UPDATE ON THE FNIH OSTEOARTHRITIS BIOMARKERS CONSORTIUM PROJECT



THURSDAY, APRIL 30, 2015 9:00 AM - 12:00 PM



















OARSI World Congress Workshop

AGENDA

9:00 AM – 9:10 AM	Welcome and Opening Remarks David J. Hunter (USydney), Virginia Byers Kraus (Duke)
9:10 AM – 9:30 AM	Study Design and Case/Control Selection Michael C. Nevitt (UCSF)
9:30 AM – 10:45 AM	Imaging Biomarkers David J. Hunter (USydney), Jamie E. Collins (BWH), Virginia Byers Kraus (Duke)
10:45 AM – 11:45 AM	Serum & Urine Biomarkers Virginia Byers Kraus (Duke), Elena Losina (BWH)
11:45 AM – 12:00 PM	Next Steps and Closing Remarks David J. Hunter (USydney); Virginia Byers Kraus (Duke)
12:00 PM	Adjournment

Video recording of this workshop will be available in late May

www.biomarkersconsortium.org

Osteoarthritis (OA) Biomarkers Project

2½ year, \$3.014M study; nested case-cohort (200 cases & 400 controls)

Contributions

Abbott Labs; Amgen; Arthritis Foundation; Bioiberica S.A.; DePuy Mitek; Flexion Therapeutics; GlaxoSmithKline; Merck Serono; Rottapharm Madaus; Sanofi

Principal Investigators:

- David J. Hunter, MD, PhD, University of Sydney
- Virginia Byers Kraus, MD, PhD, Duke University

Specific aims:

- To examine the relationship between putative efficacy of intervention markers (biochemical markers, imaging features on x-ray and MRI and their progression) and clinically relevant outcome over a 4-year follow-up period
- To identify the most responsive marker(s) of OA progression
- To develop a risk score based on baseline values of several biomarkers including JSN, BTI/FSA, knee alignment, quantitative and semi-q-MRI measures and biochemical biomarkers that would determine those who progress rapidly to case status

Image Analysis

	Imaging Biomarker	Analytic Group	Parameter(s) Measured
Radiography			
	Minimum joint space width (JSW) & joint space area (JSA) and bone trabecular integrity (BTI) by fractal signature analysis (FSA)	Duke Image Analysis Lab (DIAL)	Medial and lateral & minimum JSW and JSA; medial & lateral BTI/FSA
MRI			
	Quantitative cartilage morphometry	Chondrometrics	Cartilage volume, thickness, denuded surface area
	Quantitative bone morphometry	Qmetrics	Bone area, bone curvature, bone/cartilage interface signal contrast
	Quantitative bone morphometry	Imorphics	Area of bone covered by cartilage (tAB) & volume of osteophytes
	Semi-quantitative whole joint scoring	Boston Image Core Lab (BICL)	Assessment of the joint organ morphology using the MRI OA Knee Score (MOAKS) system
	Quantitative cartilage and meniscus morphometry	Biomediq	Cartilage and meniscus volume

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Panel of OA-Related Biomarkers						
Biomarker	Process (preliminary)	BIPEDS Classifications	Surrogacy Based on Human Clinical Trials (preliminary)			
urinary CTX-II	type II collagen degradation	Knee: BPED Hip: BPD	characterization: changed significantly in 3 pharmacologic trials that met primary clinical endpoints (Christgau 2004, Gineyts 2004, Manicourt 2006)			
serum COMP	cartilage degeneration	Knee: BPD Hip: BPD	exploration: not used to date in pharmacologic trial			
serum HA	osteophyte burden, synovitis	Knee: BPED Hip: P	demonstration: changed significantly in one pharmacologic trial that met primary clinical endpoints (Manicourt 2006)			

Knee: D(u)

Knee: E(s), D(u)

Knee: D(s),B(u),P(u)

Hip: none

Hip: B(s)

Hip: D(s)

Knee: D(s)

Knee: BPD

Knee: P(u),E(u)

Knee: B(u), D(s/u),

2005)

Manicourt 2006)

Hip: none

Hip: P(s)

Hip: none

Knee: P

Knee: E

Hip: none

Hip: none

P(u)

Hip: B(s)

Types I and II collagen

degradation

degradation

degradation

synthesis

synthesis

type II collagen

type II collagen

type II collagen

Type II collagen

bone resorption

bone resorption

cartilage aggrecan

synthesis/turnover

joint tissue

degradation

protease involved with

C1,2C

C₂C

serum and urine

serum and urine

serum and urine

Coll2-1NO2

serum CPII

Serum PIIANP

urine/serum NTX-1

Urine CTXI alpha

and beta/serum

serum CS846

serum MMP-3

CTX-1

ELISA assay

type

competitive-

competitiveinhibition &

sandwich protein

binding assay

competitive-

competitive-

competitive-

competitive-

competitive-

competitive-

competitive-

competitive-

sandwich for total

MMP-3 assay

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

sandwich

exploration: nonsignificant change in one pharmacologic

demonstration: nonsignificant change in one pharmacologic

trial that met primary clinical endpoint (Mazzuca 2006)

trial that met primary clinical endpoint (Mazzuca 2006)

exploration: nonsignificant change in one pharmacologic

demonstration: changed significantly in one pharmacologic

trial that met primary clinical (WOMAC) endpoint (Spector

exploration: nonsignificant change in one pharmacologic

trial that met primary clinical endpoint (Mazzuca 2006) but

characterization: changed significantly in two pharmacologic

trials that met primary clinical endpoints (Lohmander 2005,

trial that met primary clinical endpoint (Mazzuca 2006)

exploration: not used to date in pharmacologic trial

exploration: not used to date in pharmacologic trial

exploration: not used to date in pharmacologic trial

changed associated with concurrent JSN

OA Biomarkers Project Team

- Neil Bodick, MD, PhD (Flexion Therapeutics)
- Jamie Collins, PhD (Brigham and Woman's Hospital)
- Sahar Dawisha, MD (FDA/CDRH)
- Klaus Flechsenhar, MD (Sanofi)
- Fiona Germaschewski (GSK)
- Ali Guermazi, MD (Boston University Medical Center)
- Yves Henrotin, PhD (Univ. of Liege)
- Steve Hoffmann, MS (FNIH)
- David J. Hunter, MBBS, PhD (Univ. of Sydney)
- Joanne Jordan, MD (Univ. of North Carolina at Chapel Hill)
- Jeffrey Katz, MD, MS (Brigham and Woman's Hospital)
- Virginia Byers Kraus, MD, PhD (Duke University)
- Kent Kwoh, MD (Univ. of Arizona)
- Christoph Ladel, PhD (Merck Serono)
- Jonathan Larkin, PhD (GSK)
- Gayle Lester, PhD (NIH/NIAMS)
- Elena Losina, PhD (Brigham and Women's Hospital)
- John Lynch, PhD (Univ. of Calif, San Fran)
- Helena Martinez, MSc (Bioiberica S.A.)
- Gloria Matthews, PhD (Genzyme/Sanofi)

- Janet Maynard, MD, MHS (FDA/CDER)
- Charles McCulloch, PhD Univ. of Calif, San Fran)
- Michael Nevitt, MD, PhD (Univ. of Calif, San Fran)
- Nikolay Nikolov, MD (FDA/CDER)
- Amanda Niskar, DrPH, MPH, BSN (Arthritis Foundation)
- Bill Parrish, PhD (DePuy Mitek)
- Stefano Persiani, PhD (Rottapharm Madaus)
- **Frank Roemer, MD** (Klinikum Augsburg)
- **Lucio Rovati, MD** (Rottapharm Madaus)
- **Roger Sabata** (Bioiberica S.A.)
- Linda Sandell, PhD (Washington University, St.L)
- Csaba Siffel, MD, PhD (Arthritis Foundation)
- Valorie Thompson, PhD (OARSI)
- Wayne Tsuji, MD (Amgen)
- Josep Vergés, MD, PhD (Bioiberica S.A.)
- Susanne Wang, MD, PhD (AbbVie)
- Yingtao Zhou, MS (Arthritis Foundation)





Statistical Analysis Center

- Analytic Group serves as an independent statistical center
 - Dr. Elena Losina, PhD (Center Director)
 - Dr. Jamie Collins, PhD (Principal Statistician)
 - Dr. Jeffrey N. Katz, MD, MSc (Clinical Epidemiologist)



- Statistical Analysis Plan (SAP) Development:
 - 1. Conceptual SAP based on original OA Biomarkers Project Plan
 - 2. Specific biomarker SAPs incorporate:
 - Draft analysis plans proposed through collaborative efforts of Statistical Center and Project Team Core Group
 - Vendors provide assay kit information or prepare brief presentation(s) of methodologies and analytical systems tailored for specific sets of biomarkers
 - 3. Following consensus Core Group approval, final SAP shared with the entire OA Biomarkers Project Team
 - Monthly meetings to monitor analytical progress and review results

ALL STATISTICAL ANALYSES ARE PERFORMED INDEPENDENTLY FROM VENDORS

Acknowledgements

Scientific and Financial Support

























NIH Osteoarthritis Initiative



















In-Kind Project Support



Alere







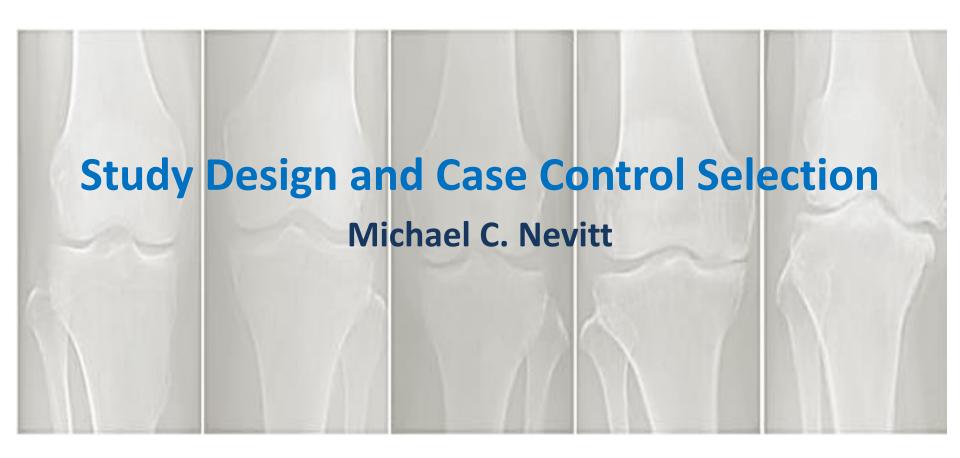








and Diagnostic Products









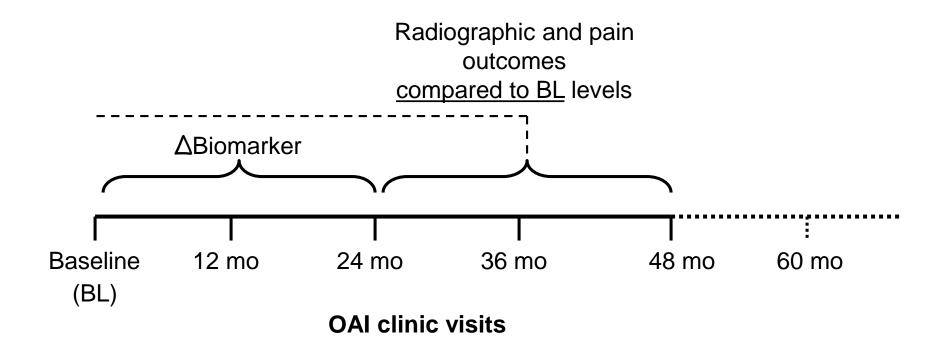


Overview

- Using data from the first four years of the Osteoarthritis Initiative (OAI), perform a <u>nested case-control</u> study to determine the predictive and concurrent validity and responsiveness of Δstructural and Δbiochemical biomarkers for radiographic and pain progression in knees with mild to moderate T-F OA.
- OAI is a longitudinal cohort study of 4,796 men and women ages 45–79 with, and at high risk for, knee OA that contains a repository of serial knee images and blood and urine biospecimens and extensive longitudinal clinical profile data.

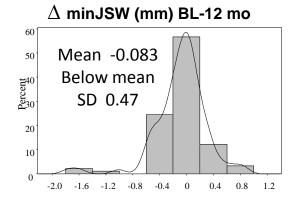
Biomarkers and Outcomes from OAI Study Visits

- Biomarkers (imaging, biochemical) assessed using data from BL, 12 mo and 24 mo visits
- Radiographic and pain progression outcomes assessed using data from 24, 36, 48 mo (and for pain, 60 mo) compared to BL



Radiographic (X-ray) Progression

- Radiographic progression = loss of medial minJSW ≥ 0.70 mm from BL to 24, 36 or 48 mo
- Annual knee radiographs using PA "fixed-flexion" protocol
 - minJSW in medial TF compartment assessed with automated software (Duryea, 2013, Osteo Cart)
- Study-specific smallest detectable change determined from serial OAI images
 - 90 reference cohort knees, KLG = 0 and no pain BL to 24 mo
 - ΔMinJSW from BL to 12 mo (no real change expected)



	Probability that change <x due="" error<="" is="" measurement="" th="" to=""></x>						
	2.5% 5% 10% 25% 50						
∆minJSW BL-12m (mm)	< -1.02	< -0.87	<-0.70	< -0.49	< 0.08		

Knee Pain Progression

- Knee pain progression = <u>persistent</u> increase vs. baseline in total WOMAC pain score above MCID (≥9 pts on 0-100 scale)
 - Persistent = increase at ≥2 timepoints from 24 to 60 mo

MCID references

- 1. Angst F, et al. Smallest detectable and minimal clinically important differences of rehabilitation intervention with their implications for required sample sizes using WOMAC and SF-36 quality of life measurement instruments in patients with osteoarthritis of the lower extremities. *Arthritis Rheum* 2001; 45: 384-391.
- 2. Angst F, et al. Minimal clinically important rehabilitation effects in patients with osteoarthritis of the lower extremities. *J Rheumatol* 2002; 29: 131-138.
- 3. Tubach F. et al. Minimum clinically important improvement and patient acceptable symptom state in pain and function in rheumatoid arthritis, ankylosing spondylitis, chronic back pain, hand osteoarthritis, and hip and knee osteoarthritis: Results from a prospective multinational study. *Arthritis Care Res* 2012; 64:1699-707.

Case – Control Knees: Definitions

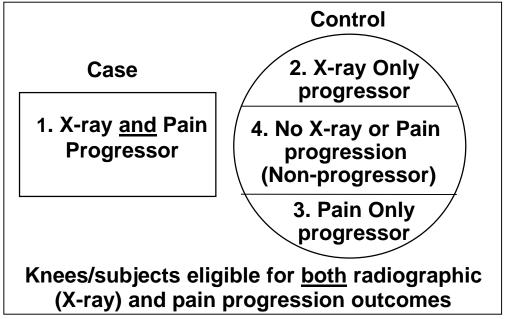
Primary <u>case</u> definition = knee having <u>both</u> radiographic (X-ray) and pain progression (**Progressor**)

Primary <u>control</u> definition = knee eligible for X-ray and pain progression that <u>does not reach criteria for both</u> endpoints

- Knee with X-ray progression but <u>not</u> pain progression (X-ray only progressor)
- Knee with pain progression but <u>not</u> X-ray progression (Pain only progressor)
- Knee with <u>neither</u> X-ray nor pain progression (<u>Non-progressor</u>)

Sampling Design

- Eligible knees
 - KLG 1-3 at BL
 - JSW and pain data at BL-48 mo
 - Knee MRI, serum and urine at BL and 24 mo
- Eligible knees classified into four outcome groups, cases and controls



Pre-specified group sizes

N = 200

Sampling Design (Cont.)

