Molecular profiling of GBM patients developed pseudoprogression after chemoradiation treatment

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Introduction

Pseudoprogression (psPD) is now recognized following radiotherapy with concurrent temozolomide (RT/TMZ) for glioblastoma multiforme (GBM). The purpose of this study was to explore biomarker expression profile of GBM patients with psPD.

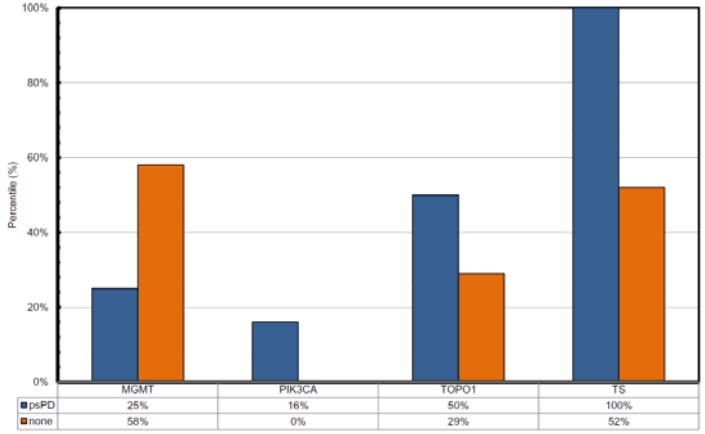
Methods

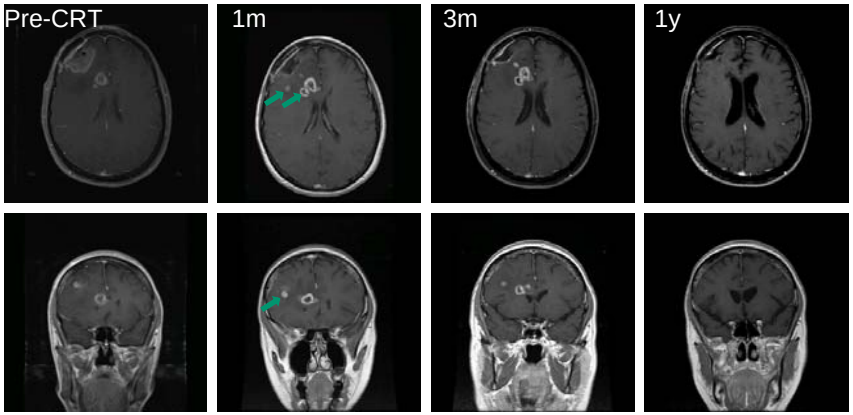
•28 newly diagnosed GBM patients
•Treatment between 01/2012 and 05/2013
•Tumor profiling provided by Caris Life Sciences.
•Immunohistochemistry, FISH, CISH, MGMT promoter methylation and NextGen SEQ (Illumina TruSeq) were performed on formalin-fixed, paraffin-embedded tumor samples.
•MRI images were performed at least every 2 months after finishing chemoradiation treatment.
•The psPD was defined per Revised Assessment in Neuro-Oncology (RANO) criteria.

Results

•A total of 12 patients (41%) developed psPD after chemoradiation (CRT) treatment.
•MGMT methylation was less frequent in patients with psPD as compared to those do not develop psPD, 25% vs 58%, respective.
•TOPO1 expression was more frequent in patients with psPD, 50% vs 29%.
•TS was found to uniformed expressed in patients with psPD (100%), while only expressed 52% of patients without psPD.
•PI3KCA mutation was more frequent in patients developed psPD , though the incidence is still low, 16%. No PI3KCA mutation was found in patients without psPD.
•The expression and mutation rate of other genes examined were similar between patients with and without psPD.

Patient Characteristics	
Age	
Median	60
Range	43-86
Gendar	
Male (%)	26 (62)
Female (%)	16(38)
Extent of Surgery	
Gross total (%)	27
Subtotal (%)	73
Tumor Histology (n)	
Glioblastoma	39
Gliosarcoma	2
Clear Cell Glioblastoma	1
Location (n)	
Frontal	18
Parietal	7
Temporal	14
Occipital	1
Basal Ganglia	3
Cerebellar	1
Tumor Size (cc)	
Median	32.1
Range	8.8-61.4
Avg. FLAIR extent(cc)	
Median	89.6
Range	17.2-410.7





Example of a patient with psPD.

Conclusions

Our findings demonstrate different gene expression profile of GBM patients with pseudoprogression. The observed gene expression profile will be confirmed with a validation data set. This may help identifying patients with pseudoprogression, and thus direct more appropriate treatment.

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