[1]. **Pandey RP**, Kumar S, Ahmad S, Vibhuti A, Raj VS, Verma AK, Sharma P, Leal E, 2020, Use Chou's 5-steps rule to evaluate protective efficacy induced by antigenic proteins of *Mycobacterium tuberculosis* encapsulated in chitosan nanoparticles, Life Sci**.**,256,117961.

The study focuses on whether antigenic proteins encapsulated in biopolymeric nanoparticles can augment protective efficacy. Chitosan nanoparticles (ChN) were prepared by ionic gelation method and Culture Filtrate Proteins (CFP) - CFP-10 and CFP-21 of *Mycobacterium tuberculosis* (Mtb) were encapsulated in ChN. The binding efficiency of nanoparticles with CFP-10 and CFP-21 proteins was confirmed by UV-Spectrophotometer. The efficacy of nanoparticles-encapsulated antigenic proteins administered intraperitoneal against Mtb aerosol infection was evaluated in Balb/c mice. Protection study was done by bacterial counts [CFU]. CFP-10 and CFP-21 proteins primed cells demonstrated a Th1 bias T cell response in an ex vivo assay. ChN-CFP10 and ChN-CFP21 nanoparticles have both protective and therapeutic potential against Mtb. In the group of mice immunized with CHN-CFP-10 the number of colonies reduced significantly from day 15 to day 60. ChN-CFP-21 showed maximum protection in ChN-CFP-21 immunized mice. ChN-CFP-10 and ChN-CFP-21 clearly showed enhanced protection against Mtb.

[2]. Miglani M, Rain M, Pasha Q, Raj VS, Thinlas T, Mohammad G, Gupta A, **Pandey RP**, Vibhuti A, 2020, Shorter telomere length, higher telomerase activity in association with Tankyrase gene Polymorphism contribute to High-altitude pulmonary edema, Hum Mol Genet**.,** 29,3094-3106.

High-altitude pulmonary edema (HAPE) is a noncardiogenic form of pulmonary edema, which is induced upon exposure to hypobaric hypoxia at high altitude (HA). Hypobaric hypoxia generates reactive oxygen species that may damage telomeres and disturb normal physiological processes. Telomere complex comprises of multiple proteins, of which, tankyrase (TNKS) is actively involved in DNA damage repairs. We hence investigated the association of TNKS and telomeres with HAPE to delineate their potential role at HA. The study was performed in three groups, High-altitude pulmonary edema patients (HAPE-p, n = 200), HAPE-resistant sojourners (HAPE-r, n = 200) and highland permanent healthy residents (HLs, n = 200). Variants of TNKS were genotyped using polymerase chain reaction-restriction fragment length polymorphism. Plasma TNKS level was estimated using enzyme-linked immunosorbent assay, expression of TNKS and relative telomere length were assessed by reverse transcription-quantitative polymerase chain reaction (RT-qPCR), and telomerase activity was assessed by the telomere repeat amplification protocol assay. TNKS poly-ADP ribosylates the telomere-repeat factor (TRF), which is a negative regulator of telomere length. Consequently, TRF expression was also measured by RT-qPCR. The TNKS heterozygotes rs7015700GA were prevalent in HLs compared to the HAPE-p and HAPE-r. The plasma TNKS was significantly decreased in HAPE-p than HAPE-r (P = 0.006). TNKS was upregulated 9.27 folds in HAPE-p (P = 1.01E-06) and downregulated in HLs by 3.3 folds (P = 0.02). The telomere length was shorter in HAPE-p compared to HAPE-r (P = 0.03) and HLs (P = 4.25E-4). The telomerase activity was significantly higher in HAPE-p compared to both HAPE-r (P = 0.01) and HLs (P = 0.001). HAPE-p had the lowest TNKS levels (0.186 ± 0.031 ng/μl) and the highest telomerase activity (0.0268 amoles/μl). The findings of the study indicate the association of TNKS and telomeres with HA adaptation/maladaptation.

