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Mesenchymal stem cells contribute to glioblastoma: A new protocol for isolation emanated from the integrative analysis of public available gene expression data

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Objective

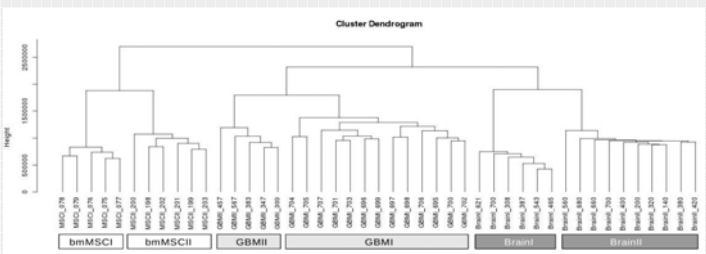
Malignant gliomas have been described as heterogeneous tumors which recruit a broad variety of host progenitor cells. Analyzing public available data for glioblastoma, brain, and mesenchymal stem cells (bmMSCs), we investigated correlations in gene expression. Thus, it was emphasized that MSCs are incorporated in glioma tissue (gbMSCs).

Material and Methods

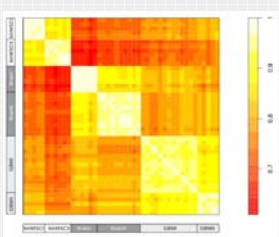
Selected public available data generated in individual experiments with normal brain, glioblastoma (GBM) and bmMSC material on Affymetrix hgu133plus2 arrays were integrated and analyzed in a combined expression matrix. A new protocol for purification of gbMSCs was established, followed by intense FACS analysis and differentiation assays.

Results

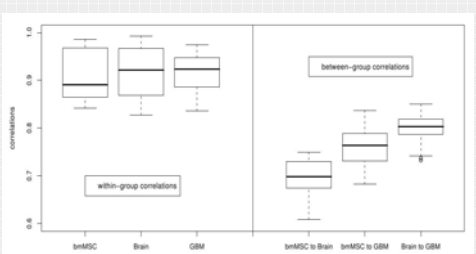
Fig. 1: Combined rank transformed expression data



Hierarchical clustering of the combined rank transformed expression matrix



Map of correlation matrix



Boxplot

Fig. 2: Mean and SD of the selected 66 probesets

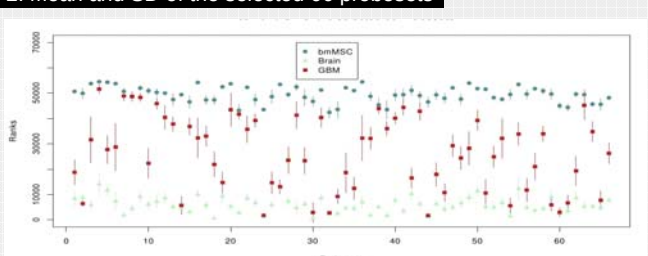
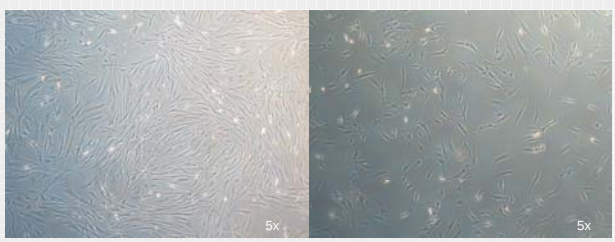
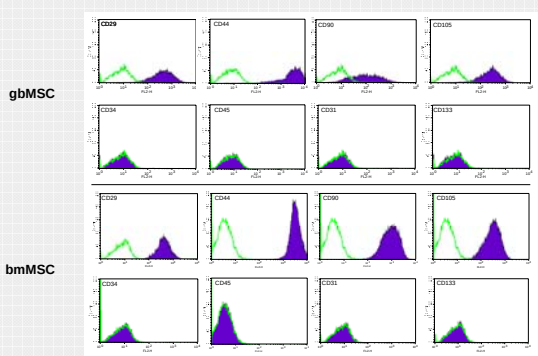


Fig. 3:Spindle morphology of gbMSCs and bmMSCs



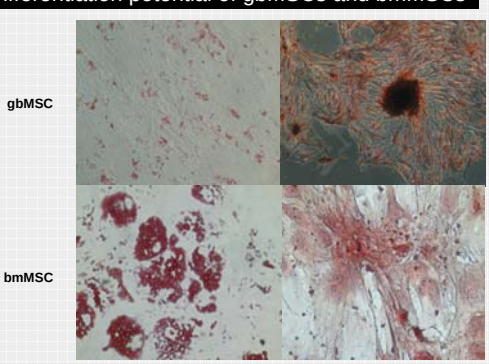
gbMSC bmMSC

Fig. 4: Surface marker profile of gbMSCs and bmMSCs



Flow cytometry analysis

Fig. 5: Differentiation potential of gbMSCs and bmMSCs



adipocyte differentiation osteogenic differentiation

Summary

The correlations of the glioblastoma samples to the bmMSC samples were significantly higher than the correlations of the normal brain group to the bmMSC samples. The majority of these probes (67%) showed significantly higher expression in glioblastoma compared to normal brain. Isolation of gbMSCs was successful in all glioblastomas. Surface marker expression analysis (FACS) and differentiation assays of gbMSCs showed close similarities to bmMSCs.

Conclusion

By intense comparative analysis of public available expression datasets we found close similarities between mesenchymal stem cells and glioblastoma tissue. Demonstrating the presence of gbMSCs in malignant gliomas, we established a new protocol for isolation and expansion of mesenchymal stem cells from tumor tissue. Further studies can now be performed to analyze the functional roles of gbMSCs, contributing to biological properties of malignant gliomas.

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