Volume 7 Issue 2 2021

ISSN 2454-3055

**INTERNATIONAL
JOURNAL OF
ZOOLOGICAL
INVESTIGATIONS**

***Forum for Biological and
Environmental Sciences***

Published by Saran Publications, India

Insights from the Predicted Motifs in the *Taenia saginata* Genome Parasitizing Domestic Water Buffalo, *Bubalus bubalis* from India

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Received: 25th September, 2021; **Accepted:** 20th October, 2021; **Published online:** 23rd October, 2021

<https://doi.org/10.33745/ijzi.2021.v07i02.058>

Abstract: *Taenia saginata* is a zoonotic digenetic trematode belonging to the order Cyclophyllidea. It has wide range of geographic distribution with zoonotic significance and several cases of its infection to humans have been reported. It is of interest to report the DNA motif analysis of 18S rDNA of *Taenia saginata* collected from the domestic water buffalo, *Bubalus bubalis* in India. This data forms a framework for an in-depth analysis of the parasite biology and development, immune evasion strategies, virulence and long-term survival within the definitive host.

Keywords: *Taenia saginata*, Digenetic, Buffalo, Immune, Motifs

Citation: Chauhan Bhumika, Sharma Akshat, Tyagi Manaswita, Tyagi Anju, Misra Monica and Sharma Bindu: Insights from the predicted motifs in the *Taenia saginata* genome parasitizing domestic water buffalo, *Bubalus bubalis* from India. Intern. J. Zool. Invest. 7 (2): 740-750, 2021.

<https://doi.org/10.33745/ijzi.2021.v07i02.058>

Introduction

Livestock has a key role in the Indian economy making up 16% of the income of the under-privileged farmers living in villages. About 20.5 million people are dependent upon livestock for their subsistence and buffaloes have been of great economic importance as they are in close association with the day-to-day activities of resource-poor rural farmers and provide with the demands of milk, meat, skin, manure, and traction

(Rajabloo *et al.*, 2014).

Taenia saginata is a beef tapeworm and its infection occurs worldwide but especially in cattle-raising regions of the tropics and subtropics in Asia, Africa, the Middle East, Eastern Europe, Mexico, and South America that has been found parasitizing a large group of animals. In August 2019, 10 cases of its zoonosis were reported from the Republic of Korea (Song *et al.*, 2019). *Taenia* is

a genus of the Taeniidae family of tapeworms. They are morphologically ribbon-like and composed of series of segments known as proglottids. Based on the maturation state the proglottids are further classified into three types: immature, mature, and gravid proglottids. Cattles are intermediate hosts for *T. saginata*. Humans are infected by eating cysticerci (larval form) in raw or undercooked beef. The larvae mature in about 2 months to adult worms that can live for several years; usually, only 1 or 2 adult worms are present. Adult *T. saginata* tapeworms are usually 4 to 12 meters in length but can be as long as 25 meters.

The advent and integration of high throughput ‘-omics’ technology has greatly provided new opportunities for global, molecular level investigations of parasites biology (Chauhan *et al.*, 2020). Genomics centralizes on the function, mapping, structure, evolution, and editing of genomes. It also analyzes the genomes using next-generation sequencing (NGS) and bioinformatics to analyze and assemble the structure and function of the entire genome (Tyagi *et al.*, 2021). Through genomics, we not only understand biology but also recognize how the system of components works together to embrace the functioning of cells in organisms (Lockhart and Winzeler, 2000). The explosion of information about protein structures, ligand-binding affinity, parasite genome projects, and biological activity of millions of molecules have unlocked the possibility to correlate this scattered information for designing small-molecule drug. Computational methods have shown their potential in drug discovery and development allied with *in vitro* and *in vivo* methodologies (Azevedo *et al.*, 2009). The present study reports the DNA motif analysis of 18S rDNA of *Taenia saginata* collected from the domestic water buffalo, *Bubalus bubalis* in India.

Materials and Methods

Sequence:

The DNA sequence 18S rDNA of *Taenia saginata* was retrieved from NCBI (National Centre for

Biotechnology Information) database (<http://www.ncbi.nlm.nih.gov>) under accession number MZ747450.

Motif analysis:

The motifs were analyzed using GLAM2 Web tool and TRANSFAC Motif tool.

