Emerging from the Pandemic:

An outbreak of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was detected in mainland China in December of 2019 and has swept the world since then. Every continent in the world has been affected by Covid-19, this highly contagious disease caused by SARS-CoV-2. With over 100 million confirmed cases of Covid-19, including 2.5 million deaths, in over 200 countries worldwide as reported by the World Health Organization (1).

The pandemic has been challenging for countries and societies on various levels and aspects, representing an extraordinary medical challenge with massive economic and societal impacts. Despite these numerous challenges, it has led to extraordinary scientific breakthroughs and created collaborations between academics, universities and organizations to a level that has not been seen before. It forced the development of necessary infrastructure and behavioural change that would have taken a decade to achieve at any other time, introducing the citizenary to the concepts of self test and remote use of diagnostics. People have created unprecedented unions of central and localised lab capacity. The pandemic led to revolutionisation of the national capacity for lateral flow manufacture. It led to the creation of a validation framework for a wide range of point-of-care and self-test systems. We have disintermediated clinicians and created logistics chains to deliver mail-order diagnostics, and report data via smartphones. We have in short 'democratised' diagnostics.

Covid-19 has shown the combined role of the citizen and the diagnostic in managing public health, but has a deeper impact on how personal health will be tracked, and improved for the future. There is no Holy Grail solution but the availability of high street, mail-order and digitally-enabled diagnostics coupled with a disrupted post-pandemic establishment, lab capacity, skills and a flow of venture capital into the sector give the UK momentum and purpose to create new market, muscle and meaning for the industry over the next 20 years.

The collaboration and infrastructural changes brought about by the pandemic can also be seen in the use of next generation sequencing and genomic surveillance. On January 10, 2020 the first SARS-CoV-2 genome sequence was made widely available. This allowed the classification of the virus as a coronavirus and provided fine-scale detail on gene content and organisation (2).

Access to SARS-CoV-2 sequence data has since influenced vaccine design by providing a basis for the selection of genes as vaccine targets, and has supported the development of molecular diagnostic tests for COVID-19. SARS-CoV-2 genome sequences have been generated and shared at an unprecedented rate, with over 500,000 sequences available via the *global initiative on sharing avian flu data* (GISAID), and almost 300,000 available in the UK via MRC-CLIMB portal generated by the COVID-19 Genomics UK (COG-UK) Consortium, permitting genomic surveillance of the unfolding pandemic (3).

Genomic surveillance and the use of pathogen genomes on this scale to track the spread of the virus internationally, study local outbreaks (e.g. care homes and hospitals) and inform public health policy have signified a new age in virus genomic investigations (4). In addition to epidemiological understanding, sequencing has enabled the recent identification of emerging SARS-CoV-2 variants and the characterisation of sets of mutations potentially linked to changes in viral properties that might have biological and/or clinical significance. This includes changes to viral transmissibility, disease severity, interactions with the human immune system, and how the performance of diagnostic tests could be impacted. Genome sequencing is set to become an on-going contributor to our efforts to control the pandemic.

References:

- 1) WHO Coronavirus Disease (COVID-19) Dashboard | WHO Coronavirus Disease (COVID-19) Dashboard (02.03.2021)
- 2) Holmes E. Initial genome release of novel coronavirus 2020 [14 January 2020]. Available from: http://virological.org/t/initial-genome-release-of-novel-coronavirus/319
- 3) Meredith, L. W., W. L. Hamilton, B. Warne, C. J. Houldcroft, M. Hosmillo, A. S. Jahun, M. D. Curran, S. Parmar, L. G. Caller, S. L. Caddy, F. A. Khokhar, A. Yakovleva, G. Hall, T. Feltwell, S. Forrest, S. Sridhar, M. P. Weekes, S. Baker, N. Brown, E. Moore, A. Popay, I. Roddick, M. Reacher, T. Gouliouris, S. J. Peacock, G. Dougan, M. E. Torok and I. Goodfellow (2020). "Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study." Lancet Infect Dis 20(11): 1263-1272.
- Rambaut, A., E. C. Holmes, Á. O'Toole, V. Hill, J. T. McCrone, C. Ruis, L. du Plessis and O. G. Pybus (2020). "A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology." <u>Nature Microbiology</u> 5(11): 1403-1407.