Meningioma immune response

Meningiomas are known to be infiltrated by immune cells including microglia, macrophages, B-cells, and T-cells. Several mechanisms contribute to decreased anti-tumor immune response, allowing tumor growth and evasion of the immune system.

The tumor microenvironment of meningiomas often includes post germinal center B cell populations. These tumors invariably include a selected, antigen-experienced, effector T cell population enriched by those that express markers of an exhausted phenotype.

In a study, Wang et al. used single-cell RNA sequencing to perform the first characterization of both non-tumor-associated human dura and primary meningioma samples. First, they revealed a complex immune microenvironment in human dura that is transcriptionally distinct from that of meningioma. In addition, they characterized a functionally diverse and heterogeneous landscape of non-immune cells including endothelial cells and fibroblasts. Through imaging mass cytometry, they highlighted the spatial relationship among immune cell types and vasculature in non-tumor-associated dura. Utilizing T cell receptor sequencing, they showed significant TCR overlap between matched dura and meningioma samples. Finally, they reported copy number variant heterogeneity within the meningioma samples [1)].

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Wang AZ, Bowman-Kirigin JA, Desai R, Kang LI, Patel PR, Patel B, Khan SM, Bender D, Marlin MC, Liu J, Osbun JW, Leuthardt EC, Chicoine MR, Dacey RG Jr, Zipfel GJ, Kim AH, DeNardo DG, Petti AA, Dunn GP. Single-cell profiling of human dura and meningioma reveals cellular meningeal landscape and insights into meningioma immune response. Genome Med. 2022 May 10;14(1):49. doi: 10.1186/s13073-022-01051-9. PMID: 35534852.