

Effects of Processing Delays on Global Gene Expression Patterns in PBMCs

Michael Barnes, PhD

Director, Cincinnati Biobank Core Facility (Pathology)

Research Associate, Rheumatology

Cincinnati Children's Research Foundation

Cincinnati Children's Hospital Medical Center

Overview

- 1. Project – Our interest**
2. Sample handling and processing
3. Study results

Gene Expression in Pediatric Arthritis (NIAMS: P01AR048929)

Overall Objective: Use gene expression analysis to investigate peripheral blood samples from patients with JIA

1. Determine differences **between** controls and current JIA classes
2. Assess heterogeneity **within** the current JIA classes

8 sub-classes of JIA

- 1. Persistent Oligoarticular (< 5 joints ever)**
2. Extended Oligoarticular (evolves to ≥ 5 joints)
- 3. RF- Polyarticular (≥ 5 joints)**
4. RF+ Polyarticular (≥ 5 joints)
5. Enthesitis related arthritis (ERA): Arthritis with enthesitis, HLA-B27+
6. Systemic: Arthritis with systemic features
7. Psoriatic arthritis: Arthritis with psoriasis
8. Undifferentiated: Do not fit any category or fit more than 1 category

Why study peripheral blood?

- Has been previously used to investigate gene expression
- “Surveys” entire body
- Easily obtainable
 - Collected from patients in clinic
 - Often collected during routine blood draws
 - Minimal risk
- Alternatives
 - Synovial fluids (few)
 - Synovial tissues (very few)
- Appropriate for diagnostic testing

Multi-Center Study

- Power analysis: ~280 subjects
- Single institution
 - Not enough patients
- 5 clinical centers

Collaborating Centers

- Cincinnati Children's Hospital (CCHMC)
- Children's Hospital of Philadelphia (CHOP)
 - David Sherry, MD
- Children's Hospital of Wisconsin
 - Judyann Olson, MD
- Schneider Children's Hospital (New York)
 - Beth Gottlieb, MD MS
 - [Normal Ilowite, MD (Montefiore)]
- Toledo Children's Hospital
 - Thomas Griffin, MD, PhD

Our study: issues with multi-center

- Power analysis: ~280 patients
- Single institution
 - Not enough patients
- 5 clinical centers
 - Lab locations



Our study: issues with multi-center

- Power analysis: ~280 patients
- Single institution
 - Not enough patients
- 5 clinical centers
 - Lab locations
 - Specific research lab Vs GCRC
 - Research group Vs Single person

Overview

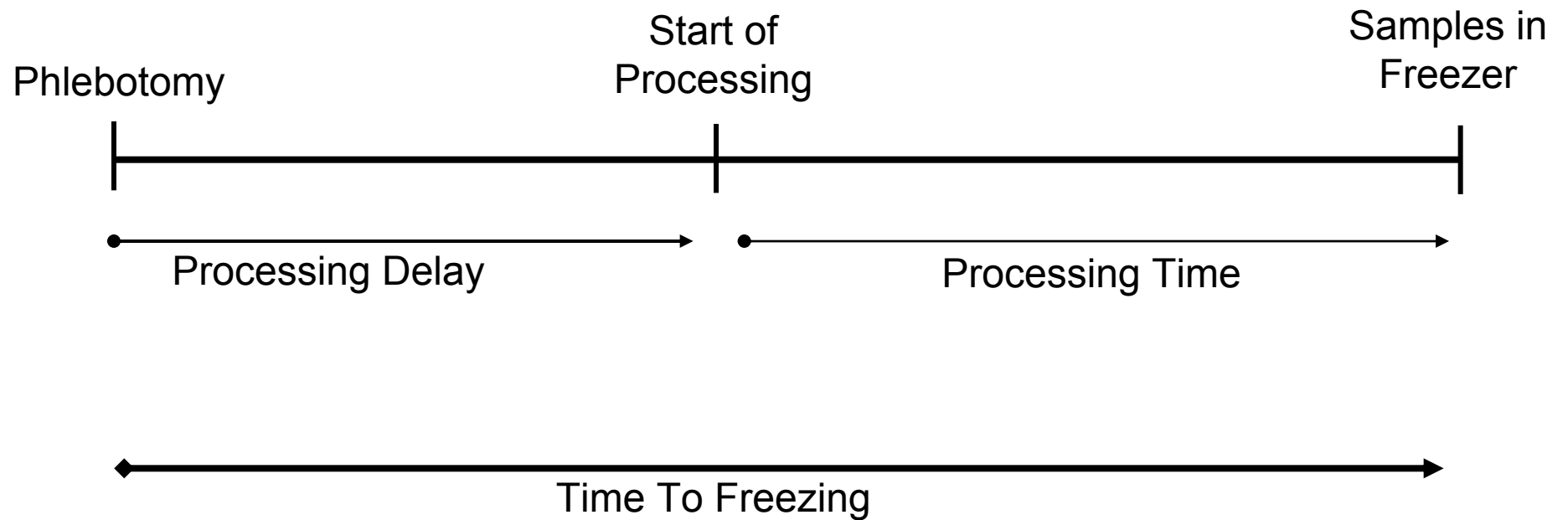
1. Project

- A. Determine differences between and within JIA subclasses
- B. Gene expression from peripheral blood
- C. Multi-center study

