therapies remain a distant prospect. Digital approaches to care, and self-management, show considerable promise but integrating such approaches into a traditional healthcare system has proven challenging.

The prognosis of heart failure has improved dramatically for many patients over the past 30 years –but the residual risk of mortality and urgent hospitalisation means that there is much work to be done.

REFERENCES

1. Conrad N, Judge A, Tran J, *et al*. Temporal trends and patterns in heart failure incidence: a population-based study of 4 million individuals. *Lancet* 2018;**391**:572–580.
2. Chronic heart failure in adults: diagnosis and management (NG106). National Institute for Health and Care Excellence, September 2018. Available at: https://www.nice.org.uk/guidance/ng106
3. Failure to Function: a review of the care received by patients who died in hospital following an admission with acute heart failure. National Confidential Enquiry into Perioperative Deaths, November 2019. Available at: https://www.ncepod.org.uk/2018report2/AHF%20full%20report.pdf

4 ADVANCES IN PALLIATIVE CARE

Ros Taylor. *Former Clinical Director at Hospice UK*

10.1136/postgradmedj-2019-FPM.4

Palliative care is at a pivotal point in its trajectory. For the last 50 years there has been a focus on service development for the new specialty, the safer use of opioids and obtaining the evidence that palliative care makes a difference, the earlier the better.

However the next 50 years will be a massive challenge, but also an opportunity. There will be a shortage of all physicians, not just palliative physicians and this is a perfect storm with our increased longevity, frailty and comorbidities.

The lecture will focus on potential solutions, drawing on global innovation and imagination. Having braver conversations about the future is all very well but we also need practical options to improve the care of dying people in all settings not just five-star hospices, and we need to be less risk-averse about supporting patient and family goals of care in a culture dominated by compliance rather than comfort and care!

5 NEW GUIDELINES FOR MANAGING TUBERCULOSIS

Paul Nunn. *Director, Global Infectious Diseases Consulting Ltd*

10.1136/postgradmedj-2019-FPM.5

In 2018, tuberculosis (TB) was still among the top 10 leading causes of death, and the leading infectious agent, above HIV/AIDS. An estimated 10 million cases occurred in 2018, with 1.2 million deaths in people uninfected with HIV, and another 250,000 cases of HIV-associated TB. Among all TB cases, 8–6% were HIV infected; 57% were men, 32% women and 11% children (<15 years). About 500,000 cases of rifampicin resistant RR-TB also occurred. Between 2000 and 2018 TB incidence fell on average about 1.6% annually, and 2% between 2017 and 2018. The new global control targets will be presented and recent changes to guidelines positioned in this new scenario.

Guidelines for TB management from the UK, US and WHO were reviewed for recent changes. NICE's 2016 guidance not to screen contacts of non-pulmonary TB met with widespread criticism, but has recently been supported by a cost-effectiveness analysis. A 2019 meta-analysis of the seminal 2014 studies, OFLOTUB, ReMOX and RIFAQUIN trials showed that while none of those trials showed non-inferiority of a four month fluoroquinolone-containing regimen in all patients, those with low smear grade or no cavitation may be treated with 4-month rifampicin containing regimens. ATS/CDC/IDSA guidelines reflect this, but had not been accepted in the UK by October 2019. WHO has recently recommended the use of new agents in the treatment of rifampicin and multi-drug resistant TB. The rapidly-evolving picture of treatment recommendations for MDR-TB will be explained.

6 TRANSLATING GENOMICS FOR CLINICAL BENEFIT

[1,2]Mark Caulfield. [1]*Chief Executive and Chief Scientific Officer, Genomics UK*; [2]*Co-Director and Professor of Clinical Pharmacology, William Harvey Research Institute, Barts and the London*

10.1136/postgradmedj-2019-FPM.6

The UK 100,000 Genomes Project has focussed on transforming genomic medicine in the National Health Service using whole genome sequencing in rare disease, cancer and infection. Genomics England partnering with the NHS established 13 Genomic Medicine Centres, the NHS whole genome sequencing centre and the Genomics England Clinical Interpretation Partnership (3337 researchers from 24 countries). We sequenced the 100,000th genome on the 5th December 2019 and completed an initial analysis for participants in July 2019. Alongside these genomes we have assembled a longitudinal life course dataset for research and diagnosis including 2.6 billion clinical data points for the 3000 plus researchers to work on to drive up the value of the genomes for direct healthcare. In parallel we have partnered the NHS to establish one of the world's most advanced Genomic Medicine Service where we re-evaluated 300,000 genomic tests and upgraded 25% of tests to newer technologies with an annual review. The Department of Health have announced the ambition to undertake 5 million genome analyses over the next 5 years focused on new areas tractable to health gain.

Poster presenter abstracts

7 ASSESSING MELANOMA BRAF STATUS THROUGH DDPCR OF CFDNA

Lauren Passy, Shobha Silva, Ian Brock, Greg Wells, Angela Cox, Sarah Danson. *University of Sheffield*

10.1136/postgradmedj-2019-FPM.7

Introduction Treatment of recurrent and metastatic melanoma has been revolutionised by targeted therapy. Inhibitors of mutant BRAF are a systemic treatment offered for patients with stage III/IV melanoma who are known to carry a mutation in BRAF. Currently patients' BRAF mutation status is assessed through molecular analysis of tissue specimens.

Cell-free DNA (cfDNA) released from tumours can be used to non-invasively detect active disease and predict survival in

melanoma. cfDNA also provides a method for detecting BRAF mutations. This project aimed to ascertain BRAF mutation status in cfDNA through digital droplet PCR (ddPCR) of plasma samples from patients with melanoma. We aimed to assess the relationship between cfDNA BRAF positivity and disease relapse and progression.

