, as a possible crucial element for the physical properties of hair shafts. Journal of Dermatological Science. 2014; 74(1):39-47.

Gong H, Zhou H, Forrest RH, Li S, Wang J, Dyer JM and Hickford JG. Wool keratin-associated protein genes in sheep-a review. Genes. 2016; 7(6):24.

Gong H, Zhou H, McKenzie GW, Yu Z, Clerens S, Dyer JM and Hickford JG. An updated nomenclature for keratin-associated proteins (KAPs). International Journal of Biological Sciences. 2012; 8(2):258.

Khan I, Maldonado E, Vasconcelos V, O'Brien SJ, Johnson WE and Antunes A. Mammalian keratin associated proteins (*KRTAPs*) subgenomes: disentangling hair diversity and adaptation to terrestrial and aquatic environments. BMC Genomics. 2014; 15(1):1-19.

Li S, Zhou H, Gong H, Zhao F, Wang J, Liu X and Hickford JG. Identification of the ovine keratin-associated protein 22-1 (KAP22-1) gene and its effect on wool traits. Genes. 2017; 8(1):27.

Li W, Gao F, Kan J, Deng J, Wang B and Hao S. Synthesis and fabrication of a keratin-conjugated insulin hydrogel for the enhancement of wound healing. Colloids and Surfaces B: Biointerfaces. 2019; 175:436-444.

Liu YX, Shi GQ, Wang HX, Wan PC, Tang H, Yang H and Guan F. Polymorphisms of KAP6, KAP7 and KAP8 genes in four Chinese sheep breeds. Genetics and Molecular Research. 2014; 13(2):3438-3445.

MacKay DJ. Information theory, inference and learning algorithms. Cambridge University Press. 2003.

Mendoza MN, Raudsepp T, More MJ, Gutiérrez GA and Ponce de León FA. Cytogenetic mapping of 35 new markers in the alpaca (*Vicugna pacos*). Genes. 2020; 11(5):522.

Rogers MA, Langbein L, Praetzel-Wunder S and Giehl K. Characterisation and expression analysis of the hair keratin associated protein KAP26. 1. British Journal of Dermatology. 2008; 159(3):725-729.

Rogers MA, Winter H, Langbein L, Wollschläger A, Praetzel-Wunder S, Jave-Suarez LF and Schweizer J. Characterisation of human KAP24. 1, a cuticular hair keratin-associated protein with unusual amino-acid composition and repeat structure. Journal of Investigative Dermatology. 2007; 127(5):1197-1204.

Tamura K, Stecher G and Kumar S. MEGA11: molecular evolutionary genetics analysis version 11. Molecular Biology and Evolution. 2021; 38(7):3022-3027.

Ullah F, Jamal SM, Zhou H and Hickford JG. Variation in the KRTAP6-3 gene and its association with wool characteristics in Pakistani sheep breeds and breed-crosses. Tropical Animal Health and Production. 2020; 52:3035-3043.

Wang J, Che L, Hickford JG, Zhou H, Hao Z, Luo Y and Li S. Identification of the caprine keratin-associated protein 20-2 (KAP20-2) gene and its effect on cashmere traits. Genes. 2017; 8(11):328.

Wu DD, Irwin DM and Zhang YP. Molecular evolution of the keratin associated protein gene family in mammals, role in the evolution of mammalian hair. BMC Evolutionary Biology. 2008; 8(1):1-15.