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Original article

Computational Analyses of Amino Acid Molecules in PDE7A for Elucidating their Evolutionary Diversity and Protein Interactions in Multiple Mammalian Species

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ABSTRACT

This study explores the protein interactions and evolutionary conservation of phosphodiesterase type 7A (PDE7A) across different species, to identify the species with the highest similarity to humans, which has important applications in many fields such as pharmacology, comparative biology, biochemistry, oncology, endocrinology, and reproductive sciences. Computational analyses of the amino acid sequence of this enzyme revealed a common evolutionary relationship between the selected species and humans, but camels show the most variable evolutionary lineage in their PDE7A protein over time. In searches for homologous proteins, identity analysis results for four returned amino acid sequences were as follows: 91.81 ± 4.25% (mean ± SD), while the similarity between the sequences was 94.66% ± 4.55, and analysis of BLOSUM62 (Blocks Substitution Matrix 62) yielded a minimum value of 0.901 ± 0.055. All species have closely related physicochemical properties. The computational analyses revealed conserved amino acid residues of the gene across the studied species, which likely contribute to the similar expression patterns of the PDE7A gene in various animals. The findings also suggest that rats are a suitable model for gaining deeper insights into human biology.

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INTRODUCTION

Cyclic nucleotides, including cyclic adenosine monophosphate (cAMP) and cyclic guanosine monophosphate (cGMP), are important intracellular second messengers that regulate various cellular processes. The cAMP pathway is involved in hormone signaling, glycogen, and lipid metabolism, and its impact on gene and protein expression [1, 2]. Meanwhile, it is also implicated in several conditions and diseases, such as inflammation [3], myocardial atrophy [4], endocrine diseases, and cancers [5] involving the pituitary [6], thyroid [7], and testes [8]. PDEs are ubiquitous enzymes and the only way for a cell to terminate a cyclic nucleotide signal, at least in eukaryotic cells [9]. Furthermore, PDEs are largely responsible for restricting cyclic nucleotide signals to specific locations and preventing their diffusion throughout the cell [10]. Therefore, they have been exploited pharmacologically to modulate cyclic nucleotide signaling in a way that prevents or treats certain human diseases.

One of the most attractive members of the cAMP-specific PDEs recently is PDE7, as PDE7 has a high affinity for cAMP with a Michaelis constant value (Km) between 0.1 and 0.2 μM [11], and its inhibitors have no side effects in the digestive system like PDE4 inhibitors [12]. This family is classified into two types, PDE7A and PDE7B which share more than 70% sequence similarity and have been found in mice, rats, and humans. Each enzyme is thought to have a specialized role in a particular tissue due to its uneven distribution [13]. However, selective inhibitors for the PDE7 family are not currently available, the regulators are still unknown, and physiological functions remain unclear [14]. Therefore, many questions remain to be answered, including whether this gene is conserved in mammals regarding evolutionary mechanisms that influence function over time.

PDE7A has been shown to be activated by the cAMP/PKA signaling pathway in neurons [15], testicular Leydig cells [16], and immune cells [17]. Different proteins are involved in multiple molecular interactions to ensure appropriate pathway activation. Thus, studying protein-protein interactions (PPIs) is important to know different biochemical cascades in signaling pathways and to understand how proteins function in cells or organisms [18]. Moreover, a wide range of human illnesses, including infectious diseases, cancer, and neurological diseases, are associated with abnormal PPIs [19]. The targets of conventional drugs are usually receptors, ion channels, or enzymes. Recently, research has shown that PPIs are a promising target for intervention in refractory conditions and that regulating them is a workable strategy for medication development. To this end, various bioinformatics tools have been widely used to simplify the visualization of molecular interactions occurring in protein networks. At present, PDE7A serves as an attractive drug target against central nervous system diseases [20] and chronic lymphocytic leukemia [21]. Therefore, this study conducted computational analyses of the protein PDE7A sequences retrieved for mice, rats, camels, and humans to better understand the evolutionary diversity and protein interaction variations associated with the gene in the selected species to facilitate their exploitation as models for human PDE7A. Consequently, our work will soon offer an appropriate platform for further molecular docking research by other researchers.

METHODS

In this paper, many bioinformatics tools were applied to the determination of the evolutionary relationship of the PDE7A protein among species, examination of similarities of sequences, determination the physicochemical properties of a PDE7A peptide, and analysis of PPI.

Determination of the evolutionary relationship of the PDE7A protein among species.

