

# Muscle quality issues explained by metabolomics

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# Outline

**Introduction**

**Outcome of the study**

**Metabolomics**

**Hypothesis**

**White Striping**

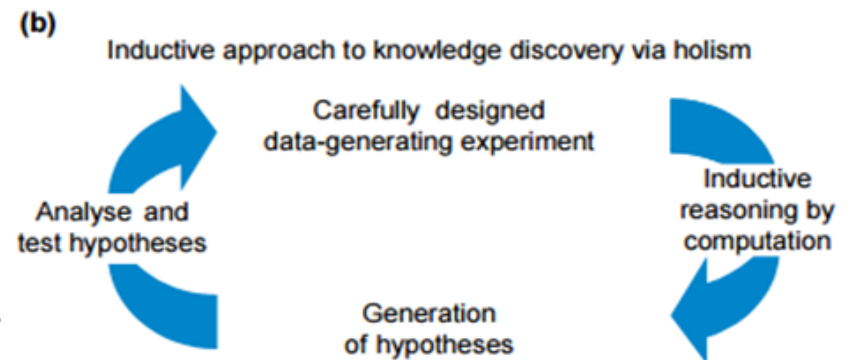
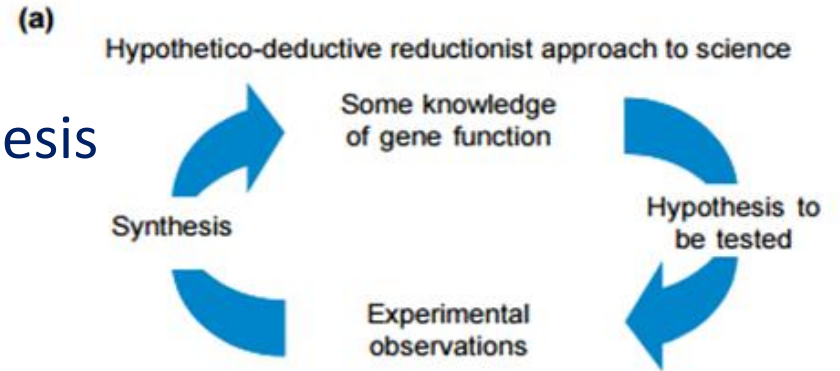
**Hypothesis testing**

**Application of  
metabolomics**

**Conclusion**

# Solving biological problems

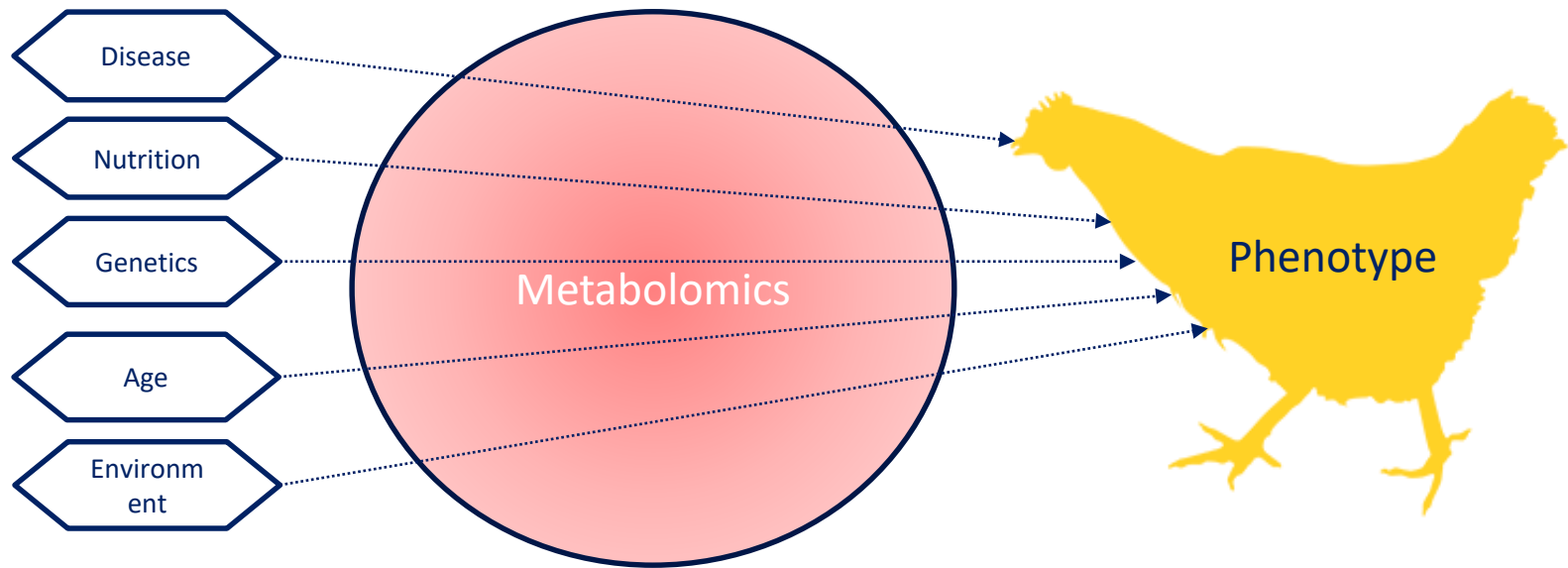
- Traditional cycle:
  - Background knowledge → hypothesis
  - Test experimentally
  - Hypothesis is starting point
- Inductive cycle:
  - No real hypothesis
  - Use data to generate hypothesis



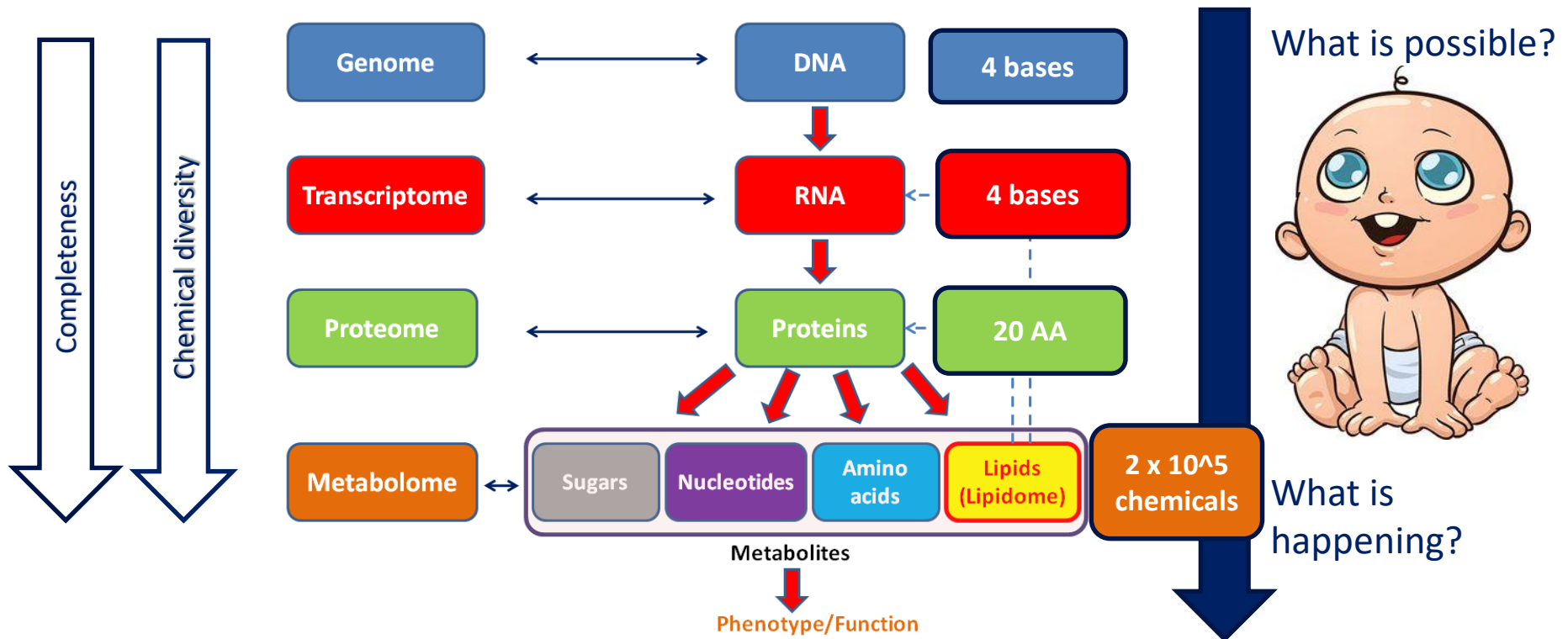
*TRENDS in Biotechnology*

# Study as many metabolites as possible

- Ideal for an inductive approach
- Level regarded as ultimate response of system
- Time sensitive → Changes quickly

