# Investigating Prognostic Biomarkers of Radioresistance Across Various Cancers: Integrating The Cancer Genome Atlas and Genome-wide, Computational Approaches


## Abstract

Radioresistance (RR) refers to the inefficacy of radiation therapy (RT) in controlling the excessive proliferation of cells seen in cancer. Investigations in the molecular underpinnings of RR exist but are scattered across journals. Moreover, while the transcriptomic basis is abundantly explored, the genomic factors contributing to RR are sparse. The current study aims to employ genome-wide association study (GWAS) techniques to identify genomic variants associated with the occurrence of RR across multiple cancers, available in The Cancer Genome Atlas. 13 Cancer types included clinically annotated datasets for response to RT. These were subjected to quality control (QC) measures, statistical association analysis (Fisher's Exact Test, Multiple Testing Corrections) and functional and pathway analysis. Four cancers (Brain Low Grade Glioma, Head and Neck Squamous Cell Carcinoma , Prostate Adenocarcinoma and Lung Adenocarcinoma) were identified to possess multiple variants significantly associated with RR. Moreover, these variants were involved in key pathways of cancer and RR, including DNA damage repair mechanisms and the immunological landscape of the tumour microenvironment. These candidate variants can be subjected to polygenic risk score analysis and experimental validation to allow for clinical implementation of these findings.