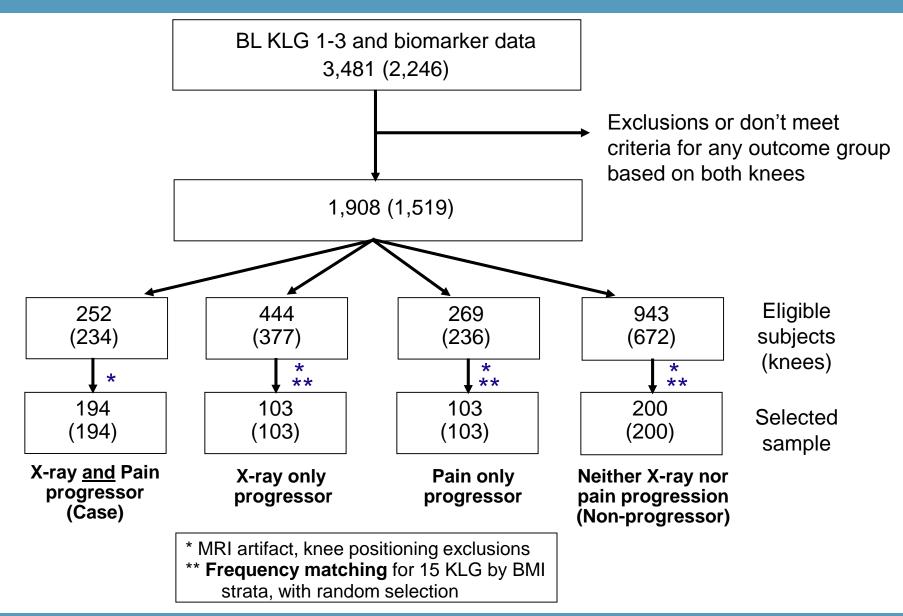
- Outcomes and imaging biomarkers are knee-specific measurements
 - One index /study knee selected per subject
- Exclusions: knees
 - Unable to progress: minJSW < 1.0mm or WOMAC pain >91 (0-100)
 - MRI artifacts likely to affect image analysis
 - Poor radiograph quality or positioning (poor or variable tibial rim alignment)
 - Controls: BL lateral JSN and/or lateral radiographic progression
- Exclusions: subjects (biochemical markers are subject-level measurements; take both knees into account)
 - Either knee meets primary case definition by 12 mo
 - TKR or THR up to 24 mo (effects on biochemical markers)

Sampling Design (Cont.)

- Exclusions: subjects (Cont.)
 - If both knees have same outcome: one randomly selected
 - If outcomes in a subject's knees are discordant
 - E.g. one knee is a pain only progressor and the other is a X-ray only progressor

...then subject excluded

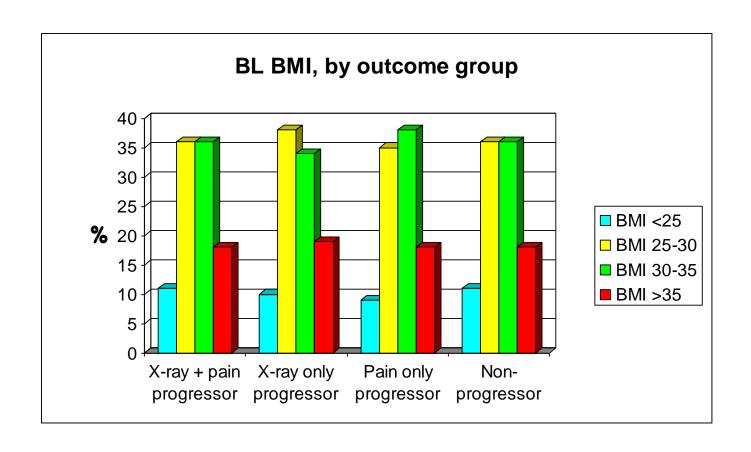
Knee (Subject) Selection Flow Diagram



Frequency Matching

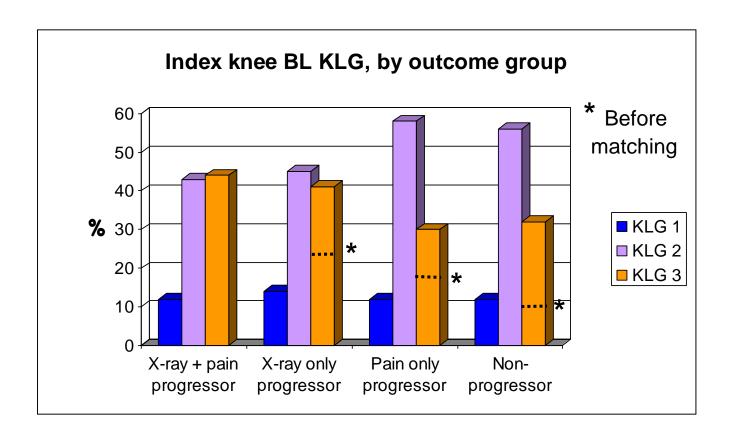
- Frequency matching of control BMI and KLG to radiographic and pain progressors (composite cases)
 - Cases: greater % in high BMI groups and KLG 3
- Goal: better balance among groups for covariate adjustment
- 15 BMI by KLG strata
 - BMI <25; 25 to <27.5; 27.5 to <30; 30 to <35; ≥35
 - KLG 1; KLG 2; KLG 3
- Difficult strata to match e.g.
 - Pain only progressor and nonprogressors with KLG = 3

Frequency Matching: Baseline BMI



Good balance achieved for BMI groups

Frequency Matching: Baseline KL grade



- Improved balance in baseline KLG
- Pain only progressors and non-progressors, fewer KLG 3 knees
- KLG a covariate in analyses

Baseline Subject Characteristics

	X-ray + pain progressor	X-ray only progressor	Pain only progressor	Non- progressor	P-value
Age (SD)	62.0 (8.8)	63.1 (8.3)	58.0 (8.7)	61.5 (9.1)	0.011
Male	43%	55%	35%	35%	0.003
Nonwhite	20%	12%	28%	22%	0.029
Pain meds for knees most days, past year	32%	21%	36%	28%	0.088
Glucosamine most days, past mo	33%	33%	29%	26%	0.290

Baseline Index Knee Characteristics

	X-ray + pain progressor	X-ray only progressor	Pain only progressor	Non- progressor	P-value
Hx of knee injury*	35%	40%	37%	33%	0.874
WOMAC knee pain (SD) (0-100)	20 (26)	33 (40)	19 (27)	26 (32)	0.002
Medial JSN gr 2 (vs 0-1)	44%	41%	28%	31%	0.009

^{*} self-report of knee injury causing difficulty walking for >= 2 days

Limitations

- Partial overlap of ΔBiomarker and progression outcome assessment periods combines predictive and concurrent validity
 - Analyze <u>early</u> (BL-24mo) vs. <u>late</u> (BL -36/48 mo) progressors
 - Analyze ΔBiomarkers from BL to 12 mo as predictors
- Other definitions of pain progression may give different results

Strengths

- Clinically relevant outcomes (structure + pain) and assessment intervals
 - ΔBiomarkers over 24 mo and progression outcomes over 48 mo
- Large sample size
- Can compare biomarker performance for progression outcomes defined in several ways
- Publicly available data
 - Link biomarker and outcome data of study subjects and knees to all other OAI variables

Pre-Specified Analyses

Primary analysis

Case: knees with both X-ray and pain progression (n=194) vs.

Control: knees that <u>did not have both</u> X-ray and pain progression (n=406)

Secondary analyses

Method 1

Comparison of 4-level outcome groups

X-ray + pain	X-ray only	Pain only	Non-progressors
progressor	progressor	progressor	
(n=194)	(n=103)	(n=103)	(n=200)

Method 2

All progressors (n=400) vs. non-progressors (n=200)

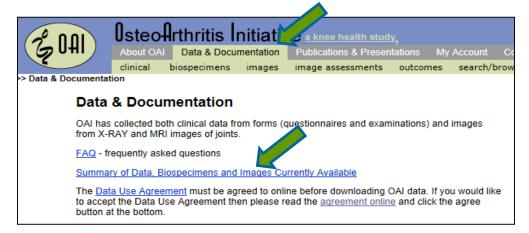
Method 3

X-ray progressor (n=297) vs. X-ray non-progressors (n=303)

Method 4

Pain progressor (n=297) vs. Pain non-progressors (n=303)

FNIH OA Biomarkers Consortium Project - Data Access on the OAI Database





http://oai.epi-ucsf.org/datarelease/

Option 1:

- Click on the Data & Documentation tab at the top of the page
- Once on the Data & Documentation page, click on the Summary of Data, Biospecimens and Images Currently Available link
- Scroll down to OA Biomarkers Consortium FNIH Project and click on that link
 - This takes you to the dedicated FNIH page on OAI Online
 - Requires you to re-enter logon credentials and then redirects to data pages

Option 2:

- Alternatively, you can just bookmark/click on this link:
 - https://www.oai.ucsf.edu/datarelease/FNIH.asp
 - This takes you to the OAIOnline logon page then immediately redirected to the FNIH page.

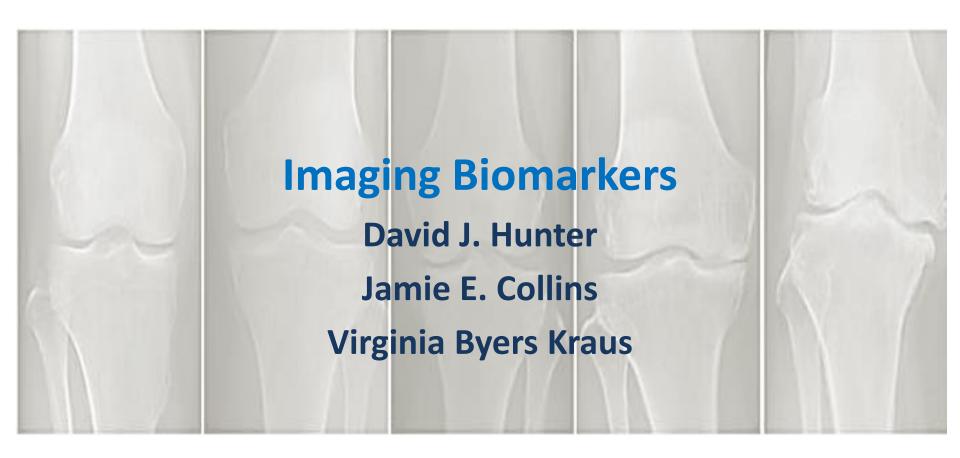










Image Analysis

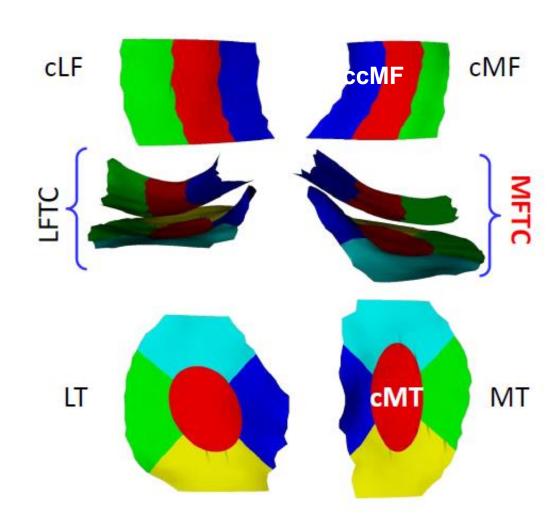
	Imaging Biomarker	Analytic Group	Parameter(s) Measured
Radiography			
	Minimum joint space width (JSW) & joint space area (JSA) and bone trabecular integrity (BTI) by fractal signature analysis (FSA)	Duke Image Analysis Lab (DIAL)	Medial and lateral & minimum JSW and JSA; medial & lateral BTI/FSA
MRI			
	Quantitative cartilage morphometry	Chondrometrics	Cartilage volume, thickness, denuded surface area
	Quantitative bone morphometry	Qmetrics	Bone area, bone curvature, bone/cartilage interface signal contrast
	Quantitative bone morphometry	Imorphics	Area of bone covered by cartilage (tAB) & volume of osteophytes
	Semi-quantitative whole joint scoring	Boston Image Core Lab (BICL)	Assessment of the joint organ morphology using the MRI OA Knee Score (MOAKS) system
	Quantitative cartilage and meniscus morphometry	Biomediq	Cartilage and meniscus volume

Analytic Overview

- Descriptive Statistics
 - n (%) for categorical variables, mean (SD) for continuous variables
- Logistic Regression for primary comparison of cases (x-ray + pain progressors) vs. controls (do not have x-ray + pain progression)
 - Multivariable models adjusted for sex, race, and baseline JSW, KL, age, WOMAC Pain
 - For continuous variables, ORs presented as the odds of being a case for each 1 SD increase in biomarker
- Multinomial Logistic Regression for secondary comparison of 4-level outcome status, with non-progressors (subjects not progressing in x-ray or pain) used as reference group

Quantitative Cartilage Morphometry

- Sagittal 3D DESSwe images (3T) @ baseline, 12 and 24 months
- analyzed by 12 readers (Chondrometrics GmbH)





Cartilage Thickness Analysis: Predictors

- 24 month change in mean cartilage thickness
 - Central medial femorotibial compartment (cMFTC)
 - Central medial tibia (cMT)
 - Central medial weight-bearing femur (ccMF)
 - Total medial femorotibial compartment (MFTC)
- Location-independent measures
 - Ordered Values
 - Cartilage change in each of the 16 subregions is computed, and then the regions are sorted by the amount of change
 - OV1: the smallest value/most negative change (the subregion with the greatest rate of cartilage thinning)
 - OV16: the largest value (the subregion with the least thinning or greatest thickening)
 - Cartilage thinning score: sum of all negative cartilage thickness changes
 - Cartilage thickening score: sum of all positive cartilage thickness changes

