National Contribution from the United Kingdom of Great Britain and Northern Ireland to the Background Information Document on New Scientific and Technological Developments Relevant to the Biological and Toxin Weapons Convention (BTWC)

Summary

This paper summarises some key points emerging from the 2017-2020 Standing Agenda Item on review of developments in the field of science and technology (S&T) related to the BTWC. It highlights some common understandings reached on the specific topics covered, as well as some areas that States Parties identified as requiring further consideration. These could provide some options for topics to be addressed in future reviews of science and technology, which are mentioned in the concluding paragraph.

I. INTRODUCTION

1. During the 2017-2020 Intersessional Programme (ISP), under the Standing Agenda Item on the review of developments in the field of science and technology related to the Convention, States Parties had the opportunity to reach common understandings and identify effective action on a wide range of relevant scientific topics. The review process included not only the provision of information on progress in various fields, but also consideration of the implications of developments on potential risks and benefits for the Convention, and on other possible measures such as:
    - Biological risk assessment and management;
    - Voluntary codes of conduct and other measures to encourage responsible conduct by scientists, academia, industry and civil society;
    - And education and awareness raising about the risks and benefits of life sciences and biotechnology.

2. Many areas relating to S&T also have relevance to Article VII and Article X of the Convention. As such, reference will be made when cross cutting themes are also relevant to Articles VII and X, as they are intimately linked to S&T.

II. GENOME EDITING

3. During the 2017-2020 ISP one particular scientific field became the ‘hot topic’ of discussion among BTWC States Parties, and indeed the world. Genome Editing dominated discussions and working papers throughout this ISP. Genome editing is a term encompassing many different molecular techniques for making changes to the genetic sequence of a given organism. These can range from restriction enzyme based techniques such as Transcription activator-like effector nucleases (TALENs), endonuclease techniques such as

zinc-finger nuclease (ZFN), and the most widespread approach, Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR). CRISPR technology exploits the functionality of Cas (CRISPR-associated) proteins such as Cas9. The rapid rise in CRISPR-Cas9 technology has led to an explosion of research in this area. The potential applications, both for eukaryotic gene editing and prokaryotic 'recombineering', means that more and more groups are investing in CRISPR-Cas9. However, with the dawn of this new technology, there are rising concerns about the ethics of gene editing, how to regulate it now and its future use in gene therapy, agriculture and gene drives. CRISPR-Cas has the potential to enable editing of any gene, by deletion, insertion or control of expression, in virtually any organism. This has produced many start-up companies aiming to use CRISPR-Cas as a gene therapy for acquired or inherited diseases from HIV and cancer to muscular dystrophy and sickle cell anaemia. However, concerns over the use of CRISPR-Cas to make heritable changes to the human genome and lack of regulation surrounding "gene drives", also highlight a potential for misapplication or deliberate misuse. Easy access to CRISPR-Cas9 reagents and the simplicity of the technology portends towards ever more widespread use, with CRISPR-Cas9 quickly becoming a standard molecular microbiology tool in laboratories around the world.

4. A key advantage of using CRISPR-Cas9 is its simplicity, allowing it to be utilised in any molecular biology laboratory without the need for additional specialist equipment. There are a huge number of CRISPR-Cas9 tools are widely available online and are accessible to all, including non-professional scientists and so-called 'biohackers'. The inventors of the technology have made all of their tools open access, including full step-by-step guides to planning and executing CRISPR experiments. However, despite the easy access to online protocols, some tacit knowledge and experience of molecular biology techniques, and access to reagents such as restriction enzymes and competent cells, is still required.

5. Genome editing has the potential to provide benefits across an increasing number of areas, including in human health, agriculture and the environment. There could also be benefits of relevance to implementation of the BTWC, for example, providing support or assistance in response to a violation of the Convention under Article VII, and development and application of scientific discoveries to the prevention of infectious disease under Article X.

6. CRISPR technology has been developed to prevent and treat disease in humans, to modify plants to deal with the impacts of climate change and plant pathogens, and to halt the spread of viruses in animal populations. It can also be used to edit germline cells in embryos, introducing genetic changes that will be passed on to future generations and which could have potential in the

treatment of genetic disorders. Some specific examples of beneficial genome editing applications given in a Royal Society Conference Report include[1]:

- conferring resistance to porcine reproductive and respiratory disease virus in pigs and to the infectious pancreatic necrosis virus in Atlantic salmon;
- targeted mutagenesis to prevent rice blast disease;
- creation of improved cellular and animal models of disease to understand disease pathways, identify and validate novel drug targets and test the efficacy of new medicines;
- targeting the genes involved in the symbiosis signalling pathway in barley to help understand their function. This may allow engineering of the pathway for cereal recognition of nitrogen-fixing bacteria, and support the development of nitrogen-fixing cereals, which could play an important role in global food sustainability.

