

Predicting meningioma recurrence using spectrochemical analysis of tissues and subsequent predictive computational algorithms

Taha Lilo^{1,*}, Camilo L.M. Morais², Katherine M. Ashton¹, Charles Davis¹, Nihal Gurusinghe¹, Francis L Martin²

¹Royal Preston Hospital, Lancashire Teaching Hospitals NHS Trust, Preston PR2 9HT, UK

²School of Pharmacy and Biomedical Sciences, University of Central Lancashire, Preston PR1 2HE, UK

*taha.lilo@me.com

Introduction Meningioma recurrence remains a clinical dilemma [1]. There is a marked range in the variation amongst surgeons in the follow-up arrangements for their patients even within the same unit. This dilemma comes with a price. It has a significant clinical, logistical and huge financial implication. Hence, the search for predictors for meningioma recurrence has become an increasingly urgent research topic in recent years.

Objective Using spectrochemical analytical methods such as attenuated total reflection Fourier-transform infrared (ATR-FTIR) spectroscopy, our primary objective is to compare the spectral fingerprint signature of WHO grade I meningioma *vs.* WHO grade I meningioma that recurred. Secondary objectives compare WHO grade I meningioma *vs.* WHO grade II meningioma and WHO grade II meningioma *vs.* WHO grade I meningioma recurrence.

Materials and Methods Our selection criteria included convexity meningioma only restricted to Simpson grade I & II only and WHO grade I & grade II only with a minimum 5 years follow up. With appropriate ethics, we obtained tissue from tumour blocks retrieved from the Brain Tumour NorthWest (BTNW) biobank. These were sectioned onto slides and de-waxed prior to ATR-FTIR or Raman spectrochemical analysis. Derived spectral datasets were then explored for discriminating features using computational algorithms in the IRootLab toolbox within MATLAB [2]; this allowed for classification and feature extraction.

Results After analysing the data using various classification algorithms such as PCA-LDA or SVM with cross-validation to avoid over-fitting of the spectral data, we can readily and blindly segregate those meningioma samples that recurred from those that did not recur in the follow-up timeframe. The forward feature extraction classification algorithms generated results that exhibited excellent sensitivity and specificity, especially with spectra obtained following ATR-FTIR spectroscopy. Our secondary objectives remain to be fully developed.

Discussion We demonstrate a reagent-free, non-destructive and low-cost tool that could give predictive information regarding the propensity of a meningioma to recur. This has enormous clinical potential with regards to being developed for intra-operative real-time assessment of disease.

References

1. Gajjar K *et al.* (2012) *Anal Methods* **5**:89-102.
2. Trevisan J *et al.* (2013) *Bioinformatics* **15**:1095-1097.