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Effective protein extraction combined with data independent acquisition analysis reveals a comprehensive and quantifiable insight into the proteomes of articular cartilage and subchondral bone

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SUMMARY

Objective: The objectives of this study was to establish a sensitive and reproducible method to map the cartilage and subchondral bone proteomes in quantitative terms, and mine the proteomes for proteins of particular interest in the pathogenesis of osteoarthritis (OA). The horse was used as a model animal.
Design: Protein was extracted from articular cartilage and subchondral bone samples from three horses in triplicate by pressure cycling technology or ultrasonication. Digested proteins were analysed by data independent acquisition based mass spectrometry. Data was processed using a pre-established spectral library as reference database (FDR 1%).
Results: We identified to our knowledge the hitherto most comprehensive quantitative cartilage (1758 proteins) and subchondral bone (1482 proteins) proteomes in all species presented to date. Both extraction methods were sensitive and reproducible and the high consistency of the identified proteomes (>97% overlap) indicated that both methods preserved the diversity among the extracted proteins. Proteome mining revealed a substantial number of quantifiable cartilage and bone matrix proteins and proteins involved in osteogenesis and bone remodeling, including ACAN, BGN, PRELP, FMOD, COMP, ACP5, BMP3, BMP6, BGLAP, TGFB1, IGF1, ALP, MMP3, and collagens. A number of proteins, including COMP and TNN, were identified in different protein isoforms with potential unique biological roles.
Conclusion: We have successfully developed two sensitive and reproducible non-species specific workflows enabling a comprehensive quantitative insight into the proteomes of cartilage and subchondral bone. This facilitates the prospect of investigating the molecular events at the osteochondral unit in the pathogenesis of OA in future projects.

Introduction

Osteoarthritis (OA) is the final stage of joint failure with chronic inflammation of synovial tissue, subchondral bone (SB) damage and cartilage erosion, but the temporal relationship of the pathological events in OA is still largely unknown[1]. Experimental data have shown perforations in the SB plate in the early phases of OA, followed by increased vascular invasion into the cartilage, and cartilage fibrillation[2–6]. Other studies showed simultaneous onset of OA pathology in articular cartilage and SB[7,8]. Although loss of cartilage is a prominent feature of OA, it is now commonly accepted that all layers of the osteochondral unit – the articular cartilage, SB, and the calcified layer in-between – are affected, and that a cross-talk at the bone-cartilage interface is involved in the pathogenesis[9,10]. Given that cartilage and bone pathology are strongly

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associated in OA initiation and progression, it is of great importance to understand the molecular changes in the osteochondral unit. A focus paper from 2016[11] emphasized the need of high-throughput proteomics methods to study the disturbances in SB and the bone-cartilage crosstalk in OA, but also recognized the technical challenges of protein extraction from especially bone, due to the high abundance of collagens and minerals. Various homogenization, extraction, and separation protocols have been tested for this purpose, but with varying and relatively low protein yield[12–18]. Major disadvantages of the techniques used so far are the high amount of tissue needed, that some techniques are very time consuming, and/or that some cause selective or partial loss of specific groups of proteins. New homogenization and extraction methods are thus warranted. A recent refined method based on pressure cycling technology (PCT) has proved useful for reproducible, rapid, and effective extraction of proteins from various biological samples, even with minimal sample amount[19]. Another method successfully used to disrupt small tissue samples and extract proteins is based on ultrasonication (US)[20]. These two methods displayed consistent and comparable results when processing soft tissue[20], but the efficiency when processing harsher material, such as cartilage and SB, has not been investigated.

Mass spectrometry (MS)-based proteomics enables detection and quantification of thousands of proteins across various biological samples in an unbiased fashion and circumvents the use of antibodies. The new generation of mass spectrometers and improvement of bioinformatics tools have facilitated the development of the analysis approach called data independent acquisition (DIA). Compared to the standard MS methods, where the proteins precursor ions are selected for analysis based on abundance, DIA is based on analysis of *all* precursor ions, thus giving a more comprehensive and reliable coverage of the proteome. Protein identification relies on comparing the DIA spectra to annotated sets of spectra in a spectral library and quantification is based on the extracted precursor intensity of the DIA spectra[21].

Biological events that lead to progressive joint degradation are difficult to evaluate in humans[22]. While use of smaller mammals is most common as animal models in OA research, large animal models provide more clinically relevant results[23,24], and the horse has been suggested to be the most relevant of all model animals[25,26]. Similar to humans, the horse is a long-lived, athletic species, which shows low intrinsic capacity for repair of cartilage defects[27].

In this study, we used either PCT or US in combination with DIA-MS analysis to obtain and investigate the equine articular cartilage and SB proteome. The robustness and sensitivity of the two workflows were evaluated, and the proteomes mined for proteins of particular interest for the pathogenesis of OA. Using these workflows, we have mapped the hitherto most comprehensive quantitative cartilage and SB proteomes for horses.

Method

Articular cartilage and SB from three biological replicates (Suppl. 1), each in three technical replicates, were independently homogenized by PCT and US followed by DIA-MS analysis and data processing based on a pre-established spectral library (Fig. 1, Suppl. 2).

