INNOVATING CROSS-DOMAIN SOLUTIONS TO DETECT EMERGING BIOLOGICAL THREATS

Pathogen X Detection Using One-hour Screen In Austere Environments

Paula Millirons GeneCapture, Inc. **Megan Roegner** GeneCapture, Inc. **Katherine Presz** GeneCapture, Inc.

Background: Pathogen X scenarios require that a pathogen, whether natural or engineered, is identified quickly so that mitigation and countermeasures can begin. The earliest days of an outbreak are often missed as testing is too costly, time-consuming, and distant from the affected population. The first 14 days are highly asymmetric in terms of Patient 0 and the spread of disease. The GeneCapture lab is developing a one-hour, affordable, portable pan-viral identifier to provide networked decision making across Military and Civilian domains, using a One Health paradigm. Rapid diagnoses impact readiness, warfighter health and bio-threat mitigation.

Purpose: Identifying the family that a newly encountered virus belongs to allows novel outbreaks to be quickly spotted to prevent spread, facilitates rapid targeted sequencing and intervention, and provides immediate important information on the correct countermeasures to protect warfighter health and readiness.

Objective: To provide medics, warfighters, first responders and farmers with access to a networked portable ‘sample to answer’ instrument that will identify the viral family in one hour.

Rationale: GeneCapture’s rapid CAPTURE ID technology is affordable and portable for austere and remote applications. The use of a highly multiplexed pre-amplification technique coupled with microarray identification should allow rapid genotypic screening across most viral families.

Relationship to Other Areas of Study: This pan-viral screen is a subset of the rapid pathogen identification that is currently being developed for far forward infection management, supported by DTRA, DHA and Army.

Methods: Sequences from a broad array of coronaviruses and influenza viruses infecting humans and animals have been aligned to find conserved regions that can be amplified and ‘captured’ with minimal degeneracy. Primers and probes are being tested/refined to allow pan-family and sub-family (e.g., pan-FluA) detection, with the detection of additional viral families planned.

Preliminary results: Amplification/primer sets for pan-influenza (A, B, C, D), pan-FluA, and pan-FluB have been designed to cover viruses infecting avian, porcine, bovine, and human hosts (among others.) These sets have been tested and verified against 13 strains of influenza, including the novel bovine H5N1 2.3.4.4b clade. Pan-coronavirus primers/probes have been designed to cover 38 strains including all human viruses and those known to infect 14 animal species. Many of these strains were provided for testing through a collaboration with Prof. Gregory Gray, University of Texas Medical Branch, Galveston, TX.

Preliminary Conclusions: Although viruses are broadly divergent, sufficient sequence conservation is present in genes encoding essential viral functions to allow amplification and detection at the family level with the system under development. The use of such a pan-influenza test on dairy farms in the US could have discovered the causative agent of the bovine H5N1 outbreak much earlier.

Impact to JSTO Mission and Joint Force: Pathogen X remains a threat to warfighter readiness and global civilian health as demonstrated by the COVID-19 and influenza pandemics. Easy-to-use, broadly implemented, affordable, and networked screening, such as reported here, can begin to counter such a diverse threat.

SBIR funding from the Defense Threat Reduction Agency