



**PHYLOGENETIC ANALYSIS OF HISTONE H3 PROTEIN IN *CHARYBDIS LUCIFERA***

**Monika M. and Shoba K.\***

Department of Biochemistry, D.K.M College for Women (Autonomous), Vellore, Tamilnadu, India.

**\*Corresponding Author: Shoba K.**

Department of Biochemistry, D.K.M College for Women (Autonomous), Vellore, Tamilnadu, India.

Article Received on 28/12/2018

Article Revised on 19/01/2019

Article Accepted on 10/02/2019

**ABSTRACT**

A single male adult specimen of the indo pacific portunid crab *charybdis lucifera*. Colour yellowish brown with two large white spots on either branchial region, cheipeds scarlet pink, the tips light brown, extreme tips whitish. The species is met with on both coasts of india, Ceylon, java and siam. The nucleotide and protein sequence of histone h3 from *charybdis lucifera* is retrived from NCBI database. The highly expressed genes are selected on the basis of CAI value using ACUA tool. Similarity search was carried out for highly expressed gene sequence. Finally the phylogenetic and evolutionary relationship of highly expressed sequences were done through using Amigo, t-coffee.,etc

**KEYWORDS:** Histone h3, NCBI, ACUA, t-coffee, highly expressed sequence, CAI value, phylogenetic analysis.

**INTRODUCTION**

Crabs are decapod crustaceans which have a very short tail and are covered with a thick shell, or exoskeleton and are armed with a single pair of claws. Crabs are invertebrates (animals without a backbone). Their exoskeleton protects them from predators and provides support for their bodies. They have flattened bodies, two feeler antennae, and two eyes located on the end of stalks, and they are 10-legged animals that walk sideways. There are about 6,793 species of crab. *charybdis lucifera* habitat: Sandy or muddy bottom. distribution: India, Sri Lanka, East Asian Countries, Australia and Japan. description: The carapace is very much broader, its length being muchless than two-thirds its breadth. A sharply dentiform lobule at the outer end of the lower border of the orbit. The chelipeds in the male are not very much more than twice the length of the carapace. The posterior border of the propodite of the last pair of legs are serrated throughout. The sixth male abdominal segment has its sides parallel or even slightly divergent in atleast two-thirds of its extent. In the anterior male abdominal appendages, there is no bend near the fringe of hairs on the distal part of the outer margin also. The fingers of the larger cheliped are shorter than the palm. remarks: Colour yellowish brown with large white spots on either branchial region, chelipeds scarlet pink, the tips light brown, extreme tips whitish.

**METHODOLOGY**

The sequence of histone h3 protein in *charybdis lucifera* is retrieved from NCBI database. The retrieved sequence

is submitted to following server, to know the evolutionary relationship of histone h3 protein. The retrieved sequence is submitted to clustal w to know the multiple sequence alignment of histone h3 protein. The retrieved sequence is submitted to phyml, t-coffee, palm server to know the phylogenetic analysis of selected sequence with histone h3 protein. The retrieved sequence is submitted to ACUA server to know the CAI value of evolutionary related sequence with histone h3 protein. The retrieved sequence is submitted to protein prediction server, protein variability server to know the protein protein interaction of histone h3 protein.

**RESULTS AND DISCUSSION****Gene Expression Analysis – ACUA: Table:01**

The above table shows the gene expression of the histone h3 protein with evolutionary Related sequence.