2. Sample handling/processing

3. Study results

Definitions

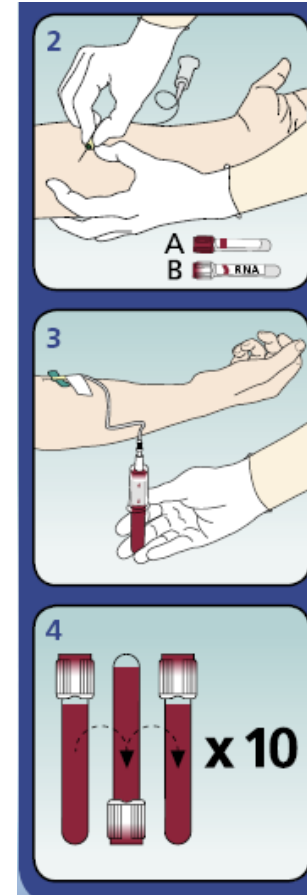


Ficoll isolation of PBMC

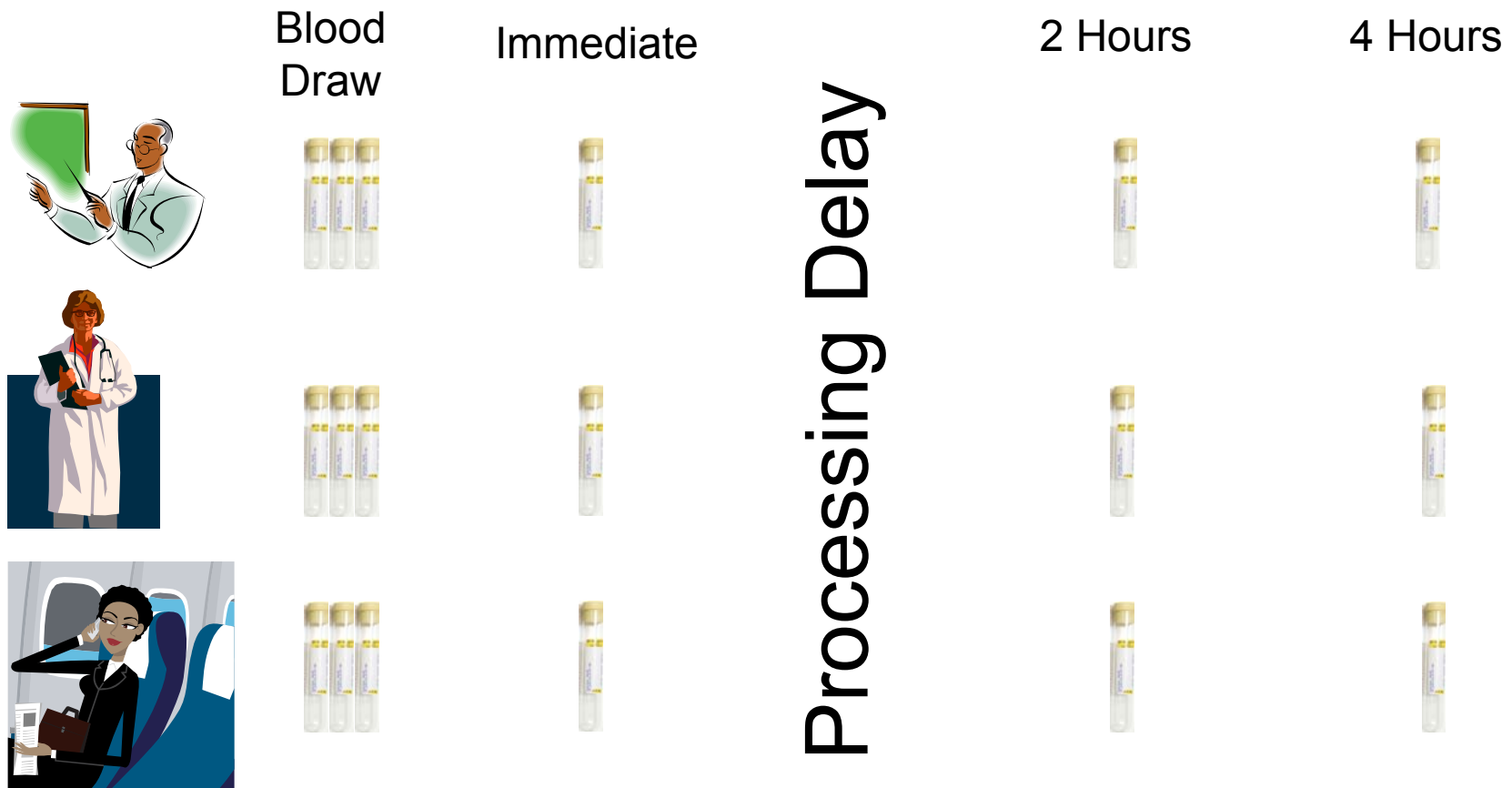
- Positive
 - Standard protocol with long history
 - Cells for downstream applications (flow, FACS, transformation, etc)
- Negatives
 - Ficoll takes time
 - Processing delay: Sample transport (Variable)
 - Processing time (into Trizol): ~1-1.5 hours
 - Cells activated and expression profiles can change
 - RNA not stabilized until samples put in Trizol

PAXgene

- PAXgene Blood RNA
 - Positive
 - Simple
 - “Instant” stabilization
 - Processing delay 1 minute
 - Processing time 1 minute
 - Stable over time
 - Negative
 - Must be done **X** fast
 - Does not collect cells for flow cytometry, FACS
 - Globin correct
- Tempus did not exist (launched August 31, 2004)