To identify the homologous genes of PDE7A within or between selected species, we used the National Center for Biotechnology Information (NCBI) database, which can be accessed at URL: https://www.ncbi.nlm.nih.gov/; [22]. The analysis involved the use of the sequences of the amino acid retrieved for the selected species including human (NP_001229247.1), mouse (NP_001116231.1), rat (NP_112342.1), and camel (XP_010985465.2). One protein sequence per gene was selected and downloaded in FASTA format. Because the PDE7A protein possesses more than one reference sequence, we chose only the longest isoform for every entry. The isoform (c) of PDE7A protein from human was used as a query sequence. For the sequences alignment, the retrieved sequences were subjected to alignment and hierarchical clustering using Multalin version 5.4.1 [23], http://www-archbac.u-psud.fr/genomics/multalin.html. The result was confirmed using MUSCLE in Molecular Evolutionary Genetics Analysis (MEGA 11) software [24], https://www.megasoftware.net/, and the cluster method used was UPGMA. The phylogenetic tree was constructed using the Maximum Likelihood method and the Dayhoff matrix-based model [25]. There was a total of 471 positions in the final dataset of the retrieved sequences, which were analyzed in 1000 bootstraps using MEGA-11 software. The evolutionary distance of PDE7A protein sequences was estimated from the alignment data by a bootstrap procedure (p-distance model) using MEGA 11 software [26].

There was also a determination of sequences identities and similarities using Sequence Identity and Similarity (SIAS) program from the Immunomedicine Group at Universidad Complutense Madrid, Spain [24], (http://imed.med.ucm.es/Tools/sias.html), using the default BLOSUM62 scoring matrices, and the cost for creating the gap, Po was set at 10 and the cost for extending the gap, Pe was set at 0.5. The physicochemical properties of a PDE7A peptide including the molecular weight (Mw) and theoretical values of isoelectric point (pI) were calculated using the compute pI/Mw tool (https://web.expasy.org/compute_pi/), the protein hydrophobicity and netcharge were predicted by using the Expasy ProtParam online server (https://web.expasy.org/protparam/; [27]. To search for known and predicted PPIs and functional enrichment, the proteins were imported into the online search tool version 12.0 of the STRING database [28]; http://string-db.org. Interactions between proteins reflect functional associations.

Statistical analysis

The Statistical Package for the Social Sciences (SPSS) version 26 was used to generate descriptive statistics of the amino acid frequencies and the physical and chemical properties of PDE7A.

RESULTS

This study retrieved the amino acid sequence of humans (NP_001229247.1), compared with mice (NP_001116231.1), rats (NP_112342.1), and camels (XP_010985465.2). Phylogenetical diversity analysis indicated that the animals studied shared a common evolutionary relationship with humans regarding the PDE7A amino acid sequences (Figure 1). Camels show the most variable evolutionary lineage in their PDE7A protein over time. The result also showed that the most conserved bases fell between 41 and 343 bases (Figure 2).

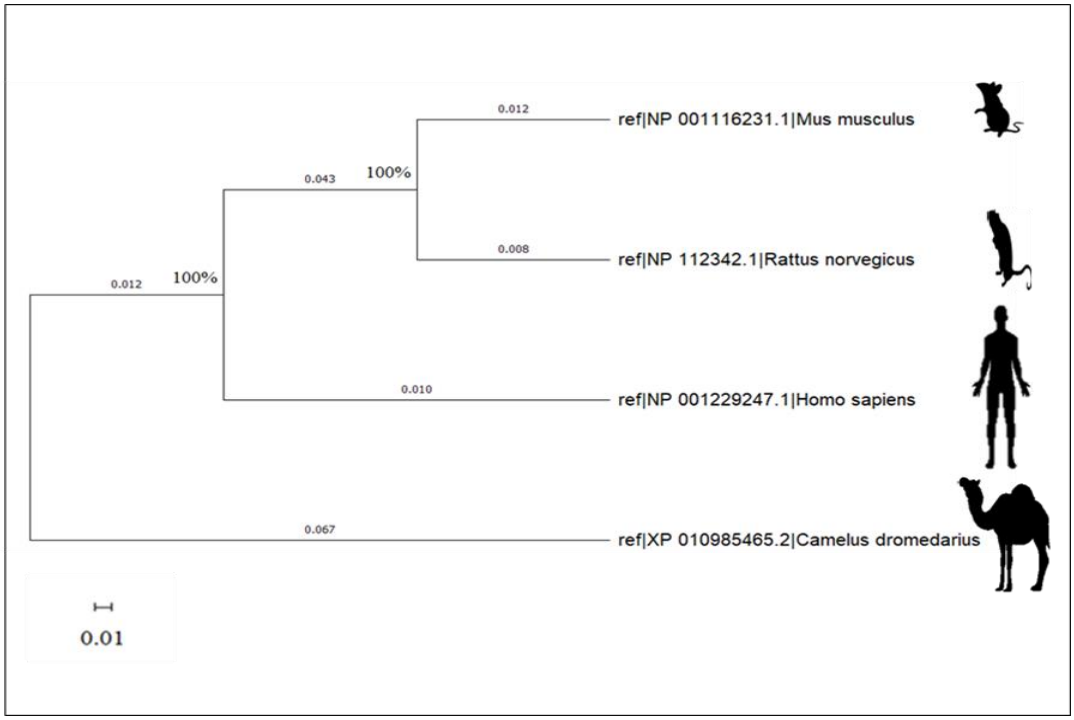


Figure 1. The dendrogram of evolutionary relationships using the PDE7A protein sequences among the selected species. Mouse (Mus musculus), rat (Rattus norvegicus), human (Homo sapiens), and camel (Camelus dromedarius). The Maximum Likelihood method and Dayhoff matrix-based model were used to construct the evolutionary relationship. The evolutionary rate differences between sites were modeled using a discrete Gamma distribution [5 categories (+G, parameter = 4.8621)]. The branch lengths of the scaled-up tree were expressed as the number of substitutions per site.