7. The broader debate on the socio-economic implications of genome editing has tended to focus on the key ethical, moral and public perception aspects, though there has been some consideration of potential security concerns. In October 2017, the InterAcademy Partnership (IAP) convened an international workshop to assess the security implications of genome editing technology. Its major goal was to enable members of the research, security and policy communities, with wide geographical representation, to discuss potential benefits, security implications associated with intended misuse, and what might be done to prevent or mitigate potential harm[2]. Discussions focussed on specific applications of genome editing, including: human cell editing; agriculture (plants and animals); gene drive applications; and microbial applications. Participants identified beneficial applications similar to those mentioned in the Royal Society report; additional examples included:
    - developing gene drives to control insect vectors of diseases such as malaria;
    - transgenic cattle for increased resistance to tuberculosis;
    - development of screens for biological processes or disease;
    - increased understanding of CRISPR functionality in bacteria revealing new opportunities to tackle pathogens, including the major therapeutic goal to avoid development of antimicrobial resistance.

8. At the workshop, potential security concerns, specifically intentional misuse, were explored taking account of developments in the specific applications. Issues included:
    - Human cell editing concerns such as: influencing future human generations; misuse potential for ‘off-label’ use, for example using a medical product for a muscle disorder for enhancement of military

[1] https://royalsociety.org/-/media/events/2018/03/crispr-revolution-tof/TOF-crispr-revolution-report.pdf?la=en-GB&hash=6BEBEE3995AFE423F97A5F213E91882E

[2] Fears R and ter Meulen V (2018) Assessing Security Implications of Genome Editing: Emerging Points From an International Workshop. Front. Bioeng. Biotechnol. 6:34. doi: 10.3389/fbioe.2018.00034

capabilities; risk of genome editing viral vectors reaching unintended recipients;
- Microbial applications have the potential for misuse to construct or alter pathogens suitable for weaponisation - this would be of concern in both human health and agriculture;
- Gene drive applications could potentially be misused to create threats to human health (e.g., by increasing the transmission of infectious disease by insect vectors) and agriculture (e.g., by increasing insect pests and plant damage).

9. In assessing both potential benefits and risks, it is also important to consider the present and future limitations of the technology and what barriers would have to be overcome to address the challenges. Some examples of limitations include:
    - unwanted off target effects which can confound research experiments and present problems for therapeutic applications; development of more specific variants of CRISPR system enzymes could minimise these effects;
    - pre-existing immune responses in humans to proteins in the CRISPR-based technology; this may hinder use to treat disease and could cause significant toxicity to patients; utilisation of alternative enzyme variants may address this;
    - delivery to the target population based on viral-vector systems, which have limitations on size of insert, efficacy and specificity; new approaches being explored include utilisation of gold nanoparticles complexes to improve delivery.

III. THE COVID-19 PANDEMIC

10. The spread of SARS-CoV-2 has resulted in an infectious disease outbreak on a scale not experienced in living memory, and it is not yet over. As we experienced with the Ebola Virus Disease outbreak of 2014, there are many lessons to be identified from biological events such as large scale infectious disease outbreaks. Lessons are still being learned and some may not yet be identified. Areas of technological progress that have direct relevance to the COVID-19 pandemic, or that have come about as a result of responding to the pandemic, and as such have relevance to Article VII include;
    - the requirement to strengthen national capacities for response and preparedness; Ensuring the WHO has an appropriate and implementable mandate for responding to and investigating outbreaks;
    - strengthening infectious disease surveillance, monitoring and early warning systems;
    - improving information sharing;
    - investing in new research and development.

A. Disease Surveillance and Monitoring

11. The requirement for effective disease surveillance and monitoring has been of critical importance throughout the COVID-19 pandemic. The UK Health Security Agency (UKHSA) carry out detailed variant surveillance analyses, which contribute to the variant risk assessments and designation of new variants of concern (VOC) and variants under investigation (VUI). Many factors of viral evolution are monitored to determine new variants and subsequently assess their impact on diagnostic and therapeutic targets and biological risk assessment and management measures. Data covering a wide range of biological properties are assessed including; changes in transmissibility, severity or immune evasion, growth rate and transmissibility, which could lead to a displacement of the current dominant variant. These reports which detail information covering genomic diversity, epidemiology, growth rates, secondary attack rates and hospitalisation are published by UKHSA on a regular basis[3,4].

