Malaysian J Pathol 2019; 41(3) : 373 – 414

The Annual Scientific Meeting of College of Pathologists, Academy of Medicine of Malaysia: Opportunities and Challenges in Laboratory Medicine, was held at Riverside Majestic Hotel, Kuching, Sarawak on 27-28 June 2019. Abstracts of K. Prathap Memorial Lecture, plenary, symposium and paper (poster) presented are as follows:

K Prathap Memorial Lecture:
Opportunities and challenges for laboratory professional in patient safety

Yasmin Ayob
National Blood Centre & National Heart Institute, Kuala Lumpur, Malaysia

Pathology has been the engine of healthcare system in understanding diseases and in the last few decades in monitoring therapy. However, the approach and technique we use remain very much the same. As we move into the future of the digital age and artificial intelligence, the challenge is should we continue doing the same or do we need to change and reinvent the discipline and the service we provide. To remain relevant, we have to embrace the change and move with the times. The digitization of pathology laboratories makes the specialty more efficient, specimen more reproducible and the work of pathologists less cumbersome. New technologies that produce biomedical "big data" (next generation sequencing, multiparameter / multiplex flow cytometry, high-throughput proteomics and metabolomics, systems biology analysis) have also caused us to rethink the best approach to diagnostics. While these opportunities and challenges seem daunting, we still have to grapple with old challenges of funding and leadership.

Plenary 1:
Challenges in diagnosis of monoclonal gammopathy

Pavai Sthaneshwar
University of Malaya (UM), Kuala Lumpur, Malaysia

The monoclonal gammopathies (MG) are a group of disorders characterised by the proliferation of clonal plasma cells to produce resulting in a detectable abnormality called monoclonal component or M-protein or paraprotein. Direct measurement of the M-protein spike by electrophoresis and immunochemical measurements of specific isotypes or free light chains pairs has provided useful information about the quantity of M-protein. Nonetheless, quantitation of M-protein by electrophoretic method gives suboptimal measurements on small M-proteins. In addition, measurements by electrophoresis of M-proteins migrating in the β- and α-regions are difficult due to the presence of normal serum proteins in those regions. The nephelometric quantitation of immunoglobulins (Igs) is a simple automated method that uses anti-human Ig antigen binding fragments (Fabs) that target the constant region of Ig. The method measures both monoclonal and polyclonal immunoglobulins, and therefore, its diagnostic use for identification of monoclonal proteins is not recommended and is also of no value for biclonal and triclonal gammopathies. Use of the serum free light chain (FLC) immunoassay, has led to improvements in the diagnosis and monitoring of patients with plasma cell dyscrasia and other monoclonal gammopathies. Not all MG secrete excess FLC. Abnormal serum FLC ratios have only been detected in 90–95% of intact Ig multiple myeloma and 40% of MGUS. Since these two patient groups can be easily diagnosed by serum M-proteins by protein electrophoresis, a combination of tests is needed to detect all MGs. Nephelometric methods using antisera specific for Ig heavy and light chain epitopes separately quantitate IgG kappa and IgG lambda, IgA kappa and IgA lambda, and IgM kappa and IgM lambda and may be useful for monitoring monoclonal proteins migrating in the beta fraction. The heavy-light, isotype-specific kappa to lambda ratio has been proposed as a potential monitoring method for IgA or IgM M-proteins migrating in the beta fraction. Although the assay is not sensitive enough to use as a routine screening method for MM, a 97% sensitivity observed in IgA MM and IgA MGUS indicates that almost all IgA MM patients can be monitored by HLC for both detection of the disease clone and quantitation using the IgA HLC assay. A 24-hour urine collection allows the quantitation of both the albumin and M-protein that has been rapidly cleared by the kidneys. The potential broad use of mass spectrometry for MG has been recently demonstrated by the application of matrix assisted laser desorption ionization – time of flight instruments (MALDI-TOF) for detecting monoclonal proteins. The Mayo Clinic group performed a large retrospective study in which patients with an assortment of plasma cell proliferative diseases had SPE, IFE, and FLC as well as urine protein electrophoresis and IFE performed at the time of diagnosis. The study shows patients would have had M-proteins detected by the various tests singly or in combination and if urine assays are removed from the diagnostic panel, there is no decrease in sensitivity. This and other studies have led the IMWG to recommend a panel of serum protein electrophoresis, immunofixation electrophoresis and FLC to screen for a MG; the inclusion of diagnostic urine testing is only recommended if amyloidosis is suspected, which simplifies collection for the patient and workflow for the laboratory and reduces costs as well.

GP-87. The role of Epstein-Barr nuclear antigen 1 (EBNA-1) gene expression in nasopharyngeal carcinoma chromosome rearrangement

Tan Siew Huang[1], Tay Siow Phing[2], Sim Sai Peng[1]
Departments of [1]Paraclinical Sciences & [2]Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Malaysia

Introduction: Nasopharyngeal carcinoma (NPC) is a cancer of the nasopharynx epithelium. Epstein-Barr virus (EBV) is one of the factors that contributes to NPC. However, its direct role is still unclear. The Epstein-Barr virus nuclear antigen 1(EBNA-1) is the only latent protein expressed in all EBV-carrying malignancies. Expression of EBNA-1 was found to result in genomic instability, possibly through reactive oxygen species (ROS) production. ROS is known to induce apoptosis-mediated chromosome breaks within the *AF9* gene. Therefore, we hypothesise that, EBNA-1 expression may induce ROS production and subsequently results in chromosome breaks within the *AF9* gene, which eventually contributes to chromosomal rearrangement. This study focused on *AF9* gene situated at 9p22 which is a common deletion region in NPC. Besides, *AF9* gene is also commonly translocated with the *MLL* gene in secondary leukaemia. The main objective is to evaluate the role of EBNA-1 expression in the production of ROS and subsequently the generation of chromosome breaks within the *AF9* gene. *Materials & Methods:* NP69 was transfected with EBNA-1 gene expression plasmid using Lipofectamine 3000. Western blot was performed to ensure the expression of EBNA-1. Oxidative stress assay was performed using 2',7'-dichlorofluorescein diacetate (DCFH-DA) method. Oxidative stress assay data were statistically analysed with t-test. *Results & Discussion:* Oxidative stress level was significantly higher in NP69 cells transfected with EBNA-1 as compared to the control ($p \leq 0.05$). In addition, chromosome breaks within the *AF9* gene were analysed by inverse polymerase chain reaction (IPCR). It was found that, the cleavage frequency in EBNA-1 transfected cells were significantly higher than the control ($p \leq 0.05$). *Conclusion:* EBNA-1 expression induced oxidative stress and resulted in chromosome breaks within the *AF9* gene.