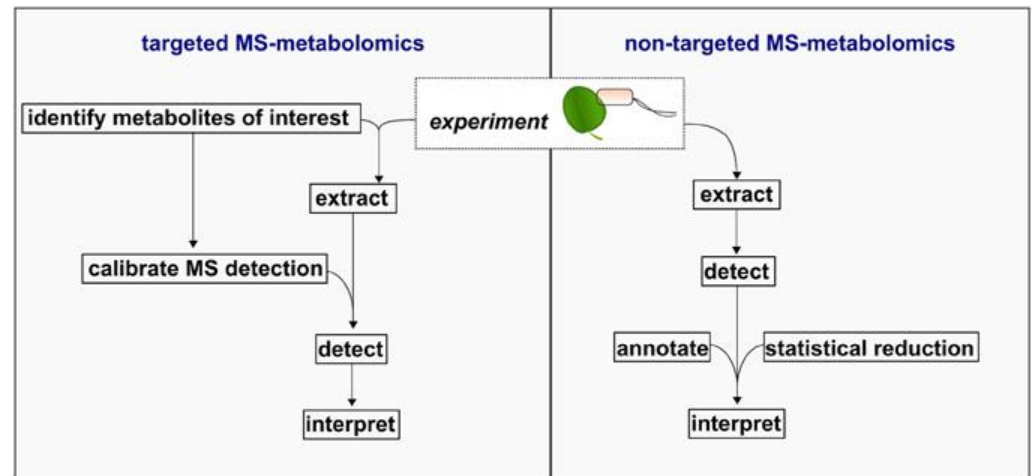


# Metabolomics can give insights into biochemical origin of problem: avenue for solutions

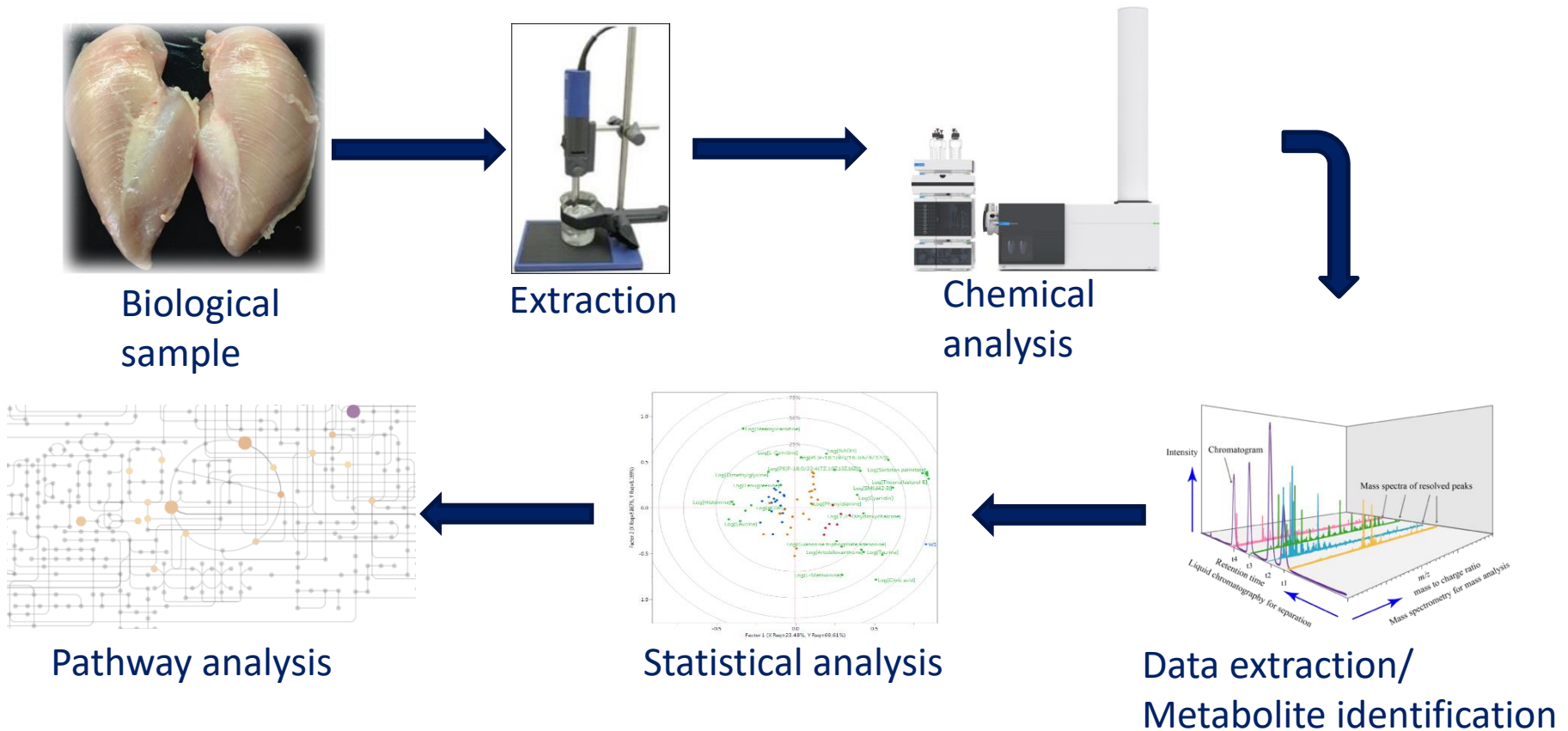


# Targeted vs Untargeted

- Two methods to perform metabolomics analysis
  - Targeted/quantitative
    - Select group of metabolites
    - Precise quantification
  - Untargeted
    - Global snapshot/fingerprinting



# Metabolomics workflow



# Metabolomics in practice: White striping



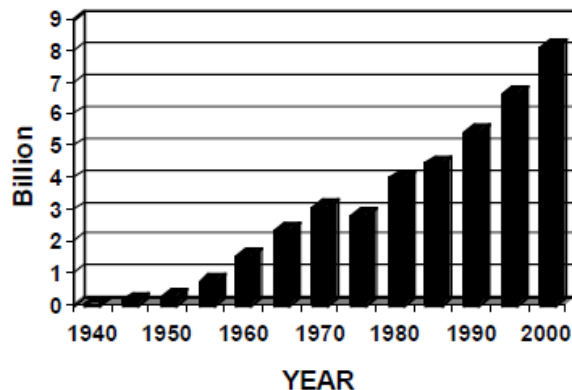
- White stripes on breast muscles
  - Various degrees
- Run parallel to direction of muscle fibers
- Unknown etiology