Cartilage Thickness: Primary Analysis Results

Change in Cartilage Thickness [mm] over 24 Months by Case-Control Status

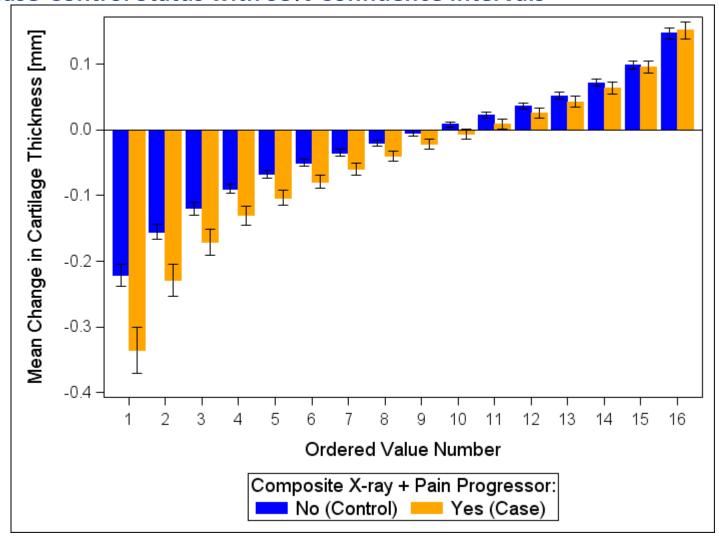
Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p-value*
Central medial femorotibial compartment (cMFTC)	-0.32 (0.40)	-0.12 (0.28)	1.9 (1.6, 2.3)	<.0001
Central medial tibia (cMT)	-0.12 (0.19)	-0.05 (0.13)	1.6 (1.3, 1.9)	<.0001
Central medial weight- bearing femur (ccMF)	-0.21 (0.28)	-0.08 (0.20)	1.8 (1.5, 2.2)	<.0001
Total medial femorotibial compartment (MFTC)	-0.18 (0.24)	-0.06 (0.18)	1.9 (1.6, 2.4)	<.0001
Cartilage thinning score	-1.26 (0.93)	-0.84 (0.65)	1.3 (1.1, 1.5)	0.0085
Cartilage thickening score	0.48 (0.37)	0.51 (0.38)	1.0 (0.8, 1.2)	0.9765

^{*}Adjusted for BL JSW, BL WOMAC Pain, BL age, BL BMI, BL KLG, BL pain medication use, sex, and race

Odds Ratio = Odds of being a composite x-ray and pain progressor vs. not having both x-ray and pain progression for each 1 SD increase in biomarker

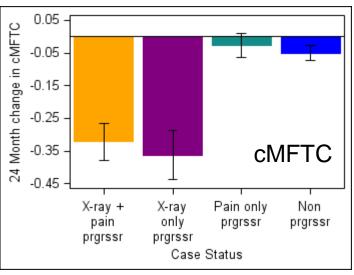
Cartilage Thickness: Primary Analysis Results

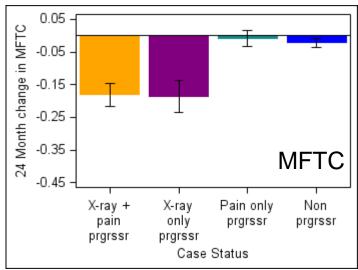
24 Month Ordered Values for Change in Cartilage Thickness by Case-Control Status with 95% Confidence Intervals

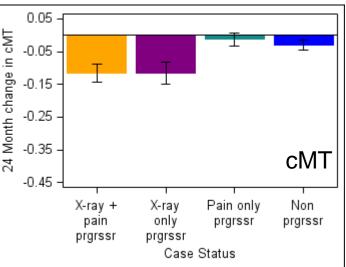


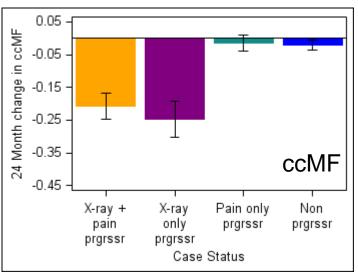
Cartilage Thickness: Secondary Analysis Results

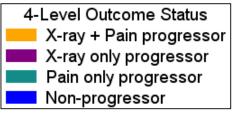
Change in Cartilage Thickness [mm] over 24 Months by Case Status (95% CI)





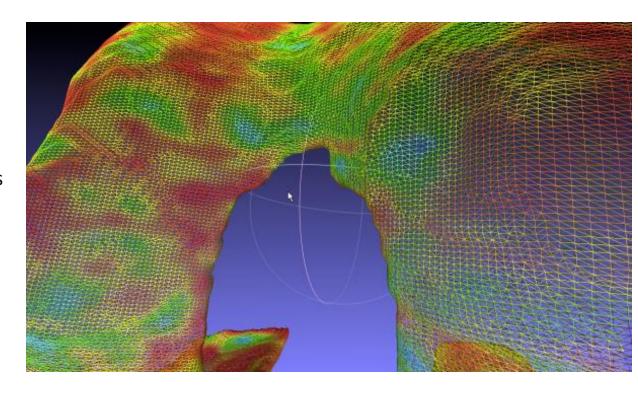






Quantitative Subchondral Bone Plate Morphometry

- Automated segmentations¹
 were reconstructed as 3D
 surfaces
- Measurements were taken at thousands of individual points across the surface
- Statistical Descriptors (Mean, Std. Dev., Low and High tails)
 were provided for Medial / Lateral Central Femur and Tibia





1: Tamez-Peña JG, Farber J, González PC, Schreyer E, Schneider E, Totterman S. Unsupervised segmentation and quantification of anatomical knee features: data from the Osteoarthritis Initiative. IEEE Trans Biomed Eng. 2012 Apr;59(4):1177-86. doi: 10.1109/TBME.2012.2186612. Epub 2012 Feb 3. PubMed PMID: 22318477.

Subchondral Bone Plate Analysis: Predictors

- Subchondral Bone Plate (SBP) Area
 - Central Medial Femur
 - Central Lateral Femur
 - Medial Tibia
 - Lateral Tibia
- Subchondral Bone Plate (SBP) Mean Curvature
 - Central Medial Femur
 - Central Lateral Femur
 - Medial Tibia
 - Lateral Tibia

SBP Area - Primary Analysis Results

Baseline SBP Area by Case-Control Status

Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p- value*
Central MedFem Area	889.3 (156.4)	891.1 (153.4)	0.83 (0.6, 1.1)	0.1969
Central LatFem Area	808.4 (136.9)	802.0 (139.9)	1.0 (0.7, 1.3)	0.9070
MedTib Area	910.8 (178.0)	911.6 (178.3)	0.82 (0.6, 1.1)	0.1625
LatTib Area	809.6 (158.0)	800.1 (161.8)	1.0 (0.8, 1.4)	0.8528

^{*}Adjusted for BL JSW, BL Pain, BL age, BL BMI, BL KLG, BL pain med use, sex, and race

SBP Curvature - Primary Analysis Results

Baseline SBP Curvature by Case-Control Status

Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p- value*
Central MedFem Mean Curvature	0.0274 (0.0064)	0.0290 (0.0059)	0.77 (0.6, 0.9)	0.0101
Central LatFem Mean Curvature	0.0255 (0.0046)	0.0264 (0.0046)	0.81 (0.7, 0.99)	0.0380
MedTib Mean Curvature	-0.0277 (0.0067)	-0.0284 (0.0062)	1.1 (0.9, 1.4)	0.2779
LatTib Mean Curvature	-0.0118 (0.0064)	-0.0117 (0.0064)	1.0 (0.8, 1.2)	0.7391

^{*}Adjusted for BL JSW, BL Pain, BL age, BL BMI, BL KLG, BL pain med use, sex, and race

SBP Curvature - Primary Analysis Results

Baseline SBP Curvature by Case-Control Status

Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p- value*
Central MedFem Mean Curvature	0.0274 (0.0064)	0.0290 (0.0059)	0.77 (0.6, 0.9)	0.0101
Central LatFem Mean Curvature	0.0255 (0.0046)	0.0264 (0.0046)	0.81 (0.7, 0.99)	0.0380
MedTib Mean Curvature	-0.0277 (0.0067)	-0.0284 (0.0062)	1.1 (0.9, 1.4)	0.2779
LatTib Mean Curvature	-0.0118 (0.0064)	-0.0117 (0.0064)	1.0 (0.8, 1.2)	0.7391

^{*}Adjusted for BL JSW, BL Pain, BL age, BL BMI, BL KLG, BL pain med use, sex, and race

SBP Area - Primary Analysis Results

24 Month Change in SBP Area by Case-Control Status

Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p- value*
Central MedFem Area	-18.4 (58.0)	-1.9 (35.6)	0.68 (0.6, 0.8)	0.0001
Central LatFem Area	-5.6 (33.4)	-5.9 (29.5)	0.98 (0.8, 1.2)	0.8667
MedTib Area	-5.4 (43.2)	0.9 (35.4)	0.85 (0.7, 1.02)	0.0779
LatTib Area	-3.6 (36.7)	-5.3 (35.3)	1.03 (0.9, 1.2)	0.7698

^{*}Adjusted for BL JSW, BL Pain, BL age, BL BMI, BL KLG, BL pain med use, sex, and race

SBP Area - Primary Analysis Results

24 Month Change in SBP Area by Case-Control Status

Predictor	Case Control (mean (sd))		OR*	p- value*
Central MedFem Area	-18.4 (58.0)	-1.9 (35.6)	0.68 (0.6, 0.8)	0.0001
Central LatFem Area	-5.6 (33.4)	-5.9 (29.5)	0.98 (0.8, 1.2)	0.8667
MedTib Area	-5.4 (43.2)	0.9 (35.4)	0.85 (0.7, 1.02)	0.0779
LatTib Area	-3.6 (36.7)	-5.3 (35.3)	1.03 (0.9, 1.2)	0.7698

^{*}Adjusted for BL JSW, BL Pain, BL age, BL BMI, BL KLG, BL pain med use, sex, and race

SBP Curvature - Primary Analysis Results

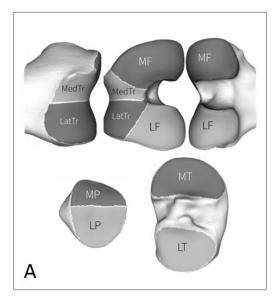
24 Month Change in SBP Curvature by Case-Control Status

Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p- value*
Central MedFem Mean Curvature	-0.0013 (0.0037)	-0.0007 (0.0028)	0.85 (0.7, 1.02)	0.0830
Central LatFem Mean Curvature	-0.0008 (0.0022)	-0.0005 (0.0019)	0.86 (0.7, 1.03)	0.1063
MedTib Mean Curvature	-0.0008 (0.0039)	-0.0002 (0.0032)	0.83 (0.7, 1.00)	0.0456
LatTib Mean Curvature	-0.0002 (0.0029)	-0.0003 (0.0028)	1.01 (0.8, 1.2)	0.9073

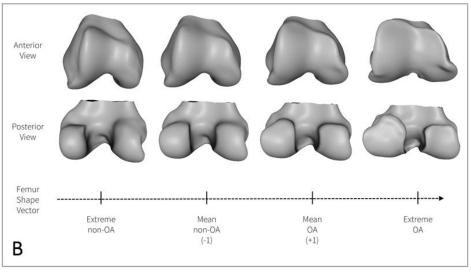
^{*}Adjusted for BL JSW, BL Pain, BL age, BL BMI, BL KLG, BL pain med use, sex, and race

Quantitative Bone Morphometry: SBP - Total Bone Area (tAB) and 3D Shape

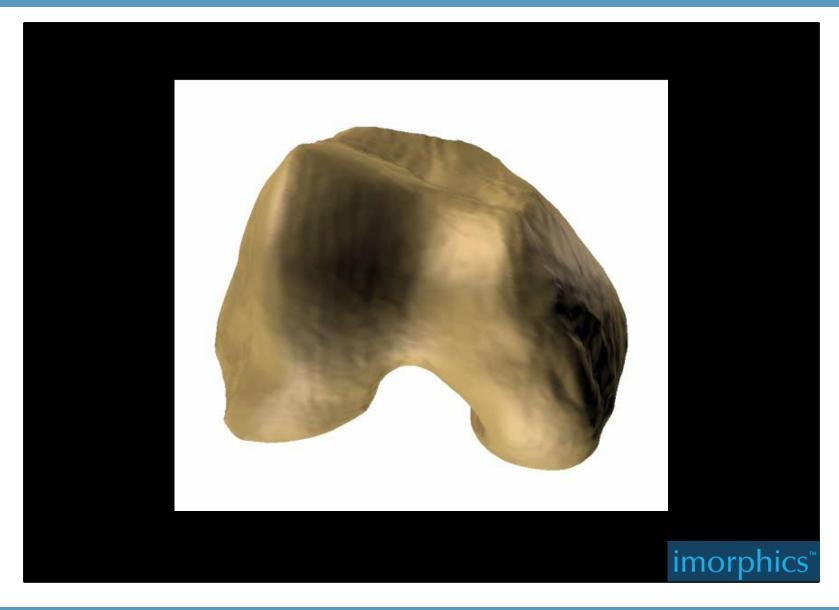
- Change in total bone area (tAB)
 on the medial and lateral femur,
 tibia and patella was measured
 directly from the automated
 segmentations.
- Overall 3D shape for the femur, tibia and patella, was obtained by projecting the shape from each segmented bone surface onto an OA vector for each bone.







Video Showing the 2 Ends of Vector



SBP - tAB and 3D Shape Analysis: Predictors

24 month change in area of subchondral bone (tAB)

Medial	Femur
	Tibia
	Patella
Lateral	Femur
	Tibia
	Patella
	Notch
Medial	Trochlea
Lateral	Trochlea

- 24 month change in position on 3D shape vectors
 - Femur
 - Tibia
 - Patella

Area of SBP (tAB): Primary Analysis Results

Change in area of bone (tAB) [mm²] over 24 Months by Case-Control Status

Predictor	Case (mean (sd))	Control (mean (sd))	OR*	p-value*
Medial Femur (tAB)	37.48 (54.82)	16.13 (41.44)	1.7 (1.4, 2.0)	<.0001
Medial Tibia (tAB)	16.99 (22.11)	10.22 (19.14)	1.4 (1.2, 1.7)	<.0001
Medial Patella (tAB)	7.25 (29.74)	3.10 (16.10)	1.3 (1.1, 1.7)	0.0160
Lateral Femur (tAB)	7.98 (47.43)	-0.45 (42.84)	1.3 (1.0, 1.5)	0.0222
Lateral Tibia (tAB)	11.01 (17.23)	5.53 (14.40)	1.5 (1.2, 1.8)	<.0001
Lateral Patella (tAB)	9.36 (37.41)	3.76 (21.21)	1.3 (1.1, 1.7)	0.0129

^{*}Adjusted for BL JSW, BL WOMAC Pain, BL age, BL BMI, BL KLG, BL pain medication use, sex, and race

Area of SBP (tAB) and 3D shape: Primary Analysis Results

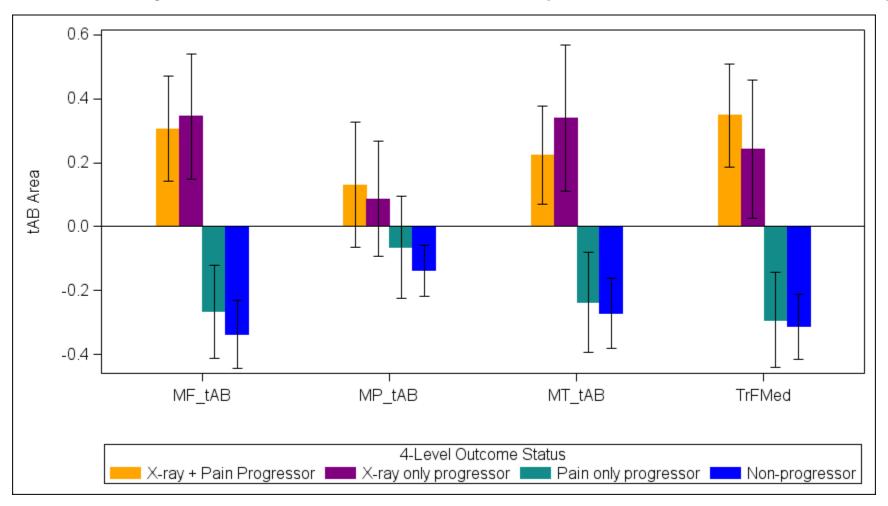
Change in area of bone (tAB) [mm²] and Bone Shape over 24 Months by Case-Control Status

