c. Statement of Research Achievements

The Central University of Punjab recognizes the best performance in research on a yearly basis and give research awards to the faculty in various categories including total cumulative impact factor >15 recently updated to >20 and the researchers who secure a grant of >1 crores. Under these Prof. Anjana Munshi has bagged the research award 7 times for the cumulative impact factor category and also securing an extramural grant of >1 crore (DBT). She has also been included in the role of honor of the University.

In addition, the review entitled **"Histone Modifications Dictate Specific Biological Readouts"** was recognized **as JGG Excellent Review Paper** for which she was given a bonus of **RMB 3000 and a medal. (2015).** This paper has been cited 184 times to date.

Munshi, A., Shafi, G., Aliya, N., & Jyothy, A. (2009). Histone modifications dictate specific biological readouts. *Journal of Genetics and Genomics*, *36*(2), 75-88.

The basic unit of chromatin is the nucleosomal core particle, containing 147 bp of DNA that wraps twice around an octamer of core histones. The core histones bear a highly dynamic N-terminal amino acid tail around 20 35 residues in length and rich in basic amino acids. These tails extending from the surface of nucleosome play an important role in folding of nucleosomal arrays into higher order chromatin structure, which plays an important role in eukaryotic gene regulation. The amino terminal tails protruding from the nuclesomes get modified by the addition of small groups such as methyl, acetyl and phosphoryl groups. In this review, we focus on these complex modification patterns and their biological functions. Moreover, these modifications seem to be part of a complex scheme where distinct histone modifications act in a sequential manner or in combination to form a "histone code" read by other proteins to control the structure and/or function of the chromatin fiber. Errors in this histone code may be involved in many human diseases especially cancer, the nature of which could be therapeutically exploited. Increasing evidence suggests that many proteins bear multiple, distinct modifications, and the ability of one modification to antagonize or synergize the deposition of another can have significant biological consequences.

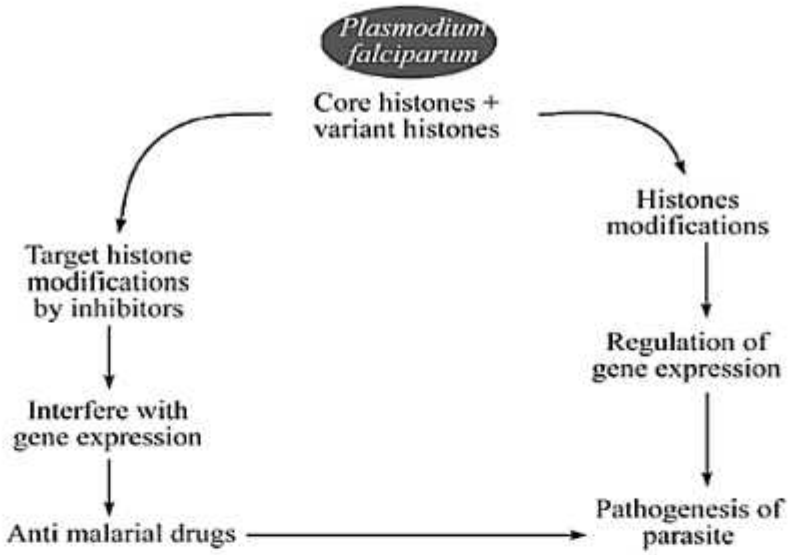

Fig: A schematic representation of how antimalarial drugs can be developed by targeting covalent modifications of the histones in the malarial parasite and thereby affecting the pathogenesis of the parasite.