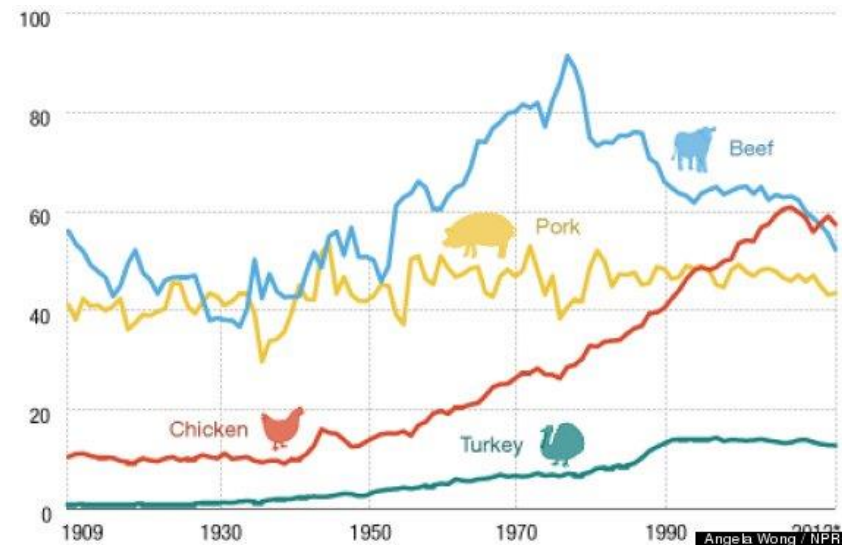
# Poultry meat consumption increased over the years

- Low cost
- Good nutritional profile
- Suitable for further processing
- Absence cultural/religious aversions

US broiler production



Meat consumption US per person in pounds



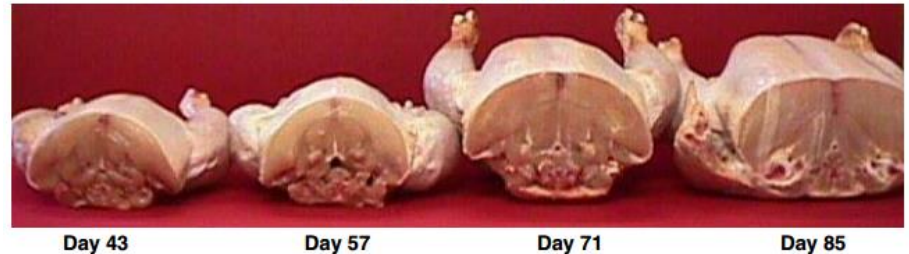
# Genetic selection made growth possible

- 85-90% due to genetic selection
  - 10-15% due to nutrition
- In 50 years:
  - Broilers 5 times larger
  - Edible carcass ↑ 12.3%
- Last 10 years:
  - Breast yield ↑ 5%

ACRBC Males - 2001 Feed

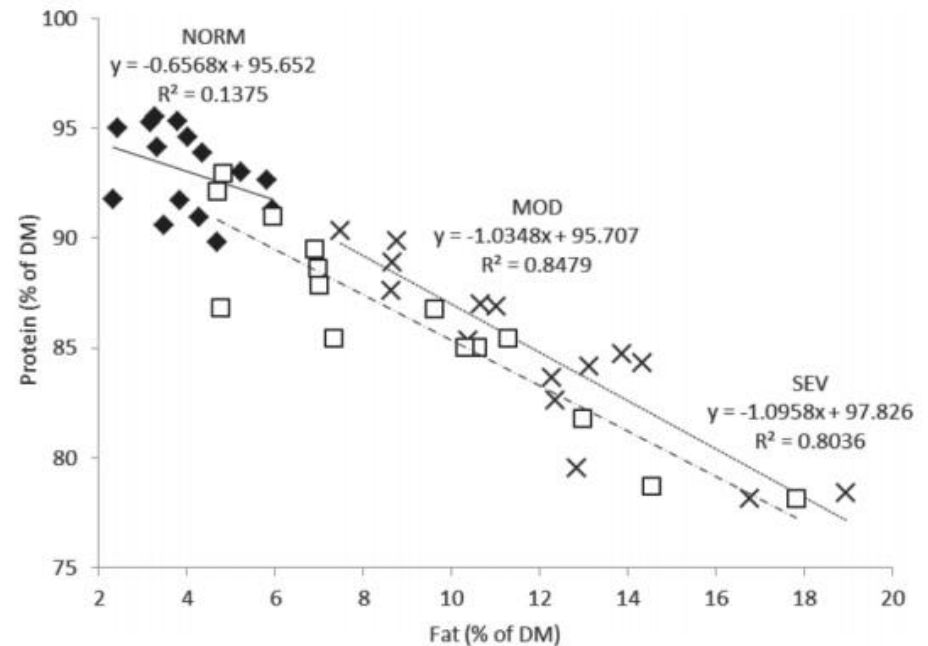


Ross Males - 2001 Feed



# White striping affects meat composition and consumer acceptance

- Pathological changes
  - Increase in fat and collagen
  - Decrease in protein
- Affects consumer acceptance
  - Perceived high fat
  - >50% would not buy



# Why Your Chicken Breast Has White Stripes + What It Means for You

LYNDSAY BURGINGER

POSTED APRIL 19, 2019

HEALTH

What Those White Stripes on Chicken Breasts Mean for Your Health

**CLUCKING HELL** This is what the white stripes in your chicken really are... and why you need to look out for them

Most people who regularly eat the nation's favourite meat will have noticed pale stripes cropping up in raw cuts of chicken breasts without really knowing what they are



You Know That White Stripe On Your Chicken Breast? Turns Out It's Bad, Very Very Bad [brobible.it/2l1qPTTr](https://brobible.it/2l1qPTTr)