Sampling

18 cartilage and 18 SB samples were obtained from the fetlock (metacarpophalangeal) of three research horses post-euthanasia from unrelated terminal studies (Suppl. 1). All sampling procedures were approved by the ethics and welfare committee of Department of Veterinary Clinical Sciences, University of Copenhagen, and

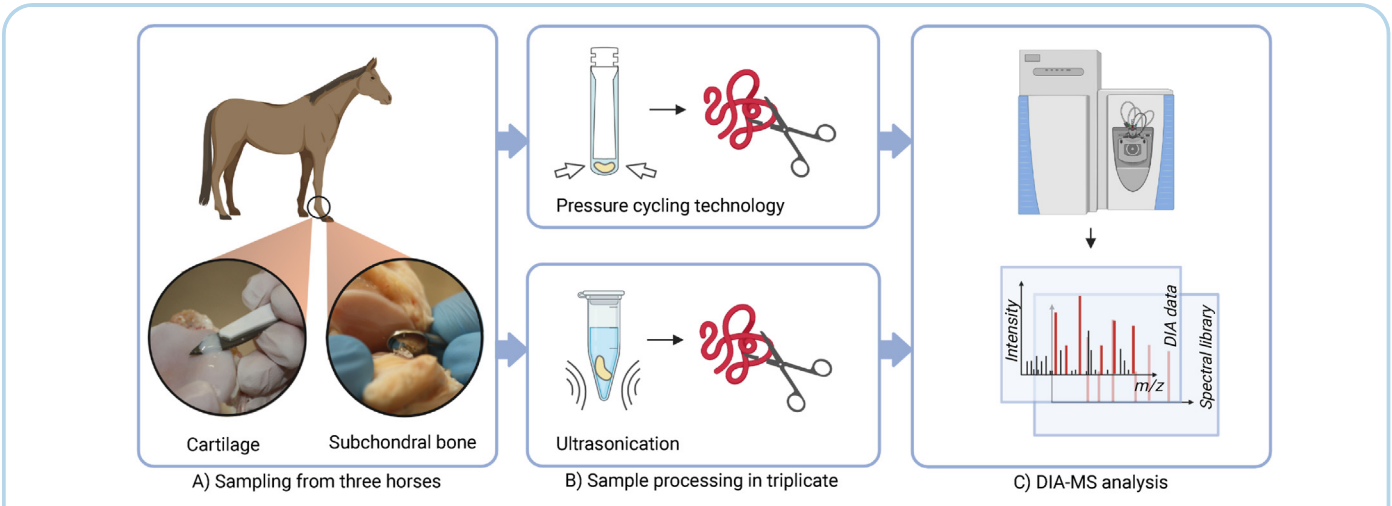

Fig. 1

Osteoarthritis and Cartilage

A) Articular cartilage was harvested by dissecting thin flakes from the surface of the joint by use of a clean scalpel blade. After careful removal of all visible cartilage from the joint surface, subchondral bone was sampled by scraping the surface using a Volkmann bone curette (see suppl. one for magnified pictures of the tissue sampling techniques). B) Samples were homogenized by pressure cycling technology or ultrasonication and the extracted proteins digested, before C) analysis by data independent acquisition (DIA) based mass spectrometry and data analysis. *Created with BioRender.com.*

procedures were carried out according to the Danish Act on animal experiments.

Within 1 h post mortem, the skin was removed and the joint carefully opened with a scalpel blade. Cartilage was harvested by dissecting thin flakes from the surface of the joint by use of a clean scalpel blade (Fig. 1, Suppl. 1) and washed in PBS to remove synovial fluid (SF). After careful removal of all visible cartilage from the joint surface, SB was sampled by curetting the surface using a Volkmann bone curette (Fig. 1, Suppl. 1). Samples were snap frozen in liquid nitrogen and stored at −80°C.

Sample processing

Homogenization by ultrasonication

Approximately 10 mg tissue was dissolved in 4 M guanidine hydrochloride (GuHCl) (Sigma–Aldrich) in 50mM HEPES (pH 7.8) (Sigma–Aldrich) and homogenized by US (Bioruptor Pico, Diagenode) for 30 min (60 cycles, 30 s ON and 30 s OFF) at 4°C. Disulphide bonds were reduced (10mM TCEP (Sigma–Aldrich), 30 min, 37°C, 300 rpm), alkylated (40mM chloroacetamide (CAA) (Sigma–Aldrich) 30 min, room temperature (RT)), and 50mM HEPES (pH 7.8) added to a final concentration of 1.2 M GuHCl. Protein C (PROC)oncentration was measured using the Bradford assay according to the manufactures protocol (http://www.bio-rad.com/webroot/web/pdf/lsr/literature/Bulletin_6835.pdf). All extracted protein was digested with Lys C (1:100 w/w) (Lysyl endopeptidase, #125-05061, Wako) (2 h, 37°C, 500 rpm), and 50mM HEPES (pH 7.8) added to a final concentration of 0.8 M GuHCl, followed by tryptic digest (1:20 w/w) (Trypsin Gold, V5280, Promega) over night (17 h, 37°C, 500 rpm). The supernatant was recovered after centrifugation for 10 min at 13,000*g* and the digestion quenched by addition of 10% trifluoroacetic acid (TFA) (Sigma–Aldrich) to pH 2–3. Samples were stored at −80 (Suppl. 3).

Homogenization by pressure cycling technology

The tissue samples (2.5–3 mg corresponding to 2–3–1 mm^3 cubes) were transferred to PCT micro-tubes, dissolved in 30 μL 4 M GuHCl in 50mM HEPES (pH 7.8), and homogenized by PCT (Barocycler 2320ETX, Pressure Biosciences Inc.) for 60 min at 4°C (60 cycles, 45 kpsi for 50s, atmospheric pressure for 10 s). Disulphide bonds were reduced and alkylated, samples diluted with HEPES and PROConcentration measured as described in the section above. All extracted protein was digested with Lys C (1:100 w/w) by PCT (45 min, 33°C (45 cycles, 20 kpsi for 50s, atmospheric pressure for 10 s)) followed by addition of 50mM HEPES (pH 7.8) to a final concentration of 0.8 M GuHCl and tryptic digest (1:20 w/w) by PCT (90 min, 33°C (90 cycles, 20 kpsi for 50s, atmospheric pressure for 10s)). The supernatant was recovered and the digestion quenched as described in the section above. Samples were stored at −80 (Suppl. 4).

