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Raman Microspectroscopy and Machine Learning: A Perspective for Tissue Remodelling Characterization

N.N. Kunchur[1,2], T.L. Hackett[3], and L.B. Mostaco-Guidolin[1,2]

[1] Carleton University/Systems and Computer Engineering, Ottawa, Canada
[2]Tissue Engineering and Applied Materials (TEAM) Hub, Ottawa, Canada
[3]University of British Columbia/Anesthesiology Pharmacology & Therapeutics, Centre for Heart Lung Innovation, Vancouver, Canada

Abstract— **Using novel technologies of the multimodal RM-SHG imaging system and machine learning (ML), we explore tissue remodelling. With ML, the imaged biochemical spatial maps of the tissues are characterized, and the main biomarkers associated with remodelling are identified.**

Keywords— Tissue Remodelling, Raman Spectroscopy, Second Harmonic Generation, Machine Learning.

I. Introduction

Tissue fibrosis is a major hallmark of several chronic diseases including atherosclerosis, COPD, cystic fibrosis and asthma. Fibrosis is characterized by the excessive accumulation of extracellular matrix (ECM) proteins; particularly collagen I [2]. Evidence suggests fibrosis leads to tissue stiffening and a reduction in organ function [3]. Traditional methods used to visualize tissue remodelling lack specificity in detailing the biochemical and structural information of ECM deposition. A novel, label-free multimodal imaging system (multimodal RM-SHG) leverages the technologies of both Raman microspectroscopy (RM) and Second Harmonic Generation (SHG) to curate high-resolution, biochemically specific maps of ECM deposition in tissue remodelling. Due to the complexity of the obtained data, the development of novel approaches based on ML strategies is necessitated.

II. Methodology

In this work, tissue sections from control and fibrotic lungs not suitable for transplantation of both sexes and varying ages are evaluated. Chemical structures of the airway tissue's epithelium (EP), basement membrane (BM), and lamina propria (LP) are acquired using RM, with simultaneous visualization of fibrillar collagen deposition through SHG (shown in Figure 1). Large area scans from a defined µm x µm bounding box, allows for the acquisition of spectra unique to the EP, BM and LP of the airways. Each pixel within the defined area is representative of a spectra unique to that location, allowing for the efficient region sampling of airway-layer specific spectra. Supervised ML and deep-learning-based models (including MLP networks and CNNs) support the generation of an open-source library of airway-specific spectral signatures. The ML workflow will support the identification of biomarkers related to fibrotic remodelling and discern the roles of active ECM-specific biomolecules.

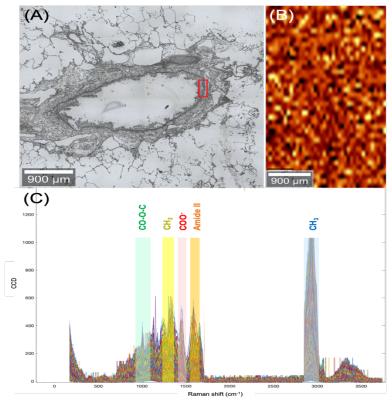

Fig. 1. (A) Representative image of a fibrotic tissue section, with a bounding box defined for the region-specific acquisition of spectra with (B) depicting fibrillar collagen identified by SHG distribution in the same area and (C) capturing the unique biochemical Raman spectra associated with each pixel within the bounding box. Common chemical signatures are identified.

III. Results

Preliminary analysis denotes spectral differences between the sectioned lung tissue layers: EP, BM and LP. Each layer presents a unique biochemical Raman signature with varying fibrillar collagen profiles. Thus, confirming the presence of specific ECM proteins associated with the dysregulation of tissue remodelling.

IV. Conclusions

With the novel combination of multi-modal RM-SHG and ML, we can objectively characterize the role of ECM proteins in chronic respiratory diseases, often characterized by fibrotic response. With the distinction of ECM protein activity amongst the three tissue layers, therapies capable of minimizing tissue scarring observed in the onset of fibrosis can be minimized with greater specificity.

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Conflict Of Interest

The authors declare that they have no conflict of interest.

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