A

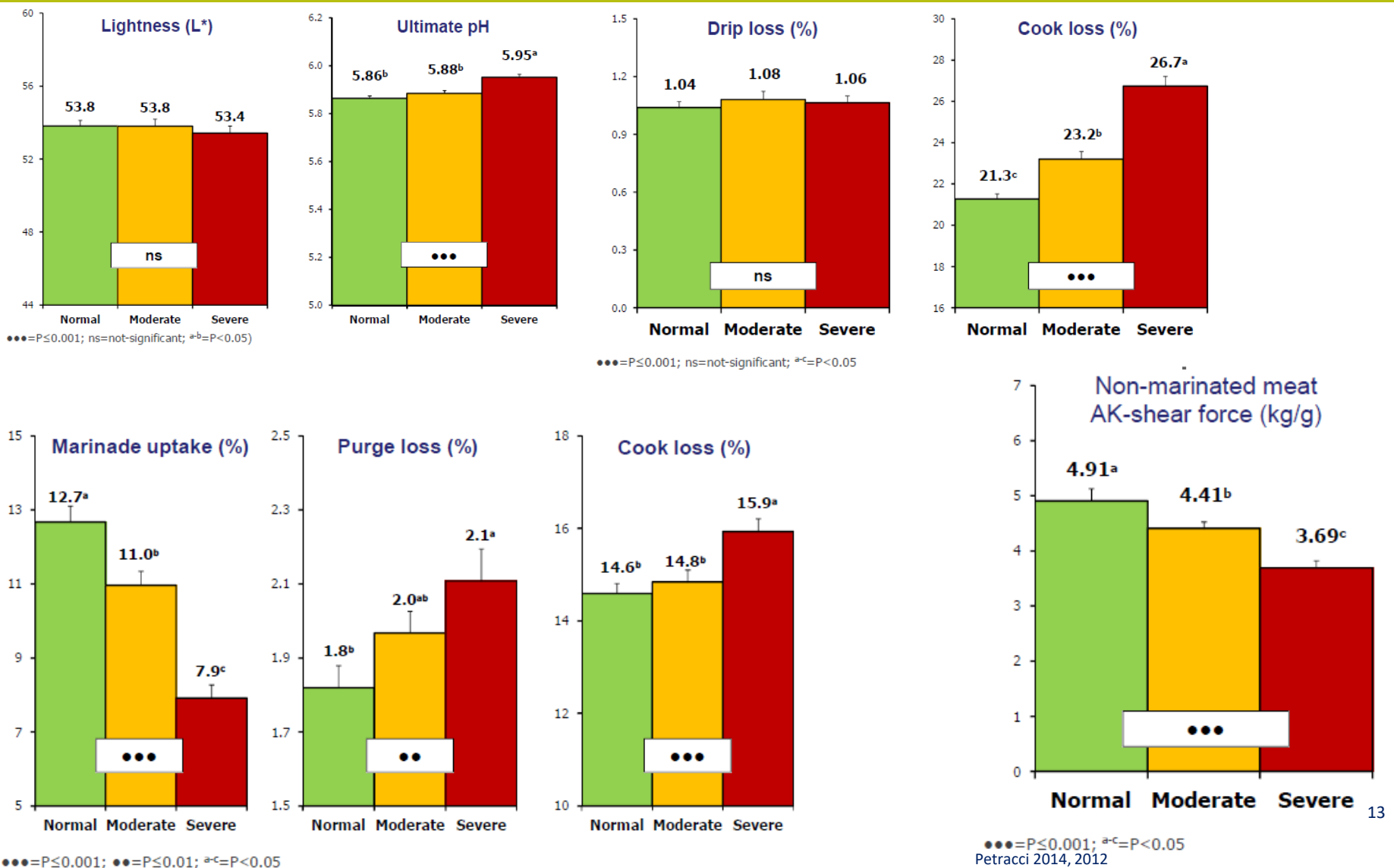


B



C

# Petracci showed influence on meat quality



# No clear etiology

- Factors linked to the occurrence of the disease

Live production factors	Mode of action on white striping occurrence	References
<b>Genotype</b>	High > standard breast-yield	Petracci et al. (2013b)
		Lorenzi et al. (2014)
<b>Sex</b>	males > females	Kuttappan et al. (2013a)
		Lorenzi et al. (2014)
<b>Growth rate</b>	higher > lower	Kuttappan et al. (2012a; 2013b)
		Lorenzi et al. (2014)
<b>Diet</b>	high > low energy diet	Kuttappan et al. (2012a)
<b>Slaughtering weight</b>	Heavier > lighter	Kuttappan et al. (2013a)
		Lorenzi et al. (2014)

# Aim of the study

- Identify biological pathways involved in the underlying etiology and pathogenesis of white striping





# Trial at our poultry facility





# Sampling most important step

- Sample collection most important step in metabolomics
- Make sure to minimize variance introduction
  - Collect without bias
  - Metabolome responds to almost all outside influences
  - Sampling and handling procedures must be identical between groups
  - Tissue is still active
    - Rigorous collection + handling protocols

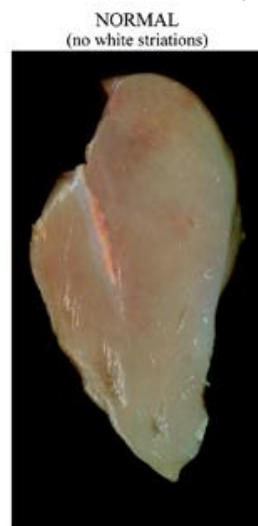


# Pectoralis major samples collected at necropsy

- ROSS 308 males
- Raised to 35 days
- 3-phase feeding using commercial feed (wheat-based)
- Final BW:  $\approx$ 2300 gr
- Pectoralis major samples (N=51) collected at slaughter
- WS scoring based on Kuttappan et al 2012

Total incidence (%)

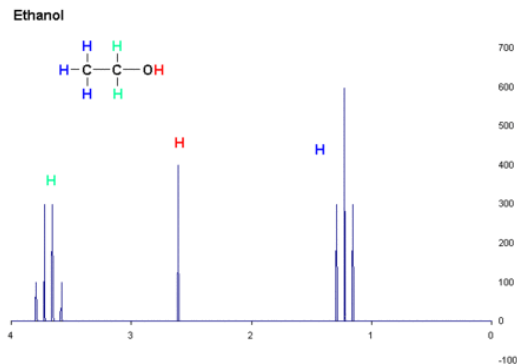
- |                   |    |
|-------------------|----|
| • Normal (N=19)   | 32 |
| • Moderate (N=24) | 59 |
| • Severe (N=8)    | 9  |



# NMR and MS to analyze samples

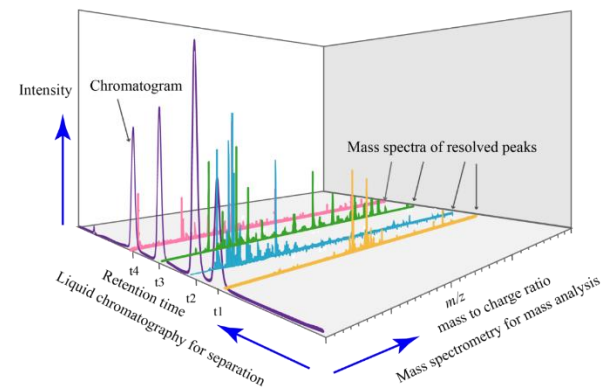
- NMR:

- Highly quantitative
- Reproducible/non-destructive
- Requires no pre-treatment
- Low sensitivity



- MS:

- High sensitivity
- Molecular specificity
- Low sample requirements
- Need for separation/purification



# Dataset

- GC-MS LC-QTOF/MS used
- Dataset contained 599 metabolites
- Retention time and molecular mass also available
- Some false annotations were removed
  - Components that could not be there
    - Alpha-tocopherol succinate