Regarding the evolutionary distance of PDE7A protein sequences between species, the values in Table 1 indicate the evolutionary divergence between humans and other species. The divergence values of mice, rats, and camels with humans are 0.0103, 0.0096, and 0.012, respectively. Table 2, Table 3Table 4) presented the identity, similarities, and BLOSUM62 comparisons, respectively. Four amino acid sequences returned exact matches in the sequence identity analysis results (min = 86.25%, max = 98.13%, and mean ± SD = 91.81 ± 4.253%). While the similarity between the sequences was (min = 88.12%, max = 100%, and mean ± SD = 94.66%± 4.555%). Analysis of BLOSUM62 yielded (min = 0.83, max = 0.98, and mean ± SD = 0.901 ± 0.055).

Table 1. Estimates of evolutionary divergence between sequences.

Organism	Evolutionary divergence between sequences			
	1	2	3	4
Human		0.010	0.009	0.012
Mouse	0.058		0.006	0.014
Rat	0.051	0.018		0.013
Camel	0.076	0.116	0.106	0.012

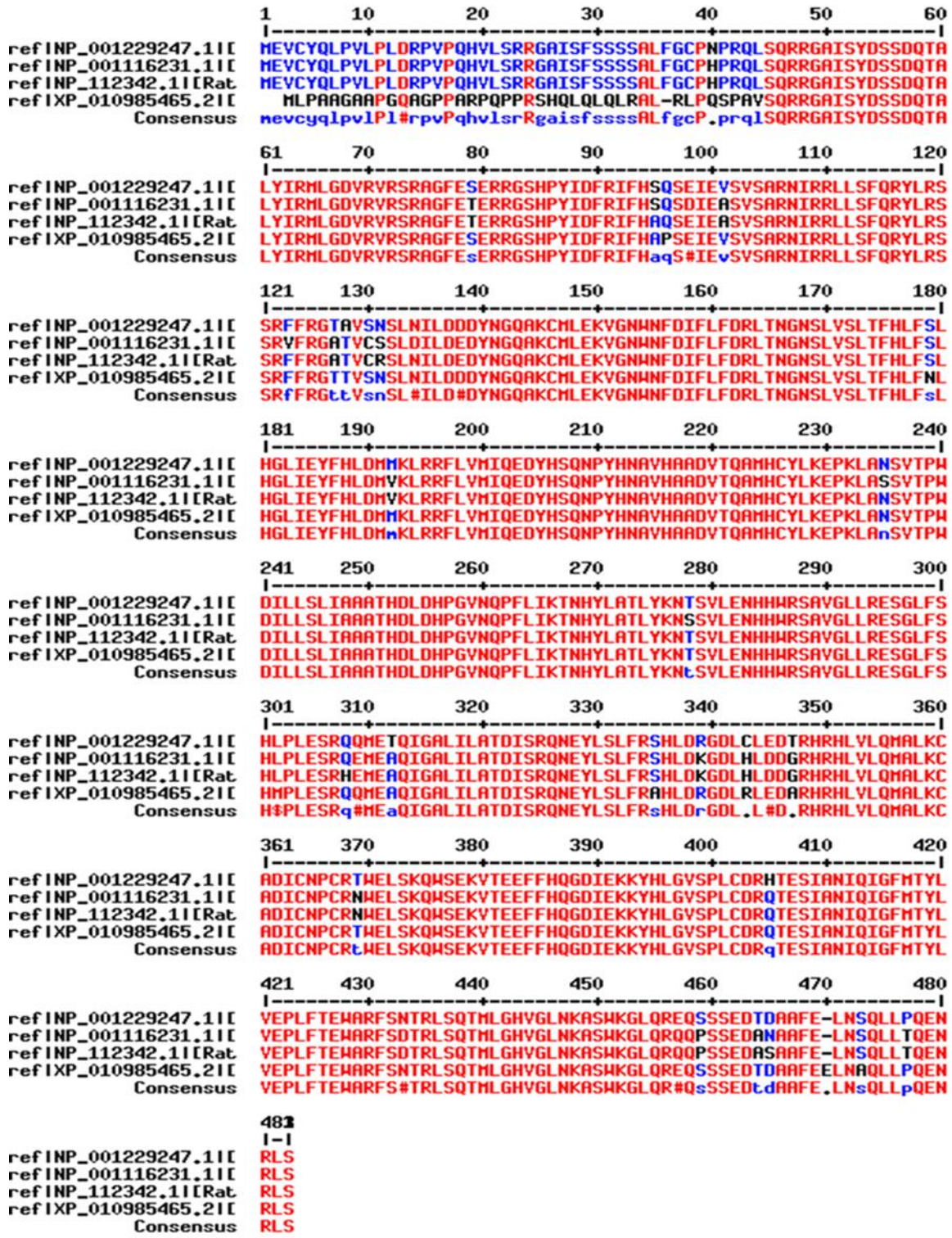


Figure 2. Multiple sequence alignment of PDE7A amino acid sequences retrieved for the species. The alignment was performed using MULTALIN. Each row represents one of the aligned amino acids sequences. ref |NP _001229247.1, human PDE7A; ref |NP_001116231.1, mouse PDE7A; ref |NP_112342.1, rat PDE7A; ref |XP_010985465.2, camel. The columns represent the locations of the sequence. The consensus sequence, "Consensus," is