JOURNAL-BASED LEARNING EXERCISES

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DEADLINE WEDNESDAY 6 JANUARY 2021

A comparison of the HAIN Genotype CM reverse hybridisation assay with the Bruker MicroFlex LT MALDI-TOF mass spectrometer for identification of clinically relevant mycobacterial species.
O'Connor JA, O'Reilly B, Corcoran GD, O'Mahony J, Lucey B. *Br J Biomed Sci* 2020; **77** (3): 152–5. doi: 10.1080/09674845.2020.1732639. Assessment No: 090120

01	*Mycobacterium avium* can be isolated from immunocompromised patients.	11	According to the authors, Genotype CM does not require mycobacteria to be pure.
02	The authors of this study concluded that MALDI-TOF MS could be a potential replacement for the HAIN assay for *Mycobacterium tuberculosis* complex but not for non-tuberculous mycobacteria.	12	It is felt that MALDI-TOF MS may offer an appropriate replacement for traditional methods used in a routine diagnostic mycobacterial laboratory.
03	The authors quote Bruker as stating that a log-score value of 2.0 or more is considered a high-confidence identification.	13	Of the three isolates that failed to identify by MALDI-TOF, all had log-scores of >1.7.
04	According to the authors, MALDI-TOF MS does not require mycobacteria to be pure.	14	All samples used in the study came from either patients or UKNEQAS.
05	Few non-tuberculosis species are considered environmental contaminants.	15	In the study, only 45% of all *Mycobacterium tuberculosis* complex isolates had a log-score of greater than 2.0.
06	The authors conclude that MALDI-TOF offers advantages over Genotype CM if high throughput of samples offsets the initial capital cost.	16	The authors quote previous research as showing that MALDI-TOF MS was superior in identifying mycobacteria from primary liquid culture as compared to a solid medium subculture.
07	In the study, all MTB complex isolates identified by Genotype CM were also identified as such by MALDI-TOF MS.	17	The Genotype CM system is unable to identify *M. xenopi*.
08	One MTC isolate that had been identified by the HAIN system was a slow-growing isolate that MALDI-TOF MS failed to identify.	18	It is recognised that rapid identification of mycobacteria facilitates early therapeutic measures.
09	The authors suggest that when choosing an empiric therapy for *M. chelonae* knowing the species is critical.	19	In the study, all *M. abscessus* isolates identified by Genotype CM were also identified as such by MALDI-TOF MS.
10	The *Mycobacterium* genus encompasses >170 species.	20	The MTC isolates used in the study included 66 *M. tuberculosis* strains.

REFLECTIVE LEARNING

01	Within your own laboratory, reflect on the methodology presently used to identify mycobacteria and whether on balance it represents the best approach.

DEADLINE WEDNESDAY 6 JANUARY 2021

Digital morphology analyzers in hematology: ICSH review and recommendations.
Kratz A, Lee SH, Zini G, Riedl JA, Hur M, Machin S. International Council for Standardization in Haematology. *Int J Lab Hematol* 2019; **41** (4): 437–47. doi: 10.1111/ijlh.13042. Assessment No: 090420

01	It is easy to access secondary consultations when using manual microscopy methods.	11	According to this article, the DI-60 is a fully integrated system involving two Sysmex XT analysers, the SP-10 Sysmex slide making/staining device and a CellaVision instrument.
02	The Diffmaster Octavia was the predecessor to the current CellaVision models.	12	WBC classification by the DI-60 was considered acceptable for normal and abnormal samples, although user verification improved performance.
03	According to Kratz's review of the DM96 at the preclassification stage, eosinophils were 29.3% less accurately identified than neutrophils.	13	For malaria diagnosis, the DI-60 has the potential to become the new gold standard.
04	According to Rollins-Raval, the DM96 had difficulty in reliably identifying immature granulocytes, plasma cells and blasts.	14	Depending on patient population, 80–90% of cases using CellaVision analysis do not require manual microscopic review.
05	Eilertsen's 2017 study of blast cell verification using the DM96 demonstrated significant differences in blast cell counts pre- and re-classification.	15	Average review times on the Nextslide system were 8.87 minutes shorter than for manual microscopy.
06	Using the DM96 ARBCA for shistocyte counting, Hervent reported a very high specificity but poor sensitivity.	16	Correlation coefficients were higher for basophils, atypical lymphocytes and bands using the Nextslide compared with the same cells using the CellaVision.
07	Direct comparisons of studies of the ARBCA can be difficult as red cell cut-off values can be manually adjusted.	17	Roche cobas M511 high-magnification module utilises a dry 50x lens for morphologic assessment.
08	In their review of the DM96, Guliati *et al.* found the sensitivity of detection of platelet clumps varied from 61.6 ± 21.2% depending upon whether the user looked for: (a) platelet clumps or fibrin strands in the WBC display only, or (b) searched all the WBC and PLT screens.	18	Agreement between the Roche cobas M511, manual microscopy and the Sysmex XN was good.
09	When examining body fluids using the DM96, Riedl *et al.* reported the correlation coefficient for post-classification accuracy of CSF analysis was 0.83–0.98 and for other fluids was 0.92–0.99.	19	Yagi and Gilbertson have published six recommendations to standardise digital image analysis.
10	According to the evidence presented in this article, the use of the DM96 for the identification of paediatric blasts is contentious.	20	For laboratories planning on introducing digital imaging, at least 100 slides covering all cell types, including abnormal cells, should be evaluated.

REFLECTIVE LEARNING

01	Using section 2.7.1 of this article as a starting point, critically discuss the practice-based opportunities that arise from research utilising digital morphology analysers.	02	Evaluate the use of digital morphology analysers in the education and training of biomedical scientists.