# Data processing to improve biological interpretability

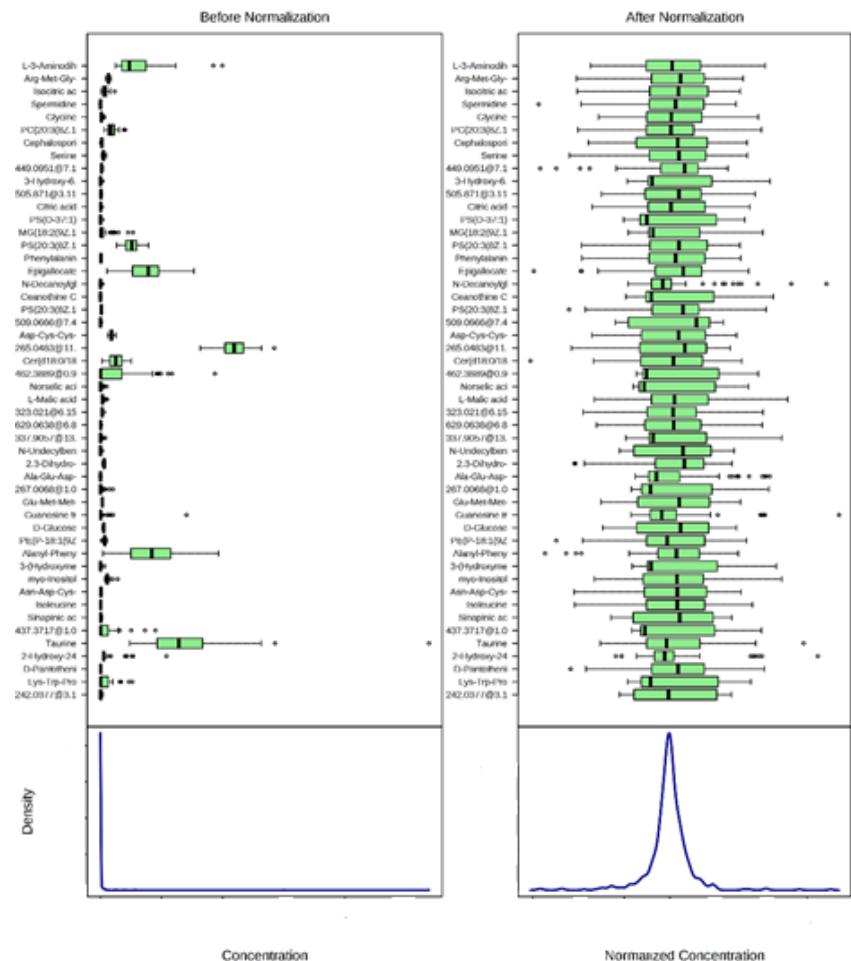
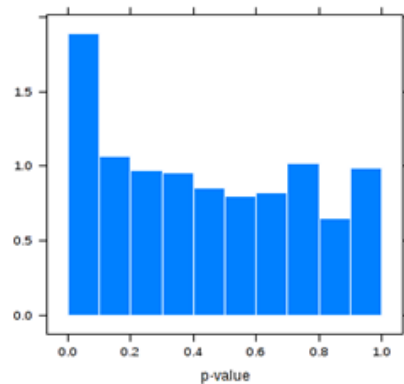
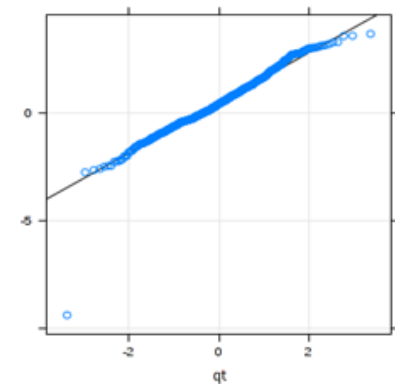
- Extracting relevant biological knowledge a major challenge
  - Unknown metabolites
  - False annotations
  - Difference in order of magnitudes
    - Signal molecules vs sugars
- Best method depends on:
  - Biological question
  - Properties of the dataset
  - Data analysis method

# 3 common steps applied in data processing

- Sample normalization
  - Reduce non-biological variation
    - Internal standard, reference sample, etc
- Data transformation
  - Remove heteroscedasticity (variability differences)
    - Log transformation, power transformation, etc
- Data scaling
  - Make variables comparable
    - Scaling by sd (auto-scaling)
    - Scaling by biological range (range-scaling)

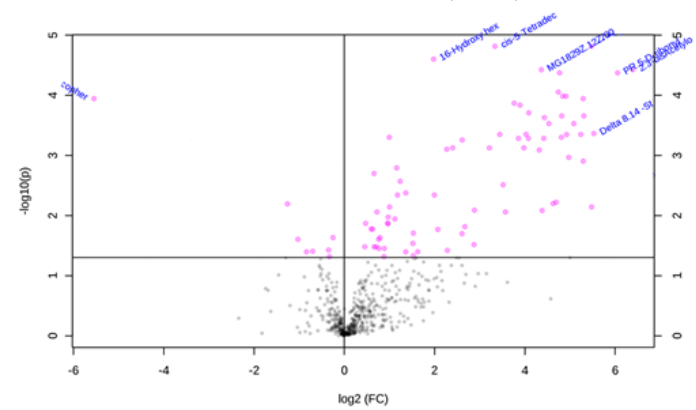
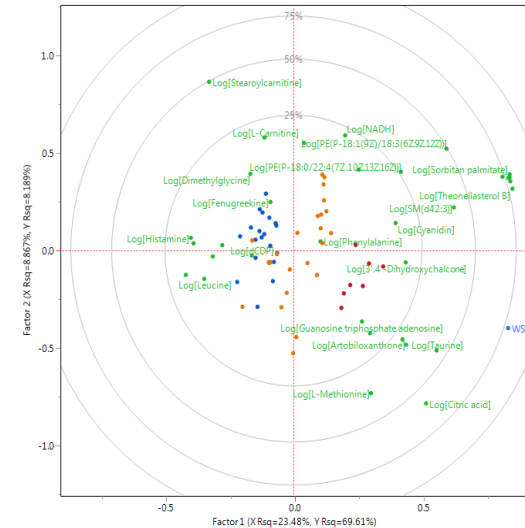
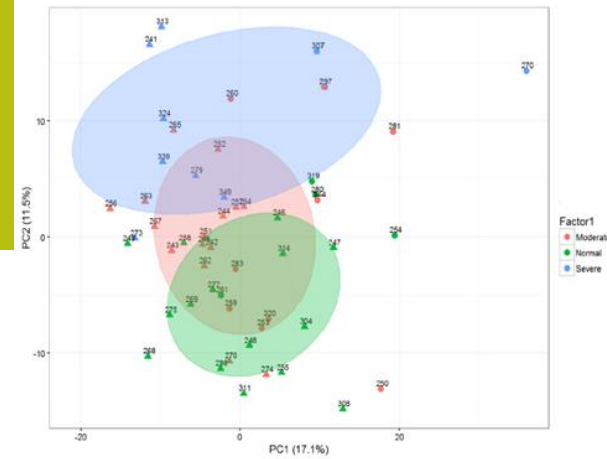
# Data processing showed improvements

- Normalized on internal standard
- Auto-scaling
- Log-transformation



# Visualization of data

- Visual representation of data + reduce dimensionality
- Principal component analysis
  - Create “super metabolites” that explain max variance
- Partial least square analysis
  - Based on max correlation
- Volcano plot
  - Significance vs fold-change