Desalting

The SOLAμ vacuum manifold and solid phase extraction (SPE) micro elution method (SOLAμ) (Thermo Scientific) was used to desalt the samples as follows. Columns were conditioned with 200 μL acetonitrile (ACN) (Sigma–Aldrich), equilibrated with 400 μL 0.1% TFA, and 250 μL of the sample was loaded diluted in 250 μL 0.1% TFA. The sample on column was washed with 500 μL 0.1% TFA, then 200 μL 0.1% FA (Sigma–Aldrich) and eluted with 2x 50 μL 50% ACN, 0.2% FA. The samples were vacuum dried and resuspended in 50 μL HPLC-water with 2% ACN 0.2% FA and synthetic peptides (1:20 v/v) (iRT peptide kit, Biognosys AG) for retention time calibration. The peptide concentration was measured by use of the Pierce Quantitative Colorimetric Peptide Assay (Thermo Scientific) according to the manufactures protocol (https://assets.thermofisher.com/TFS-Assets/LSG/manuals/23275_quantpeptide_color_UG.pdf).

Data independent acquisition mass spectrometry analysis

Samples (~1 μg) were separated on a PepMap RSLC C18 analytical column (75 μm × 50 cm, 2 μm, 100 Å, nanoViper, Thermo Scientific) using the EASY-nLC™ 1200 liquid chromatography system (Thermo Scientific) coupled in-line with a Q Exactive HF-X Hybrid Quadropole-Orbitrap mass spectrometer (Thermo Scientific). Separation was achieved by running constant flow rate of 350 nL/min in 0.1% formic acid/99.9% water and a 120 min gradient from 10% to 90% (10–30% for 90min, 30–45% for 20min, 45–90% for 1min, 90% for 10min) elution buffer (80% acetonitrile, 0.1% formic acid, 19.9% water). A DIA operated under Xcalibur 4.1.31.9 was applied to record the spectra. The full scan MS spectra (340–1400 m/z) were acquired with a resolution of 60,000 after accumulation to a target value of 3e6 and a maximum injection time of 100 ms. The MS/MS data was recorded by 32 full fragmentation scans, using an isolation window adjusted to the number of precursors (Suppl. 5). The precursor ions within each isolation window were fragmented using HCD with a resolution of 30,000 applying an AGC of 1e6 and a maximum injection time of 120 ms.

Data analysis

The DIA-MS data from cartilage and SB samples were searched as individual batches based on a pre-established spectral library. The spectral library covered joint related tissue and SF from nine horses. A detailed description of sample processing and analysis for the spectral library is included in Supplementary 2. The software Spectronaut (v13.11.200127.43655, Biognosys) was used to generate the spectral library from Pulsar and search the DIA-MS data with the equine proteome from uniprot (UP000002281 downloaded 01-23-20) as reference database. Trypsin was specified as the enzyme, up to two missed cleavages and a peptide length of 7–52 amino acids was allowed. False discovery rate (FDR) was controlled at 1% for both precursor and protein group levels. Other parameters were kept at default settings. The data was median normalized in Spectronaut and further processed in R (v4.0.2). The spectral library represented 44,922 unique peptides covering 3147 protein groups with high confidence (1% FDR) (Suppl. 2).

Venn diagrams were made in Venny v2.1, Metascape was used for GO term cluster analysis on biological processes[28], and additional graphics were created in GraphPad Prism v8.4.3. The MS data have been deposited to the ProteomeXchange Consortium via the PRIDE[29] partner repository with the dataset identifier PXD025882 and is publicly available.

Results

Using our sample preparation and MS workflows, we identified almost 2000 (1953) distinct proteins from cartilage and SB, 1232 of which were present in samples from both tissues independent of homogenization method [Fig. 2(A)].

Sensitivity and reproducibility of the workflows

Cartilage

The average amount of protein extracted per mg cartilage was similar for both processing methods (PCT: 12.2 μg/mg; US: 12.1 μg/mg). The proteome recorded from cartilage comprised 1758 different proteins, whereby PCT yielded a mean number of 1468 proteins and US 1525 protein identifications on average (Suppl. 6). For each horse, more than 77% of the identified proteins were present in all three technical replicates. The median CV for protein quantification for technical replicates processed by PCT was 18%,