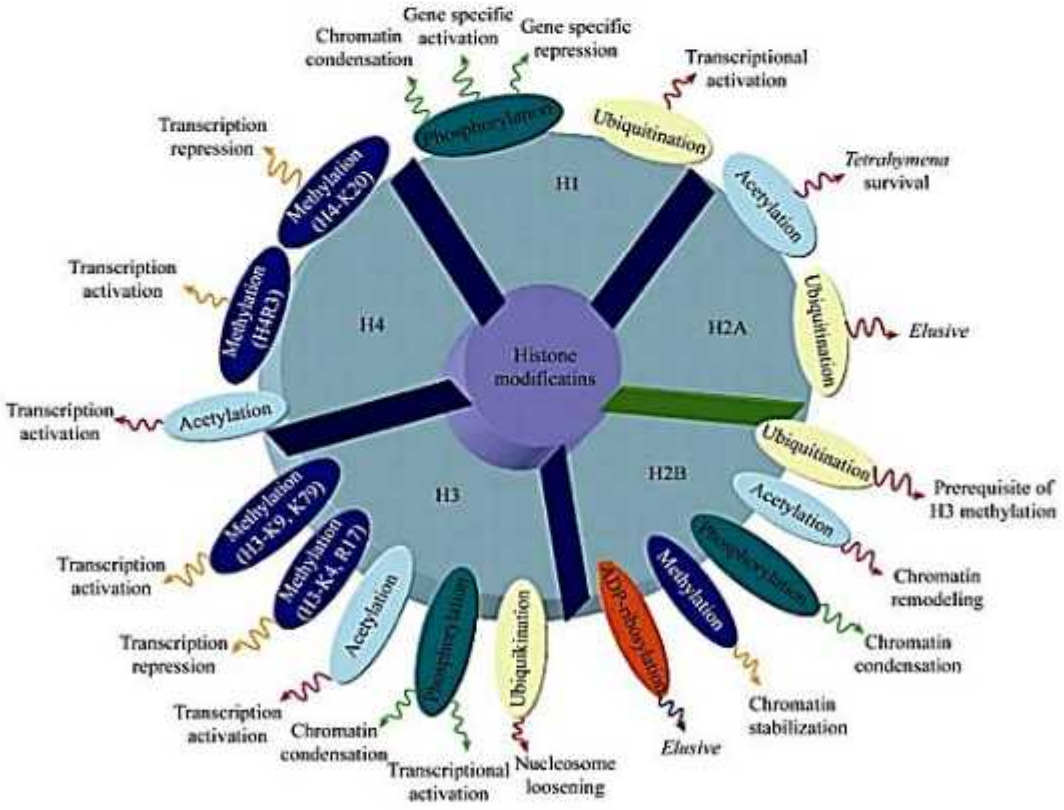

Fig: The pictorial representation of the histone modifications and their biological roles.

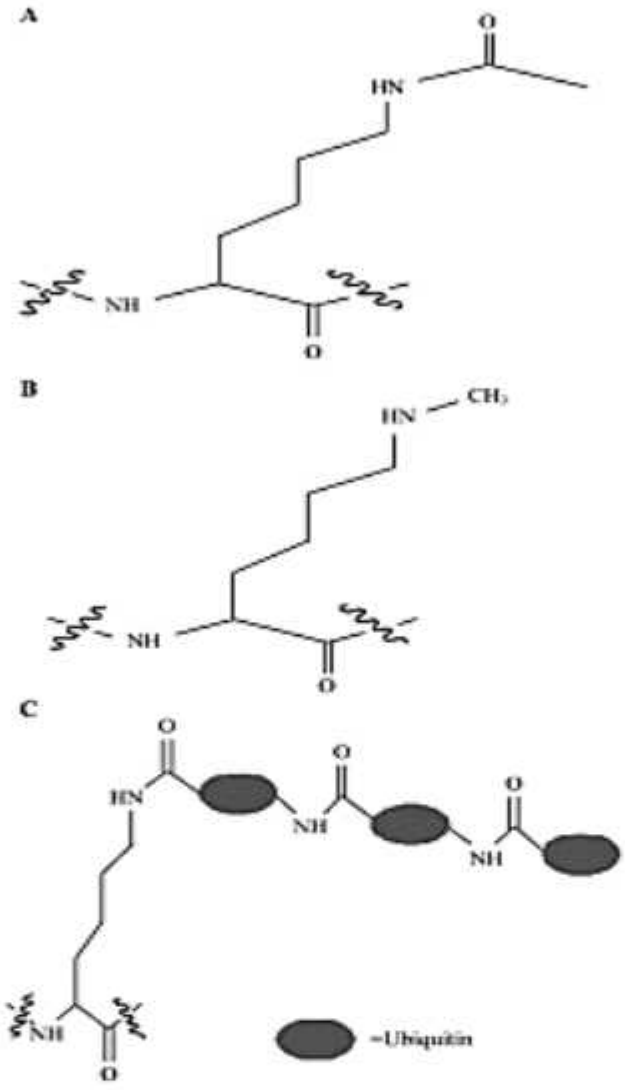

Fig: A typical example of histone acetylation (A), methylation (B) and ubiquitination (C).