[3]. Tyagi R, Srivastava M, Jain P, **Pandey RP**, Asthana S, Kumar D, Raj VS, 2020, Development of potential proteasome inhibitors against *Mycobacterium tuberculosis*, J Biomol Struct Dyn., 19,1-15.

Tuberculosis (TB) has been recently declared as a health emergency because of sporadic increase in Multidrug-resistant Tuberculosis (MDR-TB) problem throughout the world. TB causing bacteria, *Mycobacterium tuberculosis* has become resistant to the first line of treatment along with second line of treatment and drugs, which are accessible to us. Thus, there is an urgent need of identification of key targets and development of potential therapeutic approach(s), which can overcome the *Mycobacterium tuberculosis* complications. In the present study, *Mycobacterium tuberculosis* proteasome has been taken as a potential target as it is one of the key regulatory proteins in *Mycobacterium tuberculosis* propagation. Further, a library of 400 compounds (small molecule) from Medicines for Malaria Venture (MMV) were screened against the target (proteasome) using molecular docking and simulation approach, and selected lead compounds were validated in *in vitro* model. In this study, we have identified two potent small molecules from the MMV Pathogen Box library, MMV019838 and MMV687146 with -9.8 kcal/mol and -8.7 kcal/mol binding energy respectively, which actively interact with the catalytic domain/active domain of *Mycobacterium tuberculosis* proteasome and inhibit the *Mycobacterium tuberculosis* growth in *in vitro* culture. Furthermore, the molecular docking and simulation study of MMV019838 and MMV687146 with proteasome show strong and stable interaction with *Mycobacterium tuberculosis* compared to human proteasome and show no cytotoxicity effect. A better understanding of proteasome inhibition in *Mycobacterium tuberculosis* in *in vitro* and *in vivo* model would eventually allow us to understand the molecular mechanism(s) and discover a novel and potent therapeutic agent against Tuberculosis. Active efflux of drugs mediated by efflux pumps that confer drug resistance is one of the mechanisms developed by bacteria to counter the adverse effects of antibiotics and chemicals. Efflux pump activity was tested for a specific compound MMV019838 which was showing good in silico results than MIC values.

[4]. Chevillard C, Nunes JPS, Frade AF, Almeida RR, **Pandey RP**, Nascimento MS, Kalil J, Cunha-Neto E, 2018, Disease Tolerance and Pathogen Resistance Genes May Underlie *Trypanosoma cruzi* Persistence and Differential Progression to Chagas Disease Cardiomyopathy, Front Immunol., 9,2791.

Chagas disease is caused by infection with the protozoan *Trypanosoma cruzi* and affects over 8 million people worldwide. In spite of a powerful innate and adaptive immune response in acute infection, the parasite evades eradication, leading to a chronic persistent infection with low parasitism. Chronically infected subjects display differential patterns of disease progression. While 30% develop chronic Chagas disease cardiomyopathy (CCC)-a severe inflammatory dilated cardiomyopathy-decades after infection, 60% of the patients remain disease-free, in the asymptomatic/indeterminate (ASY) form, and 10% develop gastrointestinal disease. Infection of genetically deficient mice provided a map of genes relevant for resistance to *T. cruzi* infection, leading to the identification of multiple genes linked to survival to infection. These include pathogen resistance genes (PRG) needed for intracellular parasite destruction, and genes involved in disease tolerance (protection against tissue damage and acute phase death-DTG). All identified

DTGs were found to directly or indirectly inhibit IFN-γ production or Th1 differentiation. We hypothesize that the absolute need for DTG to control potentially lethal IFN-γ PRG activity leads to *T. cruzi* persistence and establishment of chronic infection. IFN-γ production is higher in CCC than ASY patients, and is the most highly expressed cytokine in CCC hearts. Key DTGs that downmodulate IFN-γ, like IL-10, and Ebi3/IL27p28, are higher in ASY patients. Polymorphisms in PRG and DTG are associated with differential disease progression. We thus hypothesize that ASY patients are disease tolerant, while an imbalance of DTG and IFN-γ PRG activity leads to the inflammatory heart damage of CCC.

