Understanding Current Clinical Scenarios for Plasma Microbial Cell-free DNA Sequencing toward Informing Diagnostic Stewardship

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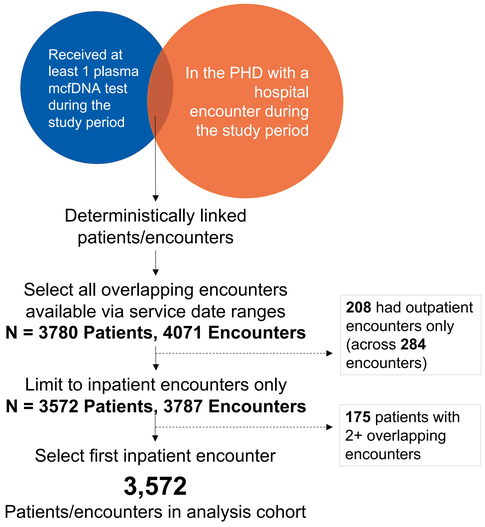
Background

Plasma microbial cell-free (mcfDNA) sequencing has emerged as a promising tool for unbiased detection of pathogens in patients with suspected infections. A systematic evaluation of the patient populations in which this test is used may provide insight into applications for clinical use. We describe demographic and clinical characteristics of patients tested with plasma mcfDNA sequencing linked to the Premier Healthcare Database (PHD).

Methods

A retrospective cross-sectional analysis was conducted using the PHD: a US hospital-based, service-level, all-payer database containing information primarily from geographically diverse communities, teaching hospitals, and health systems. Patients with plasma mcfDNA sequencing between April 1, 2018, to January 31, 2022, were deterministically linked to the PHD.

Figure 1: Patient Selection Process



Patient characteristics were collected via chargemaster data, ICD-10 diagnosis, and procedure codes. Immunocompromised (IC) status was identified via ICD diagnosis codes present during the hospital encounter and categorized using 2021 Agency for Healthcare Research (AHRQ) ICD-based definitions. The AHRQ Elixhauser Comorbidity Index score was also derived using ICD-10 diagnosis codes to indicate comorbidity burden.

Results

Patients' demographic characteristics are shown in Table 1. Ninety-two percent of patients were seen in an urban hospital, 63% at a hospital with over 500 beds, and 76% at a teaching hospital. There is a wide array of conditions that the patients were treated for during the encounter as illustrated by the distribution of primary ICD diagnosis codes (Figure 2).

Over half (N = 1,955, 55%) of the patients had evidence of being IC. Figure 3 shows the distribution of IC conditions among IC patients. Patients in this population also have a high comorbidities burden based on the distribution of the weighted Elixhauser score (Figure 4).

Table 1: Patient Demographic characteristics

Characteristic	N = 3,572[1]
Age in years, continuous	57 (39, 68)
Age in years, categorical	
<18	279 (8%)
18-34	464 (13%)
35-49	610 (17%)
50-64	1,022 (29%)
65-74	721 (20%)
75+	476 (13%)
Sex	
Female	1,490 (42%)
Male	2,082 (58%)
Race	
White	2,545 (71%)
Black	514 (14%)
Other	513 (14%)
Ethnicity	
Hispanic or Latino	496 (14%)
Not Hispanic or Latino	2,881 (81%)
Unknown	195 (6%)
Payor Type	
Commercial	1,219 (34%)
Medicaid	681 (19%)
Medicare	1,432 (40%)
Other	240 (7%)
US Census Region	
Midwest	1,093 (31%)
Northeast	21 (1%)
South	2,116 (59%)
West	342 (10%)

[1]Median (IQR); n (%). Percentages are rounded to the nearest whole number.

Figure 2: Distribution of primary ICD-10 diagnosis codes during plasma mcfDNA sequencing encounter

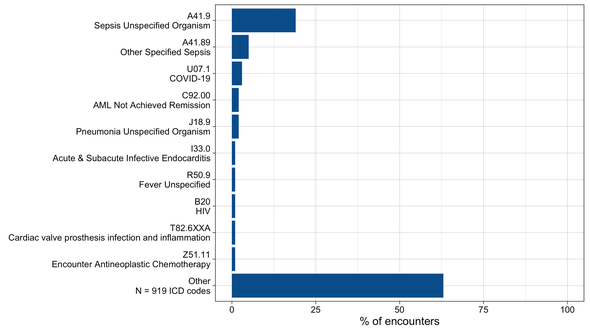


Figure 3: Distribution of immunocompromising conditions

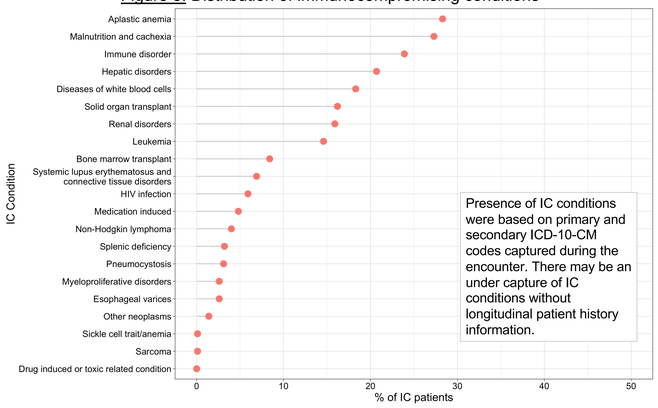
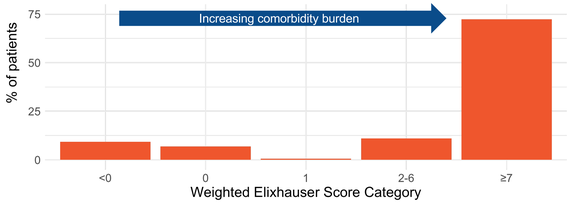


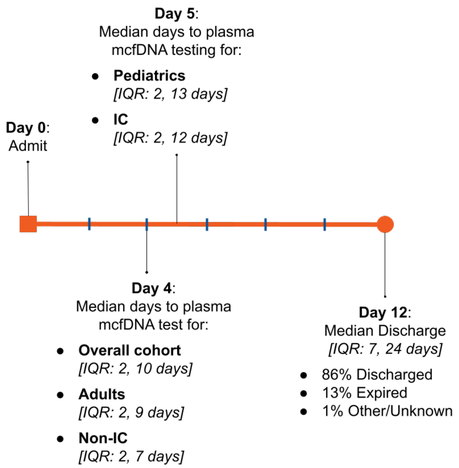
Figure 4: Distribution of Weighted Elixhauser Comorbidity Scores



Results (cont.)

Figure 5 illustrates the timing of events during a hospital encounter.

Figure 5: Timing of events during an encounter



Over half of the patients (N = 1,828, 51%) of patients had evidence of being in the intensive care unit (ICU) during the encounter, with a median of 9 days [IQR: 4, 20] spent in the ICU.

Conclusion

Plasma mcfDNA sequencing is primarily being used in the inpatient setting in a wide variety of clinical scenarios, including the seriously ill and immunocompromised patients, who tend to have broad infectious disease differentials and high morbidity and mortality risks. Understanding the current populations, indications, and timing of mcfDNA sequencing may contribute to developing diagnostic stewardship research and guidelines to optimize impact on clinical outcomes.

References

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