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1	Discoloration of Head in Sorghum due to Curvularia Lunata	Miss Sonali A. Tayade	Zoology	The Rubrics	2024	-
2	Phylogenetic analysis of Vertebrate Hepcidin	Miss Sonali A. Tayade	Zoology	Lambert Academic publishing	2024	-

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Discoloration Of Head In Sorghum Due To Curvularia Lunata

Dnyaneshwar K. Sherkar, Sonali A. Tayde,
Madhuri S. Hingankar and Megha R. Solanke
Assistant Professor,
Arts & Commerce College, Warwat Bakal, Tq Sangrampur, Buldana (MS).

FULL PAPER

Introduction:

Sorghum is an important staple food crop of Vidarbha region; it is cultivated on very large area in Vidarbha region as a cereal as well as forage crop. Sorghum is rich in carbohydrate content, as it required less amount of irrigation and other artificial nutrients; it prove to be an good alternative for wheat and rice. At the time of flowering to physiological maturity when it get a higher moisture content in the field, various fungi start to attack and grow on the head of sorghum. Due to attack of such fungi on sorghum head, it gets infected. As compare to other pathogens associated with the head of sorghum *Curvularia* species shows their dominance. More than 19 different species of *Curvularia* were reported on infected head of sorghum (Girish et al, 2011). *C. clavata, C. cymbopogonis, C. eragrostidis, C. geniculata, C. inaequalis, C. intermedia, C. ischami, C. lunata, C. oryzae, C. ovoidea, C. pallescens, C. penniseti, C. robusta, C. senegalensis, C. siddiquii, C. sorghina, C. trifolii, C. tuberculata* and *C. verruculosa* were associated with the sorghum head. Out of which *Curvularia lunata* was most dominating. Along with the Curvularia lunata, genus like *Aspergillus, Fusarium, Cladosporium, Epicoccum, ALternaria, Phoma* and *Cylindricarpons* species also reported from grain mold complex of sorghum (Kebede et al, 2023).

Sorghum seeds infected from *Curvularia lunata* shows blackish mycelial mat present on the surface of seeds, which is loosely attached to the surface. Due to such blackish mat associated with seed surface it lead to discoloration of the seeds (Rastogi et al, 1990). This reduces the quality of seeds. Histopathological study reveals that *Curvularia lunata* infects the pericarp and aleurone layer of seeds. Due to the infection of *Curvularia lunata* to sorghum seeds reduces the germination percentage and also increases the grain mold severity (Prom et al, 2003). Seed germination was hampered

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due to the infection of *Curvularia lunata*. Grain mold disease formation and its occurrence is totally depends on the differential developmental stages of sorghum plant. Wetness duration is also responsible for the attack of pathogens. Different pathogens attack on sorghum at various developmental stages. *Curvularia lunata* shows their first appearance at the stage of flowering and it shows their maximum incidence at the time of physiological maturity of sorghum (Navi et al, 2005). Sporulation in the *Curvularia lunata* and grain mold severity due to *Curvularia lunata* drastically get increased due to increase in the relative humidity and increase in the temperature (Tonapi et al, 2007). Temperature ranges from 25^0C to 28^0C increases the sporulation in *Curvularia lunata*.

Materials and Methods:-

Collection of samples:-

Samples of sorghum head were collected from different localities of Buldana district of Maharashtra. Infected samples were collected from flowering to physiological maturity stage. Collected samples were packed in zip lock bags and bringing to laboratories for further analysis.

Isolation of Pathogens:-

Pathogens associated with the sorghum head was isolated by Agar plate method (APM) and standard blotter method (SBM).

Standard Blotter paper method:-

A pair of white blotter paper was taken and jointly soaked in sterile distilled water. Pair of soaked blotter paper were placed on sterile petri dishes, and make a chamber. 5 seeds in each plate were placed in aseptic conditions. Inoculated plates were allowed to incubate for 4-5 days at room temperature.

Agar plate method:-

Potato dextrose agar (PDA) medium were prepared and poured in sterilized petri plates, allowed to solidify. 5 seeds of infected head were inoculated on each plate and plates were incubated for 4-5 days at room temperature.

Composition of PDA (Potato dextrose agar) medium:-

Peeled potato – 100gm, Dextrose 20g, Agar 20 gm and distilled water 1000ml, pH 5.6. 100 gram of potato were taken and peeled; boiled until get soft and squeeze through muslin cloth. Then dextrose was added in it and final volume of solution was made up to 1000ml. In this solution agar was added, pH was adjusted to 5.6.

