Contribution ID : **34** Type : **Poster**

Neutron scattering unravels the structure of tunable fibrin networks

Thursday, 12 November 2020 17:59 (1)

Three-dimensional (3D) in vitro cell culture in natural hydrogels has shown promising results in tissue engineering and biophysics as it mimics the native extracellular matrix [1]. However, compared to biosynthetic materials, the often uncontrollable and unstable structural and mechanical properties of natural hydrogels have hindered their wide use. Fibrin is a natural fibrous material that has drawn much interest in tissue engineering and has been employed as a scaffold for 3D cell culture because of its inherent advantages. Yet, the batch-to-batch variation, rapid degradation, uncontrollable structural and mechanical properties are the main shortcomings [2].
To overcome these shortcomings, we have established a new well-defined fibrin network with tuneable architecture and mechanical properties by employing two potent recombinant snake venom proteins. Firstly, a Procoagulant Snake Venom Protein (PSVP), which rapidly activates the thrombin precursor prothrombin, is employed for fibrin network formation; a second recombinant snake venom protein, Anti-fibrinolytic Snake Venom Protein (ASVP) is also utilized to control the fibrin degradation. Initially, confocal laser scanning fluorescence microscopy (CLSM) was employed to characterize the micro-scale structural properties. However, while CLSM can provide detailed information about the network structure, the optical resolution of CLSM is not sufficient to visualize the internal structure of individual fibers. Moreover, the fluorophores that are required for the detection can potentially interfere with the fibrin polymerization.
Therefore, we utilised combined small angle neutron scattering (SANS) and ultra-small angle neutron scattering (USANS) techniques to characterize and verify our new defined fibrin network system including internal structure of the individual fibres and the structure of the fibrin networks [3].
The combined SANS and USANS data of fibrin networks revealed details of the hierarchical structure at multiple length scales associated with the network, fibres and internal proto-fibrils, previously not accessible by CLSM, especially in the case of internal fibre structure. This data is key for correlating the network structure and the mechanical properties, which are fundamental for cellular responses including cell proliferation, migration and differentiation.

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Level of Expertise

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Yes

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Session Classification : Poster Session

Track Classification : Advanced Materials