displayed in the last row. Highly conserved amino acids (≥90%) are displayed in red, low consensus regions (≥50%) are displayed in blue, and neutral regions are displayed in black. The dot indicates that the position does not contain any conserved residues, # indicates one of these residues NDQEB.

Table 2. Comparative percentages of exact matches between PDE7A amino acid sequences aligned to specific species

Organism	Human	Mouse	Rat	Camel
Human	100%			
Mouse	94.19%	100%		
Rat	94.81%	98.13%	100%	
Camel	90.2%	86.25%	87.29%	100%

Minimum = 86.25%, Maximum = 98.13%, Mean = 91.81%, and Standard deviation = 4.253%.

Table 3. Quantitative comparison of the functional resemblances between the chosen species aligned PDE7A amino acid sequences

Organism	Human	Mouse	Rat	Camel
Human	100%			
Mouse	98.54%	100%		
Rat	95.64%	98.54%	100%	
Camel	90.83%	88.12%	88.75%	100%

Minimum = 88.12%, Maximum = 100%, Mean = 94.66%, and Standard deviation = 4.555%.

Table 4. Global block substitution matrix (BLOSUM62) similarities among the selected species aligned PDE7A amino acid sequences

Organism	Human	Mouse	Rat	Camel
Human	1	0.94	0.94	0.87
Mouse	0.94	1	0.98	0.84
Rat	0.95	0.98	1	0.85
Camel	0.86	0.83	0.84	1

Minimum = 0.83, Maximum = 0.98, Mean = 0.901, and Standard deviation= 0.055.

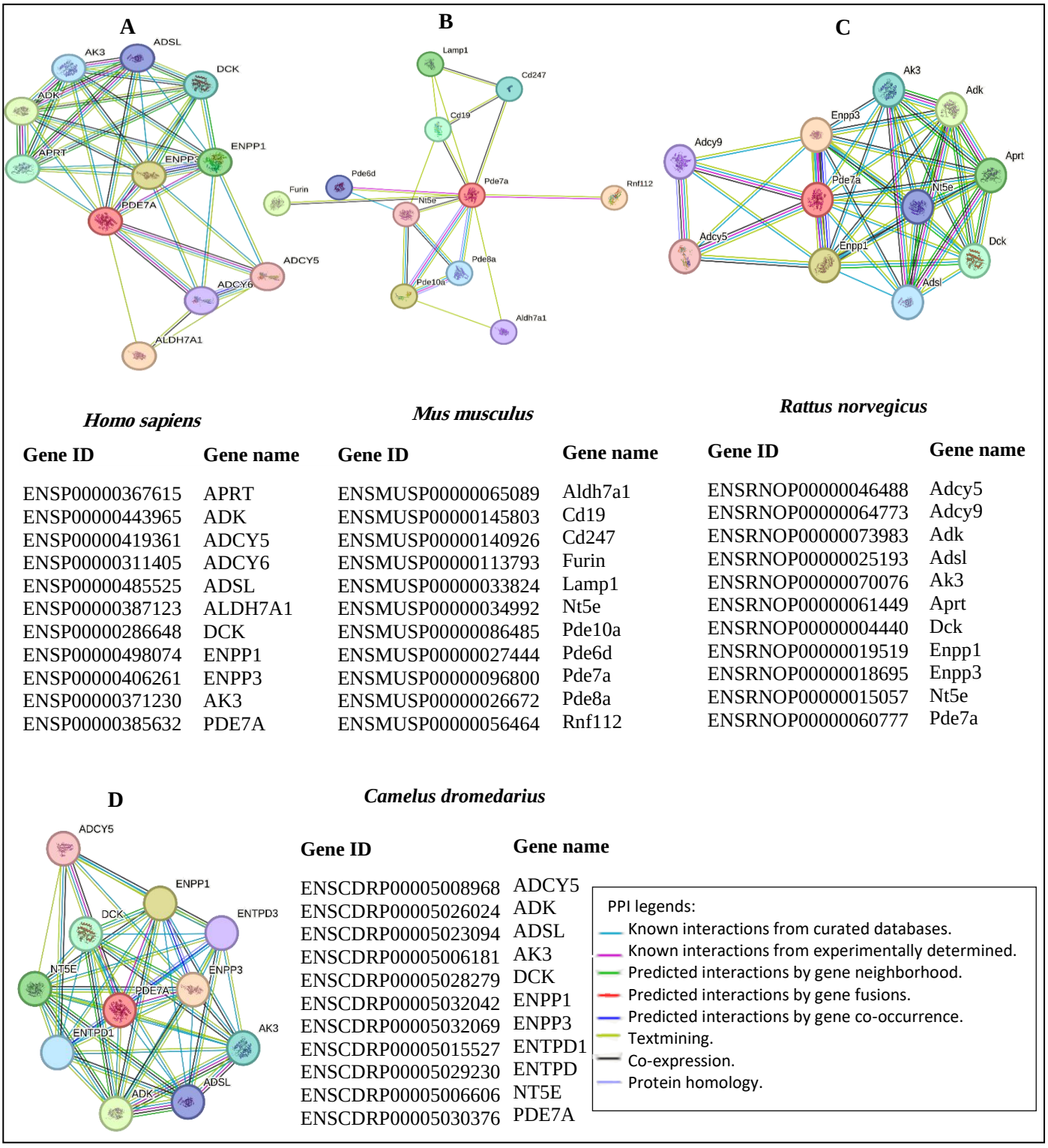
Analysis of the physicochemical properties and protein-protein interactions