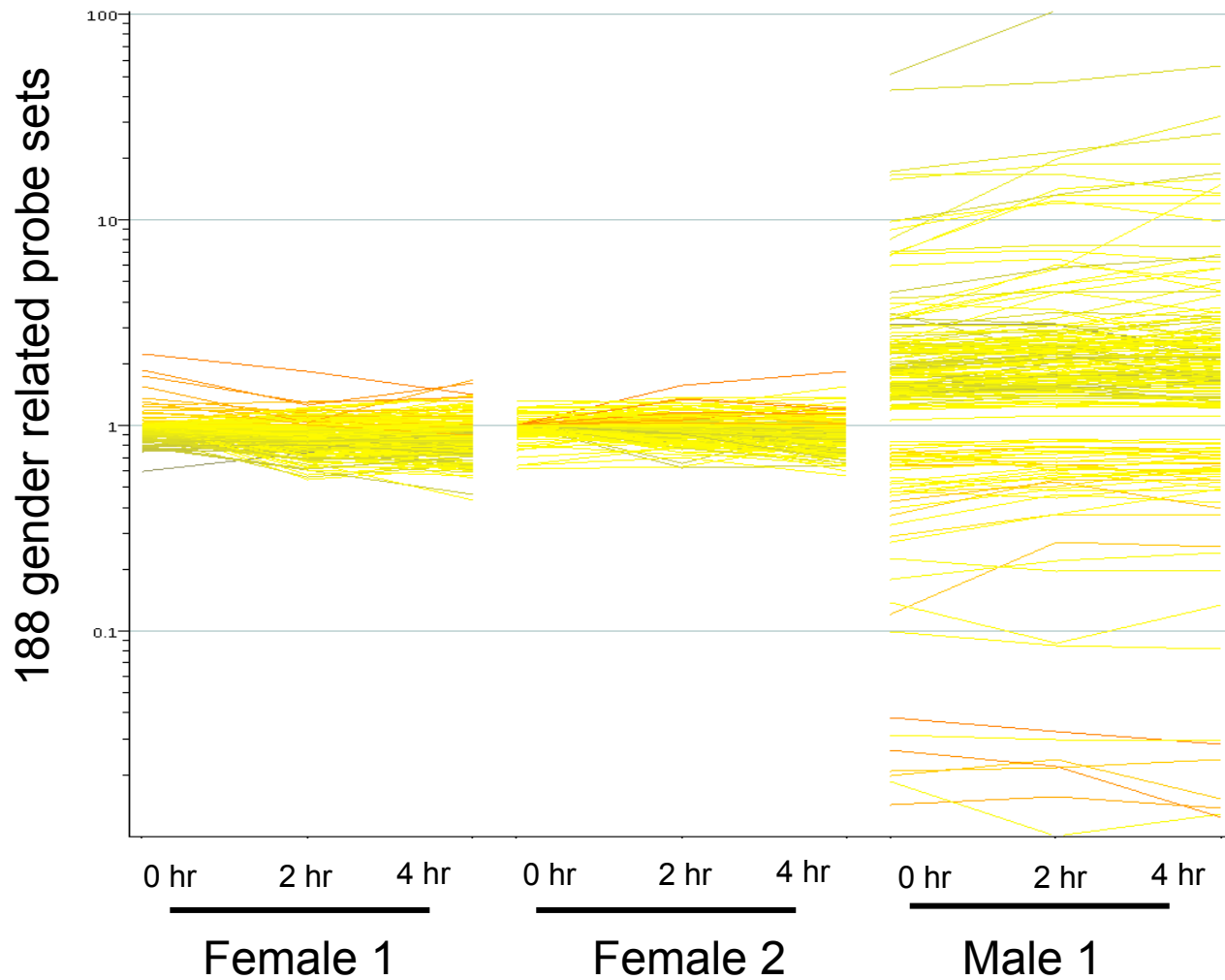


How much of an issue is variation in processing time?



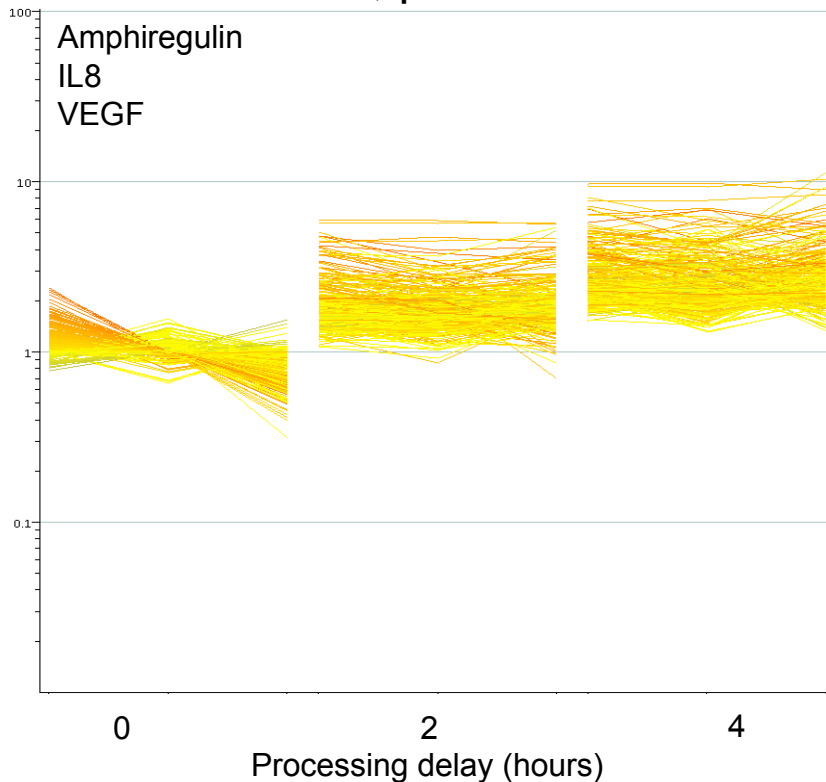
*Similar study done by EC Baechler, et al looking at effect of overnight shipping. Genes and Immunity (2004) 5, 347-353.