Name of the Species	ID	Name of the Gene	CAI
Sus scrofa	>XM_021089926.1:58-468	Histone H3	0.848
Plasmodium falciparum 3D7	>XM_961000.1	Histone H3	0.63
Oncorhynchus mykiss	>XM_021568521.1:60-470	Histone H3	0.858
Dictyostelium discoideum	>U76664.1	Histone H3	0.631
Homo sapiens	>M26150.1:557-964	Histone H3	0.741
Canis lupus familiaris	>XM_022404953.1:1986-2396	Histone H3	0.81
Neurospora crassa OR74A	>XM_951565.2:510-977	Histone H3	0.744
Saccharomyces cerevisiae S288C	>NM_001182870.1	Histone H3	0.691
Magnaporthe oryzae 70-15	>CM001235.1:301363-301575,301663-301815,301877-301921	Histone H3	0.765
Drosophila melanogaster	>NM_001032216.2:58-468	Histone H3	0.71
Bos Taurus	>XM_015463024.2:126-536	Histone H3	0.809
Oryza sativa Indica Group	>U25664.1:231-641	Histone H3	0.772
Oryza sativa Japonica Group	>GU373807.1:373-783	Histone H3	0.628
Gallus gallus	>XM_025154971.1:362-772	Histone H3	0.799
Xenopus laevis	>XM_018224168.1:17-427	Histone H3	0.862