12. Strengthening global surveillance of variants will be important in understanding the risk from new waves of disease emerging. Current genomic surveillance strategies are highly variable between countries and in many cases genomic data is not shared on public databases[5]. Strengthened and better aligned surveillance would be mutually beneficial in detecting and understanding emerging variants and their spread. BTWC States Parties should continue to proactively engage with and strengthen collaboration with the WHO, WOAH and FAO to share best practices relating to epidemiological surveillance.

B. Testing and Diagnostics

13. In response to the COVID-19 pandemic, the UK's COVID-19 testing capacity has vastly expanded through establishment of test facilities within the National Health Service (NHS), academia, universities, lighthouse facilities, the military and other private and non-profit community sectors[6]. This includes the largest network of diagnostic testing facilities in British history. Part of this capability was the establishment of several Lighthouse laboratories, which were high throughput facilities dedicated to COVID-19 testing for NHS Test and Trace.

14. Real-time PCR, from an extracted throat and nasal swab, is the gold standard used by the majority of diagnostic laboratories for COVID-19. The development of Endpoint PCR (ePCR) in a UK Lighthouse Laboratory, a technology adopted

[3]https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1063424/Tech-Briefing-39-25March2022_FINAL.pdf

[4]https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1057359/Technical-Briefing-37-25February2022.pdf

[5] Z. Chen et al. Global landscape of SARS-CoV-2 genomic surveillance and data sharing. Nature Genetics volume 54, pages499–507 (2022)

[6] https://www.gov.uk/government/news/two-new-megalabs-to-open-in-2021-to-transform-the-uks-diagnostic-facilities

from industry, is one option being utilised to scale and speed up PCR testing. A single ePCR line has the potential to run over 15,000 samples concurrently, and a testing capacity of over 150,000 samples daily. ePCR is used alongside real-time PCR in UK Lighthouse laboratories to increase testing capacity with minimal facility and operational adaptations[7]. It has been suggested that the scalability and performance of ePCR may have the potential to allow for routine whole-population diagnostic monitoring during a pandemic using few centralised testing labs[7].

15. In addition to PCR based testing, the lateral flow test is a widespread, readily accessible and user-friendly testing option based on antibody technology. Lateral flow tests have played an important role in controlling the COVID-19 pandemic in many industrialized countries as well as resource-limited settings throughout the global response to COVID-19. Most rapid point of care (POC) diagnostic tests do not meet the quality standards required to replace centralized laboratory-based tests[8]. However, lateral flow tests are a popular POC diagnostic that has been widely used in combination with PCR based techniques to confirm SARS-CoV-2 infection[9]. The widespread public acceptance and overall success of lateral flow tests for mass POC diagnostics has accelerated research into similar technologies for a whole range of infectious and non-infectious ailments, such as cancer, organ function monitoring, sepsis and concussion.

C. Genetic Sequencing

16. Whole genome sequencing (WGS) and the genotyping of variants can aid tracking disease transmission and lineages during an outbreak, especially when combined with geographical data[10]. Throughput, resolution, scalability, flexibility and affordability have continued to improve for high throughput sequencing technologies. As such, whole genome sequencing has played a pivotal role in the global response to the COVID-19 pandemic. Since the first genome sequence of a new coronavirus associated with human respiratory disease was published by Chinese scientists in early 2020, genetic sequencing of COVID-19 and subsequent variants has become commonplace in many countries[11]. The benefits of sequence monitoring were highlighted in the UK when the B.1.1.7 lineage was identified due to sequencing surveillance being conducted in London, where an increase of B.1.1.7 cases coincided with an increase in S gene target failures[12]. Other benefits include; using sequence

[7] J. Roix *et al*. Evaluation of endpoint PCR (EPCR) as a central laboratory based diagnostic test technology for SARS-CoV-2. 2021.

[8] V. Sunkara, *et al*. Lab-on-a-Disc for Point-of-Care Infection Diagnostics. Acc.Chem. res., 54 (2021);

[9] Zhou, Y, *et al*. Point-of-care COVID-19 diagnostics powered by lateral flow assay. 2021, TrAC Trends in Analytical Chemistry, Vol. 116452.