ISSN 2454-1974

Identification of Pathogens:-

Microscopic observations were taken by preparing microscopic slides for each isolates. Pathogens were identified with the help of standard literature and monographs.

Experimental results:-

Head samples of sorghum were collected from tehsil of Buldana district. All the infected samples were subjected to visual analysis. On the basis of visual symptoms appeared on the surface of seeds, seeds were categorized in different grades. All such seeds were used for the isolation of pathogens. Isolation of pathogens was done by standard blotter method and agar plate method. Out of 80 samples collected from different localities of Buldana district, 73 samples were infected by the attack of *Curvularia lunata*. As compare to other pathogens associated with this moldy samples *Curvularia lunata* prove to be dominating. Similar type of results was reported by (Girish et al, 2011). They reported more than 19 different *Curvularia* species associated with infected sorghum head. Out of which *Curvularia lunata* were more dominating, having 39% of incidence as compare to other species.

Table: - Incidence of Curvularia lunata on sorghum seeds at various developmental stages

Sr. No.	Name of Tehsil	Percent Incidence of *Curvularia lunata*	
		Flowering stage	Physiological maturity
1	Motala	20%	86%
2	Buldana	23%	94%
3	Malkapur	20%	91.5%
4	Nandura	18%	92%
5	Jalgaon Jamod	24%	89%
6	Sangrampur	21%	93%
7	Chikhali	24%	85.5%
8	Shegaon	23%	92.5%
9	Khamgaon	20%	90.5%

Samples collected at the time of flowering shows 22% incidence of *Curvularia lunata*. While samples collected at the time of physiological maturity shows 91.25 % of incidence of *Curvularia lunata*. Maximum incidence was recorded at the time of physiological maturity of plant. Samples collected from Jalgaon Jamod at the time of

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flowering stage shows highest incidence of *Curvularia lunata* (24%). While sample collected from Buldana at the time of physiological maturity shows highest incidence of *Curvularia lunata* (94%). Similar type of reports was given by (Navi et al, 2005). They show the maximum incidence of *Curvularia lunata* were observed at the physiological maturity stage. Out of all the samples collected from different localities, seed samples having black net like structure associated with them have maximum incidence of *Curvularia lunata* as compare to other pathogens. Blackish discoloration of sorghum seeds due to the attack of *Curvularia lunata* were reported by (Rastogi et al, 1990). They reported a black coloured macelial net like structure were loosely attached with the sorghum seeds. At the time of physiological maturity of sorghum plant, whenever it get a higher moisture content, *Curvularia lunata* attack on such sorghum head and causes disease. Due to its accumulation at the time of physiological maturity to harvesting, it may secrete certain toxic metabolites in seeds. Which may be reduces the quality and quantity of sorghum seeds.

Conclusions:-

From the results and observations it is concluded that *Curvularia lunata* is a serious constraint of sorghum. It attack on sorghum and responsible for the loss in yield. From visual observations, it reduces the quality and vigor of sorghum. As sorghum grains contain blackish mat along with them it is not good for human consumption. Due to continuous accumulation of *Curvularia lunata* on sorghum grain may lead to the deposition of certain harmful toxic metabolites in sorghum grain. For this reason it is recommended that such infected sorghum seeds were not good for the dietary purposes.

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Complete research work related to Botany, Zoology, Microbiology is given in this book, which has been checked by different reviews and only after thorough checking of the analysis, it has been published in this book. We are very grateful to Lambert for publishing the first volume of our Botany, Zoology and Microbiology.
Botany as a subject is related to the study of plants and a career in it would mean studying in depth about plants, fungi, algae, diseases, growth, metabolism and the structure between different groups.
Zoology deals with the animal kingdom and animal life. The history of zoology can be traced back to ancient and modern times.
Microbiology is a broad discipline of biology with works with the function, structure, uses, and the existence of the microscopic organism (microorganisms). Microbiology is a broad term studying microorganisms that includes Bacteriology, Virology, Molecular biology, Mycology, Parasitology, and other branches.

I am Dr. Shaikh Farah T. and it is my pleasure to serve as Principal of Bapumiya Sirajoddin Patel Arts, Commerce and Science College from last year. This is my ninth year to serve the society prior to become principal. My educational Qualification include Ph.D in Botany with Mycology as specialization.