Schizosaccharomyces pombe	>NM_001020112.2:139-549	Histone H3	0.618
Rattus norvegicus	>XM_006253979.2:31-441	Histone H3	0.838
[Trypanosoma brucei brucei TREU927	>XM_001218953.1	Histone H3	0.731
Danio rerio	>XM_017354221.2:88-498	Histone H3	0.841
Arabidopsis thaliana	>M17131.1:368-778	Histone H3	0.741
Leishmania major strain Friedlin]	>XM_001682084.1	Histone H3	0.751
Candida albicans SC5314	>CP017624.1:2081130-2082971	Histone H3	0.643

**Table. 02: Highly Expressed.**

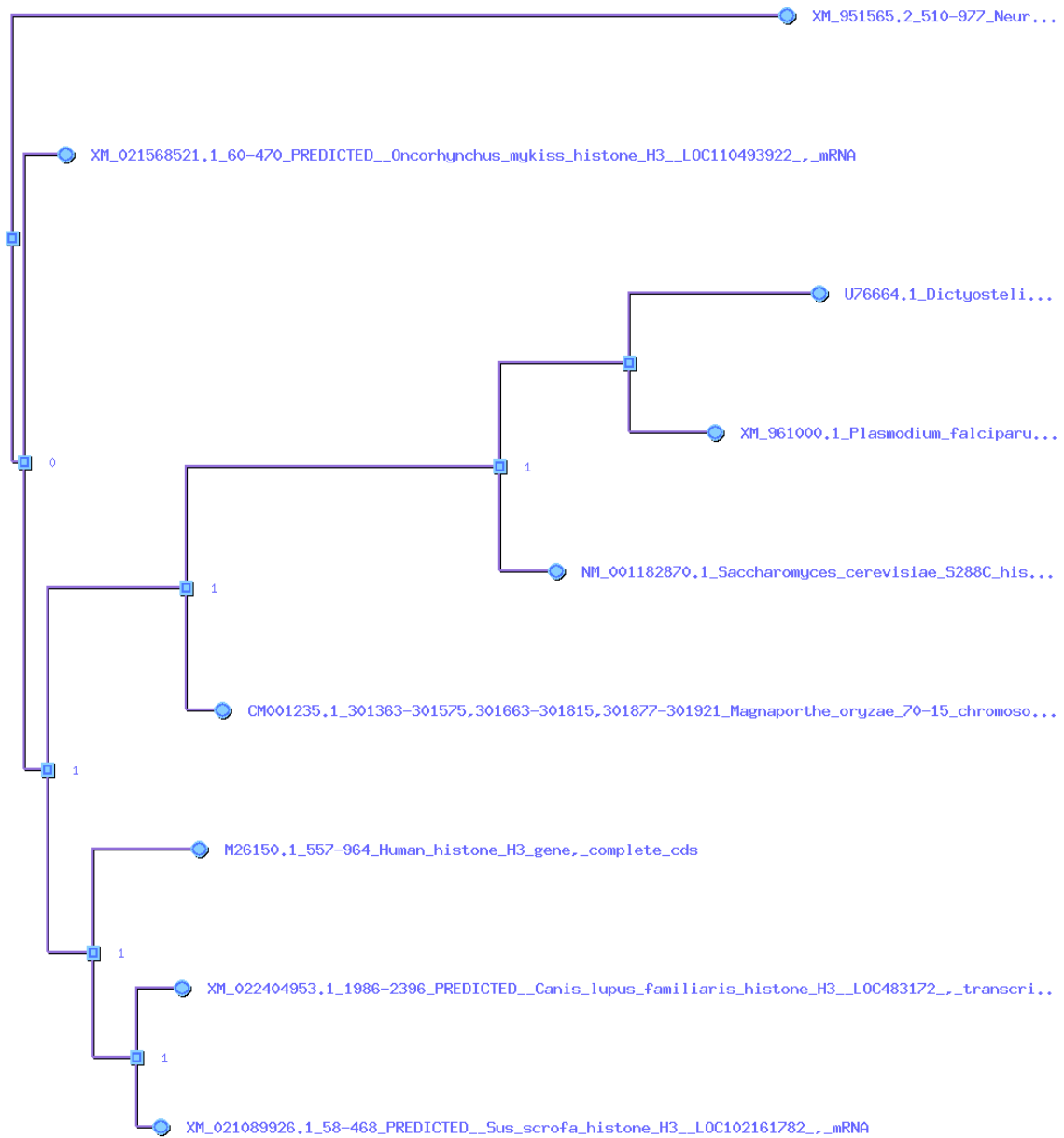
S. No	Name of the Species	ID	Name of the Gene	CAI
01	Sus scrota	>XM_021089926.1:58-468	Histone H3	0.848
02	Oncorhynchus mykiss	>XM_021568521.1:60-470	Histone H3	0.858
03	Canis lupus familiaris	>XM_022404953.1:1986-2396	Histone H3	0.81
04	Bos Taurus	>XM_015463024.2:126-536	Histone H3	0.809
05	Xenopus laevis	>XM_018224168.1:17-427	Histone H3	0.862
06	Rattus norvegicus	>XM_006253979.2:31-441	Histone H3	0.838
07	Danio rerio	>XM_017354221.2:88-498	Histone H3	0.841

