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Data Article

Characterization of the porcine synovial fluid proteome and a comparison to the plasma proteome

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ABSTRACT

Synovial fluid is present in all joint cavities, and protects the articular cartilage surfaces in large by lubricating the joint, thus reducing friction. Several studies have described changes in the protein composition of synovial fluid in patients with joint disease. However, the protein concentration, content, and synovial fluid volume change dramatically during active joint diseases and inflammation, and the proteome composition of healthy synovial fluid is incompletely characterized.

We performed a normative proteomics analysis of porcine synovial fluid, and report data from optimizing proteomic methods to investigate the proteome of healthy porcine synovial fluid (Bennike et al., 2014 [1]). We included an evaluation of different proteolytic sample preparation techniques, and an analysis of posttranslational modifications with a focus on glycosylation. We used pig (*Sus Scrofa*) as a model organism, as the porcine immune system is highly similar to human and the pig genome is sequenced. Furthermore, porcine model systems are commonly used large animal models to study several human diseases.

In addition, we analyzed the proteome of human plasma, and compared the proteomes to the obtained porcine synovial fluid proteome. The proteome of the two body fluids were found highly similar, underlining the detected plasma derived nature of many synovial fluid components. The healthy porcine synovial fluid proteomics data, human rheumatoid arthritis synovial fluid proteomics data used in the method optimization, human plasma proteomics data, and search results, have been deposited to the

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ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD000935.

Specifications table

Subject area	*Biology*
More specific subject area	*An analysis of the protein component of porcine synovial fluid, and a comparison to human plasma.*
Type of data	*Raw files and text/excel files*
How data was acquired	*Mass spectrometry liquid chromatography* *Two different high-resolution/high-accuracy mass spectrometer systems were used: TripleTOF 5600 (SCIEX) and Q Exactive (Thermo Scientific)*
Data format	*Raw and analyzed data.*
Experimental factors	*Human and porcine synovial fluid as well as human plasma was analyzed.*
Experimental features	*Synovial fluid was digested using trypsin with in solution digestion, filter aided sample preparation, and in-gel digestion protocols. Plasma was digested using filter aided sample preparation. The purified peptides were analyzed by electrospray ionization liquid chromatography mass spectrometry.*
Data source location	*Steen & Steen Laboratory, Enders Research Building, Boston Children's Hospital, 320 Longwood Ave, Boston, MA, USA.*
Data accessibility	The MS proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD000935 [2–5]. Direct download link: http://www.ebi.ac.uk/pride/archive/projects/PXD000935

Value of the data

- Increase our knowledge of synovial fluid in healthy state, usable for future studies on joints and joint disease.
- Investigate the plasma-derived nature of many synovial fluid proteins.
- Identify differences and similarities between the porcine proteome and the human proteome, usable in assessing pigs as a model system for human diseases.
- Information regarding the proteome of synovial fluid from a healthy joint will form the basis for research in joint diseases, such as osteoarthritis and rheumatoid arthritis.

1. Experimental design

Synovial fluid is an ultrafiltrate of plasma, and the two body fluids share many similarities in terms of protein composition [6,7]. To investigate the protein component of healthy synovial fluid, we analyzed the proteome of synovial fluid from healthy porcine knee joints. We used pig as a model organism, as the pig proteome is similar to humans [1]. The protein concentration in synovial fluid from healthy knee joints is approximately 25 mg/mL, and albumin constitutes approximately 12 mg/mL [8–12]. Because high-abundant proteins might hinder the identification of lesser abundant ones, most work conducted on synovial fluid has employed immunodepletion strategies and/or gel-based separation techniques [1]. However, in-gel digestion strategies are, while robust, typically not compatible with high-throughput proteome analyses