Predictor	Case (mean (sd))			p-value*
Femoral Notch (tAB)	13.09 (26.47)	6.22 (22.98)	1.3 (1.1, 1.6)	0.0045
Lateral PF Femur (tAB)	7.09 (21.04)	0.57 (18.75)	1.4 (1.2, 1.8)	0.0002
Medial PF Femur (tAB)	12.34 (14.55)	5.77 (11.24)	1.7 (1.4, 2.1)	<.0001
Femoral Vector of 3D Shape	0.30 (0.35)	0.16 (0.27)	1.7 (1.4, 2.0)	<.0001
Tibial Vector of 3D Shape	0.35 (0.45)	0.22 (0.43)	1.4 (1.2, 1.7)	0.0003
Patella Vector of 3D Shape	0.29 (0.68)	0.17 (0.68)	1.2 (1.0, 1.5)	0.0352

^{*}Adjusted for BL JSW, BL WOMAC Pain, BL age, BL BMI, BL KLG, BL pain medication use, sex, and race

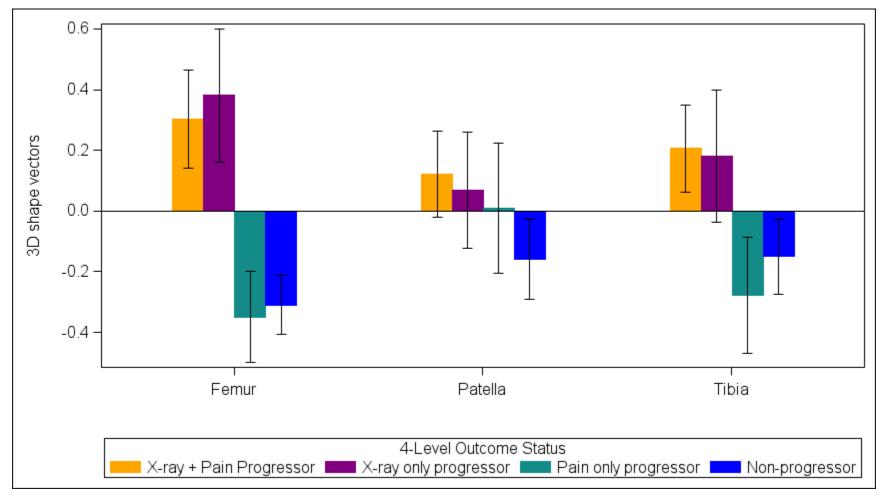
Area of SBP (tAB): Secondary Analysis Results

Change in area of the bone (tAB) in the medial compartments over 24 Months by 4-Level Case-Control Status (normalized, with 95% CIs)



SBP 3D Shape: Secondary Analysis Results

Change in 3D Shape Vector over 24 Months by 4-Level Case-Control Status (normalized, with 95% CIs)

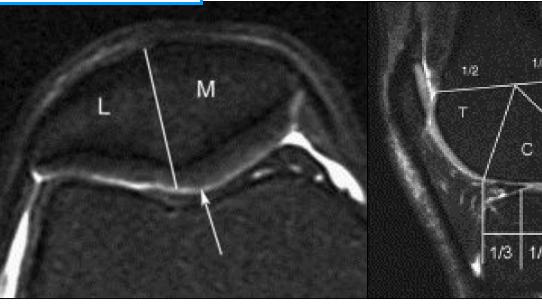


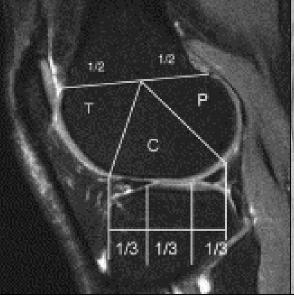
Semi-Quantitative Whole Joint Scoring

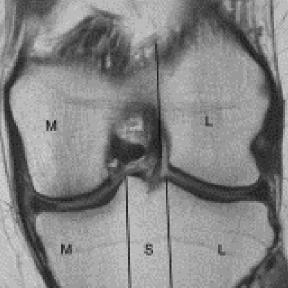
MOAKS = MRI Osteoarthritis Knee Score Osteoarthritis Cartilage 2011;19:990-1002







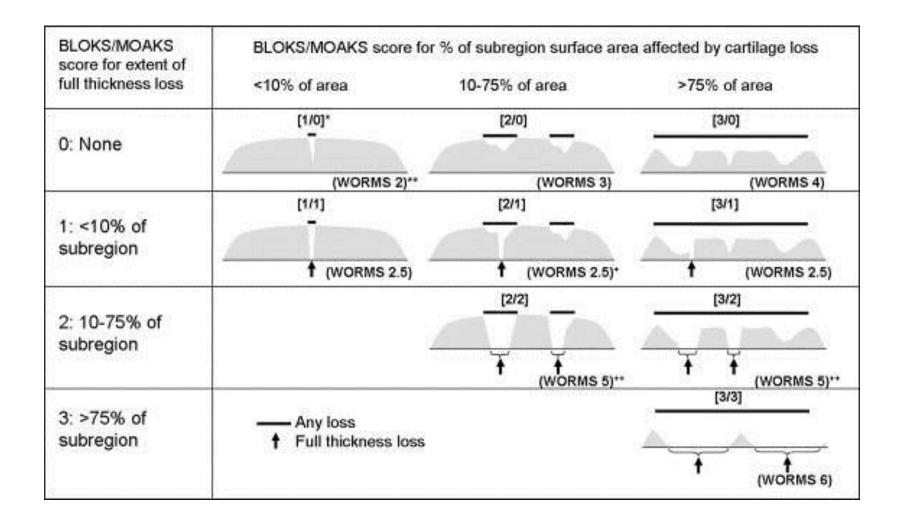




Semi-Quantitative Scoring - MOAKS

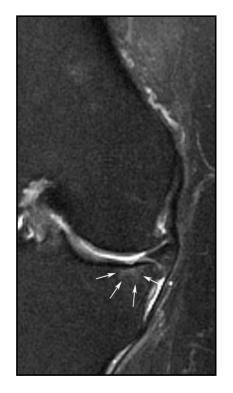
- Assessment of articular cartilage directly
- Assessment of other important structures
 - Meniscus
 - Osteophytes
 - Attrition
 - Subchondral bone marrow lesions and cysts
 - Ligaments
 - Synovium
 - Effusion
 - periarticular structures

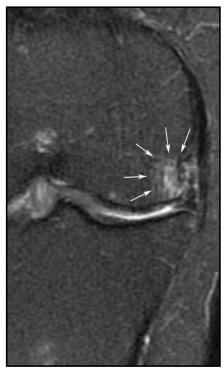
Articular Cartilage: MOAKS - 2 digit-approach



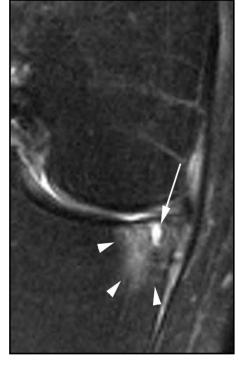
Adapted from: Guermazi et al. Nat Rev Rheumatol 2013;9:236-51

BML Scoring: MOAKS Size









Grade 1 BML

Grade 2 BML

Grade 3 BML

BML consisting of noncystic/ill-defined portion and cystic part

MOAKS Analysis: Predictors

Six Domains

- BMLs
- Osteophytes
- Meniscus
- Cartilage
- Synovitis
- Effusion

MOAKS Analysis: Predictors

Domain	Predictor (24 Month change)
BML	Change in number of subregions affected by any BML
DIVIL	Max change in BML score across all subregions
Ostoonbyto	Change in number of subregions affected by any Osteophyte
Osteophyte	Max change in Osteophyte score across all subregions in knee
Meniscus	Number of regions with worsening in meniscal morphology
Meniscus	Worsening in meniscal extrusion
	Number of areas with worsening in thickness
Cartilage	Number of areas with worsening in surface area (include withingrade change)
	Number of areas with worsening in surface area (excluding withingrade change)
Synovitis	Change in Inter-Condylar Synovitis
Effusion	Change in Whole Knee Effusion

BML - Primary Analysis Results

Variable	Category	Case	Control	OR (95% CI)	P- value
Change in	Improvement	26 (13.4%)	55 (13.6%)	1.1 (0.6, 1.8)	
Number of	No Change	95 (49.0%)	214 (52.8%)	REF	0.210
subregions affected by any BML	Worsen in 1 subregion	49 (25.3%)	105 (25.9%)	1.1 (0.7, 1.6)	0.318
	Worsen in 2+ subregions	24 (12.4%)	31 (7.7%)	1.7 (1.0, 3.1)	
	No Change	53 (27.3%)	138 (34.1%)	REF	
Max change in BML score	Within grade worsening	12 (6.2%)	24 (5.9%)	1.3 (0.6, 2.8)	0.002
	Worsening by 1 grade	81 (41.8%)	192 (47.4%)	1.1 (0.7, 1.7)	0.003
	Worsening by 2+ grades	48 (24.7%)	51 (12.6%)	2.5 (1.5, 4.1)	

Osteophyte and Meniscus - Primary Analysis Results

Variable	Category	Case	Control	OR (95% CI)	P- value
Increase in number of	No	173 (89.2%)	371 (91.4%)	REF	
subregions affected by any Osteophyte	Yes	21 (10.8%)	35 (8.6%)	1.3 (0.7, 2.3)	0.386
Max change in Osteophyte	No	151 (77.8%)	347 (85.5%)	REF	
score >=1 across all subregions in knee	Yes	43 (22.2%)	59 (14.5%)	1.7 (1.1, 2.6)	0.021
Meniscal Morphology: 24	No	140 (72.2%)	365 (90.1%)	REF	
Month any regions with worsening	Yes	54 (27.8%)	40 (9.9%)	3.5 (2.2, 5.5)	<0.001
Meniscal Extrusion Medial -	No	143 (74.1%)	369 (91.3%)	REF	<0.001
24 Month worsening	Yes	50 (25.9%)	35 (8.7%)	3.7 (2.3, 5.9)	<0.001

Cartilage - Primary Analysis Results

Variable	Category	Case	Control	OR (95% CI)	P- value	
Cartilage Morphology - worsening in thickness	No Change	82 (42.3%)	266 (65.5%)	REF	<0.001	
	Worsen in 1 subreg	49 (25.3%)	83 (20.4%)	1.9 (1.2, 2.9)		
	Worsen in 2 subreg	38 (19.6%)	39 (9.6%)	3.2 (1.9, 5.3)		
	Worsen in 3+ subreg	25 (12.9%)	18 (4.4%)	4.5 (2.3, 8.7)		
Cartilage Morphology - worsening in surface area (incl within-grade chg)	No Change	53 (27.3%)	193 (47.5%)	REF		
	Worsen in 1 subreg	54 (27.8%)	122 (30.0%)	1.6 (1.0, 2.5)	-0.001	
	Worsen in 2 subreg	39 (20.1%)	52 (12.8%)	2.7 (1.6, 4.6)	<0.001	
	Worsen in 3+ subreg	48 (24.7%)	39 (9.6%)	4.5 (2.7, 7.5)		
Cartilage Morphology - worsening in surface area (excl within- grade chg)	No Change	105 (54.1%)	277 (68.2%)	REF		
	Worsen in 1 subreg	41 (21.1%)	87 (21.4%)	1.2 (0.8, 1.9)	<0.001	
	Worsen in 2 subreg	25 (12.9%)	31 (7.6%)	2.1 (1.2, 3.8)		
	Worsen in 3+ subreg	23 (11.9%)	11 (2.7%)	5.5 (2.6, 11.7)		

Synovitis and Effusion - Primary Analysis Results

Variable	Category	Case	Control	OR (95% CI)	P- value
Change MOAKS Inter-Condylar Synovitis	Improvement	3 (1.5%)	7 (1.7%)	1.0 (0.3, 4.0)	
	No Change	158 (81.4%)	374 (92.1%)	REF	0.002
	Worsen	33 (17.0%)	25 (6.2%)	3.1 (1.8, 5.4)	
Change in MOAKS Whole Knee Effusion	Improvement	17 (8.8%)	62 (15.3%)	0.8 (0.4, 1.4)	
	No Change	98 (50.5%)	269 (66.3%)	REF	<0.001
	Worsen	79 (40.7%)	75 (18.5%)	2.9 (2.0, 4.3)	

Preliminary Results of Multivariable Models Combining Domains (1 out of 3) - Cartilage

	Model 1	
	Cartilage	
C-statistic	0.686	
Cartilage - areas with worsening in thickness	P=0.0004	
None	REF	
1 subregion	1.7 (1.1, 2.6)	
2 subregions	2.5 (1.4, 4.2)	
3+ subregions	3.2 (1.6, 6.5)	
Cartilage - areas with worsening in surface area (incl within-grade change)	P=0.0003	
None	REF	
1 subregion	1.3 (0.8, 2.1)	
2 subregions	1.9 (1.1, 3.3)	
3+ subregions	3.3 (1.9, 5.6)	

Preliminary Results of Multivariable Models Combining Domains (2 out of 3) – Cartilage + Meniscus

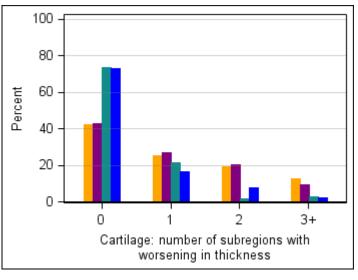
Model 1	Model 2	
Cartilage	Model 1 + Meniscus	
0.686	0.711	
P=0.0004	P=0.0028	
REF	REF	
1.7 (1.1, 2.6)	1.6 (1.0, 2.6)	
2.5 (1.4, 4.2)	2.2 (1.3, 3.9)	
3.2 (1.6, 6.5)	2.8 (1.4, 5.8)	
P=0 0003	P=0 0291	
1 -0.0003	1-0.0231	
REF	REF	
1.3 (0.8, 2.1)	1.2 (0.8, 2.0)	
1.9 (1.1, 3.3)	1.6 (0.9, 2.9)	
3.3 (1.9, 5.6)	2.3 (1.3, 4.2)	
	1.8 (1.0, 3.0)	
	P=0.0420	
	1.9 (1.1, 3.3)	
	P=0.0304	
	Cartilage 0.686 P=0.0004 REF 1.7 (1.1, 2.6) 2.5 (1.4, 4.2) 3.2 (1.6, 6.5) P=0.0003 REF 1.3 (0.8, 2.1) 1.9 (1.1, 3.3)	Cartilage