The above table shows the highly expressed sequence.

**Palm****Job Parameters**

Job ID	20190110004421994	Number of Substitution Rate Category	4
Job Note		Model Selection Criterion	AIC
Sequence Type	DNA	Optimization of Tree Topology	Yes
Number of Bootstrap	100	Optimization of Branch Length	Yes
Starting Tree	BIONJ		

## Tree Image Area



Model	-lnL	K	AIC	Delta	weight	CumWeight
GTR+G	2812.1040	9	5642.2080	0.0000	0.3566	0.3566
TrN+G	2815.5840	6	5643.1680	0.9600	0.2207	0.5773
GTR+I+G	2811.7593	10	5643.5186	1.3106	0.1852	0.7625
TrN+I+G	2815.3611	7	5644.7222	2.5142	0.1015	0.8640
TIM+G	2815.4753	7	5644.9507	2.7427	0.0905	0.9545
TIM+I+G	2815.2559	8	5646.5117	4.3037	0.0415	0.9960

The above result shows the phylogenetic analysis of histone h3 protein with evolutionary related sequence.

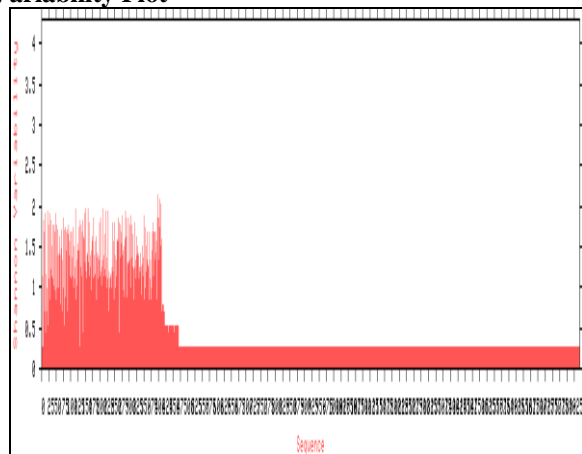
## Protin Variability Server

## Position Consensus\_Sequence Variability (H)

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1	A	0.267
2	T	-0.000
3	G	0.267
4	G	1.119
5	C	0.267
6	T	1.823
7	C	1.187
8	G	0.575
9	T	1.669
10	A	0.530
11	C	0.700
12	C	1.896
13	A	0.439
14	A	0.267
15	G	1.143
16	C	0.937
17	A	0.700
18	G	0.976
19	A	0.439
20	C	0.791
21	C	1.920
22	G	0.530
23	C	0.267
24	T	1.765
25	C	1.091
26	G	0.700
27	C	1.908
28	A	0.791
29	A	0.832
30	A	1.220
31	T	0.832
32	C	0.684
33	C	1.823
34	A	0.700
35	C	1.119
36	C	1.497
37	G	0.575
38	G	1.096
39	T	1.749
40	G	0.575
41	G	1.023
42	C	1.770
43	A	0.700
44	A	0.832
45	G	1.677
46	G	0.866
47	C	0.957
48	C	1.896
49	C	0.832
50	C	0.684
51	A	1.770
52	C	1.342
53	G	0.994
54	G	1.708
55	A	0.439
56	A	0.832
57	G	1.398

58	C	0.994
59	A	0.267
60	G	1.418
61	C	1.602
62	T	0.700
63	G	1.398
64	G	0.700
65	C	0.791
66	C	1.473
67	A	1.477
68	C	0.439
69	C	1.708
70	A	0.700
71	A	0.957
72	G	1.341
73	G	0.530
74	C	0.994
75	T	1.845
76	G	0.530
77	C	0.530
78	C	1.693
79	C	1.477
80	G	1.096
81	C	1.718
82	A	0.866
83	A	0.832
84	G	1.457
85	A	1.686
86	G	1.548
87	C	1.708
88	G	0.832
89	C	0.700
90	T	1.655
91	C	0.994
92	C	1.119
93	G	1.747
94	G	1.398
95	C	1.187
96	C	1.563
97	A	1.119
98	C	0.937
99	C	1.669
100	G	1.119
101	G	1.096
102	C	1.669
103	G	1.085
104	G	0.832
105	C	1.352
106	G	1.119
107	T	1.278
108	G	1.742
109	A	0.994
110	A	0.684

**Variability Plot**

The above result shows the protein variability in histone h3 protein.

**CONCLUSION**

Histone H3 is one of the five main histone proteins involved in the structure of chromatin in eukaryotic cells. Featuring a main globular domain and a long N-terminal tail, H3 is involved with the structure of the nucleosomes of the 'beads on a string' structure. Histone proteins are highly post-translational modified however Histone H3 is the most extensively modified of the five histones. The term "Histone H3" alone is purposely ambiguous in that it does not distinguish between sequence variants or modification state. Histone H3 is an important protein in the emerging field of epigenetics, where its sequence variants and variable modification states are thought to play a role in the dynamic and long term regulation of genes. The nucleotide and protein sequence from the genus *charybdis* is retrieved from National Center For Bioinformatics Information in fasta format. The retrieved sequence is submitted to the bioinformatics tools and server like amigo, t-coffee, palm, Acua, to know the evolutionary relationship. Further detailed analysis in other aspects is needed for promoting histone h3 protein as a therapeutic agent.

