February 20th, 2026

John Joyce, M.D.
Chairman
Subcommittee on Oversight and Investigations
Committee on Energy and Commerce

Yvette Clarke
Ranking Member
Subcommittee on Oversight and Investigations
Committee on Energy and Commerce

Dear Chairman Joice and distinguished members of the Subcommittee.

Thank you for the additional questions for the record regarding my testimony before the Subcommittee on Oversight and Investigations on Wednesday, December 17, 2025. My answers are attached in the accompanying document. Please let me know if you have any questions or concerns.

Sincerely,
Dr. Jaspreet Pannu
Senior Scholar, Johns Hopkins Center for Health Security
Assistant Professor, Johns Hopkins Bloomberg School of Public Health

1. What is the best way to assess the risk of the AI biological threat?

AI technologies could revolutionize how healthcare is organized and delivered, how medicines and vaccines are developed, how diseases are diagnosed, and the speed with which new outbreaks are detected. A subset of AI models could also increase the risk of high-consequence accidents or misuse of biology and the life sciences.

Two potential harms that are extraordinarily important to govern are AI models or tools that could currently, or in the near future, either on their own or when paired with other models or systems:

- Greatly accelerate or simplify the reintroduction of dangerous extinct viruses or dangerous viruses that only exist now within research labs that could have the capacity to start pandemics, panzootics, or panphytotics; or
- Substantially enable, accelerate, or simplify the creation of novel variants of pathogens or entirely novel biological constructs that could start pandemics, panzootics, or panphytotics.

We have previously identified specific AI model capabilities (termed "capabilities of concern") that could contribute to these harms, such as:

- Design, or modeling of directed evolution towards, transmissibility or virulence characteristics of a pathogen through genome, protein, or pathogen property alternations.
- Design of genomes, genetic pathogens or proteins that expand or target a pathogen host or tropism range.

See: https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1012975

1. a. What would be the strongest empirical evidence for assessing the likelihood that AI could help generate a novel pandemic threat virus?

Empirical evidence can, and has been, generated to assess these capabilities of concern. Through the use of AI evaluations pre-deployment (safety tests that determine whether a model possesses capabilities of concern), government and industry can be alerted of risks in advance and implement mitigations.

The strongest empirical evidence that an AI system could help generate a novel pandemic virus, is to attempt to create novel viruses. We do **not** recommend this approach given the substantial accident risks and security dilemmas this would create. Another route to generating strong empirical evidence is by testing *proxy* tasks along each step of the risk chain. These are tasks which are sufficiently similar but which do not generate a novel pandemic virus themselves. Safe proxies are also recommended by US CAISI and NIST.