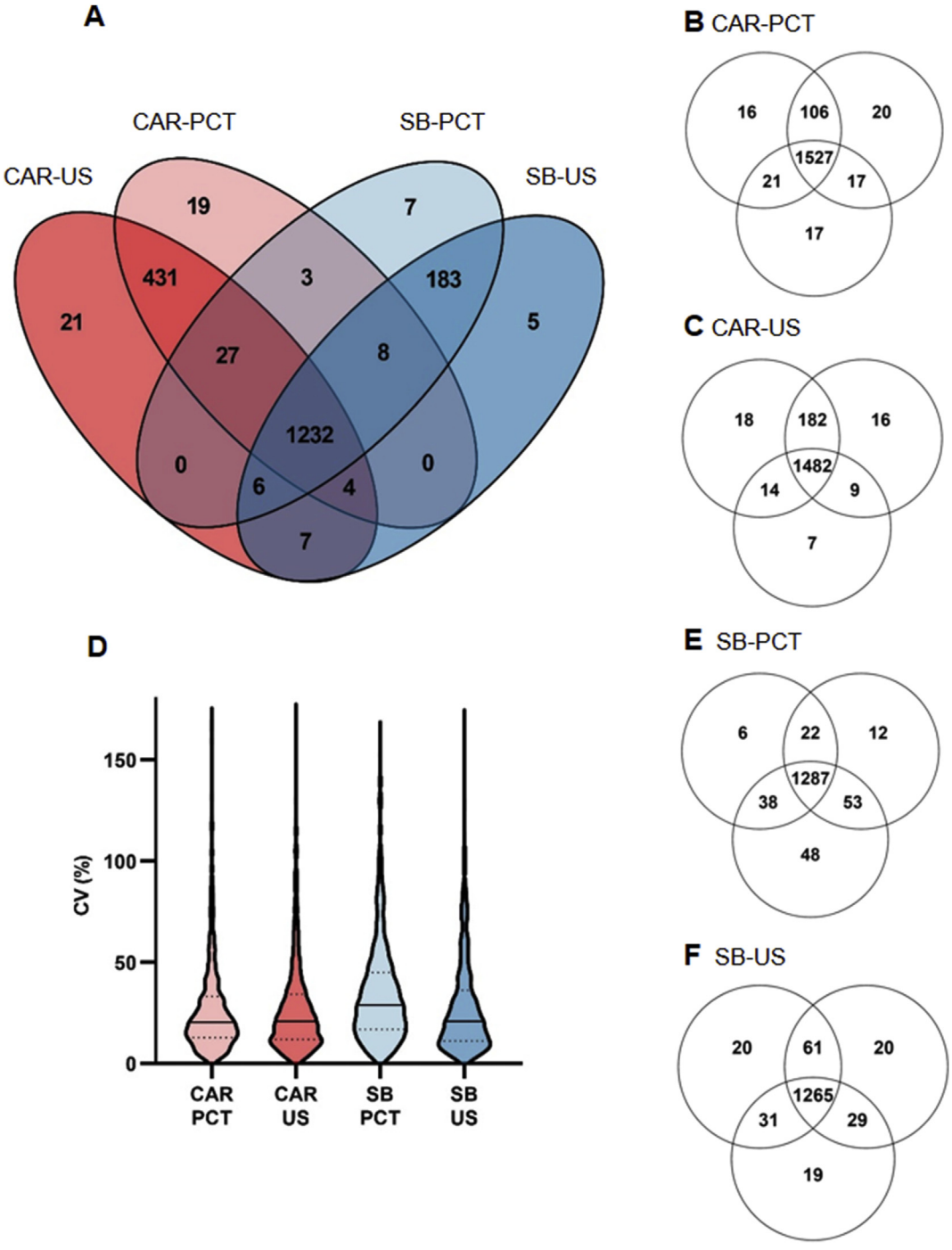

Fig. 2

Osteoarthritis and Cartilage

A) Venn diagram showing the relation between the global proteomes identified in cartilage (CAR) and subchondral bone (SB) processed by pressure cycling technology (PCT) or ultrasonication (US). B-C) CAR samples presented in Venn diagrams showing the relation of the proteins quantified in the three biological replicates (horse 1,2,3). D) The violin plot shows the distribution of CV values for the quantified proteins in the biological replicates. The line indicates the median CV, the dashed lines indicates the quartiles. E-F) SB samples presented in Venn diagrams showing the relation of the proteins quantified in the three biological replicates (horse 1,2,3).

21%, and 23% for H1, H2, and H3, respectively, and for samples processed by US slightly lower with respective CVs of 12%, 16%, and 12%. Reproducibility between biological replicates was high, with 89% (1527 out of 1724) protein identifications in cartilage samples from all three horses upon processing with PCT [Figs. 2(B)] and 86% (1482 out of 1728) in US processed specimens [Fig. 2(C)]. High qualitative reproducibility was matched with quantitative robustness as indicated by CVs between biological replicates of 20% for samples processed by PCT and 21% for samples processed by US [Fig, 2(D)]. Notably, when comparing the identified global proteomes for samples processed by PCT and US, 98% were overlapping. Only 2% (PCT: 19 proteins, US: 21 proteins) of the identified proteins were unique to each of the two preparation methods [Fig. 2(A)].

Subchondral bone

The average PROConcentration per mg tissue was 8.5 μg/mg for samples processed by PCT and 10.9 μg/mg for samples processed by US. Similar to cartilage, our workflow yielded high coverage of the SB proteome with 1482 high confidence protein identifications combined from both sample processing methods [Fig. 2(A)]. Thereby, the mean number of proteins identified was 1264 for samples processed by PCT and 1218 for samples processed by US (Suppl. 6). More than 78% of the identified proteins were present in all three technical replicates for each horse and could be quantified with median CVs of 22%, 29%, and 24% for H1, H2, and H3, respectively, when processed using PCT, and with respective CVs of 22%, 18%, and 30% upon US sample preparation. Both for samples processed by PCT and US, a percentage of 88% (PCT: 1287 proteins, US: 1265 proteins) of the identified proteome were identified in all three biological replicates [Fig. 2(E) and (F)]. The CV for biological replicates was 29% and 21% for PCT- and US-processed samples, respectively [Fig. 2(D)]. 1429 proteins were identified both in samples processed by PCT and US, accounting for 97% and 99% of the identified global proteomes, respectively [Fig. 2(A)].

Protein biological process

To increase confidence in observations even further, we only included proteins identified in at least three samples in the analyses of the proteomes. This reduced the number of proteins from 1953 to 1938.

