Correlation of ctDNA and radiographic imaging features derived from ^{18}F-FDG PET/CT for patients with metastatic melanoma treated with immunotherapy

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Background

- ^{18}F-FDG PET/CT scans are used to assess tumor response for patients undergoing immunotherapy for metastatic melanoma. Evaluating the relationship between features derived from quantitative medical image analysis and markers in blood samples such as circulating tumor DNA (ctDNA) may present an opportunity to discover imaging and blood biomarkers that can influence future patient care.
- This study evaluates the correlation of ctDNA and radiographic imaging features derived from ^{18}F-FDG PET/CT.

Methods

- Whole-body ^{18}F-FDG PET/CT scans from patients with metastatic melanoma between 2014-2020 were retrospectively collected under an IRB-approved protocol.
- Patients received pembrolizumab (n=20), ipilimumab (n=4), nivolumab (n=7), or a combination of ipilimumab and nivolumab (n=19).
- TRAQinform IQ software (AIQ Solutions) (Figure 1) identified and quantified regions of interest suspicious of cancer (lesion-ROI), extracting imaging features including SUV_{max}, SUV_{mean}, and SUV_{total} in baseline (BL) and follow-up (FU) images and the change BL to FU.

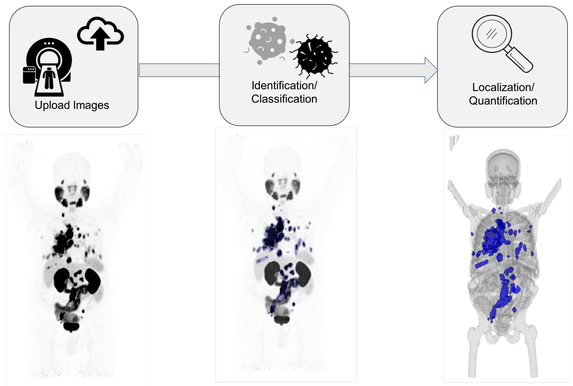

Figure 1. Illustration of TRAQinform IQ analysis process.

- Plasma ctDNA concentration (copies/ml) and frequency abundance (FA) were evaluated for the first sample (1) after immunotherapy had started (between baseline and first on-treatment scan), and the next available sample (2).
- Patients were further grouped by ctDNA mutation for analysis.
- Correlation between imaging features and ctDNA features was assessed using Spearman coefficient (ρ).

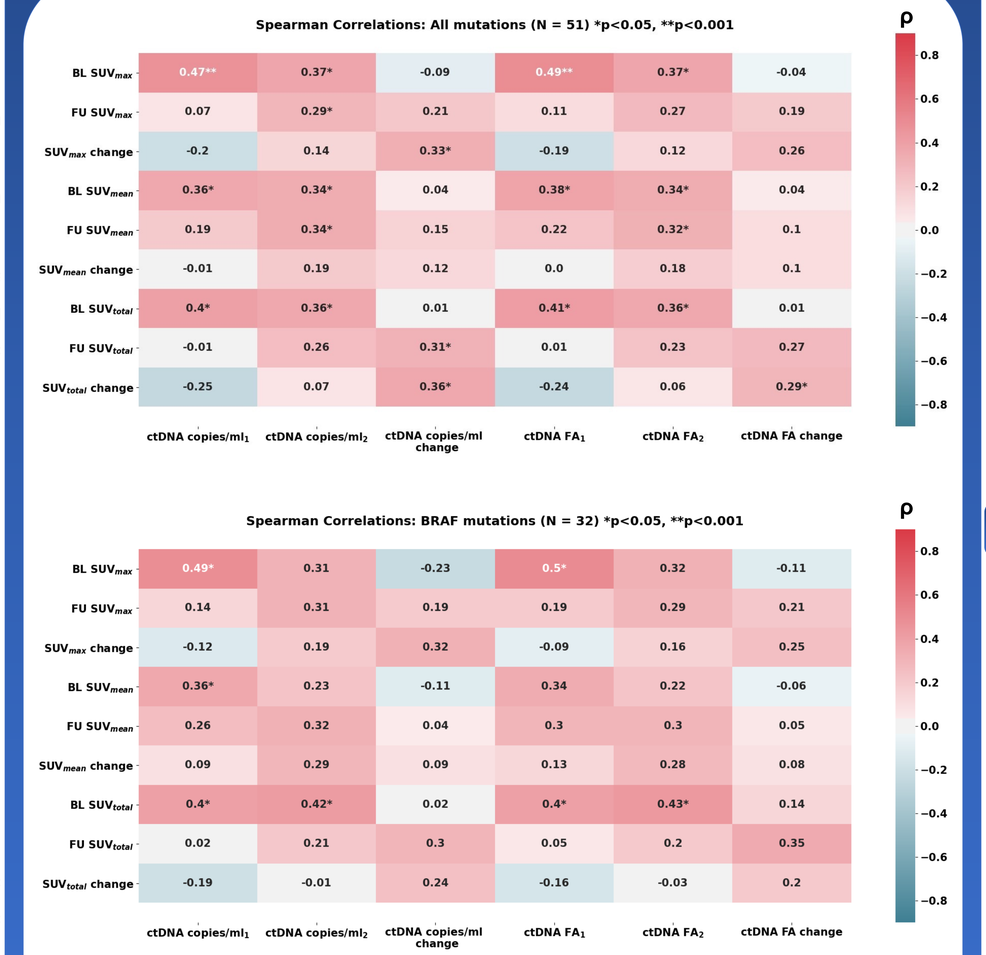

Figure 2. Heatmaps displaying the Spearman Correlation coefficients for all feature combinations.

CONFLICT OF INTEREST: OL and TP are employed by AIQ Solutions (Madison, WI, USA).
AIQ Solutions and UWA have established a collaborative, full-time research fellowship in medical imaging. MD holds one of these AIQ Solutions Fellowships.

Results

- Patient characteristics: 32 males and 19 females with average age of 62 years (range 23 ─ 83).
- For all 51 patients, a moderate correlation was observed between $SUV_{max,BL}$ and ctDNA copies/ml$_1$ ($\rho = 0.47$, $p << 0.001$), $SUV_{max,BL}$ and ctDNA FA_1 ($\rho = 0.49$, $p << 0.001$), and between $SUV_{total,BL}$ and ctDNA FA_1 ($\rho = 0.41$, $p < 0.0024$).
- In BRAF mutation patients (N=32), moderate correlations existed between $SUV_{max,BL}$ with ctDNA copies/ml$_1$ ($\rho = 0.49$, $p = 0.0041$ and ctDNA FA1 ($\rho = 0.5$, $p = 0.0035$), and $SUV_{total,BL}$ with ctDNA copies/ml$_2$ ($\rho = 0.42$, $p = 0.017$), ctDNA FA_1 ($\rho = 0.40$, $p = 0.023$), and ctDNA FA_2 ($\rho = 0.43$, $p = 0.015$).
- All the other combinations displayed weak ($\rho < 0.39$) or non-significant ($p > 0.05$) correlations.

Conclusion

This study shows that in patients with metastatic melanoma receiving immunotherapy, quantitative features from blood biomarkers such as ctDNA correlate with ^{18}F-FDG PET/CT imaging features. Combining blood biomarkers with imaging features that are spatially localizable may strengthen prognostication in this patient group. Further analysis is being performed with additional types of ctDNA mutations.