Characterizing the Biomolecular Signature of Extracellular Vesicles using (Surface Enhanced) Raman Spectroscopy

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Project description :

Extracellular vesicles (EVs) are small membrane objects that are central to cell-cell communication and exchange between the intra- and the extracellular medium of cells. Often, EVs can be separated in two main groups [1–3]: exosomes (30-100nm in diameter) corresponding to the exocytosis of endosomes, contained beforehand in multivesicular body; ectosomes or microvesicles, vesicles newly formed at the plasma membrane (100-1000nm in diameter) [1] and apoptotic bodies secreted during apoptosis (50-5000nm in diameter). The nature and content of EVs differ according to the secreting cell type, their role, mechanism and trigger of formation [4]. By recapitulating parental cell biological properties, EVs have a high potential for diagnostic [5–8] and therapeutic purpose [9–12]. Even if they are easy-to-access (for instance through the sampling of biofluids), the complexity of their biological signature made them difficult to integrate into the clinical workflow. One limitation being that biofluid analysis is usually correlated with one or several specific and known biomarkers.

Raman spectroscopy (RS) is a non-destructive laser-based technique that uses the non-linear light scattering to access information about the molecular composition of measured / imaged samples. RS was proven to be powerful for the diagnosis and characterization of several diseases, including bacterial infection [13] and cancers [14–16]. On the opposite, RS applied for the characterization of EVs is still in its infancy especially for purified EVs, with only few applications in oncology [17,18] or tissue engineering [19], where analysis were done ion dried samples. While spontaneous RS offers the advantage of being label-free, the signal may be overwhelmed by auto-fluorescence. One way to counter that is to do Surface Enhanced Raman Spectroscopy (SERS) by using nanoparticles to locally enhance the Raman signal.

The aims of this project will be to:

(1) Develop a protocol for the measurement of (wet) purified EVs using RS or SERS,

(2) Build a RS library for EVs of different origin (cancer, fibroblastic, endothelial, mesenchymal, immune, …)

(3) Identify specific signature of each EV type and build an automatic classifier using Machine Learning algorithms.

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