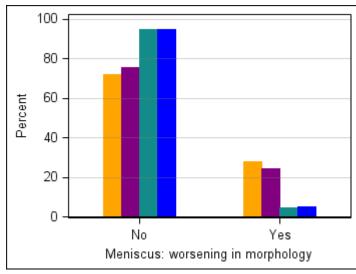
Preliminary Results of Multivariable Models Combining Domains (2 out of 3) – Cartilage + Meniscus + Effusion

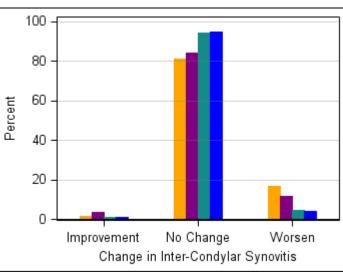
	Model 1	Model 2	Model 3	
	Cartilage	Model 1 + Meniscus	Model 2 + Effusion	
C-statistic	0.686	0.711	0.725	
Cartilage - areas with worsening in thickness	P=0.0004	P=0.0028	P=0.0087	
None	REF	REF	REF	
1 subregion	1.7 (1.1, 2.6)	1.6 (1.0, 2.6)	1.6 (1.0, 2.5)	
2 subregions	2.5 (1.4, 4.2)	2.2 (1.3, 3.9)	2.0 (1.1, 3.5)	
3+ subregions	3.2 (1.6, 6.5)	2.8 (1.4, 5.8)	2.8 (1.3, 5.7)	
Cartilage - areas with worsening in surface	P=0.0003	P=0.0291	P=0.0804	
area (incl within-grade change)	F-0.0003	P-0.0231	P=0.0604	
None	REF	REF	REF	
1 subregion	1.3 (0.8, 2.1)	1.2 (0.8, 2.0)	1.2 (0.8, 1.9)	
2 subregions	1.9 (1.1, 3.3)	1.6 (0.9, 2.9)	1.5 (0.8, 2.7)	
3+ subregions	3.3 (1.9, 5.6)	2.3 (1.3, 4.2)	2.1 (1.2, 3.9)	
Meniscus: Meniscal Morphology: Any regions		1.8 (1.0, 3.0)	1.8 (1.0, 3.0)	
with worsening (Yes vs. No)		P=0.0420	P=0.0416	
Meniscus: Meniscal Extrusion Medial		1.9 (1.1, 3.3)	1.9 (1.1, 3.3)	
worsening (Yes vs. No)		P=0.0304	P=0.1249	
Effusion: Change in Effusion Category			P=0.0010	
Improvement			REF	
No change			1.5 (0.8, 2.7)	
worsening			2.9 (1.5, 5.7)	

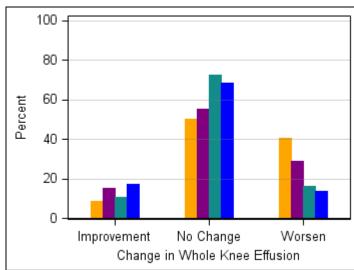
Meniscus - Secondary Analysis Results

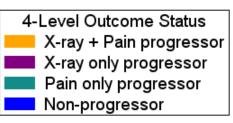
Change in cartilage and meniscus over 24 Months by 4-Level Case-Control Status









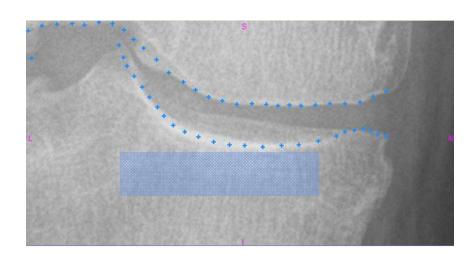


MR Imaging Biomarkers Discussion

- Associations of biomarkers with X-ray+ pain progressors and with X-ray only progressors are similar
- Associations of biomarkers with pain only progressors generally not significant
- The imaging technologies differ in the extent to which they are able to distinguish cases and controls
- Next steps: multivariable models comparing the different technologies

Bone Trabecular Integrity (BTI)

- BTI: measure of trabecular structure or 'texture'
- Measured in subchondral region of tibia
- Horizontal and vertical components





Bone Trabecular Integrity (BTI)

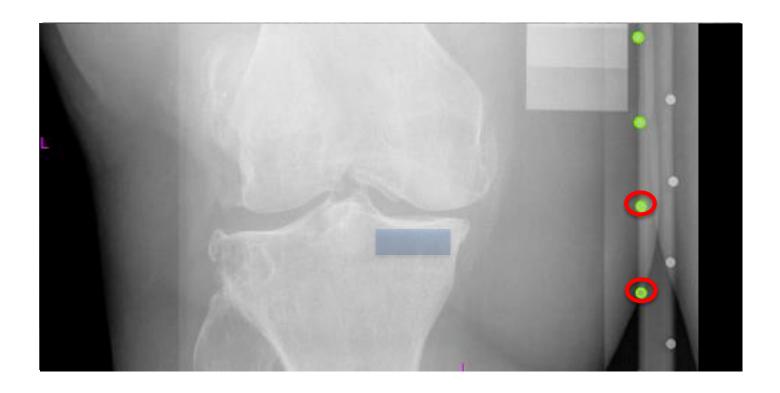
- Technique has a long publication history
 - Starting with J Lynch et al, Med Phys (1991)
- Characteristics of subchondral bone trabeculae are analyzed from knee radiographs (x-rays)
- Technique has been shown to be robust to:
 - Variations in pixel size
 - X-ray exposure
 - Patient positioning
 - Digitisation parameters

Bone Trabecular Integrity (BTI)

- BTI has demonstrated a strong association with the progression of OA based on radiographic and MRI outcomes:
 - JC Buckland-Wright et al, Rheumatology (2007)
 - EA Messent, C Buckland-Wright et al, OAC (2006)
 - VB Kraus, et al, Arthritis Rheum (2009)
 - VB Kraus, et al, Arthritis Rheum (2013)

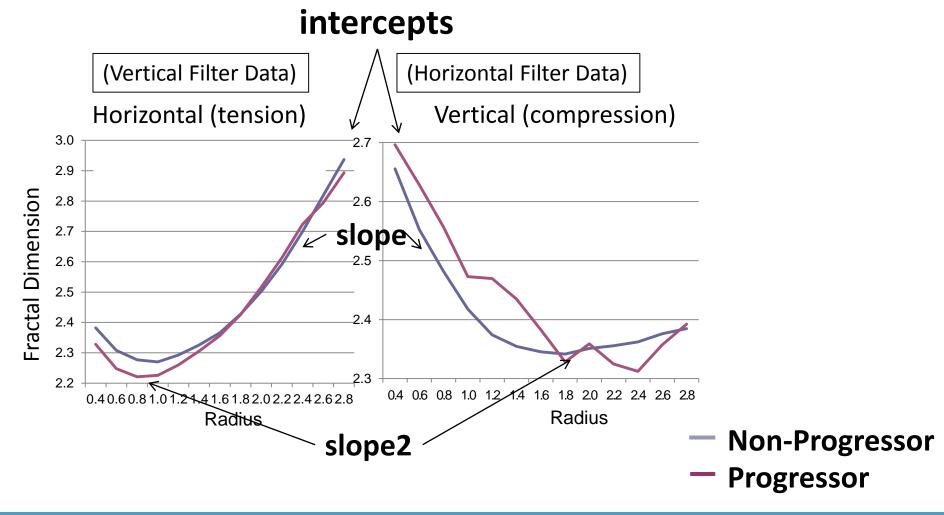
BTI: Image Analysis Implementation

- KneeAnalyzer™ markup of 6 initialisation points on x-ray
- Tibial subchondral region of interest automatically placed
- Fractal Signature Analysis (FSA) of medial compartment region
- Calibration using the Synaflexer[™] beads



BTI Analysis: 6 Predictors

Extraction of 6 BTI parameters from FSA curves



BTI Analysis: Results of Individual Parameters

Baseline Bone Trabecular Integrity by Case-Control Status

Area	Case (mean (sd))	Control (mean (sd))	OR* (z score)	p-value*
Intercept (Horizontal)	2.77 (0.20)	2.74 (0.21)	1.45 (0.9 ,2.4)	0.1337
Slope (Horizontal)	-0.18 (0.05)	-0.19 (0.05)	1.02 (0.8 ,1.3)	0.8796
Quadratic Term (Horizontal)	0.10 (0.07)	0.10 (0.06)	1.14 (0.9 ,1.5)	0.3863
Intercept (Vertical)	2.61 (0.17)	2.59 (0.16)	0.74 (0.5 ,1.1)	0.1625
Slope (Vertical)	0.03 (0.09)	0.04 (0.10)	0.99 (0.7 ,1.3)	0.9214
Quadratic Term (Vertical)§	0.25 (0.09)	0.26 (0.09)	0.72 (0.5 ,1.0)	0.0274

^{*}Adjusted for BL JSW, BL WOMAC Pain, BL age, BL BMI, BL KLG, BL pain medication use, sex, and race §Not significantly associated with any covariate

BTI Analysis: Results

Single baseline BTI parameter predicts any progression, joint space loss and pain progression over 48 months

Label	Method 2: all progressors vs non-progressors		(JSL) progres	oint space loss sors vs JSL non- ressors	Method 4: pain progressors vs non-progressors	
Intercept (Horizontal)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value OR (95% CI	
Quadratic Term (Vertical)	0.0108	0.79 (0.66, 0.95)	0.0328	0.83 (0.70, 0.98)	0.0202	0.81 (0.69 <i>,</i> 0.97)

BTI Analysis: Results of individual parameters

Baseline Bone Trabecular Integrity by Case-Control Status

Area	Case (mean (sd))	Control (mean (sd))	OR* (z score)	p-value*
Intercept (Horizontal)	2.77 (0.20)	2.74 (0.21)	1.45 (0.9 ,2.4)	0.1337
Slope (Horizontal)	-0.18 (0.05)	-0.19 (0.05)	1.02 (0.8 ,1.3)	0.8796
Quadratic Term (Horizontal)	0.10 (0.07)	0.10 (0.06)	1.14 (0.9 ,1.5)	0.3863
Intercept (Vertical)	2.61 (0.17)	2.59 (0.16)	0.74 (0.5 ,1.1)	0.1625
Slope (Vertical)	0.03 (0.09)	0.04 (0.10)	0.99 (0.7 ,1.3)	0.9214
Quadratic Term (Vertical)§	0.25 (0.09)	0.26 (0.09)	0.72 (0.5 ,1.0)	0.0274

^{*}Adjusted for BL JSW, BL WOMAC Pain, BL age, BL BMI, BL KLG, BL pain medication use, sex, and race

§Not significantly associated with any covariate

Odds Ratio = Odds of being a composite JSL and pain progressor vs. not having both JSL and pain progression for each 1 SD increase in biomarker

BTI Analysis: Results of Composite Analysis

Baseline composite BTI score predicts case status at 48 months

Model	Una	adjuste	ed	Adjusted			
	OR* (95% CI)	p-value	C statistic	OR* (95% CI)	p-value	C statistic	
Composite BTI Z-Score	1.21 (1.02, 1.45)	0.0308	0.552	1.24 (1.03, 1.49)	0.0213	0.631	
Covariates Only						0.608	

sum of all markers z-scores (vertical parameters reverse coded)

Covariates: BL JSW, BL WOMAC Pain, BL age, BL BMI, BL KLG, BL pain medication use, sex, and race

^{*}Odds of being a composite x-ray + pain progressor for each 1 SD increase in composite score.

BTI Analysis: Future

- Analyze Joint Space Area
- Analyze Anatomic Axis Angle to assess malalignment as a predictor
- Evaluate longitudinal BTI over 12 and 24 months
- BTI 6 parameter extraction now automated by Duke software that interfaces with KneeAnalyzer
- X-ray analysis and parameter extraction will require ~<30 seconds per image</p>
- Technique being developed as a point of care tool by Optasia Medical in Collaboration with Parexel

FSA/BTI Acknowledgements



DUKE IMAGE ANALYSIS LABORATORY



H Cecil Charles, PhD

 DIAL Director, Co-Director - Center for Advanced Magnetic Resonance Development, Associate Professor of Radiology

Carl F Pieper, DPH

Associate Professor of Biostatistics and Bioinformatics

Lawrence Whitley

Data Analyst, Department of Medicine



Duke University School of Medicine











C1,2C

C₂C

serum and urine

serum and urine

serum and urine

Coll2-1NO2

serum CPII

Serum PIIANP

urine/serum NTX-1

Urine CTXI alpha

and beta/serum

serum CS846

serum MMP-3

CTX-1

Solu	Soluble Bivi: Panel Analyzed									
Biomarker	Process (preliminary)	BIPEDS Classifications	Surrogacy Based on Human Clinical Trials (preliminary)							
urinary CTX-II	type II collagen degradation	Knee: BPED Hip: BPD	characterization: changed significantly in 3 pharmacologic trials that met primary clinical endpoints (Christgau 2004, Gineyts 2004, Manicourt 2006)							
serum COMP	cartilage degeneration	Knee: BPD Hip: BPD	exploration: not used to date in pharmacologic trial							
serum HA	osteophyte burden, synovitis	Knee: BPED Hip: P	demonstration: changed significantly in one pharmacologic trial that met primary clinical endpoints (Manicourt 2006)							

Knee: D(u)

Knee: E(s), D(u)

Knee: D(s),B(u),P(u)

Hip: none

Hip: B(s)

Hip: D(s)

Knee: D(s)

Knee: BPD

Knee: P(u),E(u)

Knee: B(u), D(s/u),

2005)

Manicourt 2006)

Hip: none

Hip: P(s)

Hip: none

Knee: P

Knee: E

Hip: none

Hip: none

P(u)

Hip: B(s)

Types I and II collagen

degradation

degradation

degradation

synthesis

synthesis

type II collagen

type II collagen

type II collagen

Type II collagen

bone resorption

bone resorption

cartilage aggrecan

synthesis/turnover

joint tissue

degradation

protease involved with

ELISA assay

type

competitive-

competitiveinhibition &

sandwich protein

binding assay

competitive-

competitive-

competitive-

competitive-

competitive-

competitive-

competitive-

competitive-

sandwich for total

MMP-3 assay

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

inhibition

sandwich

exploration: nonsignificant change in one pharmacologic

demonstration: nonsignificant change in one pharmacologic

trial that met primary clinical endpoint (Mazzuca 2006)

trial that met primary clinical endpoint (Mazzuca 2006)

exploration: nonsignificant change in one pharmacologic

demonstration: changed significantly in one pharmacologic

trial that met primary clinical (WOMAC) endpoint (Spector

exploration: nonsignificant change in one pharmacologic

trial that met primary clinical endpoint (Mazzuca 2006) but

characterization: changed significantly in two pharmacologic

trials that met primary clinical endpoints (Lohmander 2005,

trial that met primary clinical endpoint (Mazzuca 2006)

exploration: not used to date in pharmacologic trial

exploration: not used to date in pharmacologic trial

changed associated with concurrent JSN

exploration: not used to date in pharmacologic trial

Soluble BM: Assays

- 12 biomarkers (18 total by format) were chosen by consensus of an expert working group (Kraus VB, et al, OAC 2011)
- Selection required the biomarker be available "off the shelf" as a commercially available kit
- LabCorp Clinical Trials (San Leandro, CA)--CLIA and CAP certified division within LabCorp measured all biomarkers except urine Col2-1 NO2
- Artialis (Liege, Belgium)--Good Laboratory Practice (GLP) certified facility, measured urine Col2-1 NO2
- Duplicate analyses of baseline, 12m and 24 m samples
- Same lot of kits used for all analyses of each biomarker