[10] E.L. Stevens *et al*. The Public Health Impact of a Publically Available, Environmental Database of Microbial Genomes. Frontiers in Microbiology, 2017, 8(808)

[11] Wu, F., Zhao, S., Yu, B. *et al*. A new coronavirus associated with human respiratory disease in China. Nature 579, 265–269 (2020). https://doi.org/10.1038/s41586-020-2008-3

[12] E. Volz *et al*. Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593(7858), 266-269

data to shape emergency and longer term responses to infectious disease outbreaks, enabling preparation or predictive measures for future events, routine sequence monitoring prior to or during outbreaks could enable earlier identification of the causative agent, enabling tracking of transmission of known lineages and identification of emerging variants or variants with enhanced biological properties[10,12,13]. However, cost is still a significant limiting factor and generally, only a small proportion of confirmed positive samples are sequenced and assigned a lineage, this potentially means other circulating or new lineages may be missed[13].

17. A related well-established technology that can provide complementary high throughput data to whole genome sequencing but in a lower cost and more time efficient manner is genotyping. This uses a small panel of single nucleotide polymorphisms (SNP) to assign lineage to COVID-19 positive samples. Genotyping has been widely used in the UK and although will not produce full sequence information it can accurately assign a variant to a positive sample, which is sufficient to identify or rule out transmission routes to monitor viral spread. Using genotyping technology for real-time monitoring of COVID-19 variants can facilitate emergency responses and provide information for epidemiological studies and predicative modelling for future outbreaks. The main drawback of genotyping and a key reason why it would not be sufficient to replace the requirement for whole genome sequence surveillance is that it relies upon an up to date reference library of full genome sequences to screen against [10,13]. UK trials began with genotyping target panels in March 2021, and since then genotyping results have become a method of rapid identification of the Delta variant[14]. As of early August 2021 genotyping had been used to identify the variants Alpha, Beta, Delta and Gamma[15].

D. Big Data, Machine Learning and Artificial Intelligence

18. Rapid decision-making technologies have been in demand to facilitate the national and global response to the spread of COVID-19[16]. This encouraged the development of more intelligent, highly responsive, and efficient detection methods. Algorithms have been developed for the automatic and accurate classification of COVID-19[17]. Diagnosis can involve the detection of pneumonia in COVID-19 patients but high diagnostic accuracy is difficult[18]. Artificial Intelligence (AI) and computer vision methods have been applied to

[13] H. Harper *et al*. Detecting SARS-CoV-2 variants with SNP genotyping. PLOS ONE, 2021, 16(2), e0243185

[14] Public Health England. SARS-CoV-2 variants of concern and variants under investigation in England - Technical briefing 15. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/993879/Variants_of_Concern_VOC_Technical_Briefing_15.pdf

[15] Public Health England. SARS-CoV-2 variants of concern and variants under investigation in England - Technical briefing 21. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1012644/Technical_Briefing_21.pdf

[16] Vaishya, Raju, *et al*. "Artificial Intelligence (AI) applications for COVID-19 pandemic." Diabetes & Metabolic Syndrome: Clinical Research & Reviews 14.4 (2020): 337-339.

[17] Baghdadi, N. A., *et al*. An automated diagnosis and classification of COVID-19 from chest CT images using a transfer learning-based convolutional neural network. Computers in Biology and Medicine 144 (2022): 105383.

[18] Li D, Li S. An artificial intelligence deep learning platform achieves high diagnostic accuracy for Covid-19 pneumonia by reading chest X-ray images. I science. 2022 Apr 15;25(4):104031.

extraction of features from radiological images, to provide diagnosis ahead of pathogenic tests, thus providing disease management within the critical time[17].