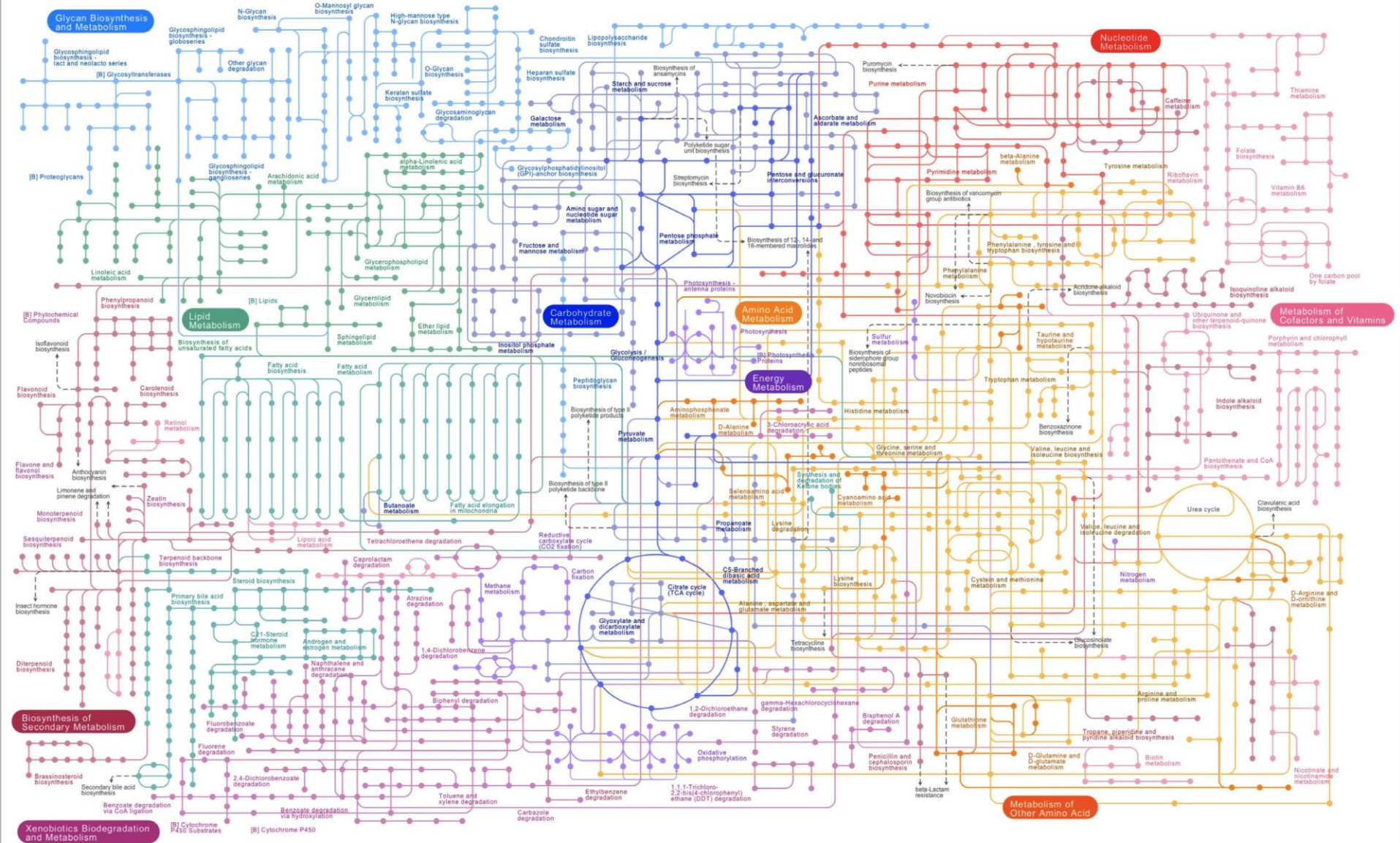




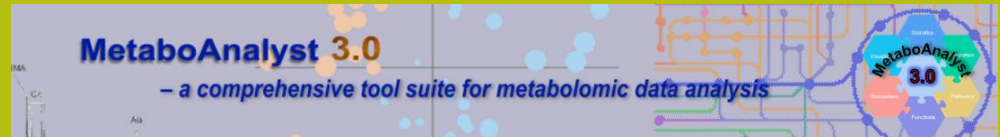
# Statistical analysis

- Analysis based on design and data distribution
- Large datasets → large amount of comparisons
  - Increased chance of false positives
- False discovery rate or Bonferroni correction
  - Reduces number of false positives

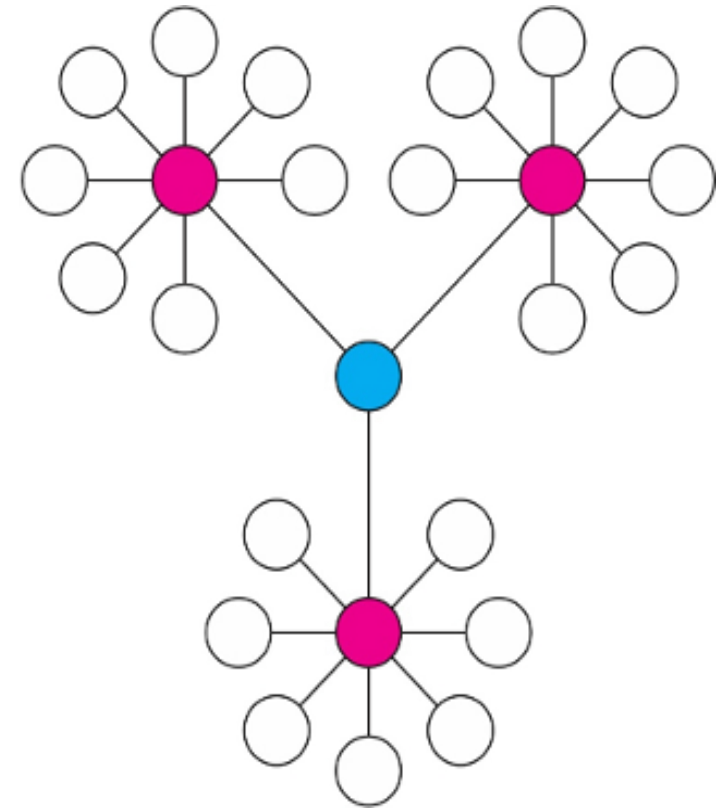
# Metabolic pathways



# Pathway visualization

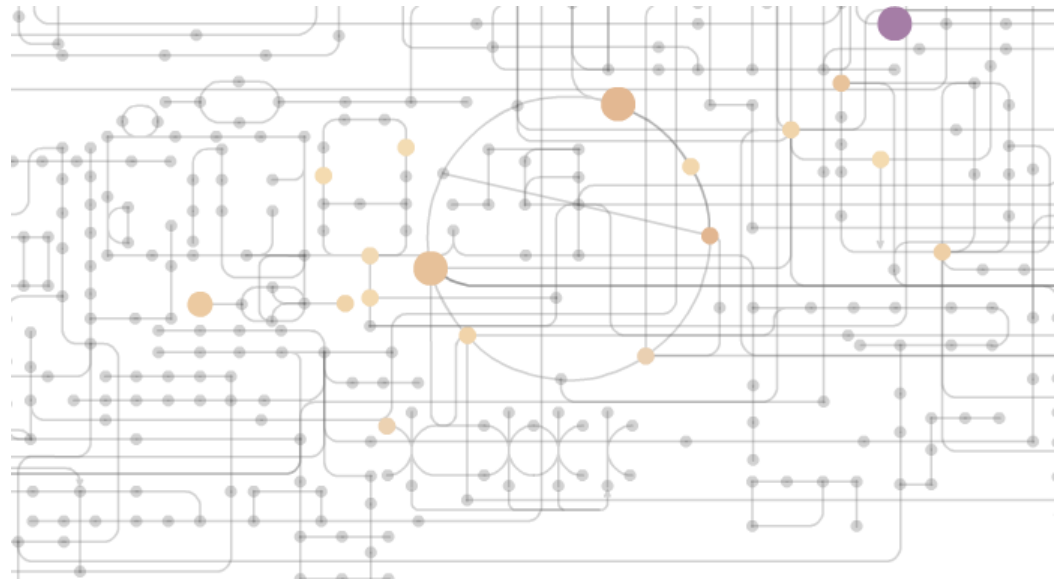


- Visualization of changes in pathways
- Pathway enrichment analysis
  - Rank lists metabolites
  - Shows subtle changes
- Pathway analysis
  - Ranks pathways based on metabolite location within a pathway
  - Betweenness centrality (blue)
  - Degree centrality (red)