Gender differences can still be detected

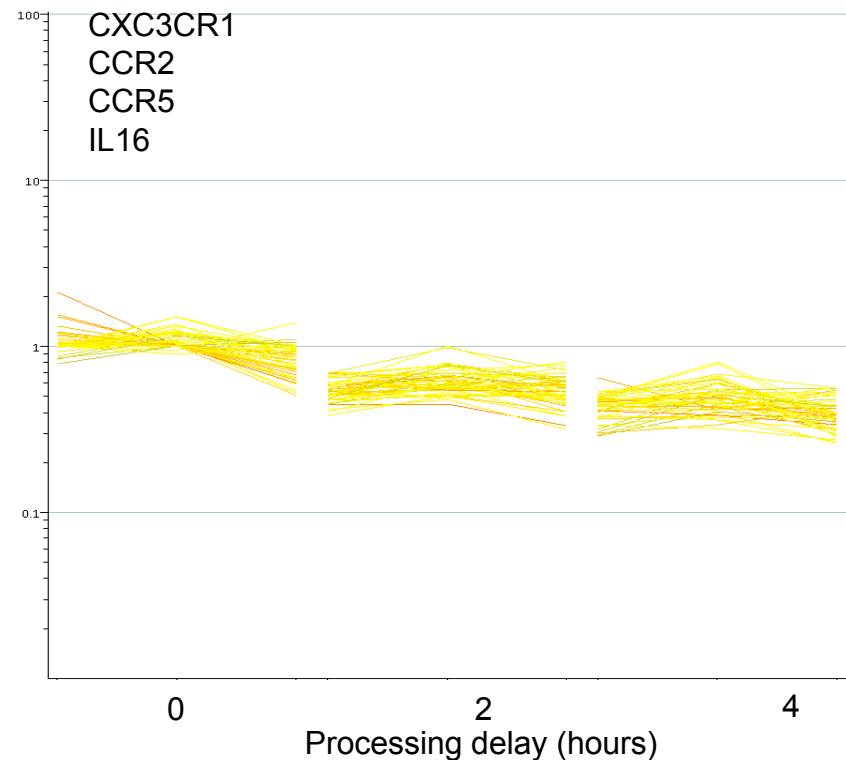


Processing Delays Cause Changes in Global Gene Expression Patterns from PBMC

311 probe sets increased
2-fold; $p < 0.05$



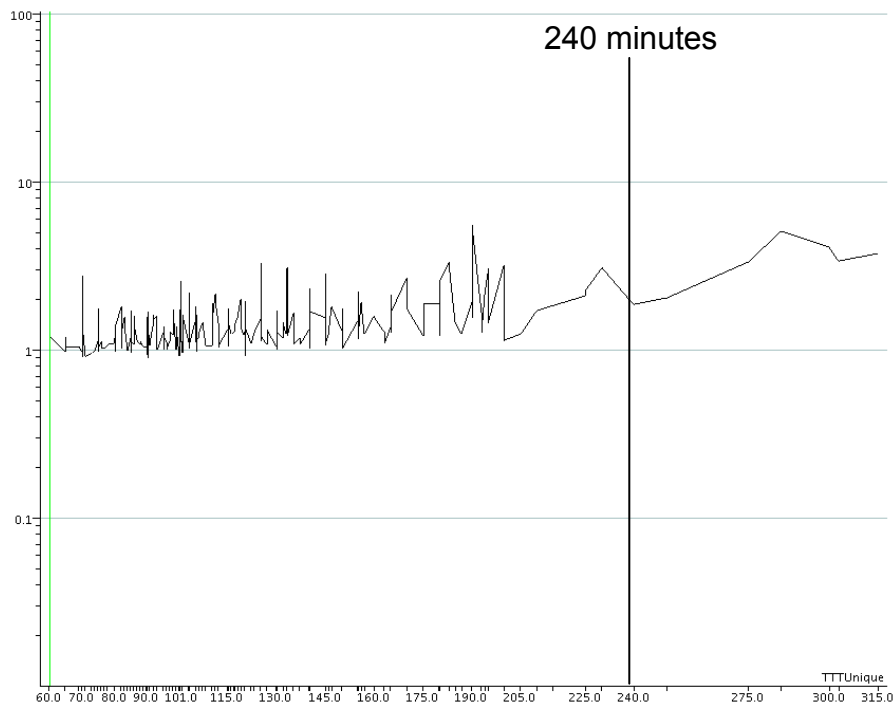
45 probe sets decreased
2-fold; $p < 0.05$



