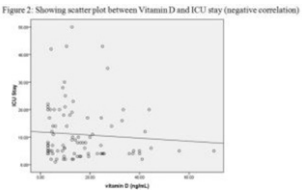

Figure 2. Showing scatter plot between Vitamin D and ICU stay (negative correlation)

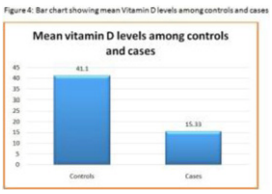

Figure 3. Bar chart showing mean Vitamin D levels among controls and cases

negative correlation. Procalcitonin levels had a positive correlation with SAPS II score, days of Mechanical Ventilation (MV), ICU LOS and mortality. The average vitamin D level in patients of sepsis in our study was 15.38 ng/dl and that of controls was 41.11 ng/dl (fig. 3) and Vit D had no significant correlation with lipid profile.

Conclusion: Deficient levels of vitamin D has a possible role in sepsis. Hence supplementation of vitamin D might have a beneficial role in sepsis management and overall outcome. Further interventional studies with larger sample size and supplementation of vitamin D is required to substantiate the findings.

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Dengue: Mathematical modelling of cytokine levels in the evoultion of severity

P. Jayasundara [1,*], N. Malavige [2], S. Perera [1], S. Jayasinghe [1]

[1] *University of Colombo, Colombo, Sri Lanka*
[2] *University of Sri Jayawardenapura, Sri Lanka, Colombo, Sri Lanka*

Background: Dengue causes considerable morbidity and mortality in Sri Lanka. Immune mediated and cytokine related factors contribute to its evolution from an asymptotic infection to severe forms of dengue. Previous studies have analysed the association of individual cytokines with clinical disease severity. In contrast, we have viewed this evolution to severe dengue as the behaviour of a complex dynamic system. We therefore analysed the combined effect of multiple cytokines that interact dynamically with each other in order to generate a mathematical model to predict the occurrence of severe dengue. We expect this to have predictive value in detecting severe cases and improve outcomes.

Methods & Materials: We analysed data on 11 adult patients with dengue fever (DF) and 25 patients with dengue haemorrhagic fever (DHF) recruited from the Colombo South Teaching Hospital, Sri Lanka. Platelet activating factor (PAF), sphingosine 1- phosphatase (S1P), IL1β, TNFα and IL10 were used as the cytokine parameters for the model. Hierarchical clustering was used to detect factors that correlated with each other. Their interactions were mapped using Fuzzy Logic mechanisms with the combination of Hamacher and OWA operators.

Results: Clustering indicated that S1P and IL1β levels were associated with each other. Since, PAF, IL-10 and TNF-α have shown to associate with severe dengue, they were combined together by allocating these cytokines a higher prominence in the model. Operator value below 0.3 in the overall model correctly predicted development of DHF with 76.6% accuracy. A region of ambiguity was detected in the model for the value range 0.35 to 0.55. However, in six instances patients with DHF indicated operator values above 0.6 and in four instances, patients with DF showed operator values below 0.35. The accuracy of this model in predicting severe dengue was 76.19% at 96 hours from the onset of illness, 75% at 108 hours and 74.07% at 120 hours.

Conclusion: The results show a robust mathematical model that explains the evolution of dengue infection to its serious forms. This model should be further improved by including additional parameters and be validated on other data sets.

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Engineering of measles virus to target cancer cells, an attempt

G. Lal [1,*], M. Rajala [2]

[1] *Jawaharlal Nehru University, New Delhi, New Delhi, India*
[2] *Jawaharlal Nehru University, New Delhi, India*

Background: Regardless of general perception as potentially dangerous pathogens, viruses have been exploited and used as vaccine agents or as carriers for gene therapy. Similar positive effects have been observed in case of cancer patients getting infected with viruses, where infection has resulted in temporary tumor regression. Hence, the development of a recombinant virus that selectively infects and kills cancer cells can be a promising anticancer tool in near future. Here we made an attempt to generate an oncolytic virus using Measles viral genome (Edmonston strain) backbone and to further arm this recombinant virus with non viral genes of known anti-proliferative activity to enhance its antitumor activity.

Methods & Materials: Genes encoding Nucleoprotein (N) and Phosphoprotein (P) of Measles virus were cloned into expression vector pcDNA(3.1+). HEK293 cells were stably transfected with viral N and P constructs to generate a packaging cell line for the recovery of recombinant virus. Gene encoding viral L polymerase (RNA-dependent RNA polymerase) was cloned in pcDNA(3.1) and co-transfected with the Measles viral full-length genome construct (Addgene #58748) in packaging cell line to enable the generation of viral negative sense genome. For arming of the virus, the gene encoding a pro-apoptotic protein BNiP3 of human origin will be inserted into the recombinant Measles viral genome upstream of Matrix gene.