Molecular profiling of short-term and long-term surviving patients identifies CD34 mRNA level as prognostic for glioblastoma survival - DTU Orbit (30/01/2019)

Despite extensive treatment, overall survival (OS) for glioblastoma (GBM) remains poor. A small proportion of patients present long survival over 3 years, but the underlying molecular background separating these long-term survivors (LTS) from short-term survivors (STS) are insufficiently understood. Accordingly, study aim was to identify independent prognostic biomarkers for survival. Study cohort consisted of 93 primary GBM patients treated with radiation-, chemo- and bevacizumab therapy, among which 14 STS (OS ≤ 12 months) and 6 LTS (OS ≥ 36 months) were identified, all confirmed being IDH wild-type. RNA expression levels in diagnostic tumor specimen for 792 genes were analyzed by NanoString technology. While no differences were found with regard to GBM subtype between LTS versus STS, comparative analysis of individual genes identified 14 significantly differently expressed candidate genes. Univariate analysis in the whole patient cohort found that 12 of these were significantly associated with OS, of which increased IFNG, CXCL9, LGALS4, CD34 and decreased MGMT levels remained significant associated with prolonged OS in multivariate analysis correcting for known prognostic variables. Validation analyses in an independent dataset from the AVAglio study confirmed CD34 as significant in comparative analysis between STS and LTS patients and as an independent prognostic factor. Analysis of this dataset further supported CD34 expression to be associated with improved bevacizumab efficacy, while CD34 immunohistochemistry indicated variation in CD34 expression to result primarily from varying tumor vascularization. Collectively, CD34 expression candidates as a prognostic biomarker in GBM able to identify survival outliers and could also be predictive for efficacy of bevacizumab.