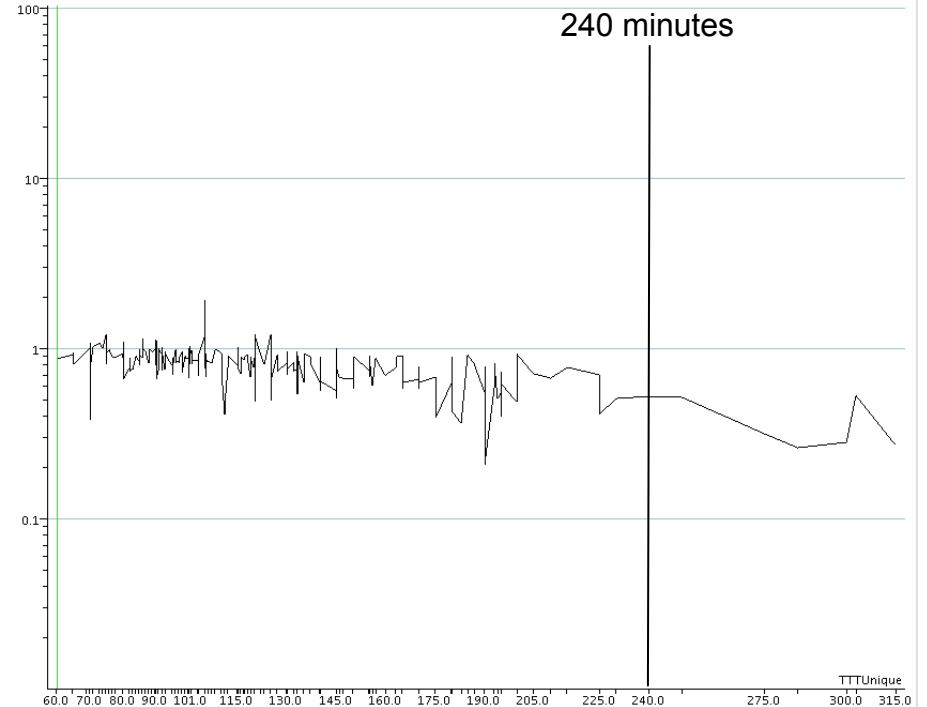
Overview

1. Project – Our interest
2. Sample handling and processing
 - A. Use Ficoll isolated PBMC
 - B. Large biological effects can still be identified
 - C. Processing time affects gene expression
- 3. Study results**

Trend in TTF genes is maintained in group of 267 arrays

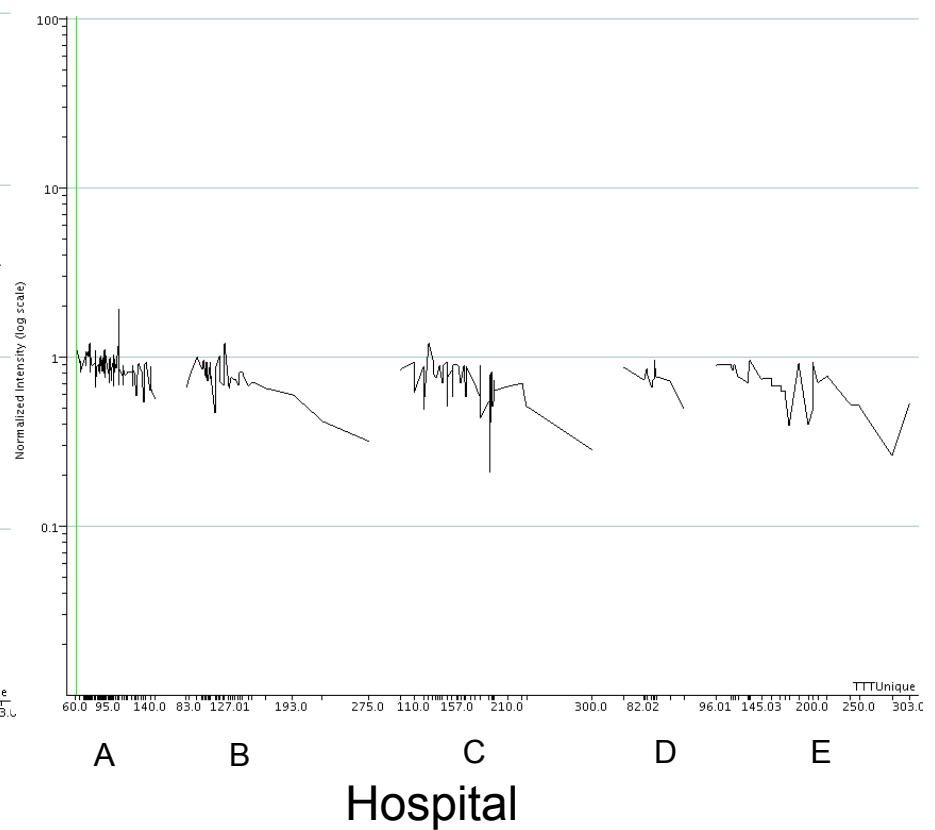
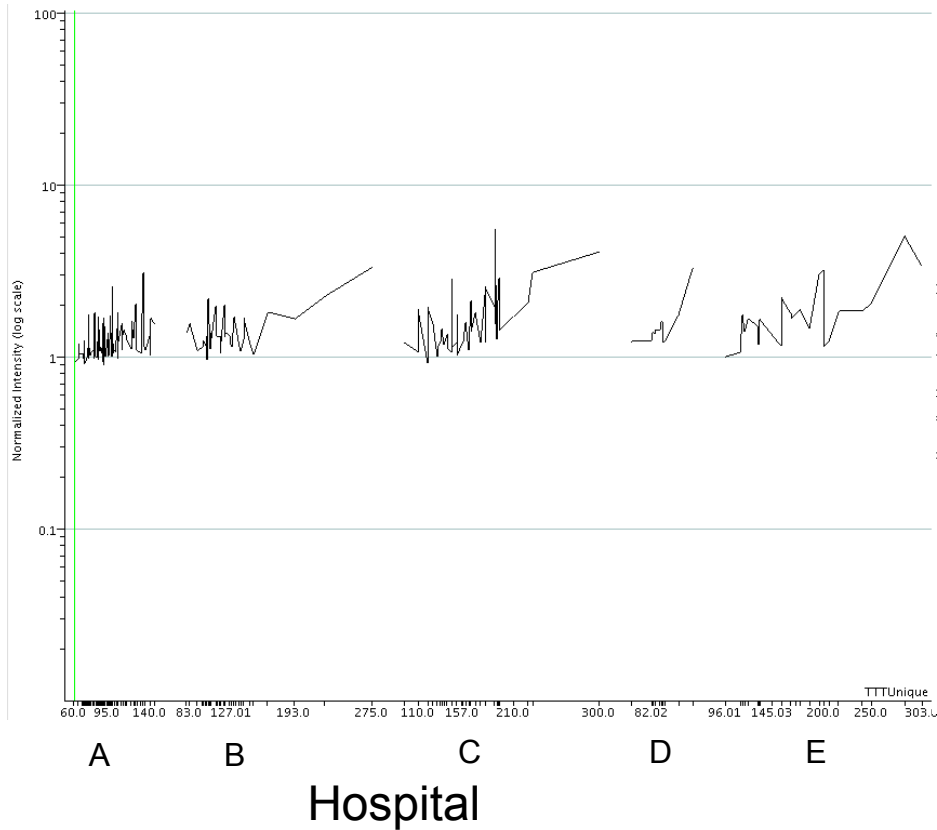