The physicochemical properties of the amino acid sequences measured included protein formula, molecular mass, pI, net electric charge, and hydrophobicity of amino acid residues. Table 5 lists Mw of protein sequences as follows: (min = 54.9 Da, max = 55.5 Da, mean =55.3 Da, and standard deviation = 0.22 Da), the IP of the protein sequence (min = 6.93, max = 7.78, mean = 6.93, and standard deviation = 0.37), and hydrophobicity as follows (min = 44.61%, max = 46.67%, mean = 45.48%, and standard deviation = 0.86%). Although the physicochemical properties of the species are closely related, the results of their protein- protein interactions indicate that PDE7A interactomes are different (**Error! Reference source not found.**A and B).

Table 5. The physicochemical properties of the amino acid sequences of PDE7A of the selected* species *by the ProtParam tool.

Species	Formula	Mass (Da)	Isoelectric point	Net charge pH (7.4)	Hydrophobicity (%)
Human	$C_{2463}H_{3830}N_{708}O_{719}S_{20}$	55.504	7.10	-1.09	44.61
Mouse	$C_{2455}H_{3818}N_{706}O_{716}S_{19}$	55.288	6.93	-2.05	45.23
Rat	$C_{2465}H_{3829}N_{711}O_{712}S_{19}$	55.425	7.38	-0.01	45.44
Camel	$C_{2440}H_{3806}N_{710}O_{708}S_{18}$	54.991	7.78	1.19	46.67
Minimum		54.991	6.930	-2.05	44.61
Maximum		55.504	7.78	1.19	46.67
Mean		55.302	7.29	-0.49	45.48
Standard deviation		0.22	0.37	1.39	0.86

The interaction network of PDE7A may reveal its involvement in various biological processes. To this end, the webtool STRING was used for the construction of PDE7A protein interaction networks for four animal species. The functional enrichment analysis and PDE7A protein-protein interaction networks for the selected species are shown in Figure 3, and the different predicted functional partners in humans, mice, rats, and camels are shown in Table 6-9), respectively.



Homo sapiens

Gene ID	Gene name
ENSP00000367615	APRT
ENSP00000443965	ADK
ENSP00000419361	ADCY5
ENSP00000311405	ADCY6
ENSP00000485525	ADSL
ENSP00000387123	ALDH7A1
ENSP00000286648	DCK
ENSP00000498074	ENPP1
ENSP00000406261	ENPP3
ENSP00000371230	AK3
ENSP00000385632	PDE7A

Mus musculus

Gene ID	Gene name
ENSMUSP00000065089	Aldh7a1
ENSMUSP00000145803	Cd19
ENSMUSP00000140926	Cd247
ENSMUSP00000113793	Furin
ENSMUSP00000033824	Lamp1
ENSMUSP00000034992	Nt5e
ENSMUSP00000086485	Pde10a
ENSMUSP00000027444	Pde6d
ENSMUSP00000096800	Pde7a
ENSMUSP00000026672	Pde8a
ENSMUSP00000056464	Rnf112

Rattus norvegicus

Gene ID	Gene name
ENSRNOP00000046488	Adcy5
ENSRNOP00000064773	Adcy9
ENSRNOP00000073983	Adk
ENSRNOP00000025193	Adsl
ENSRNOP00000070076	Ak3
ENSRNOP00000061449	Aprt
ENSRNOP00000004440	Dck
ENSRNOP00000019519	Enpp1
ENSRNOP00000018695	Enpp3
ENSRNOP00000015057	Nt5e
ENSRNOP00000060777	Pde7a

