Clinical pathology selected abstracts

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Risk estimation of severe COVID-19 based on biomarker assessment across demographics

January 2024—People respond differently to SARS-CoV-2 infection, with some having a very severe clinical course and sequelae while others recover quickly. Several research studies have used laboratory data to identify patient populations most at risk for severe outcome from COVID-19. However, many of these studies were conducted in China and did not represent the demographics of the U.S. population. Among the drawbacks of these studies were that most analyzed variance between two patient groups, yet statistical differences don't always correlate with clinically useful predictions. Furthermore, these studies used data from throughout patients' disease course, and clinicians would like to identify patients at risk during their initial interaction. The authors of this study sought to determine which demographic, clinical, and laboratory variables, at the time of initial patient contact, may help predict severe versus mild COVID-19. They studied patients from a large integrated health care delivery network that included four hospitals. Deidentified patient data were collected retrospectively for all patients who tested positive or negative for SARS-CoV-2 using a polymerase chain reaction assay from March 2020 through September 2021. The authors studied data from 14,147 patients and analyzed 58 variables, including demographics, clinical parameters, and biomarker test results. Four statistical models—inclusive, receiver operating characteristic, specific, and sensitive—were generated using backward stepwise logistic regression to predict severe disease (death or 90 or more hospital days) versus mild disease (alive and less than one hospital day). The authors found that of the 14,147 patients, including whites and Blacks and people of Hispanic ethnicity, 2,546 (18 percent) had severe outcomes and 3,395 (24 percent) had mild outcomes. The testing parameters present in all models were age, albumin, diastolic blood pressure, ferritin, lactate dehydrogenase, socioeconomic status, procalcitonin, B-type natriuretic peptide, and platelet count. The authors concluded that the biomarkers in the sensitive and specific statistical models are most useful to health care providers when they initially evaluate the severity of COVID-19. Moreover, most of the tests, including albumin, C-reactive protein, D-dimer, ferritin, procalcitonin, and platelet count, are inexpensive and readily available. Variables such as race, ethnicity, and clinical parameters did not further inform the modeling.

Kroll MH, Bi C, Salm AE, et al. Risk estimation of severe COVID-19 based on initial biomarker assessment across racial and ethnic groups. *Arch Pathol Lab Med*. 2023;147:1109–1118.

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Reducing duplicate genetic testing across a safety-net hospital system

Genetic testing has increased significantly in the past two decades. Genetic tests tend to be costly, and inappropriate use can lead to misdiagnosis and patient harm. Furthermore, repeat genetic testing performed in error can cause financial stress and undue anxiety for patients awaiting results. Because patients' germline genetics will not change during their lifetime and genetic tests have a high degree of sensitivity and specificity, duplicate testing is rarely indicated. However, it may be necessary if sample integrity is a concern, a limited panel of genetic tests is initially submitted, or mosaicism is suspected. But more often, repeat testing occurs because physicians are unable to readily review previous test results in the EHR. Duplicate genetic testing can be reduced by requiring a physician to obtain input from a genetic counselor before ordering genetic tests. However, this practice can be costly and resource intensive. An alternative approach is to provide electronic clinical decision support, which uses alerts to restrict duplicate orders. The authors conducted a study at a large safety-net hospital system as part of an effort to develop a systemwide EHR intervention to reduce wasteful duplicate genetic testing. They designed an EHR alert that would trigger when a clinician attempted to order any of 16 specified genetic tests

for which there was a previous result in the EHR system. The authors measured the proportion of genetic tests that were duplicates and alerts per 1,000 tests. Data were then stratified by clinician type, specialty, and inpatient versus ambulatory settings. The authors found that the rate of duplicate genetic testing decreased from 2.35 percent (1,050 of 44,592 tests) to 0.09 percent (21 of 22,323 tests) (96 percent relative reduction [$P<.001$]). The alert rate per 1,000 tests varied between inpatient and ambulatory orders (277 and 64, respectively). Among clinician types, residents had the highest alert rate per 1,000 tests (166) and midwives the lowest (51) ($P<.01$). Among clinical specialties, internal medicine had the highest alert rate per 1,000 tests (245) and obstetrics and gynecology the lowest (56) ($P<.01$). The authors concluded that a low-effort, high-yield EHR intervention can reduce duplicate genetic testing. Future interventions targeting departments and clinician types with higher alert rates may further reduce those rates.

Manchego PA, Krouss M, Alaiev D, et al. Reducing duplicate genetic testing in inpatient and outpatient settings across a large safety-net system. *Am J Clin Pathol*. 2023;160:292–296.

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