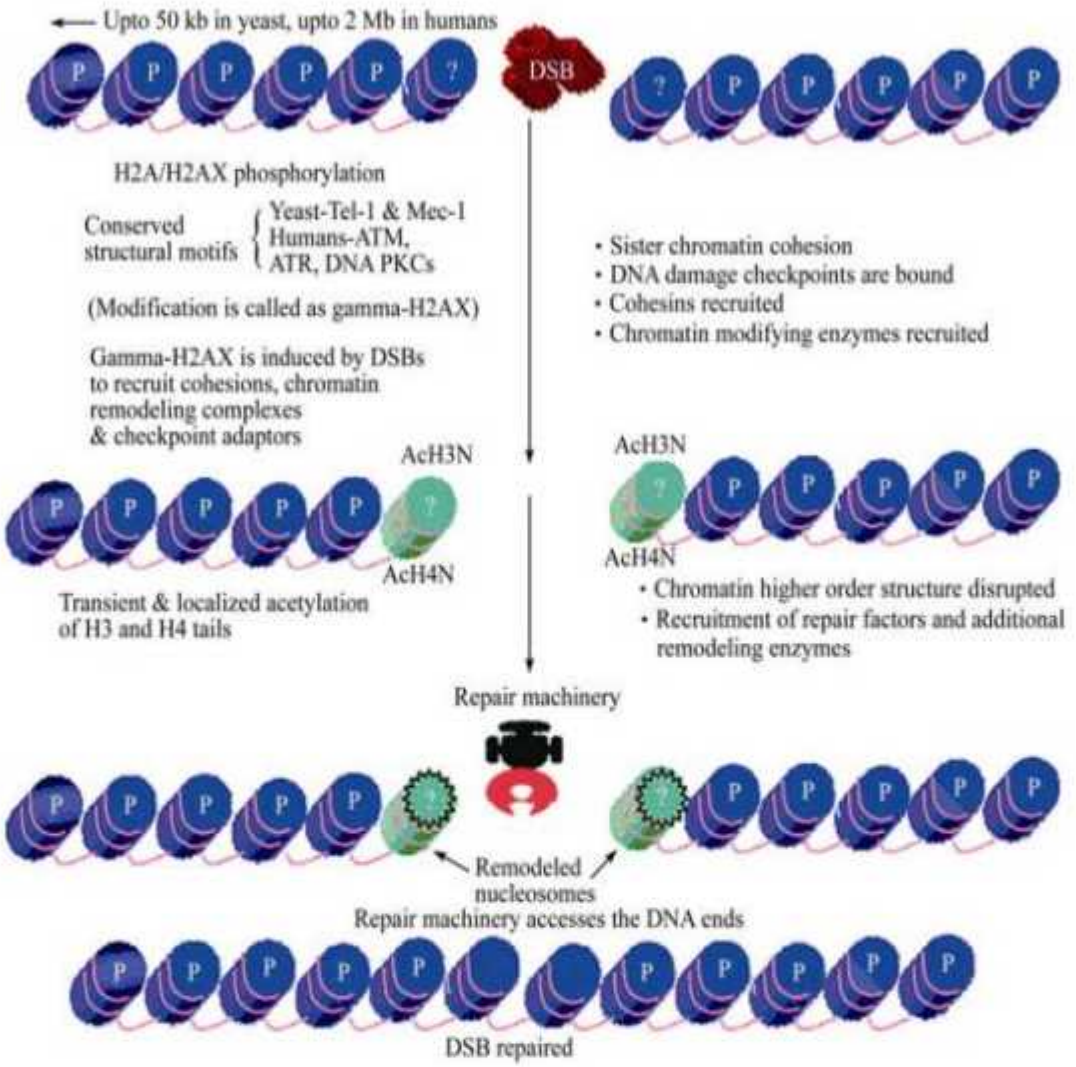

Fig: A simplified scheme of DNA damage-inducible chromatin alterations involved in double-stranded break signaling and repair.

