

the first study in the literature of more complete data for SARS-CoV-2 nucleic acid (RT-PCR) assay on sensitivity on the Abbott (Abbott Park Ill) and Cepheid (Sunnyvale CA) assays.

Methods: A retrospective search was performed for all test results for SARS-CoV-2 by RT-PCR from 3/1/2020 to 4/14/2020 at Corporal Michael J. Crescenz Medical Center, in order to evaluate the sensitivity on Abbott m2000 and Cepheid platforms. Results across multiple reference laboratories and in-house testing platforms were collated in a table with all patients clinically requiring repeat testing recorded.

Results: 114/863 patients had repeat testing. The tests were performed initially by outside reference laboratories (25 patients), on the Abbott m2000 (63 patients), and Cepheid Infinity (26 patients). 15/114 (13%) had discordant results on repeat testing. This included 1 test initially done by a reference laboratory. 8 days after the initial result from the reference lab, a positive for the same patient was identified on the Abbott platform. 11 initial Abbott results were discordant on further repeat testing on two platforms - Abbott (6 patients) and Cepheid (5 patients) 1-6 days later. In addition, 3 initial Cepheid were discordant on further repeat testing by the same Cepheid platform (1-16 days later).

Conclusion: While the instructions for use for both platforms suggest 100% sensitivity and specificity (due to the 100% positive and negative percent agreement in limited specimens), the true sensitivity is less than 100%, particularly early in the course of the infection. In our study, the positive percent agreement (surrogate for sensitivity) was 83% for initial Abbott tests, 88% for initial Cepheid tests, and 95% by Reference laboratory platform.

Assessment of Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF-MS) for Accurate Bacterial Identification in Clinical Labs

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Introduction/Objective: On behalf of the diagnostic Medical Laboratory rapid, and accurate identification of bacteria with their one-to-one anti-microbial susceptibility outlines is of ultimate importance for the management of infected patients. Contemporary microbial identification methods employed in routine clinical diagnostic laboratories relies on the use of conventional

phenotypic methods. Phenotypic methods are time consuming with minimum turn-around times of at least 24 hrs and in many occurrences of 48hrs. With the intention of accelerate laboratory processes the MALDI-TOF MS was familiarized. MALDI-TOF MS is established on proteomic profiling and permits for rapid identification of bacteria. This technology has not been widely used in Egypt, but has been regularly used in Europe for the past few years.

Methods: Two hundred forty three positive non duplicate blood cultures were accrued over a period of six months. Experimental aliquots were taken from excess sample material that was collected as part of routine clinical care. 105 were positive for Gram negative bacilli, 123 were positive for Gram positive cocci, 3 positive for Gram positive bacilli, and 7 were positive for yeast. MALDI-TOF identification was compared to conventional identification. Conventional identification consisted of a combination of MALDI-TOF identification of a subcultures colony by direct smear, biochemical reactions, Vitek 2, and molecular identification.

Results: Ninety seven of the one hundred and five blood cultures positive for Gram negative bacilli were monomicrobial. The majority of these were identified as *Escherichia coli* by conventional methods, followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Eighty-four of these monomicrobial cultures were identified by MALDI-TOF to the species level. Eighty-one of the eighty-four were concordant with the conventional identification (96.4%).

Conclusion: The MALDI-TOF proved to be useful for the rapid and reliable identification of g-ve bacteria from the clinical specimens. The difference in turnaround time for bacterial identification was significant between MALDI-TOF MS and VITEK 2 with minimal preparation for the blood cultures.

Ethnic Differences in Infection with SARS-CoV-2; a Veteran Affairs Medical Center (VAMC) Experience

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Introduction/Objective: An Institute of Medicine (IOM) report from 2002 has documented that racial and ethnic minorities have tended to receive worse health outcomes compared to non-minorities. This pattern has been demonstrated for many chronic and acute injuries and illnesses, but to the author's knowledge, there is sparse literature on this study on outcomes related to the novel coronavirus (SARS-CoV-2). SARS-CoV-2 has become a pandemic of global importance with significant impact on all elements of society. As part of quality assurance, as becoming confirmed positive for

SARS-CoV-2 would be adverse clinical news, a review was undertaken to see if there were ethnic differences in the veteran population being tested at the Veteran Affairs Medical Center (VAMC) on the risk of testing positive for SARS-CoV-2.