Camelus dromedarius

Gene ID	Gene name
ENSCDRP00005008968	ADCY5
ENSCDRP00005026024	ADK
ENSCDRP00005023094	ADSL
ENSCDRP00005006181	AK3
ENSCDRP00005028279	DCK
ENSCDRP00005032042	ENPP1
ENSCDRP00005032069	ENPP3
ENSCDRP00005015527	ENTPD1
ENSCDRP00005029230	ENTPD
ENSCDRP00005006606	NT5E
ENSCDRP00005030376	PDE7A

Figure 3. Functional enrichment analysis and PDE7A protein-protein interaction networks for the selected species. The interactive network diagram is used to display highly rated interactors. Proteins are represented by network nodes, and edges represent predicted functional enrichment associations. (A) The protein-protein interaction (PPI) network in humans; (B) The PPI network in the mouse; (C) The PPI network in rats; and (D) The PPI network in camel. The PPI legends indicate the type of interaction evidence. Proteins with known or anticipated 3D structures are associated with full notes, whereas empty notes are proteins with no known 3D structure.

Table 8

Table 6. The predicted functional partner of PDE7A in Homo sapiens.

Node 1	Node 2	Node 1 annotation	Node 2 annotation	Score
PDE7A	ADCY5	Phosphodiesterase 7A	Adenylate cyclase type 5.	0.804
PDE7A	ADCY6	Phosphodiesterase 7A	Adenylate cyclase type 6.	0.818
PDE7A	ADK	Phosphodiesterase 7A	Adenosine kinase.	0.925
PDE7A	ADL	Phosphodiesterase 7A	Adenylosuccinate lyase.	0.901
PDE7A	AK3	Phosphodiesterase 7A	Phosphotransferase AK3.	0.904
PDE7A	ALDH7A1	Phosphodiesterase 7A	Alpha-aminoadipic semialdehyde dehydrogenase.	0.949
PDE7A	APRT	Phosphodiesterase 7A	Adenine phosphoribosyltransferase.	0.909
PDE7A	DCK	Phosphodiesterase 7A	Deoxycytidine kinase.	0.905
PDE7A	ENPP1	Phosphodiesterase 7A	Ectonucleotide pyrophosphatase/ phosphodiesterase family member 1.	0.924
PDE7A	ENPP3	Phosphodiesterase 7A	Ectonucleotide pyrophosphatase/ phosphodiesterase family member 3.	0.926

Table 7. The predicted functional partner of PDE7A in Mus musculus.

Node 1	Node 2	Node 1 annotation	Node 2 annotation	Score
PDE7A	Aldh7a1	Phosphodiesterase 7A	Alpha-aminoadipic semialdehyde dehydrogenase1.	0.515
PDE7A	Cd19	Phosphodiesterase 7A	B-lymphocyte antigen CD19.	0.631
PDE7A	Cd247	Phosphodiesterase 7A	T-cell surface glycoprotein CD3 zeta chain.	0.609
PDE7A	Furin	Phosphodiesterase 7A	Furin.	0.667
PDE7A	Lamp1	Phosphodiesterase 7A	Lysosome-associated membrane glycoprotein 1.	0.66
PDE7A	Nt5e	Phosphodiesterase 7A	5'-nucleotidase.	0.506
PDE7A	Pde10a	Phosphodiesterase 7A	3',5'-cyclic phosphodiesterase 10A.	0.684
PDE7A	Pde6d	Phosphodiesterase 7A	3',5'-cyclic phosphodiesterase subunit delta.	0.55
PDE7A	Pde8a	Phosphodiesterase 7A	3',5'-cyclic phosphodiesterase 8A.	0.581
PDE7A	Rnf112	Phosphodiesterase 7A	RING finger protein 112.	0.72

Table 8. The predicted functional partner of PDE7A in Rattus norvegicus.

Node 1	Node 2	Node 1 annotation	Node 2 annotation	Score
PDE7A	Adcy5	Phosphodiesterase 7A	Adenylate cyclase type 5.	0.781
PDE7A	Adcy9	Phosphodiesterase 7A	Adenylate cyclase 9 (Predicted).	0.786
PDE7A	Adk	Phosphodiesterase 7A	Adenosine kinase.	0.923
PDE7A	Adsl	Phosphodiesterase 7A	Adenylosuccinate lyase.	0.900
PDE7A	Ak3	Phosphodiesterase 7A	Phosphotransferase AK3.	0.905
PDE7A	Aprt	Phosphodiesterase 7A	Adenine phosphoribosyltransferase.	0.506
PDE7A	Dck	Phosphodiesterase 7A	Deoxycytidine kinase.	0.684
PDE7A	Enpp1	Phosphodiesterase 7A	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1.	0.925
PDE7A	Enpp3	Phosphodiesterase 7A	Ectonucleotide pyrophosphatase/ Phosphodiesterase family member 3.	0.937
PDE7A	Nt5e	Phosphodiesterase 7A	5'-nucleotidase.	0.809

Table 9. The predicted functional partner of PDE7A in Camelus dromedarius.