[5]. Ferreira LRP, Ferreira FM, Laugier L, Cabantous S, Navarro IC, da Silva Cândido D, Rigaud VC, Real JM, Pereira GV, Pereira IR, Ruivo L, **Pandey RP**, Savoia M, Kalil J, Lannes-Vieira J, Nakaya H, Chevillard C, Cunha-Neto E,2017, Integration of miRNA and gene expression profiles suggest a role for miRNAs in the pathobiological processes of acute *Trypanosoma cruzi* infection, Scientific Reports, (Nature),7,17990.

Chagas disease, caused by the parasite Trypanosoma cruzi, is endemic in Latin America. Its acute phase is associated with high parasitism, myocarditis and profound myocardial gene expression changes. A chronic phase ensues where 30% develop severe heart lesions. Mouse models of *T. cruzi* infection have been used to study heart damage in Chagas disease. The aim of this study was to provide an interactome between miRNAs and their targetome in Chagas heart disease by integrating gene and microRNA expression profiling data from hearts of T. cruzi infected mice. Gene expression profiling revealed enrichment in biological processes and pathways associated with immune response and metabolism. Pathways, functional and upstream regulator analysis of the intersections between predicted targets of differentially expressed microRNAs and differentially expressed mRNAs revealed enrichment in biological processes and pathways such as IFNγ, TNFα, NF-kB signaling signatures, CTL-mediated apoptosis, mitochondrial dysfunction, and Nrf2-modulated antioxidative responses. We also observed enrichment in other key heart disease-related processes like myocarditis, fibrosis, hypertrophy and arrhythmia. Our correlation study suggests that miRNAs may be implicated in the pathophysiological processes taking place the hearts of acutely *T. cruzi*-infected mice.

[6]. Malik S, Sadhu S, Elesela S, **Pandey RP**, Chawla AS, Sharma D, Panda L, Rathore D, Ghosh B, Ahuja V, Awasthi A, 2017, Transcription factor Foxo1 is essential for IL-9 induction in T helper cells, Nature Communications, 9,815.

Interleukin 9 (IL-9)-producing helper T (Th9) cells have a crucial function in allergic inflammation, autoimmunity, immunity to extracellular pathogens and anti-tumor immune responses. In addition to Th9, Th2, Th17 and Foxp3$^+$ regulatory T (Treg) cells produce IL-9. A transcription factor that is critical for IL-9 induction in Th2, Th9 and Th17 cells has not been identified. Here we show that the forkhead family transcription factor Foxo1 is required for IL-9 induction in Th9 and Th17 cells. We further show that inhibition of AKT enhances IL-9 induction in Th9 cells while it reciprocally regulates IL-9 and IL-17 in Th17 cells via Foxo1. Mechanistically, Foxo1 binds and transactivates IL-9 and IRF4 promoters in Th9, Th17 and iTreg cells. Furthermore, loss of Foxo1 attenuates IL-9 in mouse and human Th9 and Th17 cells, and ameliorates allergic inflammation in asthma. Our findings thus identify that Foxo1 is essential for

IL-9 induction in Th9 and Th17 cells.The transcription factor Foxo1 can control regulatory T cell and Th1 function. Here the authors show that Foxo1 is also critical for IL-9 production by Th9 cells and other IL-9-producing cells.

[7]. Ahmad S, Khan MS, Akhter F, Khan MS, Khan A, Ashraf JM, **Pandey RP**, Shahab U, 2014, Glycoxidation of biological macromolecules: a critical approach to halt the menace of glycation, Glycobiology,11,979-90.
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[9]. Verma AK, **Pandey RP**, Chanchal A, Siddiqui I, Sharma P,2011, Encapsulation of Antigenic Secretory proteins of Mycobacterium tuberculosis in Biopolymeric Nanoparticles for possible aerosol delivery system, J. Bionanosciences, 5, 88-95.
[10]. Pal-Bhowmick I, **Pandey RP**, Jarori GK, Kar S, Sahal D, 2007, Structural and functional studies on Ribonuclease S, retro S and retro-inverso S peptides, Biochem Biophys Res Commun.,364,608-13.