Time to freezing

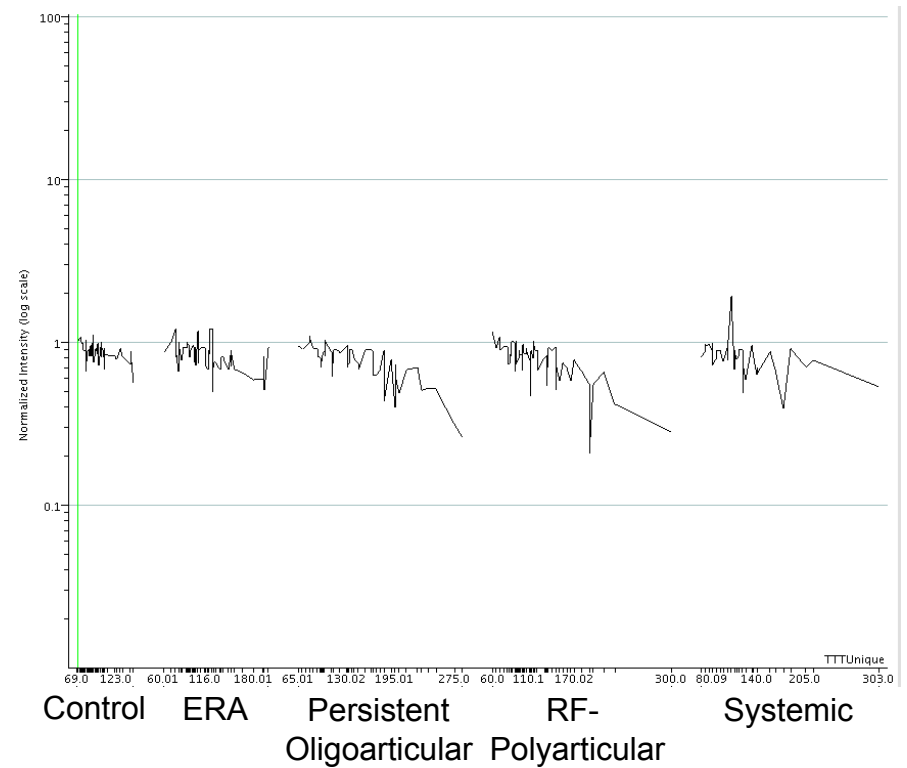
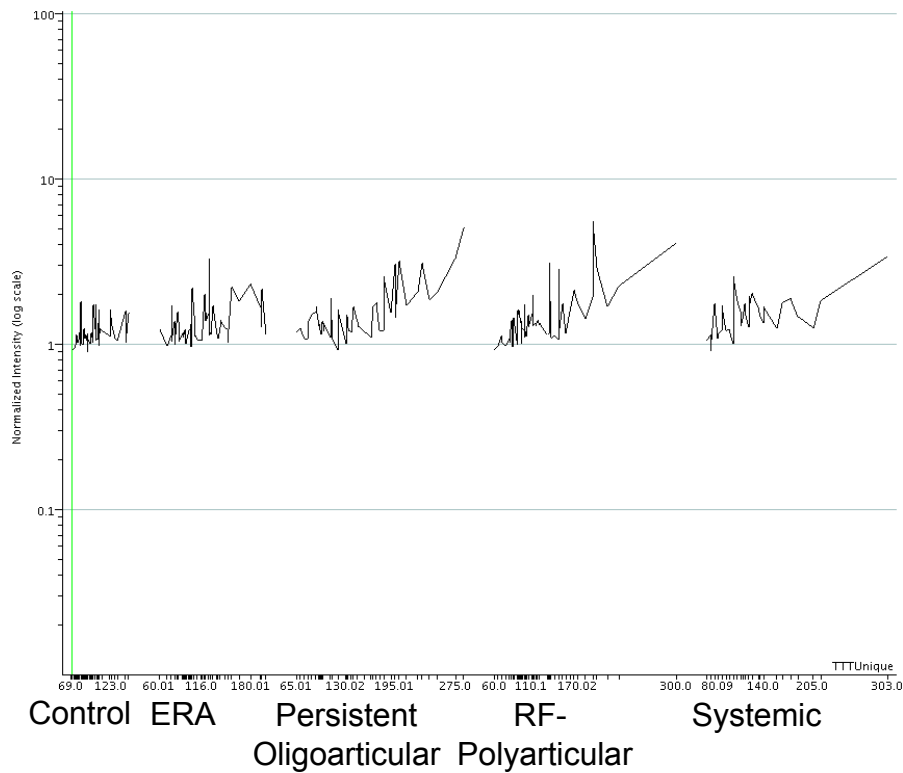