Node 1	Node 2	Node 1 annotation	Node 2 annotation	Score
PDE7A	ADCY5	Phosphodiesterase 7A	Adenylate cyclase type 5.	0.875
PDE7A	ADK	Phosphodiesterase 7A	Adenosine kinase isoform X1.	0.922
PDE7A	ADSL	Phosphodiesterase 7A	Adenylosuccinate lyase.	0.900
PDE7A	AK3	Phosphodiesterase 7A	Phosphotransferase AK3.	0.904
PDE7A	DCK	Phosphodiesterase 7A	Deoxycytidine kinase.	0.911
PDE7A	ENPP1	Phosphodiesterase 7A	Ectonucleotide pyrophosphatase/ phosphodiesterase family member 1.	0.875

PDE7A	ENPP3	Phosphodiesterase 7A	Ectonucleotide pyrophosphatase/ phosphodiesterase family member 1/3.	0.923
PDE7A	ENTPD1	Phosphodiesterase 7A	Ectonucleoside triphosphate diphosphohydrolase 1.	0.966
PDE7A	ENTPD3	Phosphodiesterase 7A	Ectonucleoside triphosphate diphosphohydrolase 3.	0.900
PDE7A	NT5E	Phosphodiesterase 7A	5'-nucleotidase.	0.900

The present study showed that there are eleven nodes found in the current network of the PDE7A protein. *Rattus norv*egicus significantly enriches interactions among the eleven genes, as indicated by a PPI enrichment p-value of 3.94e-13 (Table 10). This suggests that these genes were biologically interconnected as a group in the context of PDE7A. The network consisted of 11 nodes and 43 edges, with an average node degree of 7.82 and an average local clustering coefficient of 0.879, indicating a high degree of interconnectivity among the genes. Interestingly, humans, camels, and rats share 7 out of a total of 11 protein interactors, whereas mice share only 1 out of a total of 11 protein interactors (Figure 4). Despite their evolutionary kinship, certain species have special relationships that they do not share with others. However, further validation is required to reveal specific molecular functions between PDE7A and their protein partners.

Table 10. Network statistics of PDE7A protein.

Species	Characteristics of Network					
	Number of nodes	**Number of edges**	**Average node degree**	**Expected number of edges**	**Avg. local clustering coefficient**	**PPI enrichment p-value**
Human	11	38	6.91	11	0.879	1.82e-10
Mouse	11	19	3.45	11	0.821	0.0222
Rat	11	43	7.82	11	0.879	3.94e-13
Camel	11	51	9.27	11	0.952	< 1.0e-16

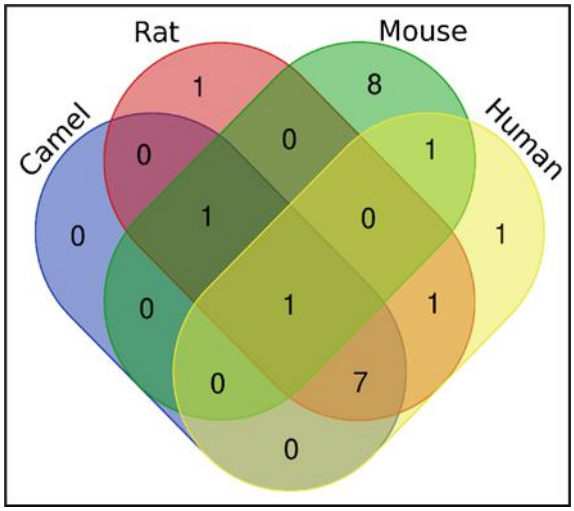


Figure 4. Venn diagram showing unique interaction similarities of PDE7A in the selected species. The data of species was collected on 12 March 2024.

DISCUSSION

Our bioinformatics investigations revealed that the sequence of PDE7A is highly conserved among mammals since mouse, rat, and camel proteins share the most amino acid alignment with humans. Phylogenetical diversity analysis revealed a common evolutionary relationship between the selected species and humans, but camels show the most variable evolutionary lineage in their PDE7A protein over time.

Given that camels and humans share 57% of the same genes compared to rats and mice that share 69% and 67% respectively, with human [29], it is not surprising that we report camels show a more distant evolutionary relationship of PDE7A protein sequences across species, while rats show a closer evolutionary relationship and a more recent common ancestor. In searches for homologous sequence proteins, camels present less identity with human PDE7A than other species. However, the physicochemical properties of the amino acid sequences of PDE7A, including Mw, pI, and hydrophobicity, indicated closely related characteristics across species.

PPIs are essential for understanding PDE7A physiology. The approach taken in this investigation used the STRING database to build the PPI network. This approach allowed us to visualize interactions between genes of interest and their potential partners in PDE7A. PPI network analysis also enabled us to identify the major clusters within the network, which may represent key regulators or mediators of PDE7A biology across species. PPI network analysis also enabled us to identify the major clusters within the network, which may represent key regulators or mediators of PDE7A biology across species.

