Discovery and validation of new osteoarthritis biomarkers using omics approaches across the spectrum of disease



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SERUM/PLASMA

URINE

OMICs
APPROACHS
in OA

SYNOVIAL FLUID

- + Target of biomarker follow-up
- Depletion of majors proteins
- Difficult to detect minor proteins

Tissues

EXTRACT

EXPLANT
SECRETOME

BONE

SYNOVIAL MEMBRANE

CELL EXTRACT

Cells

SECRETOME

MEMBRANOME

MATRISOME

CHONDROCYTES

OSTEOBLASTS

SYNOVIOCYTES

OSTEOCLASTS

- vs + Joint specificity
 - + Pathological pathways (inflammation,...)
 - Presence in serum/urine...?

⇒ complementary approachs



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GENOMIC

PROTEOMIC

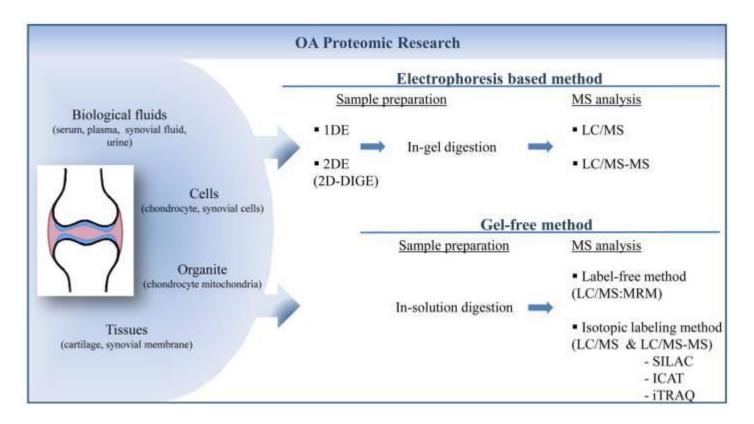
TRANSCRIPTOMIC

METABOLOMIC



Quantitative proteomics: The state of the art

Overview of the different wokflows



Gharbi M., Deberg M., Henrotin Y., Application for Proteomic Techniques in Studying Osteoarthritis: A Review, Front Physiol. 2011; 2: 90



Biomarker Discovery:

Differential proteomics analysis pipepline

Discovery

Verification / Validation

High throughput Validation

Number of sample for analysis

Number of biomarkers

- Small number of samples (3 to 10)
- Looking at ± 1000 proteins at once without any a priori
- Complex, expensive and time consuming analysis

- Average number of samples from 10 to 100
- Alternative methods
- Looking at specific proteins (10-100)
- Targeted quite complex and expensive methods

- Average number of samples greater than 100
- Immuno-based high throughput tests
- Looking at specific proteins (<100)
- Targeted and multiplex (low cost screening tests)





Exemple of proteomic application in new OA biomarker research: Identification of Fibulin-3 peptides as biomarkers of OA

Fibulin 3 peptides Fib3-1 and Fib3-2 are potential biomarkers of osteoarthritis

Henrotin Y et al Arthritis Rheum 2012, 64(7):2260-2267

- Proteomic analysis of human urines by 2D-DIGE
- Identification of proteins or fragments of interest by mass spectrometry
- Production of specific antiserum directed against identified peptides
- Development of specific immunoassay of peptides
- Validation of peptide variation in OA population



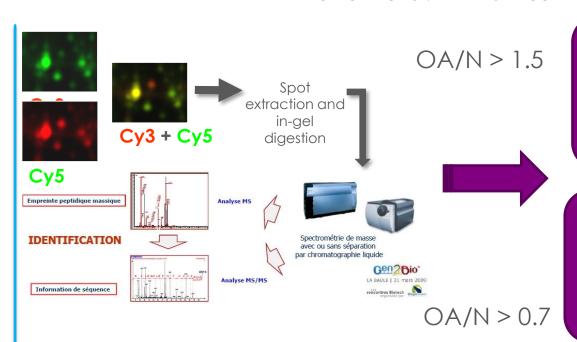




Proteomic analysis: classical workflow of protein identification

Urinary proteome

Henrotin et al. Arthritis Rheum 2012



Increased (9)

