COL4A2

The objective of a study was to explore the potential role of COL4A2 (Collagen alpha-2(IV)) in the pathophysiology of cerebral arteriovenous malformation.

Expression and localization of COL4A2 were analyzed on tissue microarrays from bAVM patients (n = 60) by immunohistochemistry. Correlations between COL4A2 levels and clinical parameters were examined with Pearson's test for normally- distributed or Spearman's Rho for not normally distributed data. Comparison between different clinical parameters was performed using a t-test, non-parametric Mann-Whitney U test or Kruskal- Wallis test. Fisher's exact test was used for categorical data.

COL4A2 was mainly expressed beneath the endothelium of vessels in the tunica media of bAVM. This pattern of expression indicates the basement membrane of the vessel walls. High levels of COL4A2 expression correlated with the age at surgery of patients ($p = 0.005$; $R = 0.393$; Spearman's Rho). The age at surgery in young (17-25 years) and old patients (55-76 years) showed a linear correlation; a greater variance of COL4A2 expression was observed in the age group between 26-54 years.

This study reports for the first time the expression of COL4A2 in bAVM and suggests a potential role of COL4A2 in bAVM pathophysiology. These findings contribute to a better understanding of the microenvironment of bAVM and may foster the development of improved therapeutic strategies for this disease [1].

Choi et al. retrospectively reviewed patients with recurrent GBM who received bevacizumab to identify biomarkers for predicting clinical response to bevacizumab. Following defined criteria, the patients were categorized into two clinical response groups, and their genetic and transcriptomic results were compared. Angiogenesis-related gene sets were upregulated in both responders and nonresponders, whereas genes for each corresponding angiogenesis pathway were distinct from one another. Two gene sets were made, namely, the nonresponder angiogenesis gene set (NAG) and responder angiogenesis gene set (RAG), and then implemented in independent GBM cohort to validate our dataset. A similar association between the corresponding gene set and survival was observed. In NAG, COL4A2 was associated with a poor clinical outcome in bevacizumab-treated patients. This study demonstrates that angiogenesis-associated gene sets are composed of distinct subsets with diverse biological roles and they represent different clinical responses to anti-angiogenic therapy. Enrichment of a distinct angiogenesis pathway may serve as a biomarker to predict patients who will derive a clinical benefit from bevacizumab [2].

1)
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2)
Choi SW, Shin H, Sa JK, Cho HJ, Koo H, Kong DS, Seol HJ, Nam DH. Identification of transcriptome signature for predicting clinical response to bevacizumab in recurrent glioblastoma. Cancer Med. 2018 Mar 23. doi: 10.1002/cam4.1439. [Epub ahead of print] PubMed PMID: 29573206.