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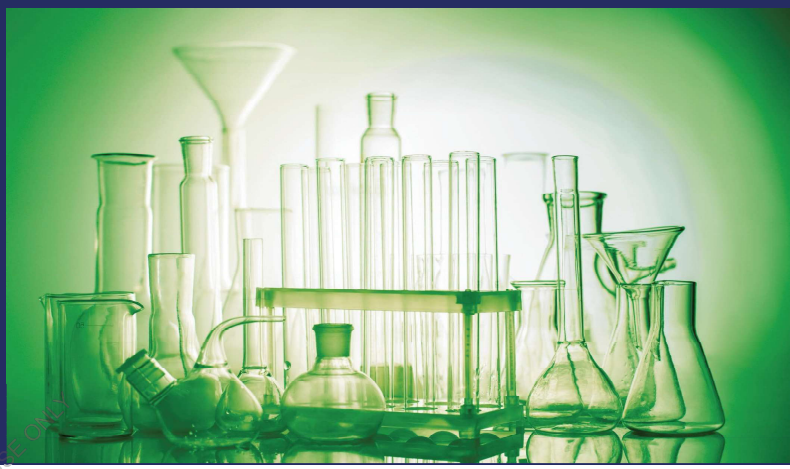

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Microbiology

Phylogenetic Analysis of Vertebrate Hepcidin

1 Sonali A. Tayade; 2Vinod K. Nagale; 3 Prajakta N. BatheAssistant Professor,
Department of Zoology,
1* Arts & Commerce College, Warwat Bakal Dist. Buldana (MS) India
sonali.tayade96@gmail.com

Abstract

The Hepcidin is an iron regulatory hormone. It is a principal regulator of iron absorption and its distribution to tissues. Originally it is identified as an antimicrobial peptide. In present study we chose 48 Vertebrate Species for phylogenetic analysis. Amino acid sequences of Hepcidin from 48 vertebrates were derived from National Center for Biotechnology Information database. Phylogenetic analysis and estimation were performed using MEGA program. The phylogenetic analysis was carried out by using distance matrix method and clustering by UPGMA (Unweighted Pair Group Method with Arithmetic Mean). In this computational study, the phylogenetic tree of Hepcidin has been investigated. Therefore, dendrograms of hepcidin were depicted. From the result of present phylogenetic study of vertebrate hepcidin, it concluded that the amino acid sequences among different vertebrate species shows slight to moderate differences without affecting its functions.

Key words: Hepcidin, MEGA, Phylogeny, Vertebrate

Introduction:

Hepcidin/LEAP-1 is called as iron regulatory hormone. Hepcidin was originally identified as an antimicrobial pepetide. Hepcidin was encoded by HAMP gene in human which has 3 exons. It is translated as 84 aa pre-propeptide in human. The hormone Hepcidin, 25 amino acid peptide, is the principal regulator of iron absorption and distribution to the tissue. It is predominantly synthesized in hepatocytes but it also synthesized in small amount in other cells and tissues such as macrophages, adipocytes and brain. Structure of Hepcidin is somewhat resembles a bent hairpin held together by four disulfide bonds. It is a main regulator of plasma iron concentration.

Iron and erythropoietic activity homeostatically regulate the Hepcidin. Excess amount of iron stimulates the production of hepcidin. Excess amount of hormone prevents further iron loading by blocking dietary iron absorption. When there is iron deficiency amount of hepcidin synthesis was suppressed which allow the more iron absorption from the diet and in this way, it replenishes the iron stores. Hepcidin production is suppressed by the increases erythropoietic activity. Molecular mechanism behind hepcidin regulation by iron and erythropoiesis are areas of intense investigation but are still incompletely understood.

According to the modern evolutionary theory, all organism on earth have descended from the common ancestor, which means that any set of species, extant or extinct are related. This relationship is called asphylogeny and is represented by phylogenetic trees, which graphically represent the evolutionaryhistory related to the species of interest.

In present study we chose 48 Vertebrate Species and performed phylogenetic analysis on hepcidin to explore the study of evolutionary relations among groups of organisms. Establishing a relation between structure, function and evolution of this protein is of paramount importance because it would provide better understanding of further possible mechanisms that the protein involves in.

