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Profiles of Short Chain Fatty Acid Metabolism as Genetic Biomarkers for Primary Brain Gliomas

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Genetic factors play a crucial role in diagnosis and treatment of glioblastoma multiforme (GBM). The key biomarker, isocitrate dehydrogenase (IDH), is associated with better survival rates in its mutated forms than in wild-type. GBM diagnosis is complex due to tumor heterogeneity and risks in sampling, and this highlights the need for non-invasive diagnostic methods. We examined the impact of glioma-specific short chain fatty acid (SCFA) transcellular flux mechanisms for energy production on genotypes and patient survival. We analyzed the genetic profiles of 10 GBM patients (5 mutants and 5 wild-types) using dynamic 18F-fluoropivalate (FPIA) PET scans focusing on 25,202(±14,337) time activity curves(TACs). We identified four distinct metabolic SCFA oxidation profiles within the lesion through time-series k-means clustering and then used deep learning to associate them with GBM genotypes. Our model accurately differentiated mutant and wild-type GBMs with a 96.75%(±3.24) accuracy, when used features extracted from the combination of the first 2 clusters'TACs only. However, its effectiveness significantly decreased when ignoring SCFA metabolism heterogeneity (i.e. the clustered metabolic profiles), as shown by the lower accuracy rates obtained using the full range of FPIA TACs(70.42%±16.25). Of note, the TACs belonging to the cluster with the lowest FPIA SUV, showed the worst performance (23.67%(±16.83)acc) confirming SCFA metabolism to be a potential biomarker of GBM genotype.

Field

Software and quantification

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