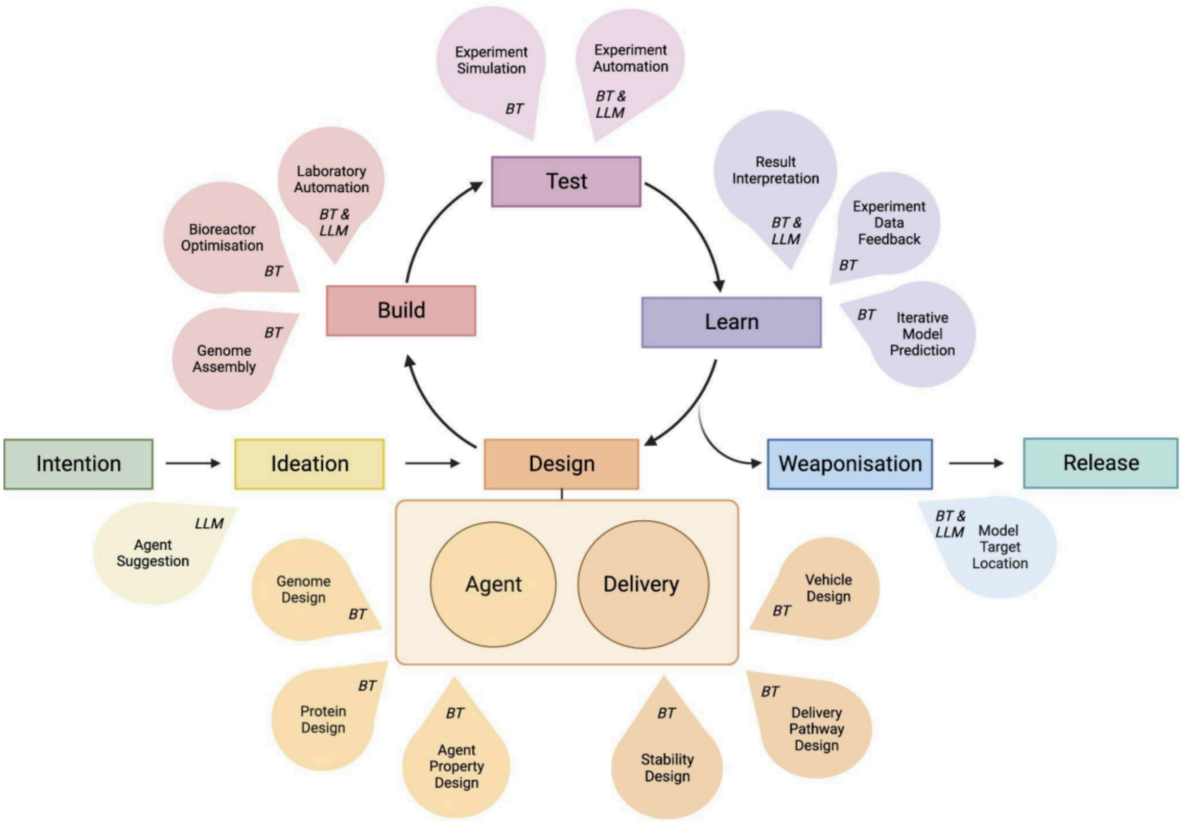

Figure 1. *Visualisation of the risk chain in biological weapon development, from malicious intention to deliberate release event. "Agent" refers to a biological agent while "Delivery" refers to the delivery mechanism, both of which pass through an iterative design-build-test-learn cycle. Rectangles represent the* ***steps*** *in the risk chain, while cones represent* ***capabilities*** *that may be accelerated by AI, with the AI-tool category of each capability specified in italics. LLM: Large Language Model; BT: AI-Enabled Biological Tool. Created with BioRender.com.*

Figure source: Center for Long Term Resilience report *Understanding AI-Facilitated Biological Weapon Development*

2. Do we have adequate visibility into the types of biological data—and volume of data—being aggregated by foreign adversaries for AI model training?

Both allied and adversary nations are investing heavily in their domestic AI capabilities. Collecting data is an integral part of that work. In my experience, it has been challenging to determine the types and volume of biological data being aggregated for AI model training. Foreign intelligence is outside my area of expertise; foreign intelligence services of the US government may be better suited to investigate this question.

3. What disease characteristics concern you most that AI could optimize in a pathogen?

Scientists and medical professionals have for decades sought to reduce the risks of scientific research that could lead, through accident or misuse, to high-consequence disease outbreaks. Scientists have carefully considered which pathogen characteristics pose greatest dual use concern when conducting wet-lab research, and the same characteristics should be considered in the case of AI. This includes:

- Transmissibility
- Virulence/toxicity
- Environmental stability and aerosolization characteristics
- Resistance to physical and medical countermeasures
- Host or tropism range
- Immune evasion and escape

The following characteristics should also be considered, but are unique to AI systems:

- Novel designs with high function homology but low sequence homology (therefore capable of circumventing gene synthesis screening)
- Autonomous (robotic) completion of protocols for de novo synthesis of pathogens

4. Can AI-enabled biological threats realistically be distinguished from a natural pathogenic outbreak if signs and symptoms became present in patients?

Currently, we lack technologies to distinguish between natural outbreaks and AI-enabled biological threats. Sequencing technologies are mature and can inform us of a pathogen's genetic sequence, but this is insufficient to determine its origin. Determining the origin of a pathogen and differentiating between natural or deliberate origin is called bioattribution. Critical gaps remain in bioattribution technologies, especially technologies that could attribute origin in real-time. The United States should prioritize sustained investment in bioattribution R&D.

5. Are there any regulations or laws preventing a researcher from modeling potentially harmful AI-enabled pathogens in a computer lab?

To my knowledge, there are no specific regulations or laws that prevent researchers from using AI to model and generate novel pathogens in a computer-only lab. Modeling pathogens for research purposes is extremely common, and any law or regulation would need to narrowly specify types of modeling that pose greatest risk; broad laws or regulations in this domain would negatively impact beneficial research.

6. Is the suitability screening of personnel to be in the Federal Select Agent Program sufficient to protect against an insider threat at a government laboratory?