E. Vaccines and Therapeutics

19. The COVID-19 pandemic has driven scientists, regulators and policy makers to take an approach to vaccine development like no other. This will no doubt provide key lessons for accelerated vaccine development and production in response to future biological threats. Emerging viruses such as SARS-CoV-2, avian influenza and Ebola in recent years have driven the research community to focus on emerging zoonotic viruses and associated vaccine development[19]. The speed with which multiple SARS-CoV-2 vaccines were developed, tested and authorised for use in the UK was influenced by; this depth of existing research into Coronaviruses and new generation vaccines, increased funding and an adapted UK approval process[20]. Lessons identified in previous outbreaks which were declared a Public Health Emergency of International Concern have been learnt and new approaches have been developed, in particular, the new regulatory pathway enabling the rapid approval for emergency use of vaccines to treat COVID-19. The Human Medicine Regulations (MHR) 2012 is the UKs core legislation which regulates medical products, changes were made to this in 2020 to allow temporary authorisation of a unlicensed product (COVID-19 vaccine), subject to safety, quality and efficacy as defined by the MHRA[22]. In 2020 the UK's Medicines and Healthcare products Regulatory Agency, the MHRA, used a regulatory process known as a 'rolling review'. A 'rolling review' can be used to complete the assessment of a promising medicine or vaccine during a public health emergency in the shortest time possible. Data on the safety, quality and effectivity of the Pfizer mRNA vaccine, including lab and clinical trials, manufacturing and quality control was submitted to the MHRA between 1st October and 2nd December. The MHRA expert scientists and clinicians reviewed data from the laboratory pre-clinical studies, clinical trials, manufacturing and quality controls, product sampling and testing of the final vaccine and also considered the conditions for its safe supply and distribution. This process lead to the first COVID-19 vaccine for the UK, developed by Pfizer/BioNTech, being granted temporary authorisation from MHRA on 2nd December 2020 for use in the UK[21]. Temporary authorisation is not the same as standard marketing authorisation that is required for medicines to be marketed, under temporary authorisation the product is not considered to be fully licenced. Temporary authorisation lasts a fixed year, within which terms and obligations are defined, such as the

[19] D. Van Riel and E. De Wit. Next-generation vaccine platforms for COVID-19. Nature Materials, 2020, 19(8), 810-812.

[20] P. Ball. The lightning-fast quest for COVID vaccines — and what it means for other diseases. *Nature*, 2020, 589, 16-18

[21] https://www.gov.uk/government/news/uk-medicines-regulator-gives-approval-for-first-uk-covid-19-vaccine

requirement of further studies. Temporary authorisation can be converted to standard marketing authorisation following further data being submitted[22].

20. The first COVID-19 vaccine was a new generation mRNA vaccine, despite being the first mRNA vaccine approved, years of mRNA vaccine research existed which speed up development. Existing coronavirus research into SARS and MERS, included vaccine development and the identification of the spike protein as an effective vaccine antigen and how to stabilise it. The UK's Oxford-AstraZeneca viral vector vaccine similarly benefited from prior research, including the identification of the modified adenovirus viral vector[20].

21. Other vaccine types, such as inactivated or live attenuated vaccines, require the growth of large quantities of the virus, making development and manufacture more costly and time consuming. Additionally, in the case of COVID-19, this would need to be done in a high containment facility. In comparison, next generation vaccines (e.g. mRNA and viral vector) can begin development using the viral sequence, in the absence of the physical virus. New generation vaccines are not only quicker to develop but are also more easily adaptable, another benefit when facing new emerging viruses and new variants in the future19[19]. During the pandemic, increased funding allowed companies to run multiple stages of clinical trials and manufacturing in parallel to speed up the process[20].

IV. ENABLING TECHNOLOGIES

A. Nucleic Acid Synthesis

22. The efficiency and scalability of nucleic acid synthesis technology continues to advance. A development that has progressed throughout this ISP is the advent of more efficient bench top DNA synthesizers. These have become more commonplace in life science laboratories, expanding access to nucleic acid synthesis technology at lower cost and increased sequence length, without the need to use a sequence service provider. Policy makers now need to work with the scientific community to create governance measures that will not hinder the application of this enabling technology for beneficial and peaceful purposes supporting human, animal and plant health, but that will manage the risk of misapplication and deliberate misuse.

B. Peptide synthesisers

23. A scientific advancement that has seen much progress since the eighth Review Conference in 2016 is peptide synthesis technology. This technology is rapidly advancing, and the emerging fields of peptide-based drugs and biomaterials

[22] Brodies LLP. The mechanics of medicines regulation - shining a spotlight on the MHRA vaccine approval decision. 2020

are increasing accessibility of custom peptide synthesis and driving down its cost. Peptide synthesis equipment is available at all scales, although currently from a limited number of manufacturers globally. However, companies providing custom peptide synthesis services are numerous and globally widespread. Peptide synthesis offers several advantages compared to exogenous peptide expression including: faster turnaround, removes the need for tag, reduces problems with low expression, removes risk of cloning errors, mistranslation or unwanted post-translational modification and it offers extensive modification options. There are however, some drawbacks associated with this technology and these include: limits to peptide length, lower yields for longer peptides, some peptide sequences are problematic, side reactions, secondary structure formation and problems with solubility. In addition to the advantages mentioned above, peptide synthesis can be applied to many research applications such as, research into peptide vaccines, peptide drugs, peptide based biomaterials, target validation, epitope mapping and structure and activity studies. Some recent developments of note include:

- Increased purity of commercially available amino acid building blocks increases yield and purity of peptides, which in turn allows for synthesis of longer peptides.
- The use of microwave or infrared heating and flow-based synthesis equipment has sped up the process to a matter of minutes[23,24], rather than hours, for each amino acid addition in a peptide chain. This can also increase the purity of the product.