MATERIAL AND METHOD

Amino acids sequences for the hepcidin protein of 48 vertebrate species were taken from National Center for Biotechnology Information database (http://www.ncbi.nlm.nih.gov). The phylogenetic analysis was carried out by using distance matrix method and clustering by UPGMA (Unweighted Pair Group Method with Arithmetic Mean) by using the Mega program. A phylogenetic tree

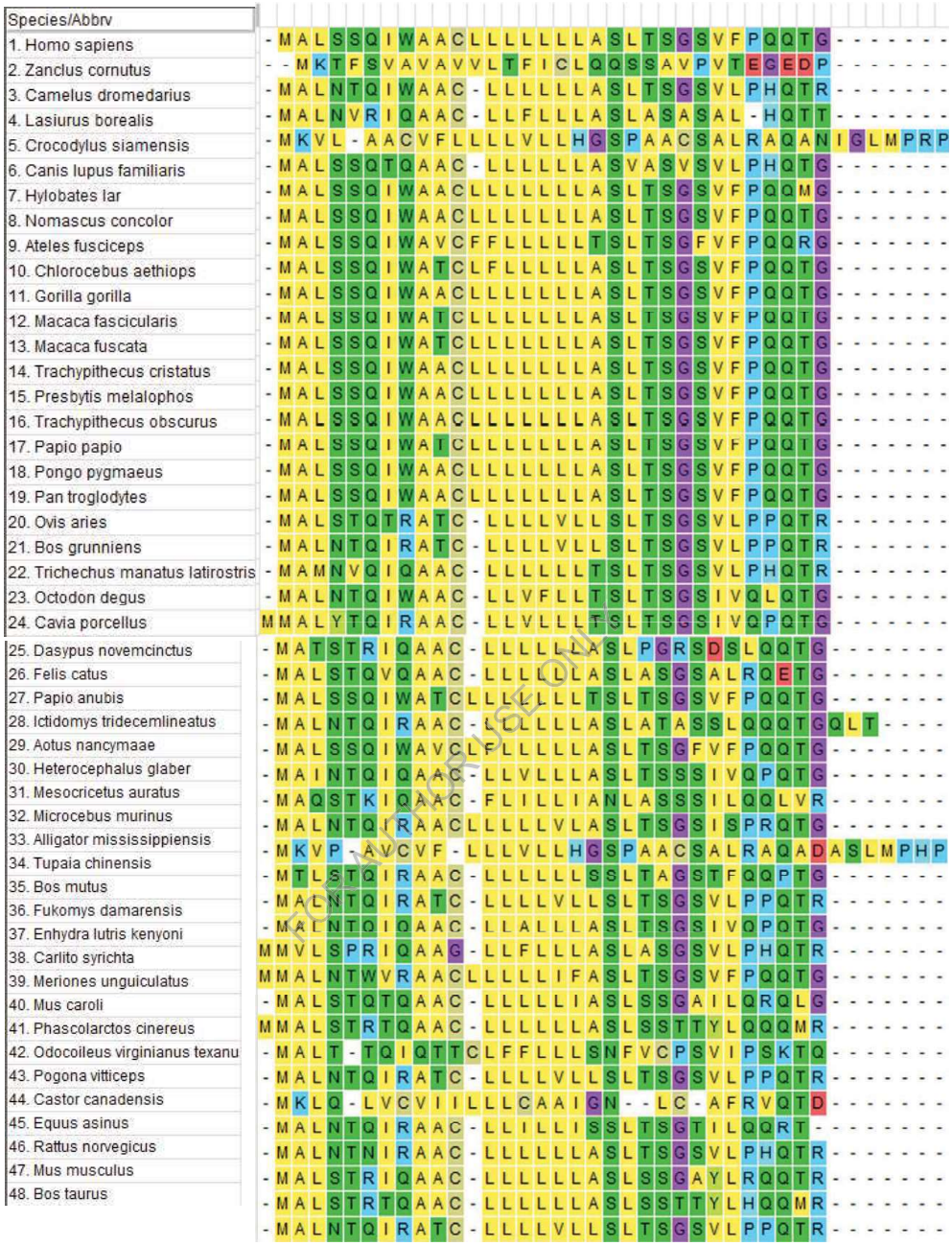
was saved and analyzed. Constructed phylogenetic tree is depicted in figure 2.