Soluble BM: Samples

- N=1785 samples were available for analysis from 600 subjects (15 of the 12 month samples missing)
- Nearly all (92-98%) serum and urine were >8 hrs fasting samples
- All samples encoded by UCSF
- Unthawed stock serum sample provided to LabCorp
- An unthawed stock urine sample was aliquoted by LabCorp and an aliquot provided to Artialis (Liege, Belgium) for Col2-1 NO2
- Freeze thaws were minimized and assays optimally sequenced per available information of biomarker stability
- Clustering of samples by individual was performed to minimize technical variability of longitudinal analyses (running all samples for a particular individual on the same plate)

Soluble BM: Imputation Strategy

- For results above the highest standard, the sample was diluted more and reanalyzed
- For results below the lowest standard
 - The kit manufacturer was consulted and when deemed appropriate,
 the sample was diluted less and reanalyzed
 - For samples still yielding values below the lowest standard, results were imputed by interpolation from the standard curve extended from the lowest standard to zero.
 - This method was deemed superior to random imputation particularly as some of the biomarkers had linear standard curves in this low range (HA and CS-846)

Soluble BM: Coefficients of Variation (from smallest to largest)

Biomarker (units)	CV
serum CTX-1 (ng/ml)	5%
serum COMP (ng/ml)	5%
serum HA (ng/ml)	7%
serum NTX-1 (nm BCE)	7%
serum MMP-3 (ng/ml)	10%
serum C2C (ng/ml)	12%
serum CPII (ng/ml)	12%
serum PIIANP (ng/ml)	12%
serum Coll2-1 NO2 (nM)	14%
serum CS846 (ng/ml)	17%
serum C1,2C (μg/ml)	23%

Biomarker (units)	CV
urine NTX-1 (nM BCE/mmol Cr)	3%
urine Creatinine (mmol/L)	3%
urine CTX-1α (μg/mmol Cr)	4%
urine CTX-II (ng/mmol Cr)	5%
urine C2C HUSA (ng/mmol Cr)	6%
urine CTX-1β (μg/mmol Cr)	8%
Urine Col-2-1NO2 (nM/mmol Cr)	9%
urine C1,2C (ng/mmol Cr)	22%

Soluble BM: Covariates

- Several of the baseline biomarker concentrations were associated with one or more demographic or baseline characteristics including sex, age, BMI, race, baseline joint space width, baseline WOMAC pain and baseline use of pain medications
- These covariates were therefore used for the final analyses but did not alter any of the results

Soluble BM: Covariates -- Serum

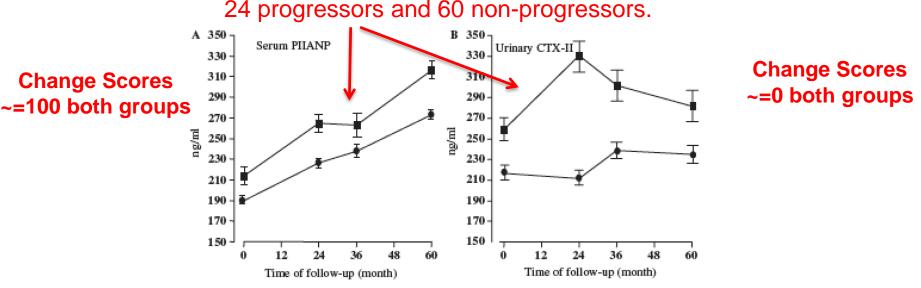
D '	6 ¥	D . D4 I *	. *	DI ICIA/+	DI MONAS	D1 4 ±	DI DAGIA
Biomarker	Sex*	Pain Meds*	Race*	BL JSW ⁺	BL WOMAC	BL Age ⁺	BL BMI ⁺
(z scored)					Pain ⁺		
serum C12C	-0.2381	0.0325	0.3425	0.0455	-0.0347	0.0552	-0.0443
	(<0.0001)	(0.4219)	(0.0404)	(0.2659)	(0.3960)	(0.1773)	(0.2799)
serum C2C	-0.2034	-0.1013	0.4871	-0.0203	0.0306	0.0359	0.0655
	(0.3710)	(0.0613)	(0.0263)	(0.6250)	(0.4613)	(0.3872)	(0.1147)
serum COLL2-1 NO2	-0.4487	-0.1273	0.5834	-0.0161	0.0522	0.0098	-0.0664
	(0.1292)	(0.1427)	(<0.0001)	(0.6986)	(0.2084)	(0.8127)	(0.1099)
serum CPII	-0.2794	-0.0741	0.7965	0.0107	0.0183	0.0269	-0.0484
	(0.5065)	(<0.0001)	(<0.0001)	(0.7962)	(0.6591)	(0.5173)	(0.2439)
serum CS846	-0.1115	-0.0212	0.0068	-0.0051	0.0186	-0.0349	0.0155
	(0.0100)	(0.6736)	(0.5599)	(0.9022)	(0.6550)	(0.4007)	(0.7084)
serum CTXI	-0.1479	0.1160	-0.1441	0.0267	-0.0427	-0.0152	-0.1228
	(<0.0001)	(0.0541)	(0.0310)	(0.5145)	(0.2970)	(0.7103)	(0.0026)
serum COMP	0.1469	0.0558	0.0809	0.0197	-0.0636	0.2454	-0.0629
	(0.0927)	(0.7808)	(0.0863)	(0.6352)	(0.1256)	(<0.0001)	(0.1301)
serum HA	0.0159	-0.0775	0.3355	-0.0993	-0.0054	0.3808	0.0483
	(0.5384)	(0.1558)	(<0.0001)	(0.0165)	(0.8965)	(<0.0001)	(0.2447)
serum MMP-3	1.0604	-0.0052	-0.1361	0.0388	-0.0774	0.0949	-0.1138
	(<0.0001)	(0.4516)	(0.0698)	(0.3497)	(0.0619)	(0.0220)	(0.0060)
serum NTXI	-0.1654	0.1755	0.0210	0.0032	-0.0024	0.0402	-0.0231
	(0.0001)	(0.8993)	(0.0898)	(0.9378)	(0.9543)	(0.3327)	(0.5791)
serum PIIANP	-0.0377	-0.0556	0.3650	-0.0100	0.0819	-0.0006	0.1517
	(0.3946)	(0.5065)	(0.5638)	(0.8066)	(0.0451)	(0.9891)	(0.0002)

Soluble BM: Covariates -- Serum

Biomarker (z scored)	Sex*	Pain Meds*	Race*	BL JSW ⁺	BL WOMAC Pain ⁺	BL Age+	BL BMI ⁺
urine Col2-1 NO2	-0.2646	-0.2250	-0.2401	0.0211	-0.0013	0.0216	-0.0103
	(0.0142)	(<0.0001)	(<0.0001)	(0.6114)	(0.9746)	(0.6019)	(0.8041)
urine C12C	0.2635	0.0324	-0.0735	0.0633	-0.0000	-0.1040	0.0745
	(0.0142)	(0.5869)	(0.5688)	(0.1268)	(0.9998)	(0.0120)	(0.0724)
urine C2C	-0.1311	0.0191	0.0247	-0.1006	-0.0308	0.2741	-0.0299
	(0.0334)	(0.8064)	(0.0131)	(0.0151)	(0.4585)	(<0.0001)	(0.4719)
urine CTXII	-0.2953	0.0630	0.2086	-0.0537	0.1057	0.1486	0.0791
	(<0.0001)	(0.0364)	(0.0381)	(0.1954)	(0.0106)	(0.0003)	(0.0564)
urine NTXI	-0.4228	0.1796	-0.1890	-0.0258	-0.0473	0.0330	-0.1075
	(<0.0001)	(0.0278)	(0.0564)	(0.5348)	(0.2539)	(0.4260)	(0.0094)
urine CTXIα	-0.2906	0.1931	-0.0233	0.0005	-0.0565	0.0039	-0.0868
	(<0.0001)	(0.0500)	(0.6575)	(0.9900)	(0.1730)	(0.9255)	(0.0363)
urine CTXIβ	-0.2977	0.1965	0.0398	0.0273	-0.0203	-0.0594	-0.0782
	(<0.0001)	(0.3447)	(0.4598)	(0.5111)	(0.6251)	(0.1523)	(0.0594)

Soluble BM: Longitudinal Biomarker Data Challenge

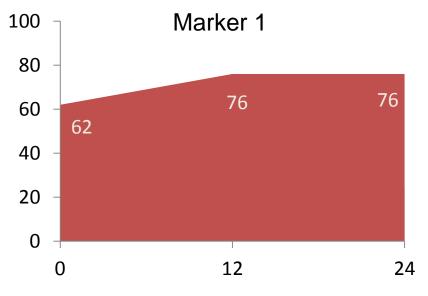
■ The dynamic nature of OA-related biochemical markers is known: Sharif M, et al, Arthritis Rheum (2004); Sharif M, et al, Rheumatology (Oxford) (2007).



Sharif, et al. (2007) Rheumatology (Oxford) 46(6): 938-943.

<u>Time-Integrated Concentrations</u> can overcome these issues and can be used to evaluate the longitudinal dynamic change in the biomarkers

Defining Time-Integrated Concentrations



Marker 1:

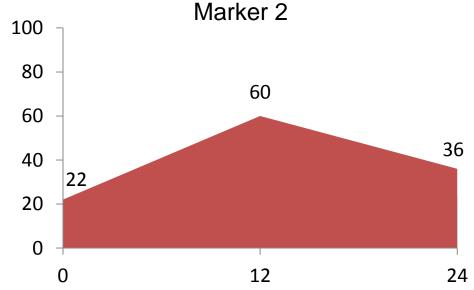
Change: 76-62=14

TIC: (62+76)/2+(76+76)/2=145



Change: 36-22=14

TIC: (22+60)/2+(60+36)/2=89



Soluble BM: Statistical Analytic Strategy

Algorithm

- Calculate Time-Integrated-Concentration (TIC) for each marker for each subject
 - Use interpolated research value
- Determine mean and SD of the TIC for each biomarker
- Convert to Z- score by subtracting the mean and dividing by SD
- Z-scores standardization helps to compare across multiple biochemical markers
- Analyzed several standardized (z-score converted) measures: baseline, 12 change, 24-month TIC for each biomarkers
 - Univariate analysis for each biomarker
 - combinatorial approach using 24-month TIC for multiple biomarkers to optimize prediction

Soluble BM: Single Biomarker Associations (adjusted for baseline covariates — Serum 1 of 2)

	Baseline Concentration (z-score)				Month TIC (Z-sc	ore)	24 Month TIC (z-score)			
Biomarker	Mean (SD) Median		OR, 95% CI,	Mean (SD) Median		OR, 95% CI,	Mean (SD) Median		OR, 95% CI,	
	Comparators	Cases	P value	Comparators	Cases	P value	Comparators	Cases	P value	
C12C	-0.03 (0.98) -0.09	0.06 (1.04) -0.02	1.08 (0.91, 1.29) 0.3868	-0.01 (1.00) -0.04	0.02 (1.00)	1.02 (0.85, 1.22) 0.8637	0.01 (1.01)	-0.01 (0.99) -0.06	0.97 (0.81, 1.15) 0.7031	
C2C	-0.02 (0.94) -0.16	0.04 (1.11)	1.05 (0.88, 1.25) 0.5778	-0.00 (0.98) -0.10	0.01 (1.05) -0.09	0.98 (0.82, 1.18) 0.8536	0.04 (0.95) 0.04	-0.07 (1.10) -0.03	0.88 (0.73, 1.05) 0.1548	
COLL2-1 NO2	0.00 (1.03) -0.18	-0.01 (0.94) -0.15	1.00 (0.84, 1.21) 0.9598	0.00 (1.00)	-0.01 (1.00) -0.18	1.00 (0.82, 1.21) 0.9930	0.02 (1.01)	-0.04 (0.98) -0.15	0.96 (0.79, 1.16) 0.6753	
CPII	0.01 (1.03) -0.12	-0.01 (0.95) -0.18	0.96 (0.80, 1.16) 0.6848	0.02 (1.00) -0.09	-0.04 (1.00) -0.18	0.92 (0.75, 1.12) 0.3963	0.05 (1.00) -0.07	-0.10 (1.01) -0.17	0.84 (0.69, 1.02) 0.0814	
CS846	-0.01 (0.96) -0.20	0.02 (1.09) -0.23	1.05 (0.88, 1.24) 0.6071	-0.01 (0.95) -0.20	0.02 (1.11) -0.28	1.04 (0.87, 1.25) 0.6637	0.00 (0.95) -0.18	-0.00 (1.10) -0.30	1.00 (0.84, 1.20) 0.9749	

Soluble BM: Single Biomarker Associations (adjusted for baseline covariates — Serum 2 of 2)

	Bas	eline Concentra	tion		12 Month TIC			24 Month TIC	
Biomarker	Mean (SD) Me	dian z score	OR, 95% CI,	Mean (SD) Me	dian z score	OR, 95% CI,	Mean (SD) Me	dian z score	OR, 95% CI,
	Comparators	Cases	P value	Comparators	Cases	P value	Comparators	Cases	P value
СТХІ	-0.05 (1.01) -0.28	0.10 (0.96) -0.04	1.18 (0.99, 1.40) 0.0642	-0.07 (0.98) -0.24	0.16 (1.04) 0.02	1.28 (1.07, 1.53) 0.0066	-0.06 (0.96) -0.23	0.12 (1.07) 0.01	1.21 (1.02, 1.44) 0.0277
COMP	0.02 (1.02) -0.12	-0.05 (0.96) -0.24	0.89 (0.74, 1.08) 0.2356	0.02 (1.01) -0.11	-0.03 (0.98) -0.24	0.91 (0.75, 1.10) 0.3446	0.03 (1.00) -0.05	-0.07 (1.01) -0.21	0.86 (0.71, 1.04) 0.1147
НА	-0.04 (1.02) -0.34	0.08 (0.96) -0.22	1.09 (0.90, 1.31) 0.3818	-0.06 (0.99) -0.35	0.12 (1.02) -0.19	1.18 (0.97, 1.43) 0.0970	-0.05 (0.96) -0.36	0.11 (1.06) -0.16	1.16 (0.96, 1.41) 0.1159
MMP-3	-0.02 (1.00) -0.22	0.04 (1.01) -0.22	1.00 (0.81, 1.22) 0.9805	-0.02 (1.01) -0.23	0.05 (0.99) -0.14	1.02 (0.82, 1.28) 0.8342	-0.02 (1.00) -0.22	0.05 (0.99) -0.13	1.00 (0.81, 1.24) 0.9876
NTXI	-0.05 (0.99) -0.20	0.11 (1.02) 0.01	1.19 (1.00, 1.42) 0.0514	-0.08 (0.97) -0.19	0.18 (1.05) 0.02	1.29 (1.08, 1.55) 0.0056	-0.05 (0.94) -0.14	0.10 (1.11) -0.01	1.16 (0.97, 1.38) 0.0951
PIIANP	0.04 (0.99) -0.03	-0.09 (1.03) -0.16	0.88 (0.74, 1.05) 0.1577	0.06 (0.98) 0.09	-0.13 (1.04) -0.18	0.83 (0.69, 0.99) 0.0431	0.07 (0.95) 0.13	-0.16 (1.09) -0.20	0.79 (0.66, 0.94) 0.0076