24. Chemistries to address problematic amino acid sequences have recently improved dramatically[25,26,27], making previously unobtainable sequences possible. Peptide ligation techniques are also advancing rapidly, which opens up the possibility of producing small proteins[28]. High throughput synthesis equipment can be used to make libraries of synthetic peptides with unlimited modification options for rapid screening to achieve desired characteristics.

25. The equipment ranges from small benchtop personal use scale, up through large benchtop research scale, high-throughput scale with multiple channels, floor standing pilot scale, and industrial scale, which can fill an entire room. The amount of crude protein produced in a single run from one of these pieces of equipment therefore ranges between milligrams and kilograms.

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[23] Hartrampf, N., *et al*., Synthesis of proteins by automated flowv chemistry. Science, 2020. 368(6494): p. 980-987.

[24] Simon, M.D., *et al*., Rapid Flov-Based Peptide Synthesis. ChemBioChem, 2014. 15(5): p. 713-720.

[25] Samson, D., *et al*., The aspartimide problem persists: Fluorenyimethyloxycarbonyl-solid- phase peptide synthesis (Fmoc-SPPS) chain termination due to formation of N-terminal piperazine-2, 5-diones. Journal of Peptide Science, 2019. 25(7): p. e3193

[26] Jaradat, D.s.M.M., Thirteen decades of peptide synthesis: key developments in solid phase peptide synthesis and amide bond formation utilized in peptide ligation. Amino Acids, 2018. 50(1): p. 39-68.

[27] Paradís-Bas, M., J. *et al*., The road to the synthesis of "difficult peptides". Chemical Society Reviews, 2016. 45(3): p. 631-654.

[28] Agouridas, V., *et al*., Native Chemical Ligation and Extended Methods: Mechanisms, Catalysis, Scope, and Limitations. Chemical Reviews, 2019. 119(12): p. 7328-7443.

26. Companies providing gene synthesis services adhere to a harmonised protocol through the International Gene Synthesis Consortium (IGSC) to screen orders for sequences associated with dual use pathogens and toxins. It may be possible to establish a similar system within peptide synthesis companies to ensure that orders are screened for toxic products. However, peptides have an added level of complexity around their modifications and folding, which play an important role in their toxicity and action, which makes screening more difficult than for DNA sequences. Since the proliferation risk from custom ordered peptides might be considerably lower than that of synthetic DNA, the introduction of screening processes that would result in a significant burden for peptide synthesis companies may be considered disproportionate at this stage.

V. CONVERGENCE OF TECHNOLOGICAL AREAS

27. Advances in a number of technology areas, including synthetic biology, bioautomation, AI, machine learning, cloud- based laboratories, materials science, quantum and energetics are rapidly converging, which may consequently increase potential risks of misuse or misapplication of bioscience research. These convergences may also give rise to questions regarding the distinction between weapons of mass destruction and conventional weapons. A topic of discussion, which States Parties may wish to consider during the potential forthcoming ISP between now and the tenth Review Conference.

VI. BENEFITS AND RISK ANALYSIS

28. As with all biological related research, there are dual use considerations for all of the aforementioned fields of biotechnology and research, so the BTWC must keep pace with these rapidly advancing areas of S&T and have balanced discussions. We must ensure that benefits of biotechnology are considered along with any potential risks and that governance is proportionate and developed in partnership with the scientific and associated communities affected by biological risk assessment and management measures.

VII. FUTURE AREAS FOR TECHNOLOGY WATCH

29. Precision medicine is a field of research that is growing considerably and has the potential to revolutionise how we treat human disease. Personalised treatments are developed taking into account genetic, environmental and lifestyle factors. In addition to the potential use of biotechnology such as gene editing in this way, BTWC States Parties should also remain mindful of the use of biometric and sequence data and consider the security implications of storing and using such data. This is an innovative field of research still in its infancy, however it does present with opportunities for technological convergence and could provide immeasurable benefits to human health on a global scale. As with

many of the tools and technologies presented herein, these benefits should not be limited by risk management and governance measures. In fact, benefits should be protected and encouraged, while early consideration of risk assessment and management measures should provide assurance that everything possible has been done to minimise the risk of misapplication or deliberate misuse of precision medicine.