Results and Discussion

Myristoylation motif were found at 17 positions within the ribosomal genome of the parasite (Fig. 1). As rDNA is evolutionary conserved and serves as a molecular machinery for protein synthesis, the identified motif will help in blocking the activity of the parasite. The role of this motif has been widely studied in coding DNA till date and coded functions include protein folding and conformational stability, antibiotic resistance and homeostasis processes, interaction with cell-surfaces, DNA repair, cell cycle control, providing innate immune response, phosphorylation sites on human lamin and in nuclear lamina structural dynamics.

Conclusion

Predicted motifs in the *T. saginata* genome were presented. We report the presence of motif N-MYRISTOYLATION sites at 51 different positions within *T. saginata* genome that will be of further consideration in drug discovery.

match_detail

1

T

C T
 G I : : :
 GCAGTT
 1

T

G

T
 G I : : :
 GTTGTG

1

C

C
 G I : : :
 GCAGCA
 1

T

T

C

G I : : :
 GTGGCT

1

T

G

A

G I : : :
 GTGAAG
 1

T

G
C

G I : : :
 GTGGCG
 .

match_score

motif information

Status: ?
pos.: 1-6

Status: ?
pos.: 7-12

Status: ?
pos.: 16-21

Status: ?
pos.: 22-27

Status: ?
pos.: 28-33

Status: ?
pos.: 34-39

1

T

Status: ?
pos.: 42-47

C T
G I : : :
GCTGTT
1

T

T

Status: ?
pos.: 48-53

C

G I : : :
GTTGCT
.

1

Status: ?
pos.: 54-59

G

C T
G I : : :
GCCCTG
1

T

Status: ?
pos.: 62-67

C

G
G I : : :
GGTGCT

1

T

Status: ?
pos.: 68-73

C T
G I : : :
GCTGTT
1

Status: ?
pos.: 74-79

G

GA A
I : : :
GACTGA

1

Status: ?
pos.: 81-86

G A
G I : : :
GGTGAA
1

Status: ?
pos.: 90-95

G
G G
G I : : :
GGGTGG
.

1

Status: ?
pos.: 171-176

G G
C C
G I: ::
GGGTGC
1

T

T

Status: ?
pos.: 180-185

G
G I: ::
GTCTGT
.

<p>Y V S V T S R R R R N N N N N N M M L K I H N G C F G R D T C G A X X S A I: :: GCTCGT</p>	Status: ? pos.: 191-196
<p>Y V S V T S R R R R N N N N N N M M L K I H N G C F G R D T C G A X X S A I: :: GCGGGT</p>	Status: ? pos.: 197-202

<p>Y V S V T S R R R R N N N N N N M M L K I H N G C F G R D T C G A X X S A I: :: GCCCCG</p>	Status: ? pos.: 205-210
<p>Y V S V T S R R R R N N N N N N M M L K I H N G C F G R D T C G A X X S A I: :: GTCGCT</p>	Status: ? pos.: 214-219

freq_pat:MYRISTYL
N-myristoylation site.
[entry]Legends: 1,
myristyl.

Fig 1: Myristoylation sites in the rDNA of *Taenia saginata*.

References

- Azevedo WF, Dias R, Timmers LFSM, Pauli I, caceres RA and Soares MBP. (2009). Bioinformatics tools for screening of antiparasitic drugs. *Curr Drug Targets* 10(3): 232-239.
- Chauhan B, Sharma B and Singh HS. (2020) SWISS-MODEL: a web based computational tool for designing of protein structures. *Biotech Today* 10(2): 34-36.
- Lockhart JD and Winzeler AE. (2000) Genomics, gene expression and DNA arrays. *Nature* 405: 827-836.
- Rajabloo M, Namazi F, Shayegh H and Alavi A. (2014) *Explanatum explanatum*: an emerging liver fluke in cattle and sheep. *Onl J Vet Res.* 18(8): 657-661.
- Song SM, Yun HS, VanBik D, Chang HH, Lee SA, Kim SW, Ryoo N, Eun DY, Lee NY, Goo YK, Hong Y, Ock M, Cha HJ and Chung DI. (2019) Ten cases of *Taenia saginata* infection confirmed by analysis of the internal transcribed spacer 1 rDNA region in the Republic of Korea. *Korean J Parasitol.* 57(4): 417-422.
- Tyagi A, Chauhan B, Sharma B and Sharma A. (2021) Integrative genomic analysis of rDNA from zoonotic gastrointestinal parasite, *Fasciola gigantica* parasitizing *Bubalus bubalis* from Bhojpur (Ghaziabad), Uttar Pradesh, India. *Intern. J. Zool. Invest.* 7(2): 486-490.