

Expression of Tissue Factor and Alternatively Spliced Human Tissue Factor in Gliomas Tom C. Zhou; Jennifer E. Hobbs PhD; James P. Chandler MD Department of Neurological Surgery, Feinberg School of Medicine, Northwestern University



Introduction

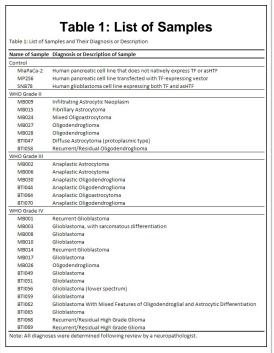
It has long been recognized that cancers, including gliomas and related brain tumors, are associated with thromboembolic diseases and activators of the coagulation cascade. Accumulating evidence has shown that tissue factor (TF), a trans-membrane activator of the blood coagulation pathway, is involved in the regulation of angiogenesis, cell migration, tumor growth and inflammation. A soluble form of TF, known as alternatively spliced human tissue factor (asHTF), is believed to promote cell proliferation and tumor growth. This project examines the expression levels of TF and asHTF in human gliomas, correlates expression levels with tumor grade and begins to assess whether these proteins may be suitable for use as diagnostic markers in the future.

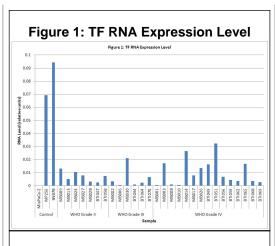
Methods

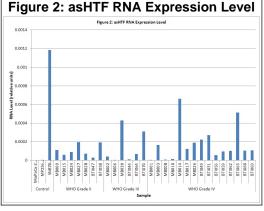
Glial tumors were collected from consenting patients who were undergoing surgical resection at Northwestern Memorial Hospital. Primary cell lines were established from these tumors and RNA was extracted. TF and asHTF RNA levels were analyzed by quantitative RT-PCR and correlated with tumor grade. In this study, 28 samples of varying histological grade (WHO Grade II, III and IV) were used, including astrocytoma, oligodendroglioma and mixed glioma. Samples and controls are shown in Table 1. All outlined approaches and tissue collections were IRB approved.

Learning Objectives

 To determine the RNA expression levels of TF and asHTF in gliomas.
To correlate the mRNA expression levels of TF and asHTF with the histological grade of the tumor.







Results

These results demonstrate the RNA expression levels of TF (Figure 1) and asHTF (Figure 2) in primary glioma cell lines. TF and ashTF expression was not detected in all samples, yet in samples that expressed TF and/or asHTF the expression levels were modest in those diagnosed as Grade II, higher in Grade III and highest expression levels were mainly observed in glioblastomas. Also, the TF expression level correlate closely with asHTF expression level in the same sample.

Conclusion

TF and asHTF have been shown to be associated with cancer progression and angiogenesis. Thus it is important to evaluate their expression levels in glioma. Here, we have screened glioma samples for TF and asHTF RNA expression levels. Further studies will help to elucidate their role in tumor development. Future analyses will examine TF and asHTF protein levels and localization as well as participation in the regulation of cell proliferation and migration. Future studies will also include examinations that will attempt to correlate corresponding patient data and therapeutic responses with TF and asHTF levels. This preliminary data coupled with planned future experiments will help to better understand how TF and asHTF may be used as a prognostic marker and for decisions related to glioma therapies.

Acknowledgements

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References

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