Utilization of comprehensive tumor profiling by race and ethnicity from real-world data of 100,000 cancer patients

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INTRODUCTION

Inequities in cancer patient outcomes and healthcare utilization by race and ethnicity are coming to the forefront. Overcoming these inequities requires a better understanding of their extent across cancer types and medical interventions.

We aimed to measure racial differences in testing for cancer therapy decision support using real-world data (RWD) from 100,000 patients who underwent tumor genomic profiling with the Tempus xT next-generation sequencing assay.

METHODS

Genetic ancestry was inferred from approximately 100,000 de-identified records of cancer patients with diverse histology who underwent tumor genomic profiling with the 648-gene Tempus xT next-generation sequencing assay between 2018-2023.

We used 654 ancestry-informative markers to infer global ancestry proportions at the continental level: Africa, Americas, Europe, East Asia, and South Asia.

To overcome race / ethnicity metadata missingness in RWD, we used a heuristic combining continental ancestry proportions to impute four race/ethnicity labels: Asian, Non-Hispanic (NH) Black, Hispanic/Latino, and NH White, showing a classification error of <2% in patients with available race/ethnicity metadata.

The difference between the expected and observed proportions in the distribution of race/ethnicity categories was calculated by comparing a) overall cohort race/ethnicity distribution or b) the United States Cancer Statistics (USCS) incidence data by state (2015-2019), with the distribution of imputed race/ethnicity in our cohort by cancer type.

When using USCS data, we combined the state level analyses weighting by USCS total incidence counts per state and adjusting by sampling rate in our cohort.

SUMMARY

- Ancestry inference from tumor genomic data can partially compensate for the lack of race/ethnicity information in RWD.
- We observed differences in patient race and ethnicity representation across cancer types, with respect to either overall cohort distributions or USCS incidence statistics that vary by cancer type.
- These differences can be the result of a complex interplay of factors, such as stage of the disease at sequencing, access to early-stage curative therapies, comorbidities/cofactors, access to care, insurance, socioeconomic status, and others.

RESULTS

Figure 1. *Racial/ethic disparities in the distribution of patients sequenced per cancer type with respect to cohort-level distributions*

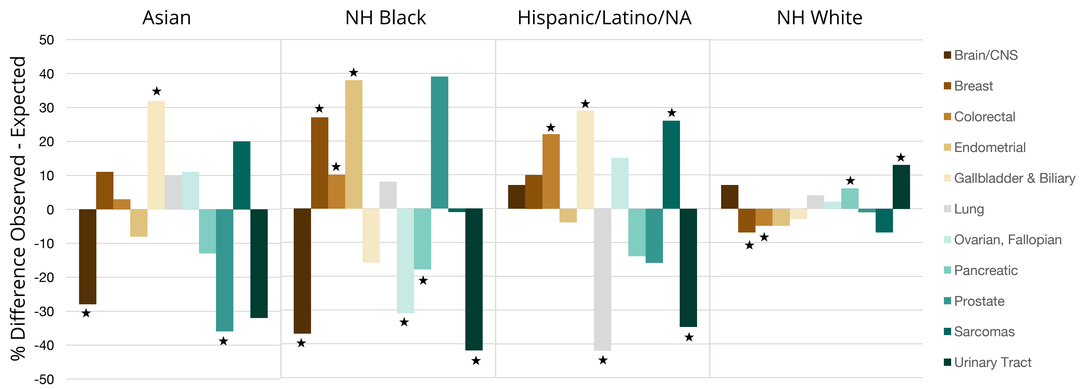

Figure 1. We observed racial/ethnic disparities in the distribution of patients of different imputed race/ethnicity as compared to expectations from the the null hypothesis of no association between race/ethnicity and cancer type (χ2 test of independence, ★ indicates $P<0.05$). The y-axis shows the percentage difference in counts as (observed – expected)/expected x 100.

Sample sizes: Asian = 2,657; NH Black = 6,327; Hispanic/Latino/NA = 4,799; and NH White = 38,299.

Figure 2. *Racial/ethic disparities in the distribution of patients sequenced per cancer type with respect to United States Cancer Statistics (USCS) database of cancer incidence*

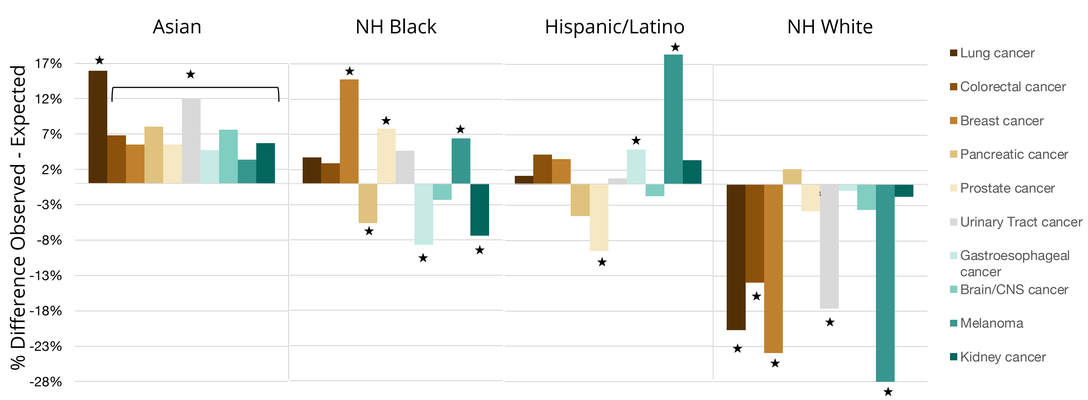

Figure 2. We assessed differences between the observed distribution of racial/ethnic categories per cancer type in our cohort and the expectation based on cancer incidence rates from the USCS database between 2015-2019 at the state level, rolled up as a weighted average adjusted by our sampling rate (number of patients in our cohort from each state). Significance was determined by a one-proportion Z-test, with p-values aggregated across states using Stouffer's Z-score method (★ indicates $P<0.05$).

Sample sizes: Asian = 2,733; NH Black = 7,168; Hispanic/Latino = 5,252; and NH White = 44,464.

Limitations: Our cohort does not represent a uniform sampling of cancer patients across the US.

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