**REFERENCE**

- Adams, A. and White, A., 1848. Crustacea. In: A. Adams, The Zoology of the Voyage of H.M.S. Samarang, 1843-1846, London
- Adams, A. and White, A., 1850. 'Samarang' Crustacea, In: A. Adams, The Zoology of the Voyage of H.M.S. Samarang, Alcock, A., 1869, J. Asiatic Soc. Bengal,
- Adams, and White, A., 1847. Zoology of the voyage of H.M.S. Samarang- Crustacea,
- Alcock, A. and Anderson, A. R., 1894. Natural history notes from H. M. Indian Marine Survey Steamer 'Investigator'. Ser. II. No. 14. An account of a recent collection of deep sea Crustacea from the Bay of Bengal and Laccadive Sea. Journ. Asiat. Soc. Bengal.
- Alcock, A., 1895. Materials for the carcinological fauna of India, No. 1, The Brachyura Oxyrhyncha. J. Asiat. Soc. Beng Alcock, A., 1895a. Description of a new species of Oxyrhynch crab of genus Parthenope. Journ. Asiat. Soc. Bengal Alcock, A., 1896. Materials for the carcinological fauna of India, No. 2, The Brachyura Oxyrhyncha. J. Asiat. Soc. Beng
- Alcock, A., 1898. Materials for the carcinological fauna of India, No. 3, The Brachyura Cyclometopa, Part 1. The family xanthidae. J. Asiat. Soc. Beng Alcock, A., 1899. - Crustacea. Part VII. Illustrations of the Royal Indian Marine Survey Ship Investigation under the command of Commander. T.H. Heming. R. N. pls 36-45. Calcutta.
- Alcock, A., 1899a. The Brachyura Cyclometopa. Part.II. A revision of the Cyclometopa with an account of the families Portunidae, Cancridae and Corystidae. Journ. Asiat. Soc. Bengal Alcock, A., 1899b. Natural history notes from the R.I.M. Survey Ship 'Investigator'. Ser. III. No.3. On some notable new and rare species of Crustacea. Journ. Asiat. Soc. Bengal
- Alcock, A., 1899c. Materials for the carcinological fauna of India, No. 4, The Brachyura Cyclometopa, Part II, A revision of the Cyclometopa with an account of the families Portunidae, Cancridae and Corystidae. J. Asiat. Soc. Beng., 68: 1-104
- Alcock, A., 1899d. Materials for the carcinological fauna of India, No. 6, The Brachyura Priniginea or Domiacea. J. Asiat. Soc. Beng., 68: 123-169. Alcock, A., 1900. Materials for the carcinological fauna of India, No. 6. The Brachyura Catometopa or Grapsoidea. J. Asiat. Soc. Beng., Alcock, A., 1901. Catalogue of the Indian Decapod Crustacea in the collection of the Indian Museum. Pt. I. Brachyura. Fasc. I. Introduction and Dromides or Dromiacea, pp. 1-80, pls. A & I-vii. Apel, M., and V. A. Spiridonov., 1998. Taxonomy and zoogeography of the Portunid crabs (Crustacea: Decapoda: Brachyura: Portunidae) of the Arabian Gulf and adjacent waters. Fauna of Arabia,
- Audouin and Savigny, 1817. Descr. Egypte Crust., Balss, H., 1922a. Diagnosen neuer japanischer Decapoden. Zool. Anz. Balss, H., 1922b. Ostasiatische Decapoden. III. Die Dromiaceen, Oxystomen und Parthenopiden. Arch. Naturgesch., Balss, H., 1922c. Ostasiatische Decapoden. IV. Die Brachyrhynchen (Cancridea). Arch. Naturgesch., Balss, H., 1934. Die Krabben der Reise J. W. Harms' nach der Christmas-Insel und dem malaiischen Archipel. Zool. Anz., Balss, H., 1935. On three South Indian crabs (Decapoda-Brachyura) of the Madras Museum. Rec. Indian Mus., 37: 45-48.
- Baker CH, Graham GC, Scott KD, Cameron SL, Yeates DK, Merritt DJ. Distribution and phylogenetic relationships of Australian glow-worms *Arachnocampa* (Diptera, Keroplatidae). Mol Phylogenet Evol. 2008 Aug; 48(2): 506-14. doi: 10.1016/j.ympev.2008.04.037. Epub 2008 May 3.