Soluble BM: Single Biomarker Associations (adjusted for baseline covariates — Urine, Creatinine adjusted)

	Baseline Concentration				12 Month TIC			24 Month TIC		
Biomarker	Mean (SD) Med	dian z score	OR, 95% CI, P value	Mean (SD) Med	lian z score	OR, 95% CI,	Mean (SD) Med	dian z score	OR, 95% CI,	
	Comparators	Cases		Comparators	Cases	P value	Comparators	Cases	P value	
Coll2-1 NO2	-0.02 (1.01) -0.27	0.04 (0.98) -0.19	1.08 (0.91, 1.28) 0.3677	-0.03 (1.01) -0.28	0.07 (0.99)	1.14 (0.95, 1.36) 0.1542	-0.01 (0.99) -0.23	0.03 (1.02) -0.20	1.07 (0.90, 1.27) 0.4447	
C12C	0.04 (1.02) -0.12	-0.08 (0.96) -0.32	0.89 (0.74, 1.07) 0.2245	0.02 (1.02) -0.11	-0.04 (0.95) -0.09	0.96 (0.79, 1.15) 0.6335	0.02 (1.03) -0.13	-0.03 (0.94) -0.13	0.95 (0.79, 1.14) 0.5848	
C2C HUSA	-0.05 (0.93) -0.20	0.11 (1.12) -0.06	1.15 (0.96, 1.38) 0.1222	-0.06 (0.97) -0.25	0.12 (1.05) -0.04	1.18 (0.98, 1.42) 0.0874	-0.06 (0.98) -0.26	0.12 (1.04) -0.07	1.17 (0.98, 1.41) 0.0885	
CTXII	-0.07 (0.98) -0.35	0.15 (1.04) -0.08	1.29 (1.07, 1.54) 0.0063	-0.08 (1.01) -0.30	0.18 (0.96) 0.05	1.34 (1.11, 1.62) 0.0020	-0.07 (1.01) -0.28	0.15 (0.97) 0.08	1.29 (1.08, 1.55) 0.0062	
NTXI	-0.06 (1.00) -0.24	0.12 (1.00) -0.05	1.22 (1.02, 1.45) 0.0301	-0.07 (0.98) -0.17	0.15 (1.03) -0.10	1.28 (1.07, 1.55) 0.0083	-0.06 (0.97) -0.18	0.11 (1.04) -0.16	1.23 (1.03, 1.47) 0.0259	
CTX-1α	-0.06 (0.98) -0.26	0.12 (1.03) -0.08	1.21 (1.02, 1.45) 0.0294	-0.08 (0.97) -0.28	0.17 (1.04) -0.01	1.29 (1.07, 1.55) 0.0063	-0.07 (0.97) -0.28	0.15 (1.05) -0.01	1.27 (1.06, 1.52) 0.0081	
CTX-1ß	-0.03 (1.01) -0.27	0.07 (0.98) -0.12	1.14 (0.95, 1.36) 0.1502	-0.06 (0.97) -0.27	0.13 (1.06) -0.10	1.27 (1.05, 1.52) 0.0123	-0.05 (0.95) -0.26	0.11 (1.09) -0.14	1.22 (1.02, 1.46) 0.0299	

Selecting Markers for Combinatorial Approach Using Measures of Discrimination

- Two stage approach
 - 1. We selected markers for multivariable modeling (combinatorial approach) based on univariate p-values (p<0.10)
 - For each marker selected we evaluated net reclassification (NRI)
 - NRI: measures the improvement in risk prediction between the old and new models by comparing number of advantageous reclassifications to the number of disadvantageous reclassifications (NRI>10%)
- Additionally we took into consideration correlation among biomarkers to avoid colinearity problems in multivariable modeling

Selecting Markers for Combinatorial Approach Using Measures of Discrimination

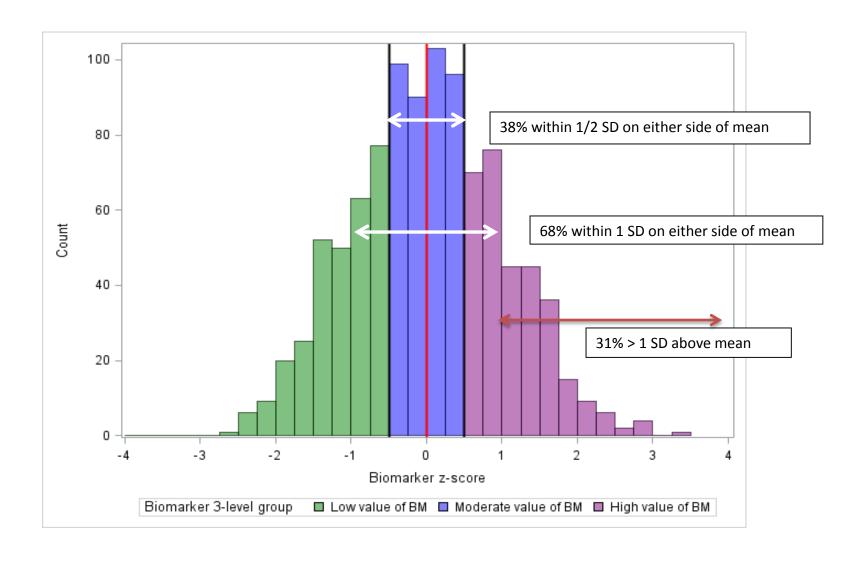
ROC analysis:

- Illustrates the performance of a set of variables as its discrimination threshold is varied
- AUC: probability that a set of markers would rank a randomly chosen case higher than a randomly chosen control (c-statistics)

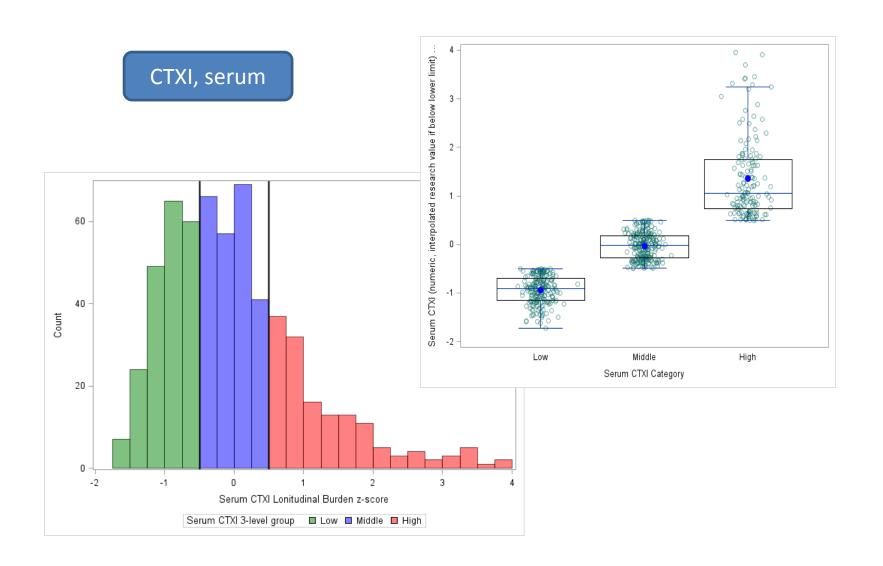
Cross-validation:

- Used 10-fold cross validation to assess the prediction error.
- Split data randomly into 10 equally-sized subsets
 - Of the 10 subsets, 9 are used as training data to estimate the model, and model performance is tested on the 10th subset
 - Process is repeated 10 times, so that each observation is included exactly ones as part of the testing dataset

Creating Clinically Meaningful Groups for Biomarkers: Theoretical Conceptualization



From theory to practice...



Soluble BM: Combinatorial Analytic Strategy

- For those biochemical markers selected for combinatorial approach we created 5-level categorical variables
- Categories were created based on z-score:
 - < 1 SD below the mean
 - between 1 and 0.5 SDs below the mean
 - within 0.5 SDs on either side of the mean
 - between 0.5 and 1 SDs above the mean
 - > 1 SD above the mean
- Each category was assigned a score: -1, -0.5, 0, 0.5, 1
- Since lower levels of Serum PIIANP should be associated with being a case, the categories were reverse coded

Results: Selecting Markers for Combinatorial Analysis Using Measures of Discrimination

						NRI	
	OR	OR 95% CI	p-value	NRI	CI	Cases - % correctly reclassified	Controls - % correctly reclassified
Serum CPII	0.84	0.69, 1.02	0.0814	0.0934	0777, .2646	23%	-13%
Serum CTXI	1.21	1.02, 1.44	0.0277	0.1924	0.0222, .3627	-3%	22%
Serum HA	1.16	0.96, 1.41	0.1159	0.1027	0718,0.2772	3%	7%
Serum NTXI	1.16	0.97, 1.38	0.0951	0.0890	0852,0.2632	10%	-1%
Serum PIIANP	0.79	0.66, 0.94	0.0076	0.2353	0.0646,0.4060	9%	15%
Urine CTX-1a (Ur_alpha)	1.27	1.06, 1.52	0.0081	0.1778	0.0039,0.3516	6%	12%
Urine CTX-1ß (Ur_beta)	1.22	1.02, 1.46	0.0299	0.0631	1110,0.2373	7%	-0%
Urine C2C	1.17	0.98, 1.41	0.0885	0.1152	0583,0.2888	12%	-0%
Urinary CTXII	1.29	1.08, 1.55	0.0062	0.2698	0.0970,0.4425	15%	12%
Urine NTXI	1.23	1.03, 1.47	0.0259	0.0326	1417,0.2069	5%	-2%

Pearson Correlations Among Selected Markers

Marker	Serum CTXI	Serum HA	Serum NTXI	Serum PIIANP	Urine C2C	Urine CTXII	Urine NTXI	Urine CTXI alpha	Urine CTXI beta
Serum CTXI		0.079	0.643	0.055	0.245	0.381	0.798	0.803	0.827
Serum HA			0.109	0.003	0.322	0.375	0.094	0.093	0.059
Serum NTXI				0.100	0.234	0.342	0.584	0.594	0.562
Serum PIIANP					0.120	0.072	0.053	0.042	0.058
Urine C2C						0.657	0.366	0.331	0.275
Urine CTXII							0.482	0.440	0.422
Urine NTXI								0.902	0.862
Urine CTXI									0.850
alpha									

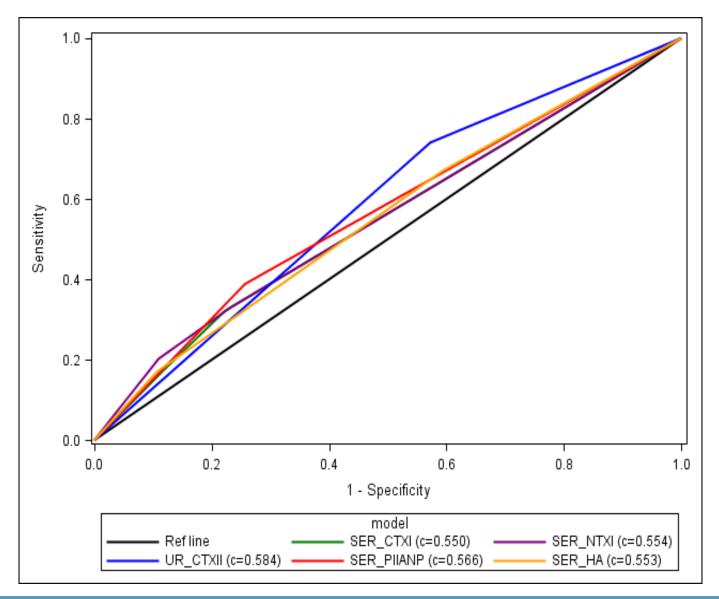
Biochemical Markers: Mechanisms and Direction

		_ I	If OA Progressing we expect	
Marker	Mechanism	High	TIC	
		vs		
		Low		
Serum_CTXI	Bone Resorption (BR)	Н	Н	
Serum_NTXI	Bone Resorption (BR)	Н	Н	
Serum_HA	Inflammation (I)	Н	Н	
Serum_PIIANP	Cartilage Synthesis (CS)	L	L	
Urine CTXII	Cartilage Degradation (CD)	Н	Н	
Urine C2C	Cartilage Degradation (CD)	Н	Н	
Urine NTXI	Bone Resorption/Turnover (BR)	Н	Н	
Urine CTX-1alpha	Bone Resorption/Turnover (BR) (new bone)	Н	Н	
Urine CTX-1beta	Bone Resorption/Turnover (BR) (old bone)	Н	Н	

Groupings for the Final Models: Predicting Case-Control Status Based on TIC

Marker	Groups
Serum CTXI Group 3-level	less than 0.5 SDs above the mean greater than 0.5 SD above the mean
Serum HA Group 2-level	Less than 0.5 SDs above the mean 0.5 SDs above the mean or greater
Serum NTXI Group 3-level	less than 1 SD above the mean greater than 1 SD above the mean
Serum PIIANP Group 2-level	Less than 0.5 SDs above the mean 0.5 SDs above the mean or greater
Urinary CTXII creatinine adj Group 2-level	at least 0.5 SDs below the mean 0.5 SDs below the mean or greater

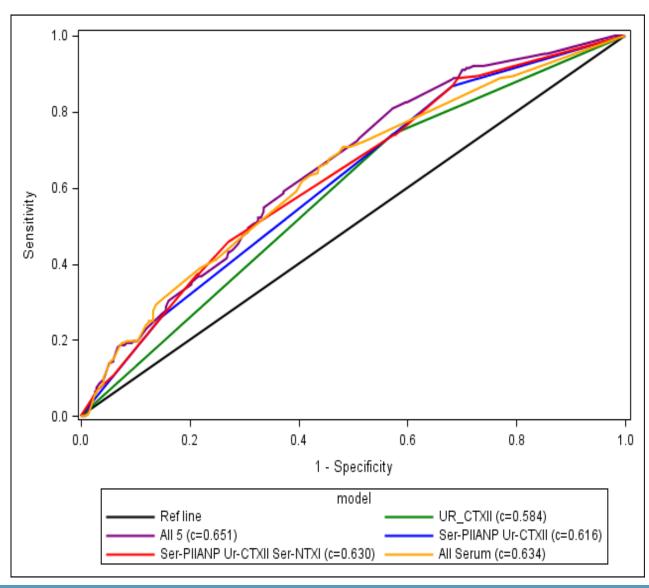
ROC for Each Individual Marker Selected for Combinatorial Analysis



