



210 - Genomic Non-specific Operational Matchmaking Enabled Systems (G-NOMES): Innovative acquisition for low-SWAP, modular, automated biological sample preparation for field forward agnostic sequencing for emerging biological threats

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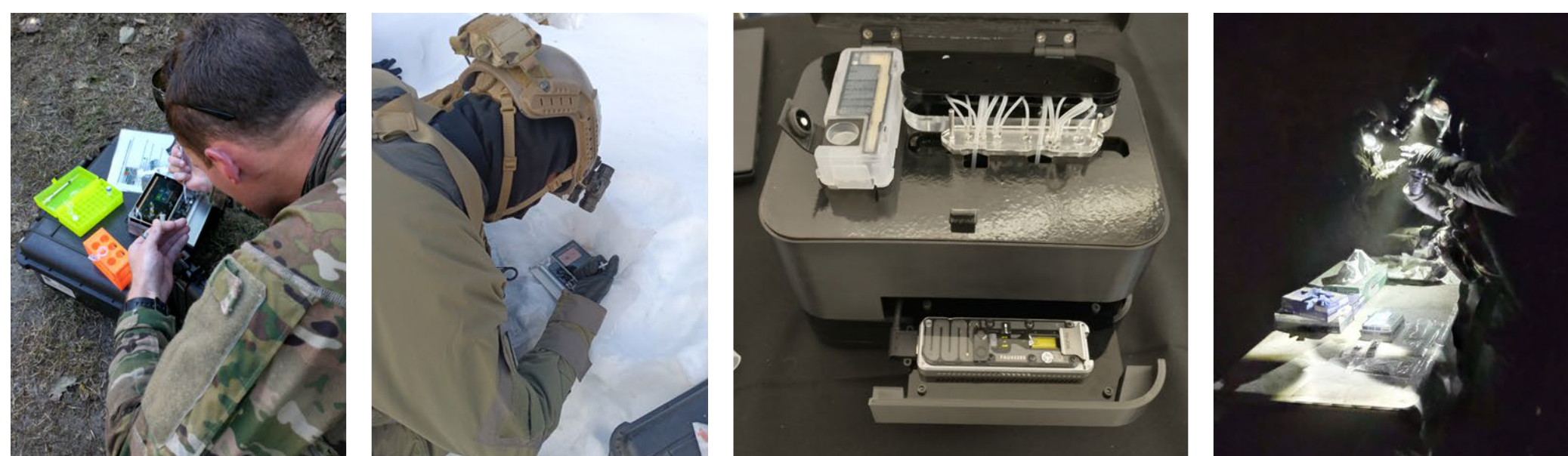
G-NOMES

Genomic
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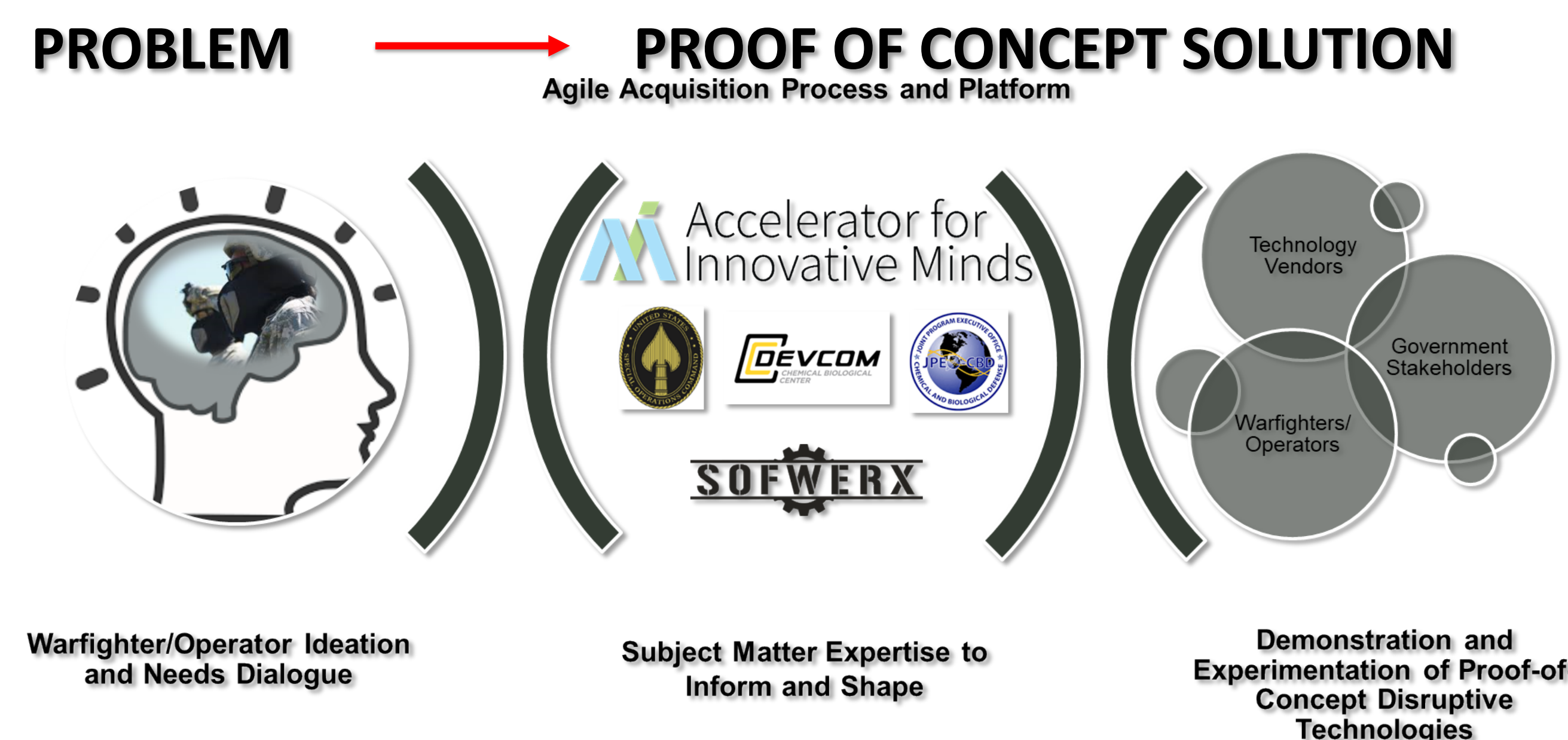
INTRODUCTION

