Integration of CT-based Qualitative and Radiomic Features with Proteomic Variables in Patients with High-Grade Serous Ovarian Cancer: An Exploratory Analysis (TCGA-OV-Proteogenomics)

Summary

Objectives

To investigate the association between CT imaging traits and texture metrics with proteomic data in patients with high-grade serous ovarian cancer (HGSOC).

Methods

This retrospective, hypothesis-generating study included 20 The Cancer Genome Atlas Ovarian Cancer Collection (TCGA-OV) patients with HGSOC prior to primary cytoreductive surgery. Two readers independently assessed the contrast-enhanced computed tomography (CT) images and extracted 33 imaging traits, with a third reader adjudicating in the event of a disagreement. In addition, all sites of suspected HGSOC were manually segmented texture features were computed from each tumour site. Three texture features that represented intra-and inter-site tumour heterogeneity were used for analysis. An integrated analysis of transcriptomic and proteomic data identified proteins with conserved expression between primary tumour sites and metastasis. Correlations between protein-abundance and various CT imaging traits and texture features were assessed using the Kendall tau rank correlation-coefficient and the Mann-Whitney U test, whereas the area under the receiver-operating characteristic curve (AUC) was reported as a metric of the strength and the direction of the association. p values < 0.05 were considered significant.

Results

Four proteins were associated with CT-based imaging traits, with the strongest correlation observed between the CRIP2 protein and disease in the mesentery ($p<0.001$, AUC=0.05). The abundance of three proteins was associated with texture features that represented intra-and inter-site tumour heterogeneity, with the strongest negative correlation between the CKB protein and cluster dissimilarity ($p=0.047$, $t=0.326$).

Conclusion

This study provides the first insights into the potential associations between standard-of-care CT imaging traits and texture measures of intra-and inter-site heterogeneity, and the abundance of several proteins.

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- TCGA-OV

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Beer, L., Sahin, H., Blazic, I., Vargas, H. A., Veeraraghavan, H., Kirby, J., Fevrier-Sullivan, B., Freymann, J., Jaffe, C., Conrads, T., Maxwell, G., Darcy, K., Huang, E., & Sala, E. (2019). **Data from Integration of CT-based Qualitative and Radiomic Features with Proteomic Variables in Patients with High-Grade Serous Ovarian Cancer: An Exploratory Analysis (TCGA-OV-Proteogenomics) [Data set]**. The Cancer Imaging Archive. https://doi.org/10.7937/TCIA.2019.9stoinf1

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