It has been shown that PDE7A has ten predicted functional partners with a suitable score in the selected species. The different interaction networks with APRT, ADK, ADCY5, ADCY6, ADSL, ALDH7A1, DCK, ENPP1, ENPP3, and AK3 were found in humans. The protein PDE7A makes the strongest interaction with ALDH7A1 with the highest confidence score of 0.949, but the weakest interaction was observed with ADCY5 with a confidence score of 0.804. It may be due to the strong interaction with ALDH7A1, which generates osmolytes and metabolizes harmful aldehydes to protect against hyperosmotic stress [30]. Moreover, ALDH1A expression in Sertoli cells was associated with its relative contribution to controlling the formation of retinoic acid (RA), the active metabolite of vitamin A, in the testis, which plays a major role in spermatogenesis and many other biological processes [31]; but the ADCY5 protein, which catalyzes the synthesis of cAMP in response to G-protein signaling [32], shows a weak interaction with PDE7A.

PDE7A interactions with Adcy5, Adcy9, Adk, Adsl, Ak3, Aprt, Dck, Enpp1, Enpp3, and Nt5e were found in Rattus norvegicus networks. The protein PDE7A has the strongest interaction with Enpp3 with the highest confidence score of 0.937. Still, the weakest interaction was observed with Aprt, with a confidence score of 0.506. The strong interaction with the Enpp3 protein, which belongs to the ectoenzyme family that hydrolyzes extracellular nucleotides such as ATP, may be due to the formation of AMP and inorganic pyrophosphate (PPi), which provide energy for many essential processes in cells [33]. Still, the Aprt protein, which helps recycle the purine adenine to generate AMP [34], shows weak interaction with PDE7A. These results underscore the potential significance of these genes in PDE7A, providing a foundation for further analysis.

The present study showed that there are eleven nodes in the current network of the PDE7A protein for all species. It may be due to all eleven interacting proteins being produced from a common encoding gene. Rats present a higher enrichment score, which might indicate an overrepresentation of the functional group of the PDE7A gene in humans. However, further validation is required to reveal specific biological processes, molecular function, and signaling pathways between PDE7A and their protein partners.

CONCLUSION

The study attempted to elucidate differences in the PDE7A protein in selected species through evolutionary diversity and PPI in gene products. This study suggests possible similarities in PDE7A function among mice, rats, camels, and humans. It was also concluded that rats are suitable models that can be exploited to study PDE7A to understand human biology. This is because the PDE7A gene could function similarly in this animal, which could accelerate research. However, there are anatomical and developmental differences between rats and humans that must be considered when extrapolating information from rat models to humans.

Conflicts of Interest

The authors declare no conflicts of interest.

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التحليلات الحسابية لجزيئات الأحماض الأمينية في PDE7A لتوضيح تنوعها التطوري وتفاعلاتها البروتينية في أنواع متعددة من الثدييات

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المستخلص

تستكشف هذه الدراسة التفاعلات البروتينية والحفظ التطوري لإنزيم فوسفوديستيريز النوع A7 (PDE7A) عبر الأنواع المختلفة، بهدف تحديد الأنواع ذات أعلى قدر من التشابه مع البشر، وهو ما له تطبيقات مهمة في العديد من المجالات مثل علم الأدوية، علم الأحياء المقارن، الكيمياء الحيوية، علم الأورام، الغدد الصماء، وعلوم الإنجاب. كشفت التحليلات الحسابية لتسلسل الأحماض الأمينية لهذا الإنزيم عن علاقة تطورية مشتركة بين الأنواع المختارة والبشر، لكن الجمال تظهر السلالة التطورية الأكثر تنوعًا في بروتين PDE7A بمرور الوقت. في عمليات البحث عن البروتينات المتجانسة، كانت نتائج تحليل الهوية لأربعة تسلسلات من الأحماض الأمينية المسترجعة على النحو التالي: 91.81 ± 4.25% (متوسط ± انحراف معياري)، بينما كان التشابه بين التسلسلات 94.66% ± 4.55، وأسفر تحليل BLOSUM62 (مصفوفة استبدال الكتل 62) عن قيمة دنيا تبلغ 0.901 ± 0.055. جميع الأنواع لها خصائص فيزيوكيميائية وثيقة الصلة. كشفت التحليلات الحسابية عن بقايا أحماض أمينية محفوظة للجين عبر الأنواع المدروسة، والتي من المحتمل أن تساهم في أنماط التعبير المتشابهة لجين PDE7A في حيوانات مختلفة. تشير النتائج أيضًا إلى أن الجرذان نموذج مناسب لاكتساب رؤى أعمق في علم الأحياء البشري.

الكلمات الدالة: إنزيم فوسفوديستيريز النوع A7، تسلسل الأحماض الأمينية، الفئران، الجرذان، الجمال.