Methods Plasma from 100 patients with active or recently resected melanoma was obtained during previous work. 85 samples had cfDNA extracted. Tissue BRAF status was known for 57 samples. cfDNA was extracted from 1–2 ml plasma with the QIAamp circulating nucleic acid kit (QIAGEN®) following manufacturer protocol, eluting cfDNA into 100µL. cfDNA was quantified with SYBR green quantitative real-time PCR (Life Technologies), based on an 87bp GAPDH gene amplicon. ddPCR™ was performed using the Bio-Rad QX200 Droplet Generator™ and Droplet Reader as per manufacturer protocol. Analysis was performed with Bio-Rad QuantaSoft Version 1.7.4.

Results Median yield of cfDNA extracted from 85 samples was 1.97 ng/ml when eluted into 100µL. This was well-correlated with previous cfDNA extraction yields from this sample set (Pearson's $r=0.6687$, $p<0.0005$), where a 200µL elution volume was used. 74 samples yielded >10,000 droplets and were included for analysis. 12 samples contained BRAF mutant positive droplets. A 74% concordance rate between tissue BRAF mutation status and the presence/absence of cfDNA BRAF mutant positive droplets was found. 7/18 tissue BRAF mutant samples contained BRAF mutant droplets, in comparison to 2/32 tissue BRAF wild-type samples. The presence of BRAF mutant positive droplets was significantly different between the tissue BRAF mutant and tissue BRAF wild-type groups ($\chi 2$ 8.3145, $p=0.004$).

Fractional abundance of BRAF mutant droplets in the samples containing mutant droplets ranged from 0.07–0.74%. When comparing BRAF mutant droplet-containing samples and samples without BRAF mutant droplets, there was no significant difference in rate of relapse ($\chi 2$ 0.0948, $p=0.758$), nor mortality rate ($\chi 2$ 3.3959, $p=0.654$).

Conclusion cfDNA provides a non-invasive snapshot of the tumour genome and any potential therapeutic targets held within. This work demonstrates that a very low volume of cfDNA can be used to detect BRAF mutations in patients with melanoma through ddPCR.

Previous work assessing BRAF status in cfDNA has used larger volumes of cfDNA. Though our concordance rates are comparable with other studies, it is possible that using a smaller amount of cfDNA in our ddPCR has resulted in some samples being below the limit of detection for ddPCR.

Longitudinal study is warranted to monitor cfDNA BRAF status and mutant fractional abundance, and whether this better correlates with relapse of disease and disease progression.

8 GENERAL SURGICAL FOUNDATION DOCTOR OPTIMISATION OF DAILY PRACTICE

[1]Emmanuel Feldano, [2]Ben Ramasubbu. [1]*NHS Grampian*; [2]*NHS Aryshire and Arran*

10.1136/postgradmedj-2019-FPM.8

Introduction Traditionally the role of a surgical foundation year 1 (FY1s) doctors consisted of long working hours, multiple on call shifts and little to rest however, the introduction of European working time directive now means that FY1s are constricted to 48 hours per week on average and various other regulations that junior doctors should abide by yet the same quantity of daily tasks remains the same. In this study we looked at the difficulties FY1s now face in their daily working day and if some of these issues could be resolved by implementing some structural changes.

Methods The study was conducted in three cycles, each lasting five days (Monday to Friday). Cycle 1 included shadowing of Surgical FY1s on wards for five consecutive days observing daily routine (arrival, lunch and departure time), task completion, communication and handovers. Following this multiple interventions were made to the structure of their daily practice to improve productivity and performance. These improvements were measured in cycle 2 (as the new model was scaffolded into place) and cycle 3 (strictly observed).

Results In cycle 1 we observed that 100% of F1s arrived to work on time, there was no set times for lunch and all of the FY1s lunches were interrupted. There was no structure for handovers and 100% of F1s stayed at work beyond there contracted hours. In second cycle, 100% of F1s had lunch between the hours of 12pm-1PM on 3/5 days and 75% on the remaining two days. 75% of F1s had uninterrupted lunches on all 5 days. Morning and afternoon handovers were completed every day. In cycle 3 the results remained as high. There was no significant difference in number of tasks between week 1, 2 and 3.

Conclusion Through the implementation of daily structure and other interventions involving the multidisciplinary team we improved the quality of F1s working day and increased the efficiency of service delivered on the surgical ward.

9 LOW FIDELITY SIMULATION IN A HIGH FIDELITY WORLD

A Scott, A Gartner. *Frimley Park Hospital NHS Foundation Trust*

10.1136/postgradmedj-2019-FPM.9

Introduction All aspects of medical training have experienced an exponential acceleration in the application of technology for learning needs.[1] Research promotes the use of high fidelity models and ever more complex training methods with organisations keen to adopt and implement new technology. Models are utilised to minimise potential risks to patients through bedside learning and refine established technique.[2] Simulation practice can also be used to develop non-technical skills pertinent to safe clinical practice.[2–4] Simulation training can be employed from early stages of undergraduate education through to use in professional postgraduate exams giving a large scope of use in a multiplicity of environments.[1 4 5]

Methods Forty Foundation Year 1 Doctors were taught clinical skills utilising Low fidelity part task training models. Four clinical skills were selected from pre-determined postgraduate curricula. Self assessment pre and post procedure were recorded with qualitative feedback sought as a secondary measure.

Results Global increases are seen across 4 sampled clinical skills. Participants self-reported increased confidence and competence. A high value was placed upon trainees perceived value in training.

Conclusion Fidelity has been shown to play an integral role in simulation.[4] The authors conclude that simple part task