12. Balss, H., 1957. Decapoda VIII. Systematick. Bronn's Kl. Ordn. Tierreichs Bd. 5, Abt. 1, Buch 7, Lelf., 12: 1505-1672.
13. Shoba.k and Dr. Mazher sultana, Three - dimensional structure and motif prediction studies on collagenase protein in fiddler crab, International journal of novel trends in pharmaceutical sciences, Issn: 2277 – 2782,volume 6, issue 4, pages 79 – 83.
14. Shoba K. , Manjuladevi M , Dr. Mazher sultana, Biochemical analysis and gene expression profiling on collagenase protein in fiddler crab, World journal of pharmacy and pharmaceutical sciences, issn 2278 – 4357, volume 6, issue 3, 747-756
15. Shoba K., Sowmiya S and Dr. Mazher sultana, World Journal of Pharmaceutical and Life Sciences, ISSN 2454-2229, Vol. 3, Issue 1, 427-436.
16. Shoba.K, Hebsibahelsie.B, insilico homology modeling ofribulose-1, 5-bisphosphate carboxylase protein in gracilariaedulis, world journal of pharmacy and pharmaceutical sciences, 2017,volume 6, issue 8, 396-406, issn 2278 – 4357.
17. Shoba.K, Lavanya.G, Identification Of De Novo Peptide And Motif Prediction On Porphyrin Protein (Hmbs) Using Insilico Tools, Universal Journal Of Pharmacy ,2018, Volume 8, Issue 1, Issn2320-303x.
18. Shoba.K, Lavanya.G, Tertiary Structural Prediction And Drug Binding Studies On Mutated Gene (Hmbs) In Human Porphyrin,International Journal Of Novel Trends In Pharmaceutical Science,2018,Issn 2277 -2782,Volume 8,Issue 1
19. Shoba K., Hebsibah Elsie B. And Bavyasri S. Insilico Peptide Modeling Studies And Structural Analysis On Ribulose -1, 5 Bisphosphate Carboxylase In GracilariaEdulis, World Journal Of Pharmacy And Pharmaceutical Sciences, 2018,Volume 7, Issue 3, 1086-1095, Issn 2278 – 4357.
20. Shoba. K, Hebsibah Elsie. B and Jayakumari. S. Sathya. R. (2018); Insilico Structural Analysis and Drug Docking Studies On Ribulose -1, 5 Bisphosphate Carboxylase In Gracilaria Edulis. International journal of advanced research. 6 (9). 159-165] (ISSN 2320-5407).
21. Hebsibah Elsie B, Subashini.G, Nithya.G and Shoba.K.; Purification and Identification of Antioxidant Peptides from the Skin Protein Hydrolysate of Marine Fish (*Aurigequula Fasciata*). European journal of Pharmaceutical and Medical Research, 2018; 5(10). 371-378.Issn No 2394-3211.
22. Shoba. K, Nithy.G and Deepa.L.; Biochemical Analysis and Peptide Modeling of Lysozyme in Indian Fenneropenaeus indicus shrimp species. International journal of advanced research, 2018; 6(9). 159-165] (ISSN 2320-5407).
23. Kalpana K., Manjuvani S., Shoba K. In Silico Comparative Modeling of Maturase K Protein in *Cymbopogon martinii* Plant. Research & Reviews: A Journal of Bioinformatics. 2018; 5(3): 30–36p.
24. Shoba K., Kalpana K., Protein Modeling and Drug Docking Studies on Potential Protein Target (E. coli–dosP) and Compound Aldehyde (Sumatriptan) using Bioinformatics Tools. Research & Reviews: A Journal of Bioinformatics. 2018; 5(3): 9–18p.