RESULTS AND DISCUSSION

The hepcidin protein sequences of 48 vertebrate species were aligned and analyzed. The phylogenetic analysis was carried out by using distance method and clustering by UPGMA (Unweighted Pair Group Method with Arithmetic Mean). A dendrogram of hepcidin drawn by using MEGA7 multiple sequence alignment of the hepcidin proteins is depicted in Figure1 and constructed phylogenetic tree is depicted in Figure 2. The evolutionary history was inferred using the UPGMA method. The optimal tree with the sum of branch length = 6.72748499 is shown (next to the branches). The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 48 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 65 positions in the final dataset.

The multiple sequence alignment of hepcidin is clear that the sequences analyzed in 48 species share the strong similarity among themselves.

The dendrogram based upon the protein sequences of Hepcidn demonstrate the presence of 13 clusters among the 48 different spacies.



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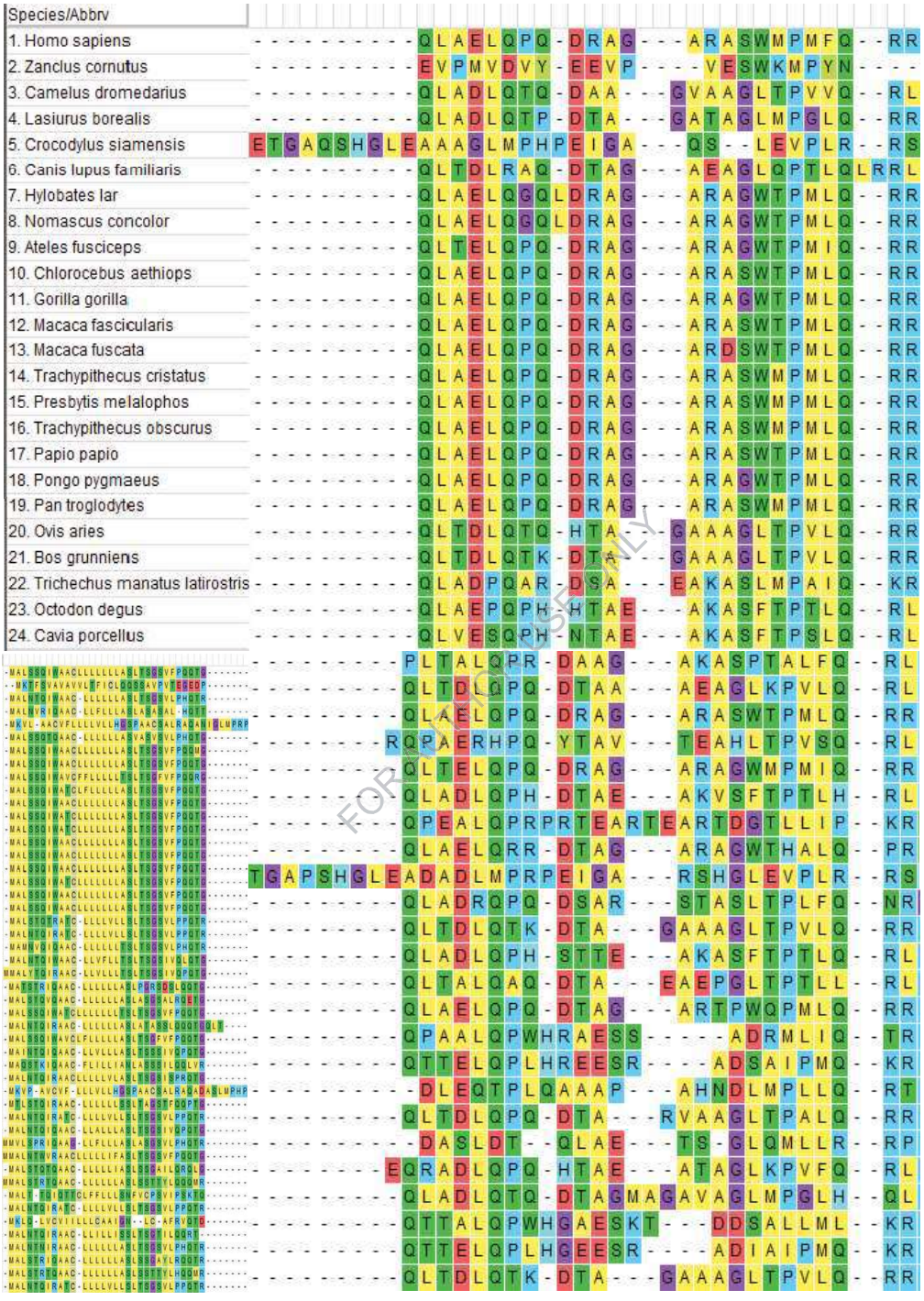