B-actin α1-microglobulin **Fibulin-3 fragments** Apoptosis inducing factor-2

Decreased (9)

Serpins \$1 et \$3 Mannan binding lectin serum proteases-2 Kinnogen 1

FBLN3_HUMAN Mass: 54604 Score: 130 Queries matched: 2

EGF-containing fibulin-like extracellular matrix protein 1 precursor (Fibulin-3) (FIBL-3)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
149	685.33	1368.64	1368.54	0.09	0	58	0.00027	1	R.CVCPVSNAMCR.E
444	965.32	1928.63	1928.73	-0.10	0	72	4.2e-06	1	R. TCQDINECETTNECR.E







Fibulin-3: relation with cartilage

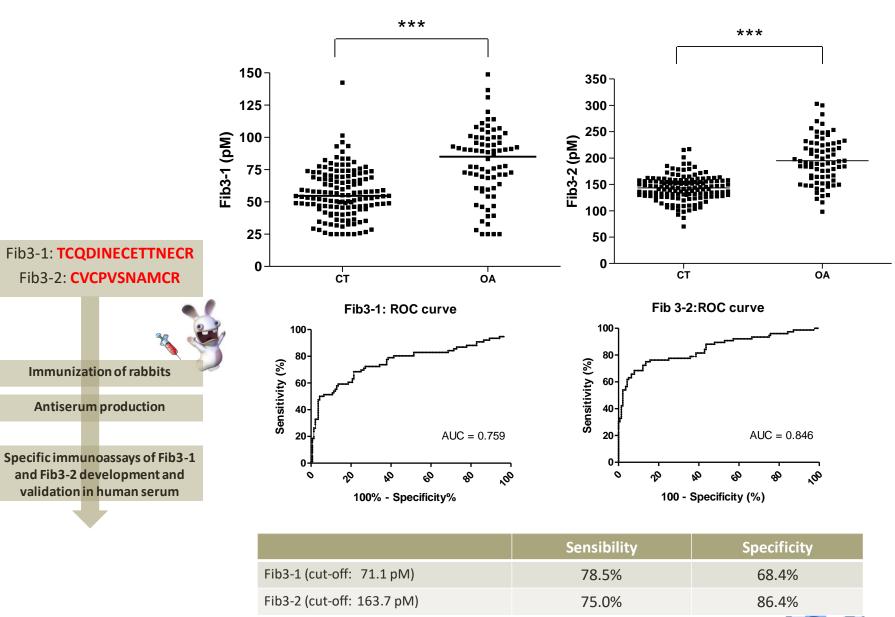
- Extracellular matrix protein highly expressed in cartilaginous tissue (Timpl, et al. 2003; Kobayashi, et al. 2007)
- Expressed in the mesenchyme giving rise to cartilage and bone, and plays a role in organizing the development of skeletal system (Ehlermann et al., 2003)
- Identified in OA cartilage by proteomic analysis (Vincourt et al., 2006)
- Intimately associated with (TIMP)-3, an inhibitor of metalloproteinases involved in the pathogenesis of OA (Klenotic et al., 2004; Kevorkian et al., 2004; Sahebjam et al., 2007)
- Negative regulator of chondrocytes differentiation (Wakabayashi, et al. 2010)

These bibliographic data suggest an implication of Fibulin-3 in the physiopathology of OA





Fibulin-3 fragments (Fib3-1 and Fib3-2): potential diagnostic biomarkers





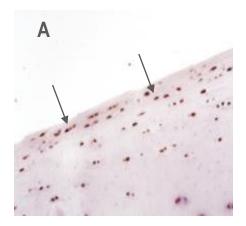
Antiserum production

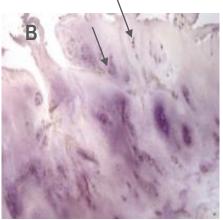
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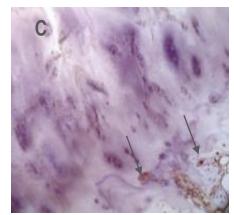