Core histones can be reversibly modified by acetylation, ubiquitination or ADP-ribosylation and these modifications Fig. 4. A schematic representation of how antimalarial drugs can be developed by targeting covalent modifications of the histones in the malarial parasite and thereby affecting the pathogenesis of the parasite. have consequences for gene activation, gene repression, heterochromatization and DNA repair and disease development. In fact, the long-standing idea that the covalent modifications of histones play a role in determining states of gene activity has been confirmed. The enzymes that bring about these modifications do not work alone but exist in multiprotein complexes. Recently, it has been reported that plants are capable of adapting their growth and development to environmental changes, such as light,

temperature, biotic and abiotic stresses by modulation of histone acetylation (Chen and Tian, 2007). So, it is quite evident that histone modifications are implicated in diverse biological processes. However, the precise mechanistic roles have started to come into focus but the picture is not clear yet. The different histone modifications act either in a sequential manner or in combination to form a "histone code", which is read by other proteins to bring about the specific biological events. Workman (2001) is of the opinion that exploitation of the histone code is likely to be new "omics". This could lead to therapeutic exploitation of histone modifications and Workman has termed this as "histonomics" (Workman, 2001). The histone modifying enzymes might turn out to be a rich source of potential targets. Any disease that is modulated by modification of histones can be targeted by interfering with the enzymes responsible for this. Therefore, the drugs that can target these enzymes and thereby treat the diseases like cancer, and some neurological conditions and other disorders might be the future treatment modalities. The better understanding of PTMs shows that many proteins undergo multiple, distinct chemical modifications. These discoveries point to the existence of complex combinatorial networks of PTMs with the potential to modulate different biological outcomes. Sorting out this 'molecular switchboard' of posttranslational events should reveal novel mechanisms for the control of biological systems and promises to open up new avenues for the exploration and manipulation of processes such as gene expression, signal transduction and cell-cycle progression. Understanding the interrelationship between multiple different modifications will be critical for unraveling the combinatorial 'code' of PTMs. The ability of one modification to antagonize or synergize the deposition of another modification can have important biological consequences, and dynamic transitions among various modification states could regulate the spatial and temporal behavior of proteins in general and histones in particular. At present, it remains to be seen what fraction of the histone molecules will experience a given set of modification events.

This has not been included in the current application and in addition to this no award has been received by the applicant on the research achievements included in this application.

Central University of Punjab

CERTIFICATE

13th Foundation Day Celebrations, 2022

Certificate of Commendation

This is to certify that based on the recommendations of the Evaluation Committee Dr. Anjana Munshi won the **Certificate of Commendation** for his/her **Research Publications with Cumulative Impact Factor of more than 15** in the year 2020-21 on February 28, 2022. The award includes Research Grant of Rs. 20,000/-.

Kanwal Pal Singh Mundra
Registrar

Central University of Punjab

CERTIFICATE

14th Foundation Day Celebrations, 2023

Certificate of Commendation

This is to certify that based on the recommendations of the Evaluation Committee Dr. Anjana Munshi won the **Certificate of Commendation for his/her Research Publication(s)** with more than 20 cumulative Impact Factor as corresponding author in the year 2021-22 on February 28, 2023.

The award includes research grant of Rs. 20,000/-.

Prof. (Dr.) B. P. Garg
Registrar (I/c)

Central University of Punjab

CERTIFICATE

14th Foundation Day Celebrations, 2023

Certificate of Commendation

This is to certify that based on the recommendations of the Evaluation Committee *Prof. Anjana Munshi* won the **Certificate of Commendation** for **securing research grant of more than Rs. 1 crore** in the year 2022 on February 28, 2023. The award includes research grant of Rs. 20,000/-.

Prof. (Dr.) B. P. Garg
Registrar (I/c)


JGG
Excellent Review
(2008 - 2012)
Awarded to
Histone Modifications Dictate Specific Biological Readouts
Anjana Munshi, Gowhar Shafi, Nishat Aliya, Akka Jyothy
J. Genet. Genomics, 2009, 36: 75 - 88
Yonghiao Xie
Editor-in-Chief