A biological process enrichment analysis based on GO classification showed that for proteins identified in cartilage only (471 proteins) the top 5 clusters were RNA splicing (GO:0000377), leukocyte degranulation (GO:0043299), regulation of mRNA metabolic process (GO:1903311), ribonucleoprotein complex subunit organization (GO:0071826) and establishment of protein localization to organelle (GO:0071826) [Fig. 3(A)]. For proteins identified in SB only (195 proteins), the top 5 clusters were ossification (GO:0001503), response to wounding (GO:0009611), skeletal system development (GO:0001501), tissue remodelling (GO:0048771), and negative regulation of hydrolase activity (GO:0010466) [Fig. 3(B), (C)].

Further mining of the obtained cartilage and SB proteomes revealed a high abundance of extracellular matrix proteins of major relevance in cartilage and SB. Fig. 4 shows a heat map of a merge of the top 50 most abundant proteins identified in all of the four different types of samples. Biglycan (BGN), fibromodulin (FMOD), prolargin (PRELP), and aggrecan (ACAN) were among the top five most abundant proteins in both cartilage and SB processed with US or PCT. Various other proteins involved in extracellular matrix organization were identified among the top 50 proteins such as hyaluronan and proteoglycan link protein 1 (HAPLN1), decorin (DCN), cartilage intermediate layer protein (CILP) and CILP2, lumican (LUM), osteomodulin (OMD), fibrillin 1 (FBN1), COL2A1, COL6A1, and COL9A1. Proteins specific to top 50 in cartilage were thrombospondin (THBS) 1, THBS4, vitrin (VIT), and mimecan

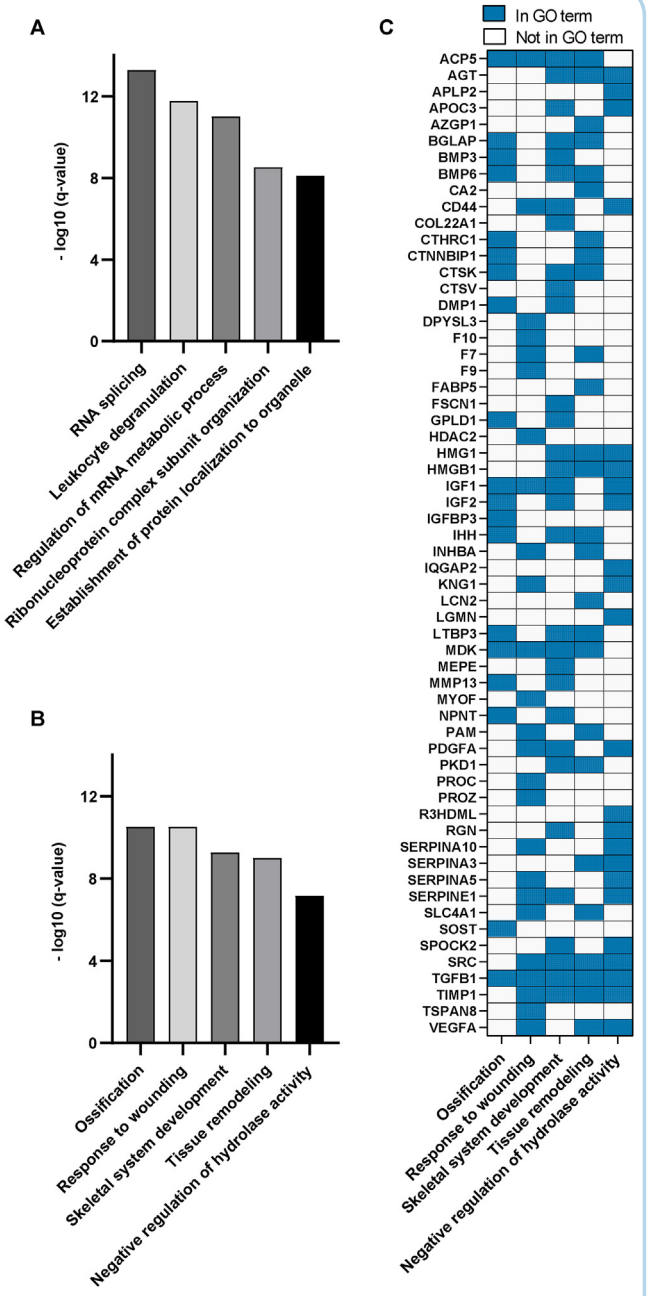

Fig. 3 Osteoarthritis and Cartilage

The column bar graphs shows A) the top five GO clusters after biological process enrichment analysis of proteins identified only in A) cartilage samples, B) subchondral bone samples. C) Proteins (represented by gene name) identified in subchondral bone mapping to the top five GO clusters. Blue: protein in GO term, White: protein not in GO term.