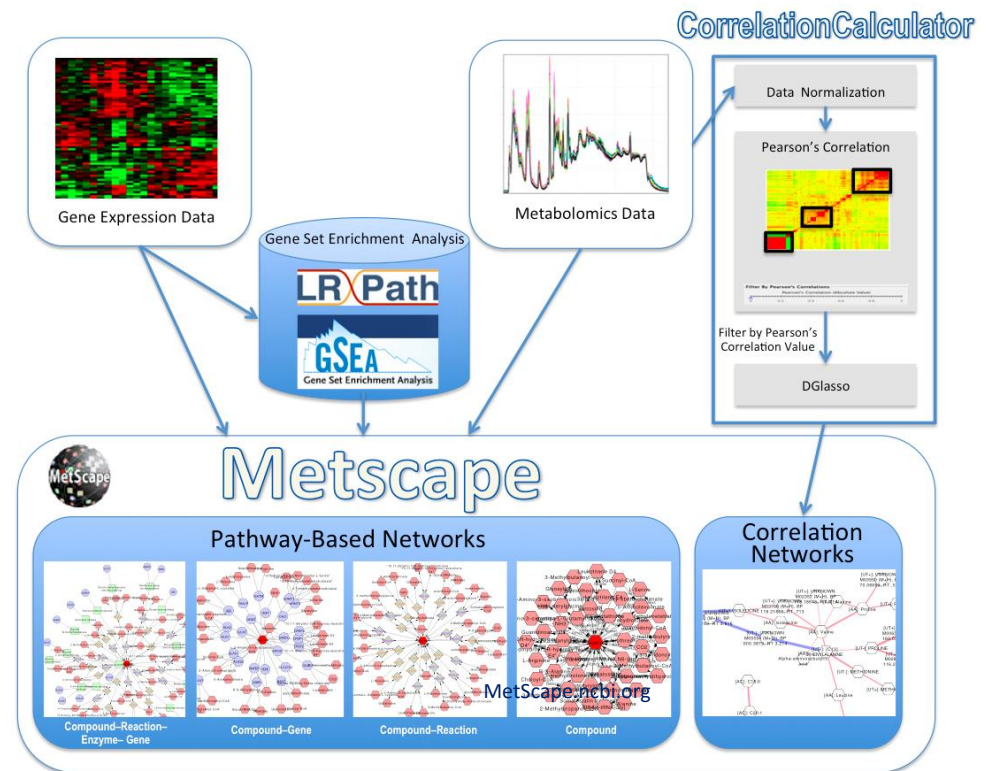
# Ipath

- Gives overview of all changes
- Shows significance and fold change
- Cons:
  - Overwhelming

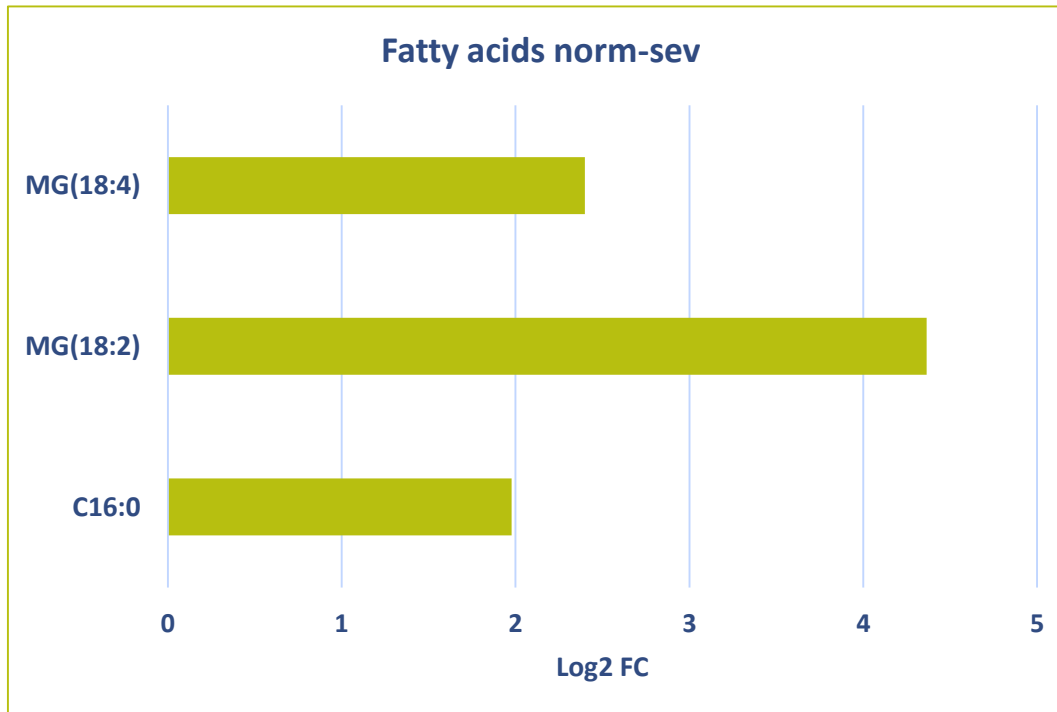


# Metscape

- Build pathway based on data
- Multiple build options
- Cons:
  - Only 3 databases (human, mouse and rat)



# Changes in lipids & carnitine in WS-affected broilers

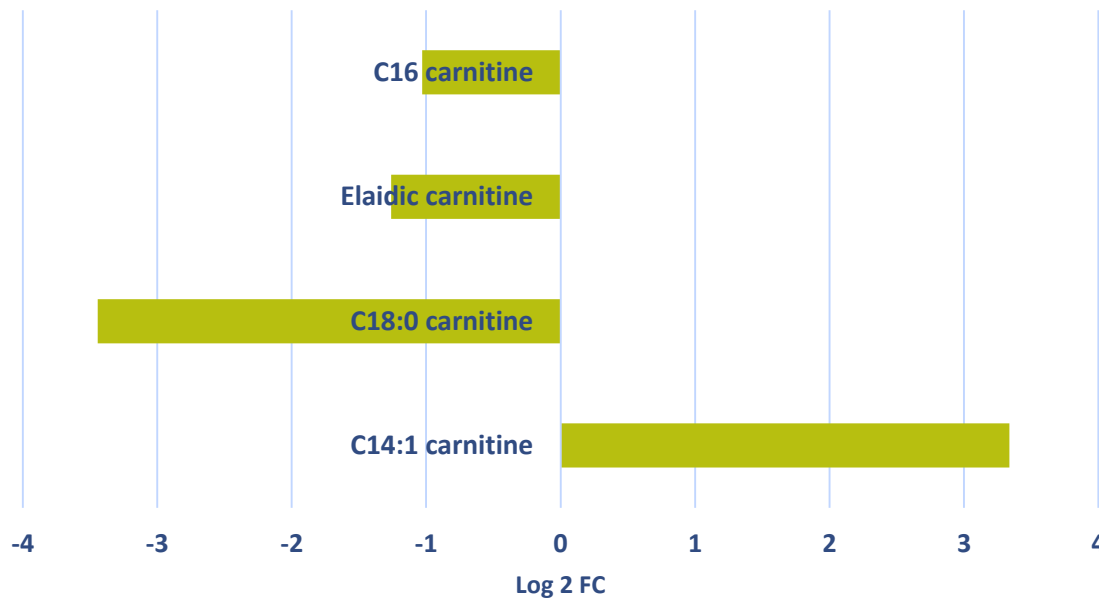


- Increase in fatty acids
- Increase in cis-5-C14:1 carnitine (marker for  $\beta$ -oxidation disturbances)
- Low levels of C16 + C18 carnitine
  - transfer LCFA from cytoplasm to mitochondria