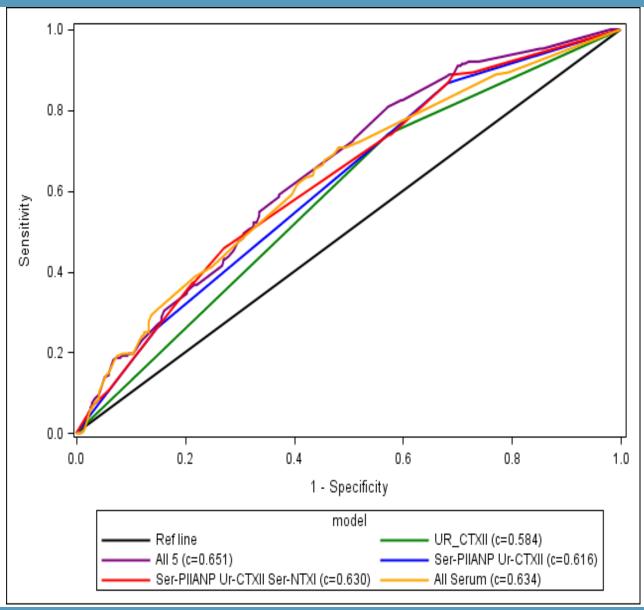
Additional Modeling Considerations

- We evaluated the performance of various combinations of biomarkers:
 - Including all 5 markers in a logistic model
 - Including only markers that were statistically significant in the multivariable model (Urine CTXII, Serum PIIANP)
 - Including all serum markers
 - Combinations of the best performing markers in preliminary analysis (Urine CTXII, Serum PIIANP, Serum NTXI)
 - For reference, we've also included the ROC curve for the best performing (by c-statistic) univariate marker Urine CTXII

ROC Analysis using Combination of Biomarkers

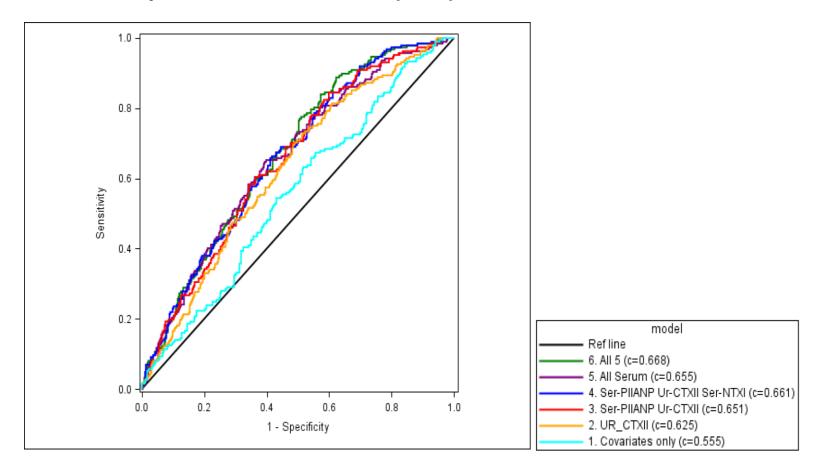


Refined ROC Analysis



Soluble BM: Combinatorial Results: Adjusted for Covariates

Receiver Operator Characteristic (ROC) Curves for 24 month TICs



Soluble BM: Combinatorial Analysis-24 month TIC Predicting Case Status with Cross-Validation

model	C-statistic (no CV)	10-fold CV C- statistic - mean	10-fold CV C- statistic – range (min)	10-fold CV C- statistic – range (max)
Covariates Only	0.555	0.511	0.488	0.535
U-CTXII	0.625	0.594	0.577	0.607
Ser-PIIANP Ur-CTXII	0.651	0.620	0.606	0.631
Ser-PIIANP Ur-CTXII Ser-NTXI	0.661	0.628	0.614	0.638
All Serum 4*	0.655	0.613	0.594	0.627
All 5	0.668	0.627	0.614	0.640

CV=cross-validation;

serum 4: PIIANP, NTXI, CTXI, HA;

all 5: serum 4+urine CTXII

BM Analysis: Conclusions I

- The catabolic biomarkers (CTXII, CTX-I and NTX-I) were positively associated with OA progression while the anabolic biomarker (PIIANP) was negatively associated with OA progression.
- These type I collagen biomarkers along with two representative of type II collagen (CTXII and PIIANP) were the most predictive of case status.
- These results are consistent with the long recognized association of OA with bone abnormalities and the promise shown for a number of bone-acting agents for treating OA.
- The inflammatory biomarker (HA) was positively but not significantly associated with OA progression on its own but did contribute to the combinatorial prediction.

BM Analysis: Conclusions II

- The dynamic nature of biomarkers necessitated appropriate approaches to longitudinal analysis including the Time-Integrated-Concentration (TIC).
- The 24 month TIC of several biomarkers (singly and in combination) was superior to baseline covariates for predicting case status at 48 months.
- Although two of the markers (CTXI and NTXI) are in vitro diagnostics approved for osteoporosis, none of these biochemical markers are yet approved for clinical use for OA.

Soluble BM: Discussion









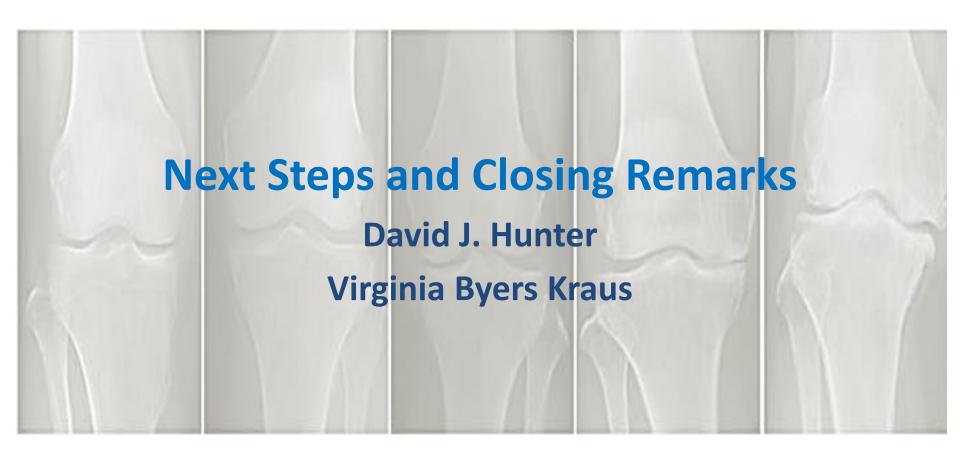




Public Data Release – OAI Database



- Imorphics, Qmetrics & Chondrometrics imaging datasets were publically released on February 27th
- BICL and BioMediq datasets were publically released on the OAI Database on April 10th
- The Scaffold files (MSBioworks) data and associated epitope mapping methodology were publically released on April 10th
 - Richard Jones has provided an instructional slide deck that walks users through downloading the free Scaffold software and opening the data files for individual use
 - Files viewed/accessed through Scaffold can be saved into Excel for further manipulation
- The Biochemical (serum/urine) and FSA datasets will be released May 29th
 - All OA Partners currently have access to these datasets; many have requested and been using them for some time
 - UCSF/OAI is working on final QC of data, uploads, etc. may be able to release a week sooner.











Thumbnail Summary of Publications

- All biomarker measurements are completed
- Statistical analyses are ongoing

Publications

- Study design paper has been published: <u>Best Practice &</u> Research Clinical Rheumatology 28 (2014) 61–71
- Preliminary Assessment of Predictive Validity Periarticular Bone Area and Shape Markers in Knee OA, #336

(Poster/Abstract, OARSI 2013)

 Establishment of Reference Intervals for Osteoarthritis Related Biomarkers – The FNIH/OARSI OA Biomarkers Consortium

(Podium Pres/Abstract, OARSI 2014)

 Preliminary Assessment of Predictive Validity of Semiquantitative MRI Biomarkers in Knee OA – The FNIH Biomarkers Consortium

(Poster/Abstract, OARSI 2014)

 Preliminary Assessment of Predictive Validity of Cartilage Thickness MRI Biomarkers in Knee OA – the FNIH OA Biomarkers Consortium

(Poster/Abstract, ACR 2014)

Best Practice & Research Clinical Rheumatology 28 (2014) 61-71



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Biomarkers for osteoarthritis: Current position and steps towards further validation



David J. Hunter a,*, Michael Nevitt b, Elena Losina c,d, Virginia Kraus e

- ^a Department of Rheumatology, Royal North Shore Hospital and Northern Clinical School, Kolling Institute, University of Sydney, Reserve Road, & Leonards, Sydney, NSW 2065, Australia
- ^b Department of Epidemiology and Bios tatistics, OAI Coordinating Ctr., University of California, San Francisco (UCSF), San Francisco, CA, USA
- ^c Orthopaedic and Arthritis Center for Outcomes Research, Department of Orthopedic Surgery, Brigham and Women's Hospital, Boston, MA, USA
- d Harvard Medical School Boston MA USA
- *Department of Medicine, Duke University, Rheumatology & Immunology, Durham, NC, USA

Keywords: Osteoarthritis

ABSTRACT

Historically disease knowledge development and treatment innovation in osteoarthritis (OA) has been considered to be slow. One of the many reasons purported as responsible for this slow pace has been the alleged lack of valid and responsive biomarkers to ascertain efficacy, which itself has been dependent upon the slow evolution of the understanding of the complex nature of joint tissue biology. This narrative review outlines the rationale for why we need OA biomarkers with regard to biomarker validation and qualification. The main biomarkers in current development for OA are biochemical and imaging markers. We describe an approach to biomarker validation and qualification for OA clinical trials that has recently commenced with the Foundation of NIH OA Biomarkers Consortium study cosponsored by the Osteoarthritis Research Society International (OARSI), With this approach we endeavor to identify, develop, and qualify biological markers (biomarkers) to support new drug development, preventive medicine, and medical diagnostics for osteoarthritis.

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Summary of Publications — Submitted & In Preparation

- PRELIMINARY ASSESSMENT OF PREDICTIVE VALIDITY OF PERIARTICULAR BONE AREA AND SHAPE MARKERS IN KNEE OSTEOARTHRITIS imorphics
 - Submitted to Annals of Rheumatic Disease 3/16
- CARTILAGE THICKNESS CHANGE AS AN IMAGING BIOMARKER OF KNEE OSTEOARTHRITIS
 PROGRESSION DATA FROM THE FNIH OA BIOMARKERS CONSORTIUM
 - Submitted to Arthritis & Rheumatology 3/25
- PREDICTIVE VALIDITY OF BIOCHEMICAL BIOMARKERS IN KNEE OA THE OARSI / FNIH OA BIOMARKERS CONSORTIUM
 - Final analysis and draft in progress
- PREDICTIVE VALIDITY OF RADIOGRAPHIC BONE TRABECULAR INTEGRITY IN KNEE OA THE OARSI / FNIH OA BIOMARKERS CONSORTIUM
 - Final analyses and draft in progress
- SEMI-QUANTITATIVE MRI ASSESSMENT IN THE FNIH BIOMARKERS CONSORTIUM STUDY:

 OVERVIEW OF METHODOLOGY AND DEFINITION OF CHANGE
 - Analysis Plan to be distributed, ongoing analysis

Summary of Publications — In Preparation

- PRELIMINARY ASSESSMENT OF PREDICTIVE VALIDITY OF SEMI-QUANTITATIVE MRI BIOMARKERS IN KNEE OA: FNIH OA BIOMARKERS CONSORTIUM
 - > Analysis Plan to be distributed, ongoing analysis
- PREDICTIVE VALIDITY OF CARTILAGE AND MENISCAL VOLUME IN KNEE OA THE FNIH OA BIOMARKERS CONSORTIUM
 - Ongoing analysis
- SUMMATIVE PROJECT MANUSCRIPT RESPONSIVENESS OF MRI MEASURES THE FNIH OA BIOMARKERS CONSORTIUM
 - Ongoing analysis
- SUMMATIVE PROJECT MANUSCRIPT IMAGING AND FLUID BIOMARKERS OF OSTEOARTHRTIS
 - Ongoing analysis



- ESTABLISHMENT OF REFERENCE INTERVALS FOR OSTEOARTHRITIS RELATED BIOMARKERS
 - > Final analyses and draft in progress



Osteoarthritis Biomarkers Project Phase 2 – BQP

David J. Hunter, MBBS, PhD
University of Sydney

Virginia Byers Kraus, MD, PhD

Duke University Medical Center











OA Biomarkers Project - Phase 2 Aims

- The overarching goal of this proposal is to pursue formal FDA and EMA qualification of OA biomarkers
- Our objective is to pursue qualification of biomarkers pertinent to knee OA for:
 - Prognostic biomarkers (baseline predicting progression of pain and structure and longitudinal burden predicting JSW change in long-term in placebo group);
 - Efficacy of intervention (predictive of treatment response) short term predicting long term response in radiograph
- This will be pursued by deploying best novel biomarker measures in extant clinical trials to determine if they have greater prognostic ability and are more predictive of treatment response than the existing gold standard of radiographic JSW

Direct Benefits of OA Biomarkers

- Will provide a rich set of qualified drug development tools
 - Stratification of OA subjects who are progressors; will allow for enrichment of clinical trials with identified progressors
 - Will provide potential biomarker surrogates to take the place of the current radiographic joint space narrowing
- Will facilitate smaller, shorter trials more closely linked to clinical outcome endpoints, thereby dramatically reducing OA clinical trial costs
- Will inform the biological and clinical context of marker performance

Timelines for Phase 2 Project

Proposal Development

- Decision on imaging and biochemical BMx to include May 2015
 - Need to establish criteria for inclusion/exclusion
- Outreach with Phase 1 data to potential funding partners
 - o Q2/Q3 2015
- Work with regulatory agency liaisons (FDA/EMA)

Concept Proposal submission to IISC

Mid 2015

Funding Commitments

- Funding commitments (letters of intent) finalized after full Project Plan approval by Biomarkers Consortium IISC and Executive Committee in Q4 2015
- Project ready for launch and contracts executed in Q1 2016

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- The OAI is a public-private partnership comprised of five contracts (N01-AR-2-2258; N01-AR-2-2259; N01-AR-2-2260; N01-AR-2-2261; N01-AR-2-2262) funded by the National Institutes of Health (NIH). Funding partners include Merck Research Laboratories; Novartis Pharmaceuticals Corporation, GlaxoSmithKline; and Pfizer, Inc. Private sector funding for the Consortium and OAI is managed by the FNIH
- NIH HHSN2682010000 21C Pivotal OAI MRI Analyses (POMA)
- In-kind donations to support biochemical tests are being provided by: Alere Inc.; ARTIALIS S.A.; BioVendor – Laboratorni medicina a.s.; IBEX Pharmaceuticals Inc.; Immunodiagnostic Systems Ltd; and Quidel Corporation





WORKSHOP SERIES 2015

8th International Workshop on Osteoarthritis

Imaging Based Measures of Osteoarthritis

ABSTRACT SUBMISSION DEADLINE: 07 July 2015

www.ismrm.org/workshops/Osteo15/



11–14 September 2015 Asilomar Conference Center, Pacific Grove, CA USA