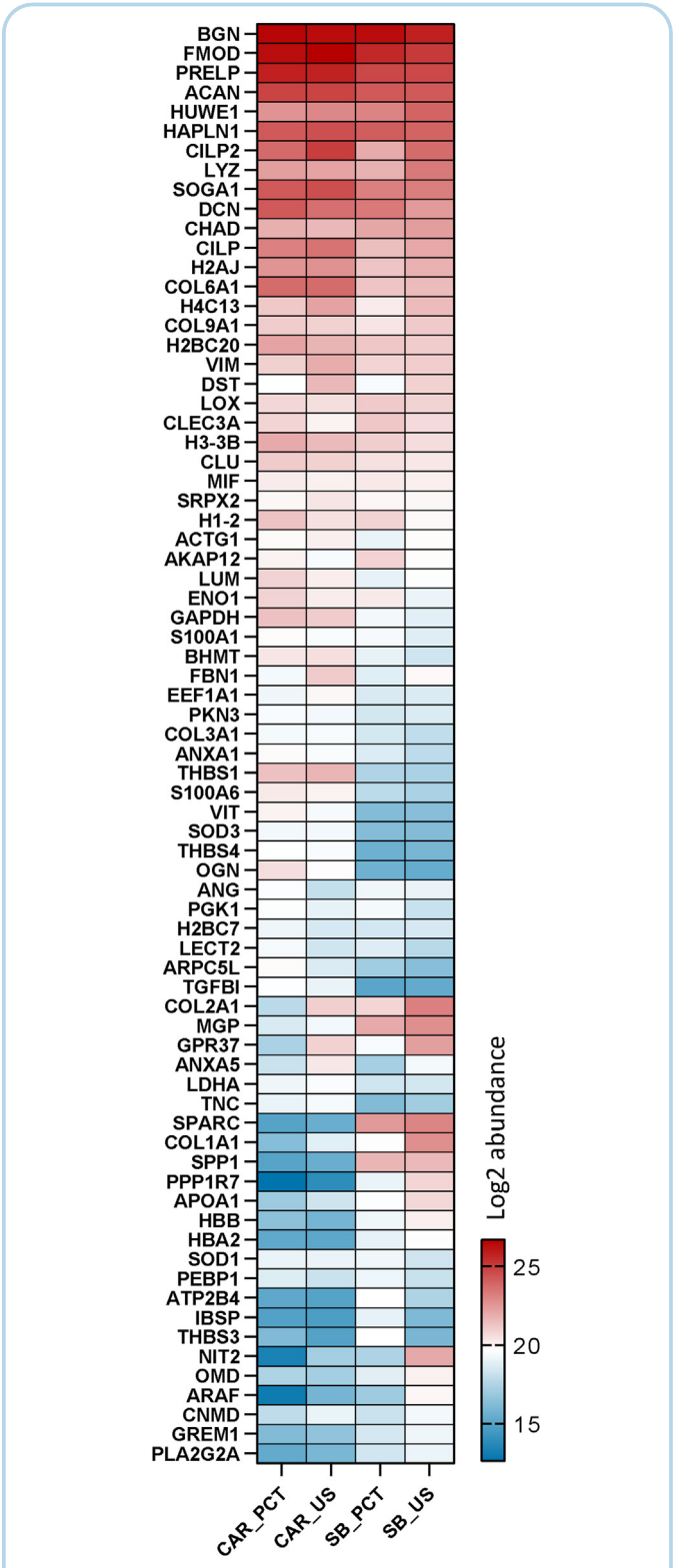

Fig. 4

The heatmap combines the log 2 transformed intensities of the 50 most abundant proteins (represented by gene name) in each of the four sample types and corresponding intensities found across the four types of samples. Cartilage (CAR), subchondral bone (SB), pressure cycling technology (PCT), ultrasonication (US).

(OGN), whereas osteopontin (SSP1), SPARC, and COL1A1 were specific to top 50 in SB.

Protein level evidence of expression of different splice variants

When aligning the identified proteins, all sequences were unique, but 62 of the proteins were identified with gene name in duplicates, three in triplicates, eight in quadruplicates, and five in quintuplicates (Suppl. 7). This may reflect either potential point mutations in the protein sequence or different splice variants of the gene. A substantial part of the proteins in the equine reference database from Uniprot is derived from transcripts nominated by genomic and transcriptomic technologies and contain alternative splice forms. Proteomics data can be used to obtain protein-level evidence of expression of the transcripts and different splice variants, an approach called proteogenomics[30]. As examples, our data provided protein level validation of sequence variants of cartilage oligomeric matrix protein (COMP) and tenascin N (TNN).

COMP was identified with two different protein sequences, accession F6U3D3 and A0A3Q2H402, in samples from both cartilage and subchondral bone [Fig. 5(A)]. More than 50 different peptides were annotated to accession F6U3D3. Three peptides were annotated to A0A3Q2H402, of which two exon–exon junction peptides were unique to this protein sequence [Fig. 5(A)]. At least one of these unique peptides was identified in all samples from cartilage, but only in five out of the 18 samples from SB.

Accession A0A3Q2LJB3 and A0A3Q2KYM7 with the common gene name TNN was identified in samples both from cartilage and subchondral bone [Fig. 5(B)]. The exon–exon peptide APTEIDSPQNLVTDR unique to accession A0A3Q2LJB3 span an alternative splice site compared to accession A0A3Q2KYM7. This peptide was identified in all samples where the protein was present (21 out of 36 samples). Accession A0A3Q2KYM7 was present in all but one sample from cartilage.

These sequence variants represent different protein isoforms and some may have unique biological roles.

Discussion

We have established two novel reproducible and sensitive workflows for quantitative studies of protein expression in cartilage and SB, based on either US or PCT for tissue homogenization coupled with DIA-MS analysis. Using these workflows, we have mapped the hitherto most extensive quantitative proteomes for equine cartilage and SB.

There was a high consistency of the identified proteomes using the two workflows (>97% overlap) for both cartilage and SB, indicating that both extraction methods preserve the diversity among the extracted proteins. For the cartilage samples the median variation across the technical replicates (12–23%) was comparable to the results from another study, where kidney biopsies were processed employing a similar workflow[31]. The slightly higher variation for samples from subchondral bone (18–30%) was expected

because it is a harder tissue and therefore more difficult to homogenize. The hard nature of the tissue may also explain why the median variation is higher than the down to 6% CV found for technical replicate PCT and US processing of spleen samples[20]. However, it is worth to notice that in that study only proteins quantifiable in samples from both extraction methods were included when calculating the CV. Pre-homogenization grinding of the tissue might decrease the variation but will increase the time of processing.

