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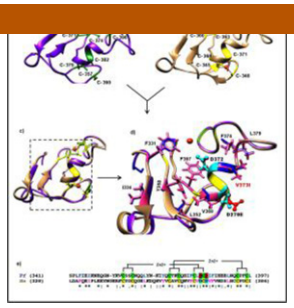

Conclusion: Presence of large number of ZFPs suggests an extensive mechanism of gene regulation in *P. falciparum*. The comprehensive genome wide analysis provides a solid platform for further investigations into the role of zinc finger proteins in development of parasite.

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Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

The level of Profilin and Interleukin-12 in obese patients infected by Toxoplasma gondii: A correlation study between Toxoplasma gondii infection and obesity

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Background: Background. Toxoplasma gondii is one of the microorganisms that causechronic inflammation. It is also thought to be associated with obesity. Profilin T. gondii is an actin cytoskeletonprotein with a molecular weight of 18 kD identified in the membraneof T. gondii. Interleukin-12 is a proinflammatory cytokine arising from the body's immune response to exposure to profilin. Profilin and IL-12 arethought to have a role in the pathomechanism of obesity.

Objective: The objective of the study was to determine the level of Profilin and IL-12 in obese individuals infected by chronic T.gondii and to examine a po

Methods & Materials: Methods. We report an observational analytical study using a cross sectional design. The subjects of the study were 57 obese individuals divided into a positive IgG T. gondii obese group and a negative T. gondiiIgG obese group. Profilin, IL-12, and IgG levels were measuredby ELISA. Differences between the two groups were examined using the independent samples t-test. Bivariate correlations between variables were examined using-Pearson's test or the Mann-Whitney test. A value of $p< 0.05$ was considered statistically significant.

Results: Results. The mean of profilin for the positiveT. gondii-IgG group was higher than that of the negative T. gondii IgG group (97.7 ± 32.6[SD] vs 64.4 ± 25.1 μg/ml; $p = 0{,}002$). The mean of IL-12 for the positiveT. gondii IgG group was higher than that of the

There was no significant correlation between Profilin and IL-12 ($r = 0.056$, $p = 0677$). However there was a positive correlation between Profilin and IgG T. gondii ($r = 0.372$, $p = 0.004$).

Conclusion: Conclusion. The level ofT. gondii Profilin and IL-12 are higher in the positiveT. gondii IgG group than in the negative T.gondii IgG group., but There is no significant correlation between the level of Profilin and Il-12 in obese individuals. Further research is needed to know the patomechanism of T gondii profilin in causing obesity.

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Comparative study between vivax and falciparum malaria in Eastern India: Breaking a myth

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Background: Plasmodium vivax has long been thought to cause benign infection which has been challenged recently. Various studies have pointed towards the rising severity of vivax infections. Till date no longitudinal study has compared vivax and falciparum malaria directly to show the final outcome. Our aim was to explore the manifestations of vivax and falciparum malaria infection and to follow them up and observe the final outcome over a period of 28 days.

Methods & Materials: In this hospital based longitudinal observational study, 89 patients attending a tertiary care hospital in Kolkata, who were positive for *vivax* or *falciparum* malaria (both complicated and uncomplicated)(confirmed by PCR) and who did not receive anti-malarial therapy from outside were consecutively recruited and their clinico-pathological, biochemical parameters and proteomics were analysed. They were followed up for a period of 28 days to observe their outcome after institution of appropriate guideline directed anti-malarial therapy.

Results: Of the 89 patients infected with either vivax or falciparum, 10 were complicated vivax and 12 were complicated falciparum. Jaundice and thrombocytopenia accounted for majority of complicated vivax whereas cerebral malaria, severe anaemia and thrombocytopenia accounted for majority of complicated falciparum infections. One of the vivax infection, complicated by jaundice and severe anaemia and two falciparum infections complicated by jaundice and cerebral malaria resulted in death. All the other patients showed improvement in their clinico-pathological and biochemical parameters over time. There was no statistically significant difference in the parameters over time when compared between complicated vivax and falciparum malaria. (p value>0.05). Of the multitude of protein changes in the serum of malaria patients, serum amyloid associated protein (SAA) and haptoglobin showed a characteristic pattern of change, with SAA being upregulated and Haptoglobin being downregulated; the alterations in

these two protein levels being much higher in the complicated vivax and falciparum infection than uncomplicated infection.