Warfighters need situational awareness of potential unknown and emerging biological threats in far forward and austere environments. Current far-forward biological identification technologies (HHA and PCR) can only detect a small number of known biological threats. Non-targeted DNA/RNA sequencing technology is needed for fully agnostic biological identification. Current methods for preparation of sequencing-ready DNA/cDNA require lengthy multi-step regimens; a process too cumbersome in time to carry out in austere, hostile environments. Thus, there is an unmet need for streamlined, low SWAP next generation modular and automated biological sample preparation for field forward nucleic acid sequencing.



ACCELERATOR FOR INNOVATIVE MINDS (AIM) : MODEL FOR ACQUISITION STRATEGIES AND TRANSITION CAPABILITY

WHAT IT IS: An established enduring, agile Hybrid Accelerator model to enhance the defense acquisition process by means of fusing best industry practices with technology disrupters and alignment with acquisition and organizational specialties to expedite technology transition driven by Warfighter needs.



WHAT IT IS NOT: AIM is not meant to take the place of any other GOV acquisition pathway.

SUCCEED EARLY

SUCCEED FAST

SUCCEED CHEAP

- Aligning organizations and people throughout the acquisition process
- Answering a problem statement and facilitating direct dialogue
- Reducing acquisition bureaucracy

WHY DO WE NEED BIOSEQUENCING?



WHAT IS FIELDIED NOW:
Current far-forward biological identification technologies (HHA and PCR) can only detect a small number of known biological threats

WHY SEQUENCING:
Non-targeted DNA/ RNA sequencing technology is needed for agnostic biological identification

HOW TO ACCELERATE G-NOMES?

ONGOING PLANS:

Far-Forward Biological Sequencing (FFBS) Program of Record at JPM CBRN SOF

- High concentrated samples with low background
- Time to answer: 30-60 min for DNA-based organisms, 60-120 min for RNA viruses
- Non-laboratory trained operators
- Incremental fielding strategy

WHAT IS NEEDED:

Rapid and automated sample preparation for DNA and RNA sequencing is required for use on target

- Current TRLs for these technologies range from 2-4
- TRL 6 is needed to begin advanced development
- Reduces time-to-answer from days/weeks to 60-90 min

*There is a need for next generation **modular** and **automated** biological sample preparation for field forward nucleic acid sequencing in **austere, hostile environments**.*

CONCLUSIONS

The AIM G-NOMES technology output will deliver warfighter-focused solutions for field forward nucleic acid sample prep that are:

1) **SAMPLE TO SEQUENCING READY:** All steps required to produce sequencing ready DNA will be included.

- Sample types include high abundance biological material with low background. Steps required include lysis of cells, extraction of nucleic acids (DNA and RNA), and library preparation resulting in sequencing ready DNA.

2) **OPERATIONALLY HARDENED:** Technology will be able to perform in outdoor environments by warfighters.

- Technology must be able to perform in extreme hot and cold outdoor environments at all levels of humidity. The exterior must be able to be easily cleaned with a decontamination solution such as bleach to ensure safety of operators.

3) **LOW SWAP:** Optimized in size, weight, and power

- Technology will fit into a cargo pocket and ideally weigh less than 5 pounds. It must use battery power and be able to heat (for one step) to 80°C. All reagents will be contained within the device.

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