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

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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

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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.

(TKI) has resulted in its use as frontline therapy. However, emergence of mutation in the *BCR-ABL* kinase domain (KD) impairs IM binding capacity thus contribute to IM resistance. Our study aims to determine the genomic landscape of *BCR-ABL* KD mutations, to determine the prevalence of these mutations in our population and to identify novel, pathological mutations. *Materials & Methods:* A cohort of 86 CML patients with IM resistance was enrolled in this study. RNA extraction was performed using QIAamp RNA Blood Mini Kit (QIAGEN, Germany). Multiplex nested reverse transcriptase PCR was performed for *BCR-ABL* gene amplification. All mutations were characterized using Sanger sequencing. *Results & Discussion: BCR-ABL* KD mutations were observed in 23 patients (27.6%). Fifteen different types of mutations have been identified: Y253H, E255K, T267A, K285I, A287T, M290R, F311I, T315I, F317L, F359V, F359I, F359C, K357T, A399T and E459K. We also discovered two patients with silent mutation at codon 389 and 401. Amongst all mutations identified, Y253H is the most common mutation found in this study. Interestingly, of all the mutations identified, four appeared to be novel mutations namely M290R, K285I, K357T and A287T. *Conclusions:* Mutation analysis of *BCR-ABL* KD is recommended in CML patients with IM-resistance. Knowing the exact mutations responsible for IM resistance will help to select the most suitable TKIs for CML patients. Furthermore, early detection may allow timely treatment intervention to prevent or overcome resistance. Therefore, this test should be offered as diagnostic platform to guide therapy for precision medicine.

HM-30. Cytokines and small molecules expression profiles in patient with acute myeloid leukaemia: A multiplexed immunoassay approach

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Introduction: Acute myeloid leukaemia (AML) is an aggressive and heterogeneous bone marrow malignancy characterized by the accumulation of somatically acquired genetic changes, altering self-renewal, proliferation, and differentiation of hematopoietic progenitor cells. It has been suggested that substantial cytokines deregulation in AML patients could be associated with pathogenesis, disease progression, and survival in AML. The aim of this study was to evaluate plasma level of multiple cytokines and small molecules (analytes) in patients with newly diagnosed AML. This approach allows multi-analytical determination from a single sample thus providing greater insight as diagnostic and prognostic markers of AML. *Materials & Methods:* We used bead-based multiplex immunoassay to simultaneously quantify 32 analytes expression level in 76 AML patients and 38 matched healthy subjects. These archived plasma samples were analyzed on the Luminex platform. The results were expressed in nanograms per litre (ng/L), micrograms per litre (µg/L) and units per millilitre (U/mL). Statistical analysis was performed using SPSS 16.0. *Results & Discussion:* Our results indicated that 15 analytes were found to be significantly deregulated (Cathepsin D, Galectin-3, Ferritin, FAPa, MIAP, SHBG, IFBP3, FGF-2, HGF, IL-8, Leptin, MIF, TGF-α, CA15-3, IL8; Mann-Whitney U-test, $p<0.001$) where 5 of them had never been reported before in AML. No significant difference was found in the levels of other evaluated analytes. *Conclusions:* These significantly altered cytokines and small molecules in AML patients reflecting the pathological state of the disease. Whether these alterations could serve as a prognostic marker for AML is not known. The knowledge gained from multiple cytokine and small molecules analysis could allow better diagnosis and disease management, since cytokines or their receptors may also represent a target for specific anticancer therapy at the molecular level.

HM-31. Correlation of initial blast and minimal residual disease with biological characteristics of acute leukaemia

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Introduction: Acute leukaemias (AL) are highly malignant neoplasms and responsible for a large number of haemopoietic cancer-related deaths. Prognosis of AL is dependent upon various biological and clinical factors. There is growing body of evidence that supports minimal residual disease (MRD) values and initial blast count (IBC) at diagnosis in predicting treatment outcome and relapse risk in AL. However, there is scarcity of data on the relationship of IBC and MRD with biological characteristics [gender, age groups, AL types and immunophenotypic aberrancy (IA)]. Therefore, this study was designed to determine the correlation of IBC, MRD (post-induction chemotherapy) and biological characteristics of AL. *Materials & Methods:* This was a retrospective study involving all the 493 AL patients diagnosed at the Flow Cytometry Laboratory of UNIMAS from 2006 to 2014. *Results & Discussion:* The AL patients comprised 44.2% children and 55.8% adults with a male predominance (55.6%). The mean ages for children and adults were 5 and 45 years old, respectively. There were more AML (55.2%) than ALL (44.8%) cases. B-ALL and AML-M2 predominated the AL subtypes in children and adults, respectively. ALL patients showed significantly higher IBC (p£0.001) and MRD (p£0.001) levels than AML. Significantly higher IBC (p£0.001) and lower MRD (p=0.014) levels were observed in children, indicating a better response to treatment, as compared to adults. However, there was no significant difference in IBC and MRD found between genders. In addition, expression of IA was more common in AML than ALL (p=0.037). *Conclusions:* To the best of our knowledge, this was the first report of a significant negative correlation between IBC and MRD (r=-0.24, p=0.001), whereas IBC and MRD did not correlate significantly with IA. As MRD studies were more routinely performed in ALL, these findings reflected the successful management of ALL patients in our local clinical settings. Future studies should be embarked to further assess the value of IBC, MRD and IA in prognosticating the disease outcome among the local AL patients.