Frontal glioma

Although every glioma patient varies in tumor size, location, histological grade, and molecular biomarkers, non-tumoral morphological abnormalities are commonly detected by a statistical comparison among patient groups, missing the information of individual morphological alterations.

Zhang et al. introduced an individual-level structural anomaly detection method for glioma patients and proposed several abnormality indexes to depict individual atrophy patterns. Forty-five patients with a glioma in the frontal lobe and fifty-one age-matched healthy controls participated in the study. Individual structural abnormality maps (SAM) were generated using patients' preoperative T1 images, by calculating the degree of deviation of voxel volume in each patient with the normative model built from healthy controls. Based on SAM, a series of individual abnormality indexes were computed, and their relationship with glioma characteristics was explored. The results demonstrated that glioma patients showed unique non-tumoral atrophy patterns with overlapping atrophy regions mainly located in the hippocampus, parahippocampus, amygdala, insula, middle temporal gyrus and inferior temporal gyrus, which are closely related to the human cognitive functions. The abnormality indexes were associated with several molecular biomarkers including isocitrate dehydrogenase (IDH) mutation, 1p/19q co-deletion and telomerase reverse transcriptase (TERT) promoter mutation. The study provides an effective way to access the individual-level non-tumoral structural abnormalities in glioma patients, which has the potential to significantly improve individualized precision medicine [1].

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Zhang G, Zhang X, Huang H, Wang Y, Li H, Duan Y, Chen H, Liu Y, Jing B, Tie Y, Lin S. Probing individual-level structural atrophy in frontal glioma patients. Neurosurg Rev. 2022 May 4. doi: 10.1007/s10143-022-01800-9. Epub ahead of print. PMID: 35508819.