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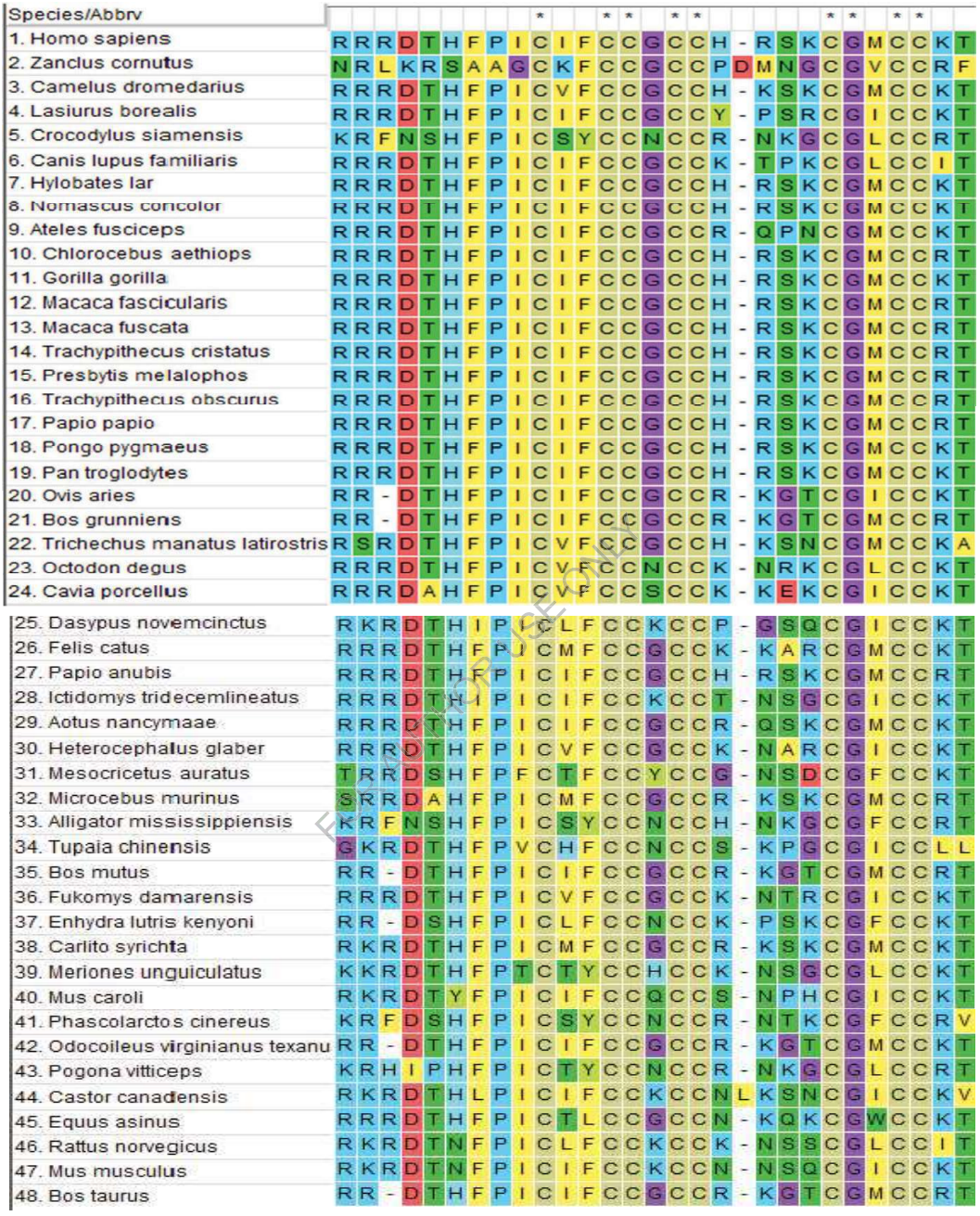