Immunolocalization of Fib3-1 and Fib3-2 (human)

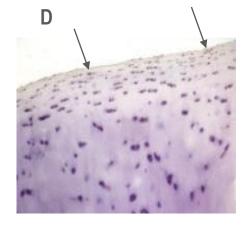
Fib3-1



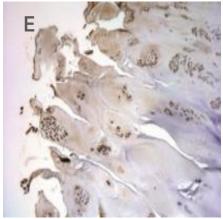




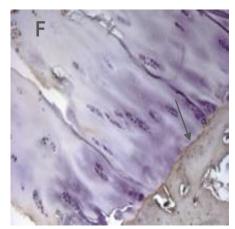
Fib3-2



Healthy cartilage



OA cartilage **Superficial layers**



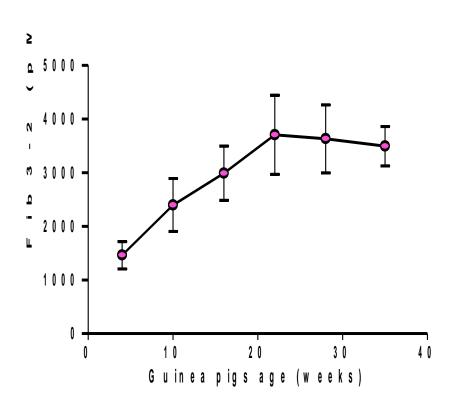
OA cartilage **Bone junction**



Guinea pig as spontaneous model of OA

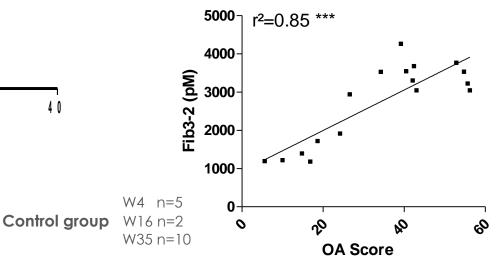








35-week old guinea pig, right knee, medial



Recommanded OARSI histological OA score for guinea pig, parametric ANOVA /Dunnett's post test





Proteomic paradox

Recovery of unknown proteins in chondrocytes - cartilage matrix

AND

Some known proteins are not found!

Example:

Rosenthal et al (2011) investigated protein pattern present in articular cartilage vesicles (AVCs) and didn't find TNALP or PC1, well known enzymes located in their membrane

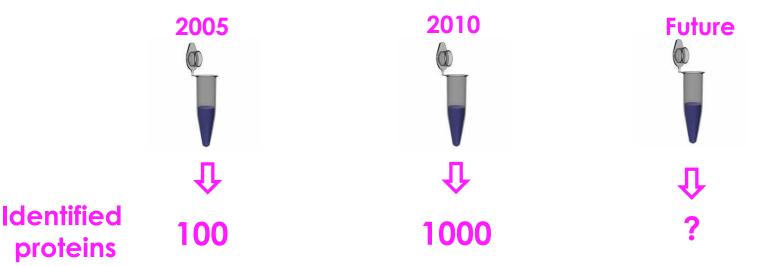
Due to their structure/composition/localisation, Lot of proteins are undetectable with current technics





Quantitative proteomics: a discipline in constant progress

- ✓ Sample preparation method / Specific depletions
- Protein labeling label free methods
- Improvement in protein separation
- Protein fractionation method
- ✓ Sensibility of detection
- Evolution of databases





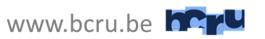
proteins



Conclusions

- New OMICs technologies flood us with new potential biomarkers
- Validation and qualification of one potential biomarker is a very long and expensive process
- It's essential to start OMICs studies with the good samples – representative – homogen...to gives us important informations - maybe on subgroups of the disease









Team

Bone and Cartilage Research Unit



Thank you!