The inclusion of three technical replicates ensured a reliable coverage of the global proteome in both cartilage and SB. The between-horse variation (20–29%) was markedly lower than the up to 45% inter-patient variation found in the comparable study on kidney biopsies[31]. Overall, this method is regarded very reproducible and with a total of 1758 unique proteins identified in cartilage and 1482 unique proteins identified in SB with high confidence, the results reveals the most comprehensive quantitative cartilage and SB proteomes in all species presented to date[12–17].

Proteins in cartilage and SB that are embedded in the solid material, insoluble, or extensively cross-linked are challenging to detect by MS. In future studies, the insight into the proteome could be expanded even further by including alternative proteases such as LysargiNase and the endoproteinases GluC and AspN to identify proteins not amenable to digestion by endoproteinase LysC and trypsin[32].

The spectral library described herein is the first published library covering joint tissue and SF samples from the horse. This high-quality dataset is a resource for the research community for bioinformatical mining, or for future DIA experiments on joint tissues and fluids. Even though this is a comprehensive spectral library, the proteome of joint-related structures is not exhaustively covered. In the future, the depth of the spectral library proteome can be further extended by including data from e.g., pre-fractionation of samples prior to LC separation[33]. The advantage of DIA is that as the spectral library is expanded with more peptide information the acquired data can be re-searched and maybe contribute

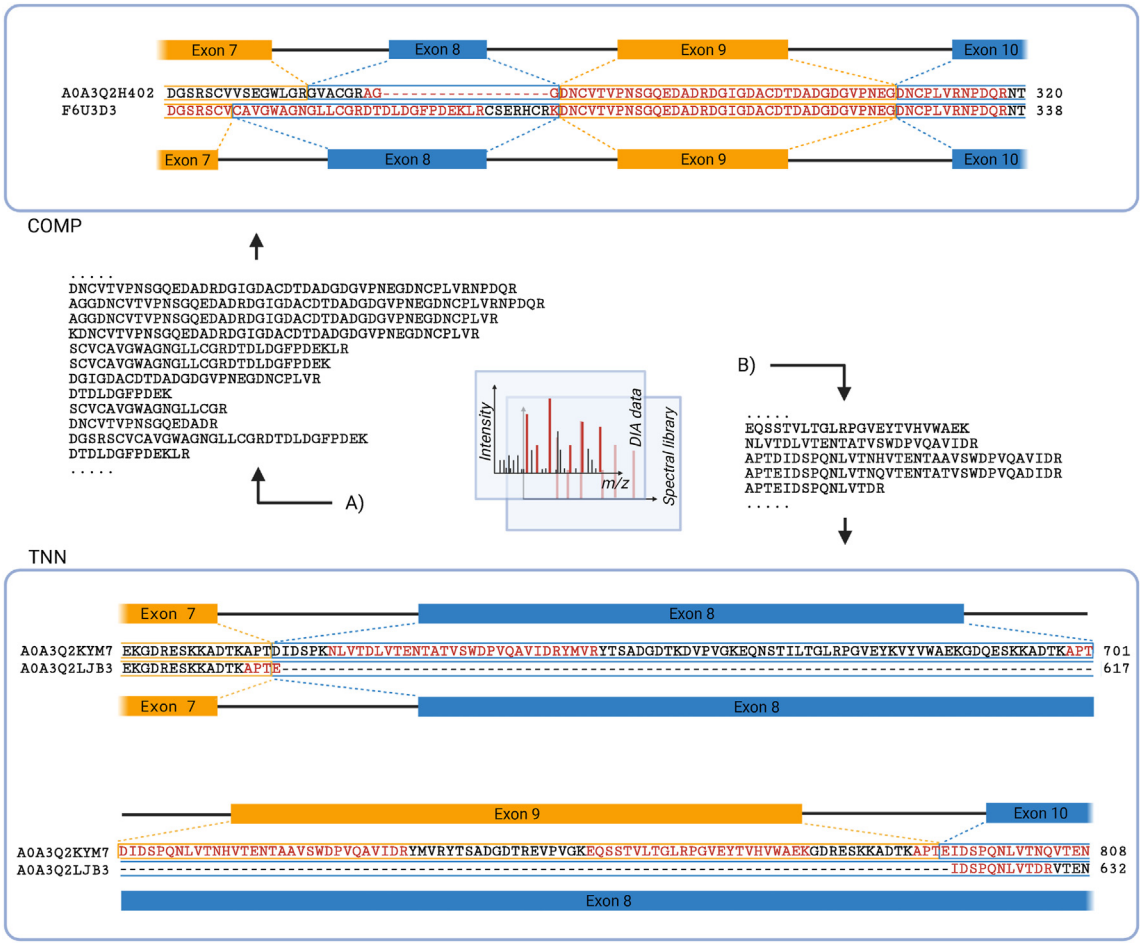

Fig. 5

Osteoarthritis and Cartilage

A) Alignment of part of the protein sequences for accession A0A3Q2H402 and F6U3D3 with the common gene name COMP in the Uniprot database, and the peptides identified in this region. The protein-coding exons are included to show sites for alternative splicing and exon–exon peptides. Peptides identified are marked in red. B) Alignment of the protein sequences for accession A0A3Q2KYM7 and A0A3Q2LJB3 with the common gene name TNN in the Uniprot database, and the peptides identified in this region. The protein-coding exons are included to show sites for alternative splicing and exon–exon peptides. Peptides identified are marked in red. *Created with BioRender.com.*