Time to freezing

Trend is not hospital specific



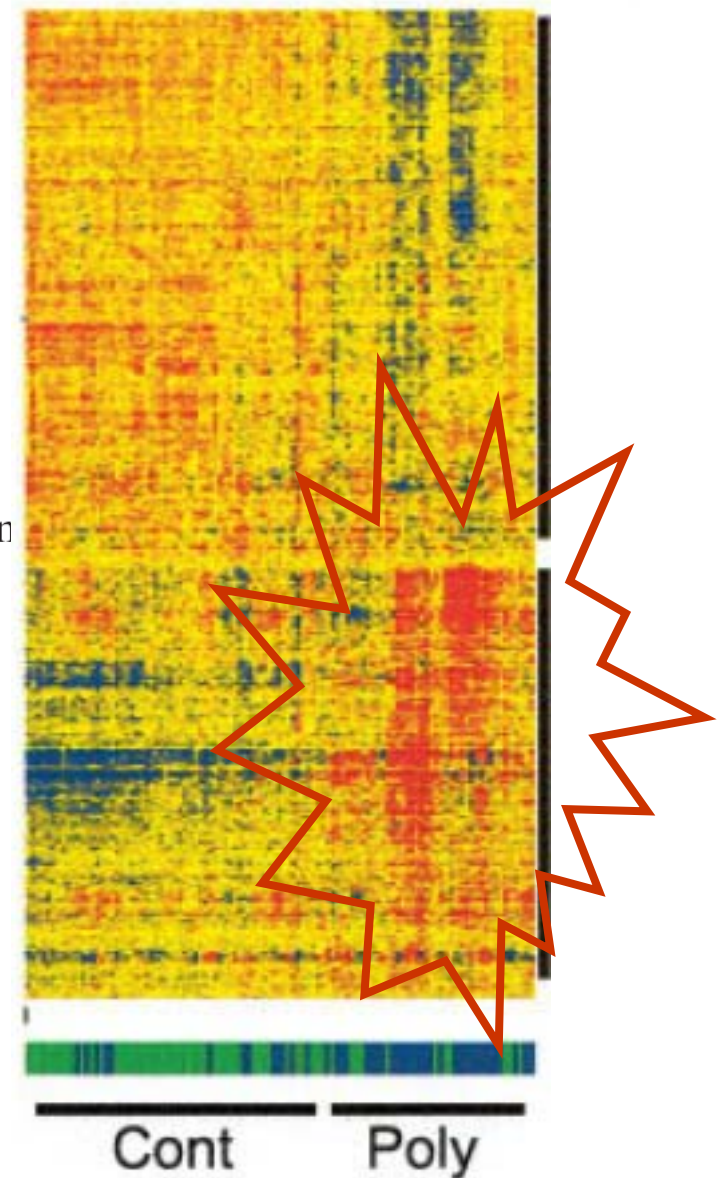
Trend is not JIA subtype specific



ARTHRITIS & RHEUMATISM
Vol. 60, No. 7, July 2009, pp 2102–2112

Subtype-Specific Peripheral Blood Gene Expression Profiles in Recent-Onset Juvenile Idiopathic Arthritis

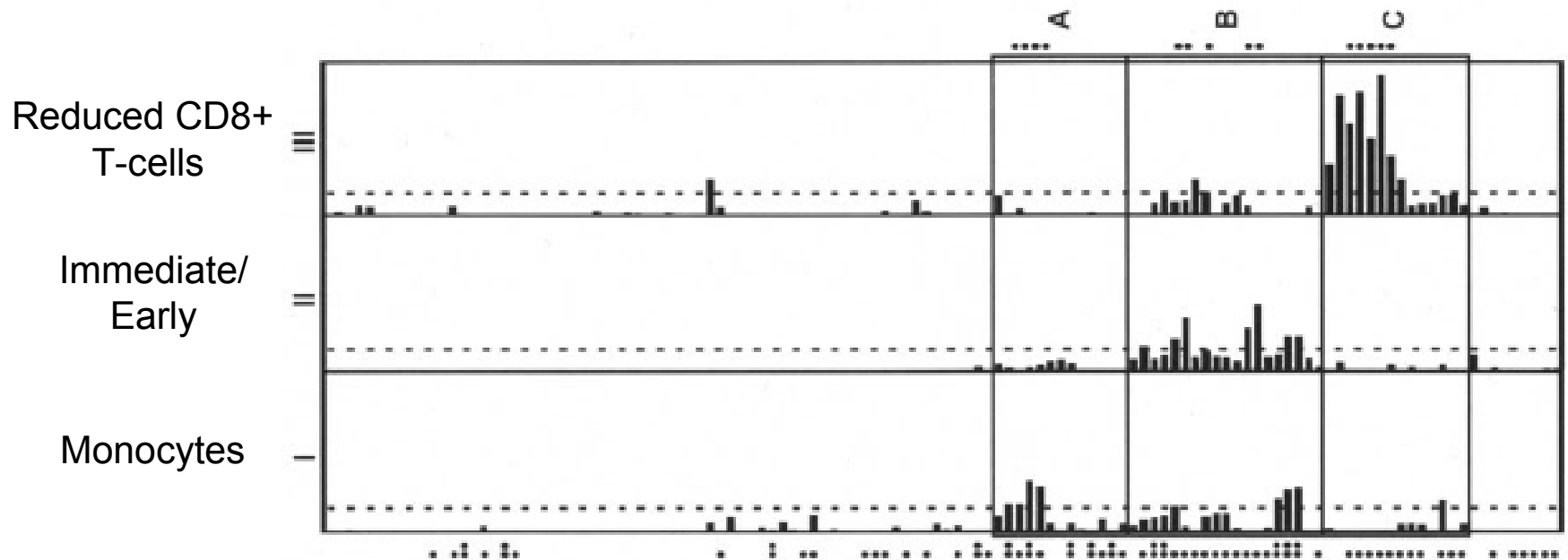
Michael G. Barnes,¹ Alexei A. Grom,¹ Susan D. Thompson,¹ Thomas A. Griffin,¹
Paul Pavlidis,² Lukasz Itert,¹ Ndate Fall,¹ Dawn Paxson Sowders,¹ Claas H. Hinze,¹
Bruce J. Aronow,¹ Lorie K. Luyrink,¹ Shweta Srivastava,¹ Norman T. Ilowite,³
Beth S. Gottlieb,⁴ Judyann C. Olson,⁵ David D. Sherry,⁶
David N. Glass,¹ and Robert A. Colbert¹



