Differences in the molecular landscape of cancer between African American (AA) and Caucasian (CC) cancer patients.

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Background: The racial and ethnic differences in the molecular pathology of cancer have yet to be fully characterized. Here we report on the molecular landscape of tumors classified by race.

Methods: DNA from formalin-fixed paraffin-embedded samples was sequenced using the Illumina NextSeq (Agilent SureSelect XT, 592 gene selected based on COSMIC database) and MiSeq (20 exons, 47 genes) to evaluate mutation and gene amplification. Immunohistochemistry (IHC) evaluated protein expression. The exome aggregation consortium database was evaluated for known exome alterations.

Results: Tumors from 355 AA and 833 CC patients were included. In both groups, the most prevalent cancer types were NSCLC (40.0% vs. 60.0%, p = 0.005), including the V600E variant (7.7% AA vs. 8.5% CC, p = 0.01), BRAF mutations were more frequent in AA than CC (14% vs. 4%, p = 0.006) but higher in Merkel (2.5% (2/67) and 6.5% (4/60), p = 0.035) and PIK3CA mutations (12% vs. 11%, p = 0.01, no difference in distribution of exon 9) was similar. In NSCLC, adenocarcinoma, BRAF mutations were more frequent in AA than CC (14% vs. 4%, p = 0.002); in NSCLC squamous cell carcinoma, PD-L1 tumor expression using SP142 (Ventana) was significantly higher in AA patients (85% in CC CRC patients but only 7.1% in AA CRC patients, p = 0.01). PIK3CA mutation is more than twice as prevalent in AA CRC tumors than with exons 9 mutations being more prevalent than each 20 mutations in both groups.

Conclusions: Differences in the molecular landscape of the most common cancers between AA and CC patients were seen. Observations such as higher BRAF V600E mutation rates in CC CRC may have clinical implications. Further investigation is warranted to explore these differences.

References