

## Empowering the Warfighter: Resilience Through Innovation

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## INNOVATIONS IN NEXT GENERATION CB THREAT CHARACTERIZATION AND ASSESSMENT FOR DECISION SUPPORT

## Genotypic And Phenotypic Analysis Of 22 Historic Francisella Tularensis Isolates Available Through The Biodefense Reference Material Repository

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Tularemia is a naturally occurring illness which is caused by the highly infectious pathogenic, gram negative bacterium Francisella tularensis. If untreated, the mortality rate among individuals exposed to the aerosolized bio-threat agent can range from 30-60 percent. Pioneering research on the bacterium sought to characterize the relationships between virulence, immunogenicity and morphology of isolated strains, and more recently, of the subspecies types A and B, which are known to cause tularemia in humans. The United States Army Medical Research Institute of Infectious Diseases' Biodefense Reference Material Repository (BRMR) contains historical and contemporary isolates derived from clinical and environmental sources of type A and B strains. We have examined the genotypic and phenotypic characteristics of 22 historic strains, which were lyophilized prior to the 1950s and more recently cultured and accessioned into the BRMR for use in Department of Defense-sponsored research activities. Our analysis reveals that, among these isolates, the type B strains grow significantly better in fructose compared to glucose and glycerol. Additionally, both types reflect high and low virulence calls in embryonated egg LD50 models, and type A strains better metabolize carbon substrates (namely, glucose and glycerol) compared to type B in Biolog microarray analysis. We are in the process of comparing and analyzing the whole genome sequence data that we obtained from each isolate and in conjunction with outcomes detailed in the recent literature, we aim to determine likely target genes, enzymes and pathways that may provide additional insight on how these subspecies compare. By accessioning, characterizing, and analyzing 22 historic strains, which played a central role in early tularemia research, we hope to aid in the development of effective treatments against the disease and provide protection across strains.