Methods: As part of a quality assurance/quality improvement project, a manual retrospective review of all SARS-CoV-2 RT-PCR tests performed at the VAMC from March 11th, 2020 to April 13th, 2020. These tests were reviewed within

the computerized medical record system to determine the age, gender, ethnicity of the patients, and test result of the patient.

Results: There were 571 patients who had tested for SARS-CoV-2. Out of these patients, 99 of these patients had a positive test result. The ethnic breakdown of the unique patients with a positive test result was 67 were African-American (68% of positive results), 2 Asian-American (2%), 1 Native Hawaiian or other Pacific Islander/Hispanic mixed (1%), 17 Caucasian (17%), and 12 declined to answer or left ethnic field unanswered. Among the 471 who had negative results, only 197 or 42% were African American and 118 were Caucasian (25%).

Conclusion: African Americans had more infections with SARS-CoV-2 compared to the other ethnic groups. Caucasians had many of the negative results, and positive results were otherwise not common in the other ethnic groups in the VAMC cohort. Given this first report in the literature of the disproportionate impact SARS-CoV-2 is having on those of African American ethnicity, appropriate clinical access and low threshold to test is essential.

Prognostic and Theragnostic Applications of Circulating Tumor DNA (CtDNA) in Metastatic Castrate-resistant Prostatic Carcinoma in Veterans: A Novel Promise in Precision Oncology

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Introduction/Objective: Utility of CtDNA in peripheral blood through liquid biopsies serves as a robust biomarker for precision oncology. Prostate cancer is most common cancer diagnosed in veterans, more commonly presenting at advanced stage with increased incidence of metastatic castrate-resistant prostatic carcinoma (MCRPC). Minimally invasive liquid biopsy is not limited by tumor site, type, tumor heterogeneity, and most importantly enables real time disease monitoring for best therapy decisions in MCRPC. The literature is sparse depicting the role of CtDNA in MCRPC in veteran patient population

with distinct demographics/frequency of Tp53 mutations. We herein aim to study role of CtDNA in liquid biopsies for prognosis, treatment decisions and outcome in veterans with MCRPC.

Methods: QA documents from Foundation One (Cambridge MA, NGS) on liquid biopsies performed for the Corporal Michael J. Crescenz Veteran Affairs Medical Center (CMCVAMC) from May 2019 to April 15, 2020 were reviewed. All liquid biopsies were performed on MCRPC with evidence of tumor progression. Statistical data for adequacy, type of mutations either altering therapy, disease course or outcome was noted.

Results: A total of 23 liquid biopsies were performed. 21/23 (91.3%) biopsies were adequate, 19/21 (90.4%) showed signature mutations for resistance to therapy, predicting prognosis, or suggesting poor outcome with decreased overall survival. 4/21 (19%) showed androgen receptor amplification (ARV7 mutation) that helped in making treatment decisions. Increased frequency of Tp53 mutations were noted (12/21 (57.1%) compared to general population (30- 40%)) indicating worse prognosis/aggressive disease course with decreased survival.

Conclusion: Combined exposure of herbicide agent orange and smoking may be a fertile soil for observed differences in type and frequency of genomic alterations in veteran patient population with MCRPC. Comprehensive genomic profiling on CtDNA through minimally invasive liquid biopsy is feasible and can be successfully implemented in veterans with multiple co-morbidities. Although ARV7 mutation is much more common in general population, veterans with advanced hormone resistant prostatic carcinoma may benefit from aggressive approach in developing targeted therapy focused on DNA repair genes, especially Tp53.

Improved Across the Board Access to SARS-CoV-2 Laboratory Testing in an Integrated Medical System; the Veteran Affairs Medical Center (VAMC) Experience

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Introduction/Objective: Due to the spread of SARS-CoV-2 – the causative pathogen behind COVID-19, a significant impact on society including significant death, morbidity, strain on the nation's medical systems, and an economic shutdown of many sectors has come to pass. While society has been affected by this virus, it has also been documented in the mainstream news that this pandemic has disproportionately affected non-white minority groups, and that access to testing for vulnerable populations have been limited. Similarly, previously published epidemiological data by Zuvekas et al. show that