Conclusion: Physicians should give equal importance to vivax as a cause of severe malaria as falciparum, with thrombocytopenia and jaundice being the most common complications. Policy makers should consider giving equal importance to severe vivax as severe falciparum and make amends in their action plan against malaria.

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Assessment of malaria transmission intensity using anti-MSP1$_{-19}$ (Plasmodium vivax) antibody as a serological marker in a previously malaria endemic district in Sri Lanka

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Background: Serological markers have been identified as good indicators of malaria transmission intensity, including in elimination settings. This study assessed the ability of using anti-malaria antibody MSP1$_{-19}$ for vivax malaria to predict changes in transmission intensity in a previously malaria endemic district in Sri Lanka i.e. Kurunegala.

Methods & Materials: Serum was collected from 637 individuals (469 females: 150 males) and was subjected to standard ELISA to determine the sero-positivity for anti-malarial antibody MSP1$_{-19}$ (P.v). Sero-conversion rate (λ) and sero-reversion rate (ρ) were estimated by fitting the optical density values obtained using ELISA to a simple reversible catalytic conversion model.

Results: Age ranged from 1 – 84 years (mean = 43.31 yrs, median = 46 yrs). Study participants were grouped into 4 age groups i.e. 1-5 years, 6-10 years, 11-20 years and >20 years. Previous exposure to malaria was low (18.8%) and the number of individuals with past history was significantly high in 11-20 and >20 years categories when compared to the younger age groups. Over 60% of the population was sero-positive for MSP1$_{-19}$ (P.v.) antibody. Sero-prevalence did not significantly differ between the District Secretariat divisions, nor between males and females. The number of sero-positive individuals below 10 years were significantly lower than the expected counts, while the number of sero-positive individuals were significantly higher than the expected counts in11-20 and >20 year age groups. The association between sero-positivity and malaria exposure was relatively poor and not significant. The age specific sero-prevalence was fitted to a simple reversible catalytic model using maximum likelihood method. The estimated annual sero-conversion for the particular area (λ_2 = 0.011/year) indicated that the transmission intensity is very low in the Kurunegala. This was significantly lower when compared to the sero-conversion rates 30 years ago where the sero-conversion rate (λ_1) = 0.101 and sero-reversion rate (ρ) = 0.030.

Conclusion: The maximum log likelihoods indicated that a reduction in *P. vivax* transmission intensity occurred approximately 30 years ago in Kurunegala district, Sri Lanka.

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In-silico analysis of Chromatin Assembly Factor 1 (CAF-1) family and production of PF3D7_0110700 protein in human malaria parasite Plasmodium falciparum

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Background: Chromatin Assembly Factor 1 (CAF-1) is a histone chaperone that promotes DNA synthesis-coupled chromatin assembly during DNA replication and DNA repair. It is a highly conserved heterotrimeric protein complex basically required for normal S-phase progression and chromatin restoration during DNA repair. Here, we report a comprehensive *In-silico* analysis of PfCAF-1 family and cloning, production and purification of PfCAF-1 gene (PF3D7_0110700).

Methods & Materials: PfCAF-1 genes sequence was retrieved from PlasmoDB and domain architecture was drawn by SMART and Pfam. Orthologs in different organisms were identified by BLASTp program. Multiple sequence alignment of PfCAF-1 was done by ClustalW. PfCAF-1 (PF3D7_0110700) was cloned in two vectors (pTEM11& pTEM30) and expressed in *E. coli* B834 cells. Recombinant protein was purified by Ni-NTA chromatography. Polyclonal antiserum was raised in New Zealand White rabbit.

Results: In the present study, five PfCAF-1 genes were identified. Out of five genes, four posses CAF1C_H4-bd and WD40 domain composition while one contains only WD40 repeats. Largest subunit of CAF-1 complex was found to be missing in *P. falciparum*. Analysis of protein expression profiles revealed three genes to be trophozoite specific at both mRNA and protein level, whereas, other two showed nonlinear relationship between transcriptome and proteome. The modelled 3-D structure of PF3D7_0110700 depicts the conserved H3-H4 binding pocket. However, multiple sequence alignment showed the variation in five residues that are important for histone binding as compared to its human homologue. PF3D7_0110700 was amplified, cloned and expressed in *E. coli* with His tag and GST tag. When induced with 0.25 mM IPTG at 16 °C, we were able to get the protein in soluble form. The recombinant protein was purified by Ni-NTA chromatography. Raised polyclonal antibodies were able to detect native protein.