figure 1: multiple sequence alignment of Hepcidn

Phylogenetic Tree:-

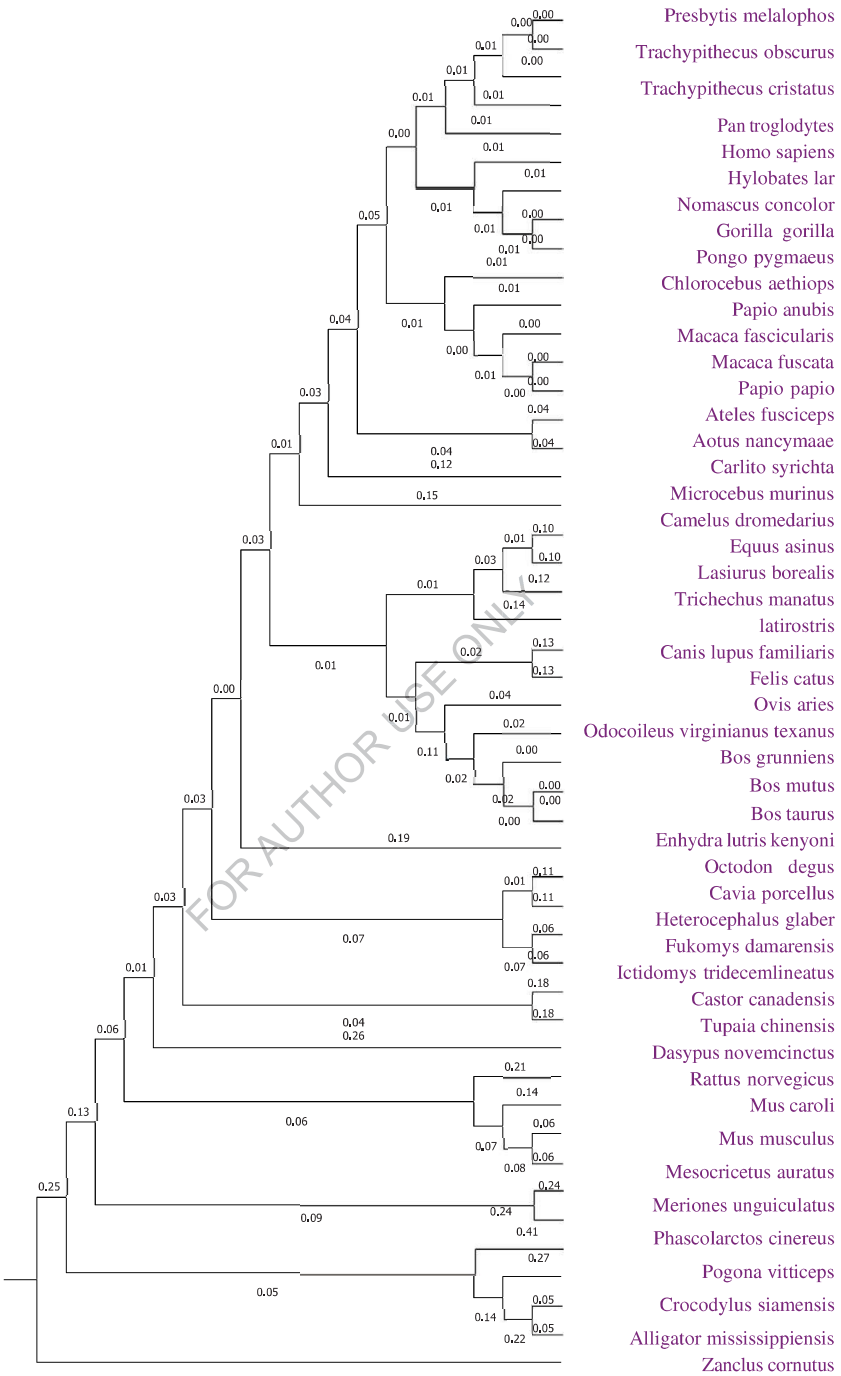

figure 2. phylogenetic tree of hepcidin in vertebrate species

CONCLUSION

From the results and discussion of present phylogenetic analysis study of vertebrate hepcidin, the amino acid sequences among different mammalian species show slight to moderate differences without affecting its function. It also concluded from the phylogenetic tree analysis that, Hepcidin in different mammalians species also have strong to moderate sequence similarities among studied vertebrates.

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