The Federal Select Agent Program (FSAP) employs a multi-layered screening process to ensure that individuals with access to high-consequence biological agents and toxins are both secure and reliable. This is composed of Security Risk Assessment (SRA), required for all personnel, and the more rigorous Suitability Assessment, required specifically for those working with Tier 1 agents. The SRA is a mandatory federal background check conducted by the FBI's Criminal Justice Information Services Division (CJIS). It is required for any individual who requires access to any select agent or toxin, and involves submitting fingerprints and checking criminal history. Further Suitability Assessment is required for agents designated as Tier 1 (posing the highest risk of deliberate misuse), which involves checking an individual's credentials, temperament, and obtaining references. These are all substantial measures that protect against insider threats at a government laboratory.

Importantly, computational work involving data pertaining to these pathogens, or AI modeling of these pathogens, is not covered by the Federal Select Agent Program, which is designed to secure physical specimens. A separate or additional policy approach would be needed to address risks from the use of AI.

7. What steps are AI companies like OpenAI taking to mitigate risks and protect their platforms from misuse related to biosecurity and terrorism?

The companies OpenAI, Anthropic, Google, Amazon, Microsoft and Meta are members of the Frontier Model Forum (FMF), an industry consortium of leading AI companies collaborating to develop and share best practices for responsible development and risk mitigation of frontier AI systems. AI companies like OpenAI and other FMF members are instituting biosafety thresholds that trigger additional safeguards when models could significantly enable non-experts to create or deploy biological threats, favoring capability- and outcome-based thresholds over compute-only measures. They assess risk using cumulative evidence like benchmarking, expert red-teaming, and uplift studies, while considering actor expertise, comparative baselines, and real-world feasibility. These assessments are often within tiered risk levels that escalate mitigations.

7. a. Are these steps effective? If not, what would you recommend AI companies do to improve risk mitigation and biosecurity monitoring?

These steps are directionally sound but not yet fully sufficient. AI companies should standardize what “significant enablement” means across industry, expand independent third-party evaluations, continuously update baselines to avoid moving goalposts, integrate end-to-end supply-chain and operational feasibility checks, and implement robust access controls, monitoring, and incident response tied to threshold findings. Government collaboration, coordinated through entities like CAISI, can strengthen this ecosystem by providing shared threat intelligence, harmonized evaluation protocols, and channels for rapid information sharing and coordinated response, helping translate model evaluation results into clear, enforceable policies and ensuring mitigations keep pace with advancing capabilities.

See:
https://www.frontiermodelforum.org/issue-briefs/frontier-ai-biosafety-thresholds/#d11cc2e0-e68c-4b71-9ba4-d2d2393111ff-link

8. How can AI interpret the DNA of a pathogen and trace its origins?

Biological AI models like protein language models (ESM3) and genomic language models (Evo2) can interpret and generate amino acid and nucleotide sequences, respectively. These models can help researchers interpret the function of sequences, among other applications.

In the case of physical pathogen specimens, AI can be used for genomic forensics, in order to determine the geographic/host source or to attempt to detect a synthetic footprint. Phylodynamics modeling reconstructs transmission trees and helps researchers understand how pathogens are evolving over time, and how they may have originated. AI can also identify geographic signatures, as pathogens accumulate mutations as they adapt to regional hosts or environments. In the case of human-designed pathogens, there are efforts being made to identify “design signatures”. Research labs often have unique habits, such as specific preferred methods. AI can be used to attempt to predict the lab of origin of an engineered pathogen.

9. Can AI help researchers identify surveillance and mitigation strategies for emerging biothreats?

Yes. AI can help researchers conduct biosurveillance and plan mitigation strategies for emerging biothreats. AI can be used to advance Biothreat Radar, especially versions of this system built on metagenomic sequencing technology. AI can also enhance early detection by integrating real-time open-source intelligence from social media, news, and mobility trends. In addition, AI supports mitigation by accelerating diagnostics and medical countermeasure development, optimizing trials and resource allocation, and improving contact tracing and risk communication, enabling faster and more targeted interventions.

10. From a clinical perspective how could AI assist public health management and preparation for biological threats?

AI can assist public health management and preparation by enabling faster diagnosis, risk stratification, and smarter resource planning. Clinically, AI models that use age, comorbidities, and biomarkers have been developed to predict severe COVID-19 risk, supporting triage and targeted interventions through real-time clinical decision support. AI can also accelerate medical countermeasure development through initiatives like the protein-structure tool AlphaFold. Finally, AI can forecast demand for critical supplies like PPE and ventilators and guide allocation during surges, improving preparedness and response.