with even more information. As expected, many proteins identified only in SB are involved in osteogenesis and bone remodelling, e.g., tartrate-resistant acid phosphatase type 5 (ACP5), bone morphogenetic protein (BMP) three and 6, osteocalcin (BGLAP), and cathepsin K (CTSK), and the top one and three biological processes assigned in the GO enrichment analysis were *ossification* and *skeleton system development*[34,35]. Proteins known to be of major importance in bone tissue were identified in SB only, this further adds to the reliability and validity of the sampling and analysis methods used in this study and emphasize that these are promising workflows for getting a better insight into the molecular events in SB. Histological studies have shown that SB is vascularized and venous plexuses exist on the border between the SB and the deep cartilage layer[36]. Activation of blood coagulation post mortem or by tearing of these small vessels upon sampling may explain the identification of coagulation factor VII, IX, and X, kininogen-1 (KNG1), vitamin K-dependent PROC, vitamin K-dependent protein Z (PROZ) in SB only, and that *response to wounding* is the top two biological process found in the GO enrichment analysis.

The five most enriched GO terms in cartilage were all related to cellular processes, and this is most likely because cartilage has a substantial number of chondrocytes compared to the more cell poor SB[10]. The proteoglycan ACAN and the small leucine-rich proteoglycans BGN, PRELP, and FMOD are all major components of the extracellular matrix in cartilage[10,37] and were also found in high abundance in cartilage. These proteins were also found in high abundance in SB and their presence in bone is in accordance with findings in previous studies[12,37].

Mining of the cartilage and SB proteomes revealed a number of proteins with mutual gene names but different sequence variants. These protein isoforms might have different biological functions.

COMP is an extracellular matrix glycoprotein expressed in a wide variety of tissues including cartilage and SB[38,39] and represents a promising marker for joint tissue degradation[40]. Interestingly, A0A3Q2H402 was identified in all samples from cartilage, but only a few samples from SB, suggesting that A0A3Q2H402 could be a more dominant COMP isoform in cartilage. However, to our knowledge, no research studies have described isoform variants of COMP in any species, but Uniprot lists different isoforms in humans and mice and mutant COMP variants specific for certain diseases exits[38]. Further research is needed to determine if these COMP isoforms have distinct tissue specificity.

TNN was another protein identified in two isoforms. TNN is an extracellular matrix protein involved in osteogenesis, and a study in mice showed that TNN was dysregulated in OA[41]. TNN was identified with a longer and a shorter sequence in both cartilage and SB comparable to the two splice variants described in mice[42]. In mice, the biological function of the two transcripts differed and it could be of high interest to investigate if the same applies to the horse and maybe have an impact on the pathogenesis for OA.

For many of the proteins with two or more transcripts the distinction were based on only one unique peptide, but according to the guidelines from the Human Proteome Organization protein quantification should rely on two unique peptides[43]. However, we found that we missed out potential important findings, e.g., some of the potential protein isoforms, by including the more strict setting of two unique peptides per protein in the search criteria. The unique peptides identified for all the different proteins are useful to build parallel reaction monitoring studies for further investigation and validation of the different transcripts, specific degradation products and the biological function or relevance for specific diseases.

A review from 2020[44] summarized the results from 11 different OA studies over the last decade on gene expression profiling of various tissues, such as cartilage, SB, and synovium from human OA and mouse OA models. They listed 87 differentially expressed genes mainly involved in matrix metabolism, bone remodeling, and inflammation pathways in OA tissue compared to normal tissue, including ALPL, OGN, IGF1, TGF-β1, TGFBI, POSTN, MMP3, MMP13, ACP5, ASPN, IHH and multiple collagens. We identified the corresponding proteins to 36 of the genes and close protein family members to 19 of the genes. The prospect of investigating the interrelation of these proteins together with the other identified cartilage and SB related proteins in one single analysis emphasizes that PCT or US homogenization combined with DIA analysis is a very promising workflow to get a valuable and deep insight into the molecular events at the osteochondral unit.

In conclusion, we have successfully developed two workflows based on either PCT or US for tissue homogenization and protein extraction coupled with DIA-MS analysis. The workflows enabled to our knowledge the hitherto most comprehensive quantitative insights into the equine proteomes of cartilage and SB, and facilitate the prospect of investigating the molecular events at the osteochondral unit in the pathogenesis of OA and other cartilage and bone related diseases in future projects in all species including humans. Both workflows were very reproducible and the high overlap of more than 97 percentage between the two workflows for both cartilage and SB indicates that the proteomes cover the true biological composition.

The proteomes and the spectral library will be open access resources for the research community for further mining of proteins of interest, and as support for development of methods for targeted analysis of specific proteins or potential protein isoforms.

Conflict of interest

The authors declare to have no conflict of interests.

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Not applicable.

Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.joca.2021.09.006.

Author contributions

LB conceived the study, sampled most of the samples, prepared all samples for analysis, interpreted the data, and drafted the manuscript. EA provided expert assistance with sample preparation for MS analysis, MS analysis, data interpretation, and revised the manuscript critically. JM conceived the study, provided expert assistance with design of the project, MS analysis, data interpretation, and revised the manuscript critically. UadK conceived the study, provided expert assistance with design of the project, MS analysis, data interpretation, and revised the manuscript critically. MW assisted with design of the project and method development, sampling, and revised the manuscript critically. SJ conceived the study, provided expert assistance with the project design and method development, sampling, data interpretation, and manuscript preparation and revision. All authors read and approved the final version of the manuscript.

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