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PPAR α agonists are in current clinical use as hypolipidaemic agents and show significant antineoplastic effects in human glioblastoma models. To date however, the expression of PPAR α in large-scale glioblastoma data sets has not been examined. Haynes et al aimed to investigate the expression of the transcription factor PPAR α in primary glioblastoma, the relationship between PPAR α expression and patients' clinicopathological features and other molecular markers associated with gliomagenesis.

Using protein immuno-blotting techniques and RT-qPCR, PPAR α was found to be significantly overexpressed in glioblastoma compared to control brain tissue (p=0.032 and p=0.005). PPARA gene expression was found to be enriched in the classical glioblastoma subtype within The Cancer Genome Atlas (TCGA) data set. Although not associated with overall survival when assessed by immunohistochemistry, cross-validation with the TCGA data set and multivariate analyses identified PPARA gene expression as an independent prognostic marker for overall survival (p=0.042). Finally, hierarchical clustering revealed novel, significant associations between high PPARA expression and a putative set of glioblastoma molecular mediators including EMX2, AQP4 and NTRK2.

PPAR α protein is overexpressed in primary glioblastoma and high PPARA gene expression functions as an independent prognostic marker in the glioblastoma TCGA data set. Further studies are required to explore genetic associations with high PPARA expression and to analyse the predictive role of PPAR α expression in glioblastoma models in response to PPAR α agonists ¹⁾.

1)

Haynes HR, White P, Hares KM, Redondo J, Kemp KC, Singleton WG, Killick-Cole CL, Stevens JR, Garadi K, Guglani S, Wilkins A, Kurian KM. The transcription factor PPARalpha is overexpressed and is associated with a favourable prognosis in IDH-wildtype primary glioblastoma. Histopathology. 2016 Dec 7. doi: 10.1111/his.13142. [Epub ahead of print] PubMed PMID: 27926792.

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