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The proteomic landscape of desmoid tumours

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Desmoid tumours are characterised by an unpredictable and variable natural history with periods of tumour growth, stable disease and even spontaneous regression. While there has been extensive research in the genomics and transcriptomics of this disease, proteomics analysis has been limited. This gap in knowledge is due in part to the analytical challenges associated with profiling of formalin-fixed paraffin embedded (FFPE) archival specimens and the relatively large sample requirements for this analytical technique. We have developed a proteomic pipeline for the analysis of FFPE tissue specimens which has been applied to >500 soft tissue tumours including a cohort of patients with desmoid tumours. In this talk, I will describe our studies to employ comprehensive proteomics to characterise, in unprecedented detail, the desmoid tumour proteome in clinical specimens from The Royal Marsden. We show that desmoid tumours have a distinct proteomic profile compared to 10 other soft tissue tumour histological subtypes with an enrichment of extracellular matrix signatures. I will also discuss our efforts to dissect the molecular heterogeneity in desmoid tumours including the identification a subset of proteins which are enriched in tumours that follow an aggressive course of disease. We anticipate that this research will deepen our biological understanding of the protein networks operating in desmoid tumours as well as contribute to the discovery of biomarkers for improved clinical management of these patients.