Letters to the Editor

[The Editor is not responsible for the views expressed by the correspondents]

The Clinical Utility of Atypical Lymphocytes, Large Immature Cells, and Rising Hematocrit in Predicting Dengue Fever Severity

SIR, — I am writing to draw attention to the clinical significance of atypical lymphocytes, large immature cells, and rising hematocrit in predicting the severity of Dengue fever — an issue of paramount importance in the field of infectious diseases.

Acute febrile illnesses, particularly Dengue fever, are prevalent from August to November. Dengue, a mosquitoborne viral hemorrhagic fever, poses a potential threat to life, primarily affecting tropical and subtropical regions. The risk of severe Dengue is heightened during secondary infection with a different serotype, where antibodies induced during primary infection facilitate enhanced viral entry into cells, triggering severe manifestations such as vascular leakage, fluid accumulation, thrombocytopenia, and hemorrhagic shock.

Natural History of Dengue Fever: Dengue fever progresses through three stages: the acute febrile phase, the critical phase following defervescence, and the recovery phase. Severe Dengue, marked by complications like vascular leakage and thrombocytopenia, typically arises in the critical phase with an increase in hematocrit and a decline in platelet counts. There is a clinical imperative to devise metrics to predict severe Dengue, aiming to comprehend its underlying pathophysiology.

Prognostic Factors : Several markers have been explored for prognostic purposes, with a focus on atypical lymphocytes, large immature cells, and rising hematocrit. Atypical lymphocytes, as proposed by Claire, *et al* (2019), demonstrate a correlation with Dengue severity. These immune cells, exhibiting anomalies under microscopic examination, could be valuable in assessing the efficacy of the immune response.

Large immature cells, indicating bone marrow response, and rising hematocrit levels, reflective of hemoconcentration, offer insights into the severity of vascular leakage and fluid accumulation during Dengue infection. These factors hold promise as early indicators of disease progression, facilitating timely intervention.

Conclusion : In conclusion, the clinical utility of atypical lymphocytes, large immature cells, and rising hematocrit in predicting Dengue fever severity presents a promising avenue for further research and application in clinical settings. If validated through rigorous research, these metrics could become valuable tools for identifying patients at risk of severe complications during the critical phase. Early recognition and intervention based on these markers may not only improve patient outcomes but also guide resource allocation in Dengue-endemic regions.

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Publication Spree in Medical Colleges. Where does this lead us in long term ?

SIR, — Publication in the medical colleges are on their all-time high pick. Writing on same topic by multiple authors which are making spree to journal for publication. There are several strange bedfellows are existing which influence the medical research publication practices¹. As Banerjee A said very well that, you can bring a horse to water, but can'tmake it drink. We are facing a similar situation. Earlier it was only for promotion in colleges, but now with accreditation and ranking competitions, it is now mandatory for all to do publications in respected journals.

The result is now a mad rush. It has now gone beyond "Publish or perish"^{2,3}. With institutes publishing articles in hundreds not having an appropriate infrastructure, questions must be asked but the genuinity of the articles. With the data generated from these publications, can a policy making body rely? To writing one research paper need a many thing. Start from thought of hypothesis and review literature and take few months to years to complete one research article. Hard work, team work and passionate work can be a fruitful and useful for the field, society and humanity but today in race of quantitative work, the qualitative work going to vanish.

How many path breaking publications have come from these forced publications?Can one enlighten. Forced publications have led to increase in predatory journals, plagiarism etc⁴. Most of the good data comes from a handful of people who are in genuine love for research and work exclusively towards that. Research work planning, performing and collecting data is not enough to complete the publication, Good language and writing skill all required to convey you research work to journals as well as others⁵. Donning multiple hats at one time doesn't do any good. If this madness does not stop, we will be sitting on a pile of truck load of garbage soon.

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Exploring the Potential of Artificial Intelligence in Diagnostic Microbiology

SIR, — Artificial Intelligence (AI) refers to the creation of a computer system capable of performing work that requires human intervention, including learning from data, recognising patterns, making decisions, and solving problems. The notion of AI traces its origins to the 1950s when British scholar A. Turing envisioned the concept that machines could evolve into smart devices, and their intelligence could be tested. John McCarthy and Marvin Minsky introduced the term Artificial Intelligence in the year 1956¹.

Use of AI in diagnostic Microbiology laboratory : Various tasks in diagnostic microbiology can be integrated with AI which includes various activities like analysis of microscopic images, screening of slides for micro-organisms, culture identification and interpretations, antimicrobial susceptibility testing and interpretation along with identification of mechanism responsible for Antimicrobial Resistance (AMR). AI systems can also be useful in molecular laboratories identifying infectious organisms.

There are algorithms used for culture identification such as Chromogenic Media Image Detectionin which positive cultures can be detected with very high specificity and sensitivity. Another algorithm is Growth versus Nogrowth discrimination by colony counting method; this algorithm is best applied on samples that may be received in bulk in the laboratory particularly urine samples for culture examination^{2,3}. Recently, the BD Kiestra[™] TLA system automates the microbiology process, from sample processing, plate transportation and incubation, to digital imaging. A deep Convolutional Neural Network (CNN) is utilized for culture analysis by investigating the urine samples through their images⁴. Colony recognition and application of expert rules; help in an easy and rapid reading of culture plates and better discriminate the negative from positive cultures^{2,3}.

Computer vision technology in AI can assess the screening for Vancomycin-resistant *Enterococcus* (VRE) and Methicillin-resistant *Staphylococcus Aureus* (MRSA). Early detection and timely intervention for such bacterial organisms are crucial for treatment and also to prevent their further spread in hospital environments³.

Microorganisms like acid-fast bacilli and protozoanlike malarial parasites can be identified by using computer vision with high precision. Furthermore, Mathison *et al.* have reported computer vision as an effective AI tool for detecting protozoal parasites and helminthic ova in trichrome-stained stool smears⁵.

Al can be utilized to predict antimicrobial resistance in vitro. Peiffer-Smadja N, *et al* 2020, have shown the application of Al algorithms to predict resistance to aminoglycosides in *Escherichia coli* and *Staphylococcus aureus*⁶.

Matrix-assisted laser desorption ionization-time-of-flight mass spectrometry (MALDI-TOF MS) could be improved by merging it with AI for the identification of microorganisms and the prediction of antimicrobial resistance⁷.

The molecular methods allow us for detailed and very precise study of microorganisms like early identification, mutations and presence of AMR genes etc. Al algorithms are effectively used for the enhancement of results in this study.

Thus, the implementation of AI in diagnostic microbiology enhances precision in microorganism identification, image analysis, and antimicrobial resistance prediction. After rigorous training and validation, AI proves to be cost-effective, utilizing existing laboratory computers for image analysis⁸. While AI partially replaces human involvement, challenges like interpretability of results, transparent models for reliability², scarcity of comprehensive datasets, and robust validation techniques are challenges to be tackled to reveal its complete potential in microbiology.

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