Gene Expression Signatures in Polyarticular Juvenile Idiopathic Arthritis Demonstrate Disease Heterogeneity and Offer a Molecular Classification of Disease Subsets

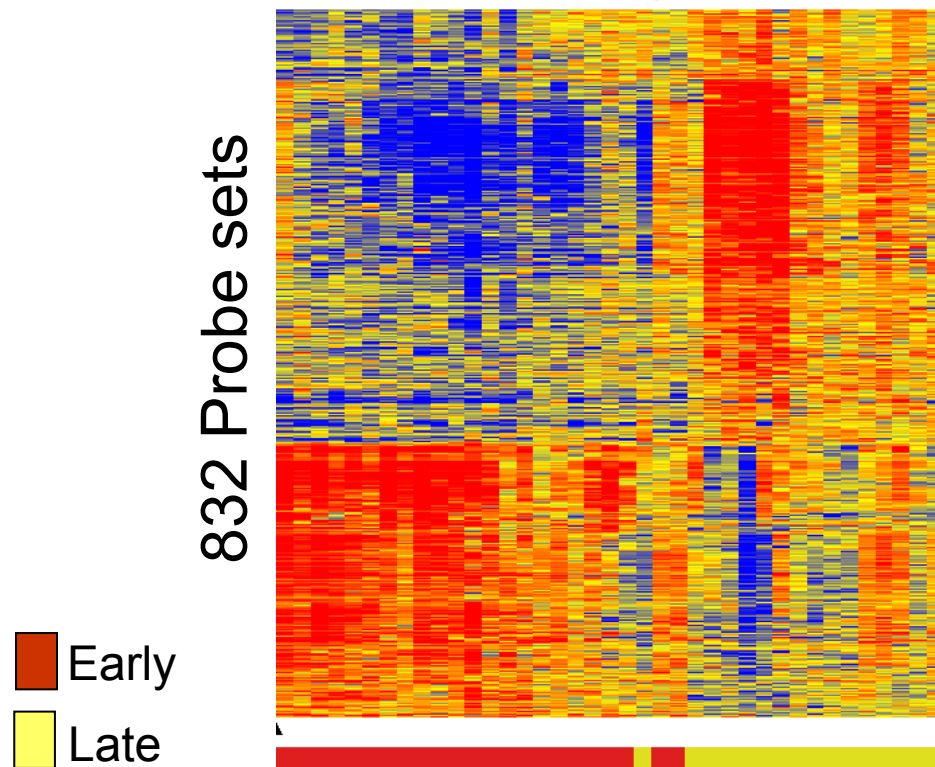
ARTHRITIS & RHEUMATISM
Vol. 60, No. 7, July 2009, pp 2113–2123

Thomas A. Griffin,¹ Michael G. Barnes,¹ Norman T. Ilowite,² Judyann C. Olson,³
David D. Sherry,⁴ Beth S. Gottlieb,⁵ Bruce J. Aronow,¹ Paul Pavlidis,⁶
Claas H. Hinze,¹ Sherry Thornton,¹ Susan D. Thompson,¹
Alexei A. Grom,¹ Robert A. Colbert,¹ and David N. Glass¹



Can we identify gene expression signatures indicative of age-at-onset?

Persistent oligoarticular



Not explained by:

- Sex
- Hospital
- Current joint count
- X-ray results
- CRP
- ANA

- No overlap with TTF genes
- No overlap with Signature II

Overview

1. Project – Our interest
2. Sample handling and processing
3. Study results
 - A. Important to track sample processing time points and include during data interpretation
 - B. A large biological effect can still be identified in spite of processing variations
 - C. Limited number of extended TTF samples have limited effect on results

How can we handle the effect of time to freezing?

- ~~Ignore the issue~~
- Only use “best” samples (< 4 hours TTF)
- Filter TTF genes¹
- Other collection tubes:
 - PAXgene/Tempus
 - Globin reduction protocols
 - Globin effect “solved” with NuGEN labeling
 - CPT
- Standardize processing delay (realistic...)
- Statistical modeling

¹Baecheler, EC. PNAS (2003) 100: 2610-2615.

Acknowledgements

- P01 group
 - Robert Colbert, MD, PhD
 - David Glass, MD
 - Tomas Griffin, MD, PhD
 - Alexei Grom, MD
 - Susan Thompson, PhD
- Lab
 - Lorie Luyrink
 - Shweta Srivastava
 - Lukasz Itert
- Groups
 - CCHMC Gene Expression Microarray Core
 - Biomedical Informatics
- Donors
 - Patients
 - Controls
- Funding
 - NIH/NIAMS
 - Arthritis Foundation
 - CCHMC