# Changes in lipids & carnitine in WS-affected broilers

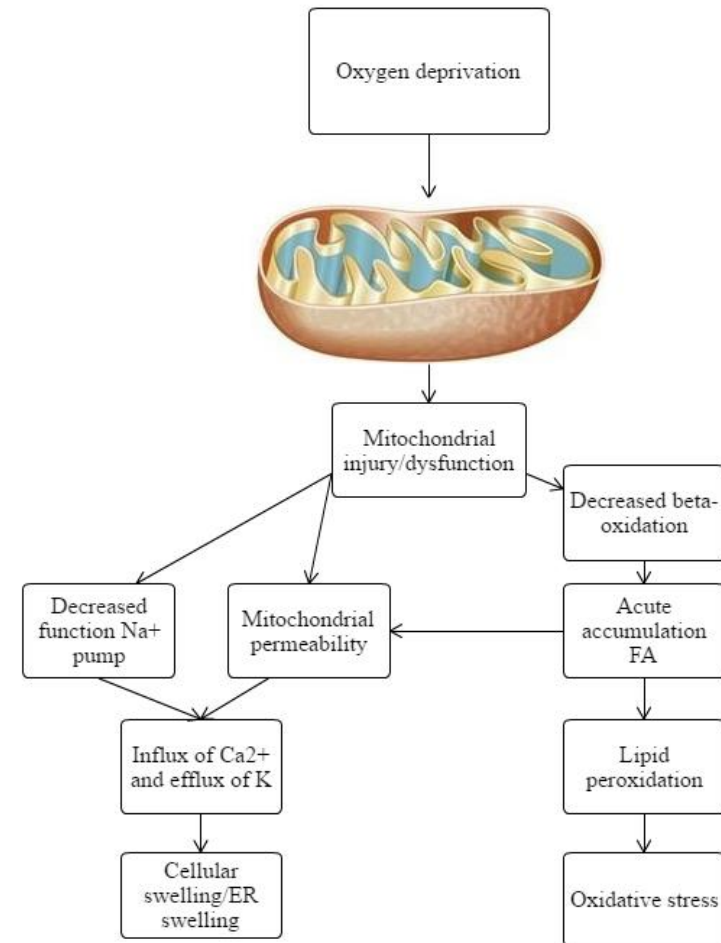
Carnitine results norm-severe



- Increase in fatty acids
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  - transfer LCFA from cytoplasm to mitochondria

# Hypoxia can explain changes in beta-oxidation

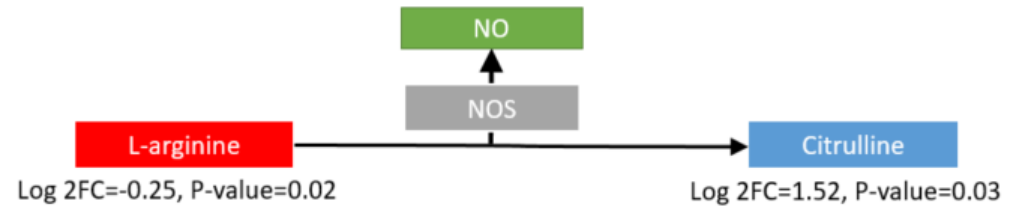
- Oxygen deprivation → mitochondrial architectural changes  
→ diminish mitochondrial beta-oxidation,  
TCA and respiratory chain → acute accumulation of FA
- Peroxisomes continue → no transporter needed →  
Accumulation of fatty acids intermediates
  - Such as monoacylglycerides → **detergents!**
- White lesions → attempt to minimize cellular damage  
from ectopic extracellular lipids





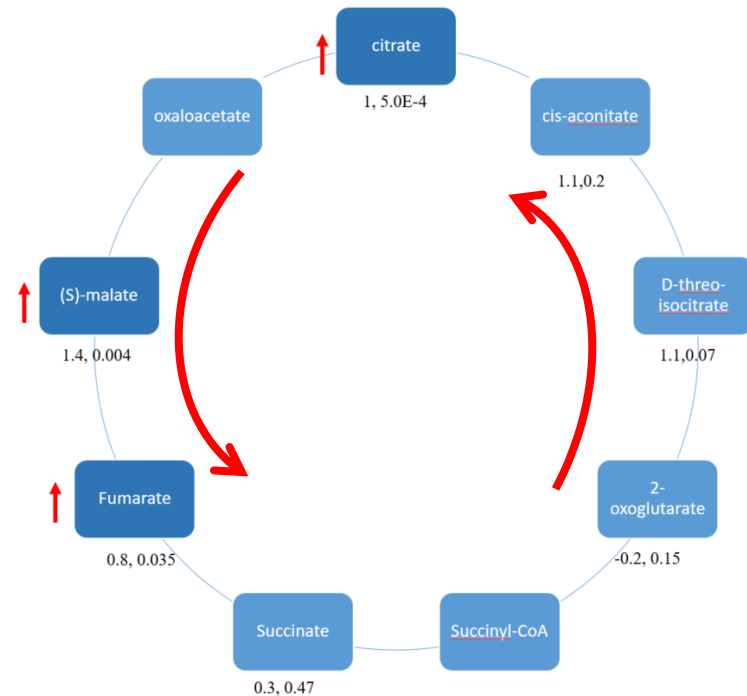
# Arginine metabolism increased for NO

- Arginine levels lowered
- Citrulline levels increased
- Increased conversion to create NO
- NO needed for enhanced blood flow
- Limited system
  - broilers unable to synthesize arginine
  - Already maxed out?!
- NO mediator of hypoxia/re-oxygenation-induced damage



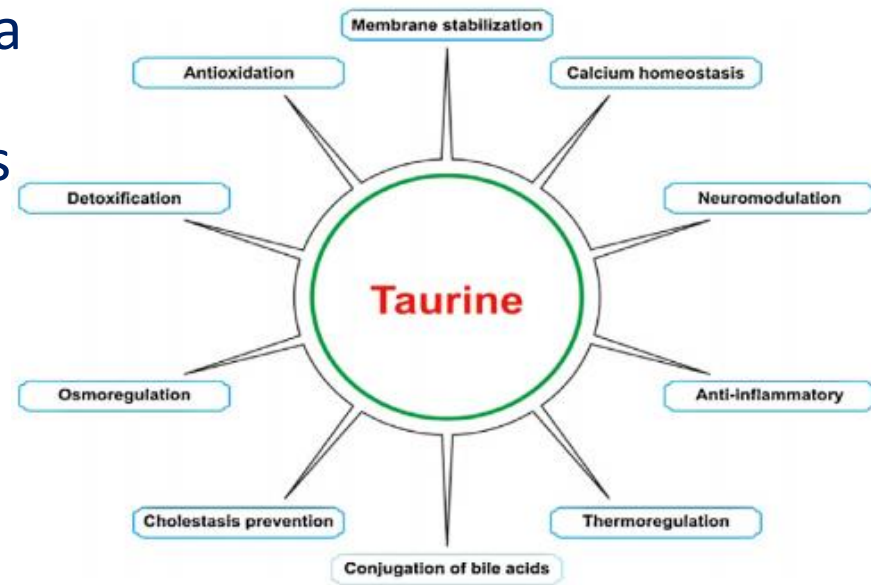
# Krebs cycle disturbed

- Increases in citrate, fumarate and malate
- Parts of TCA cycle increases
- Oxaloacetate-fumarate flux/backflux
  - Anaerobic conversion:
  - Oxaloacetate → malate → fumarate → succinate
- Citrate formed from glutamine during hypoxia
  - Glutamine → 2-oxoglutarate
  - Accompanied by increase 2-hydroxyglutarate (P:0.04)



# Increase in the osmolyte taurine to prevent damage

- Taurine levels increased 2 fold ( $P < 0.01$ )
  - Stabilization of the sarcolemma
  - Modulates potassium channels
  - Controls intracellular calcium
  - Released to prevent damage
    - especially calcium-related
  - Higher levels also upon reperfusion



# Hypothesis: blood supply is bottleneck



## Hypothesis

- Rapid tissue growth
- Blood vessel development borderline adequate
- Animal tries to compensate hypoxia by producing nitric oxide
  - Nitric oxide also leads to oxidative stress
- White striping seems to be caused by hypoxic conditions resulting from inadequate blood flow

# Conclusion: metabolomics is a great tool for meat sciences

- White striping had no clear etiology
- Metabolomics great to increase understanding
- Solution found based on metabolomics work
- Metabolomics does have unique challenges
  - Data collection needs to be well controlled
  - Targeted/Untargeted
  - Data analysis
  - Data interpretation
- Advances in the field of metabolomics are still made and hence will lower the threshold

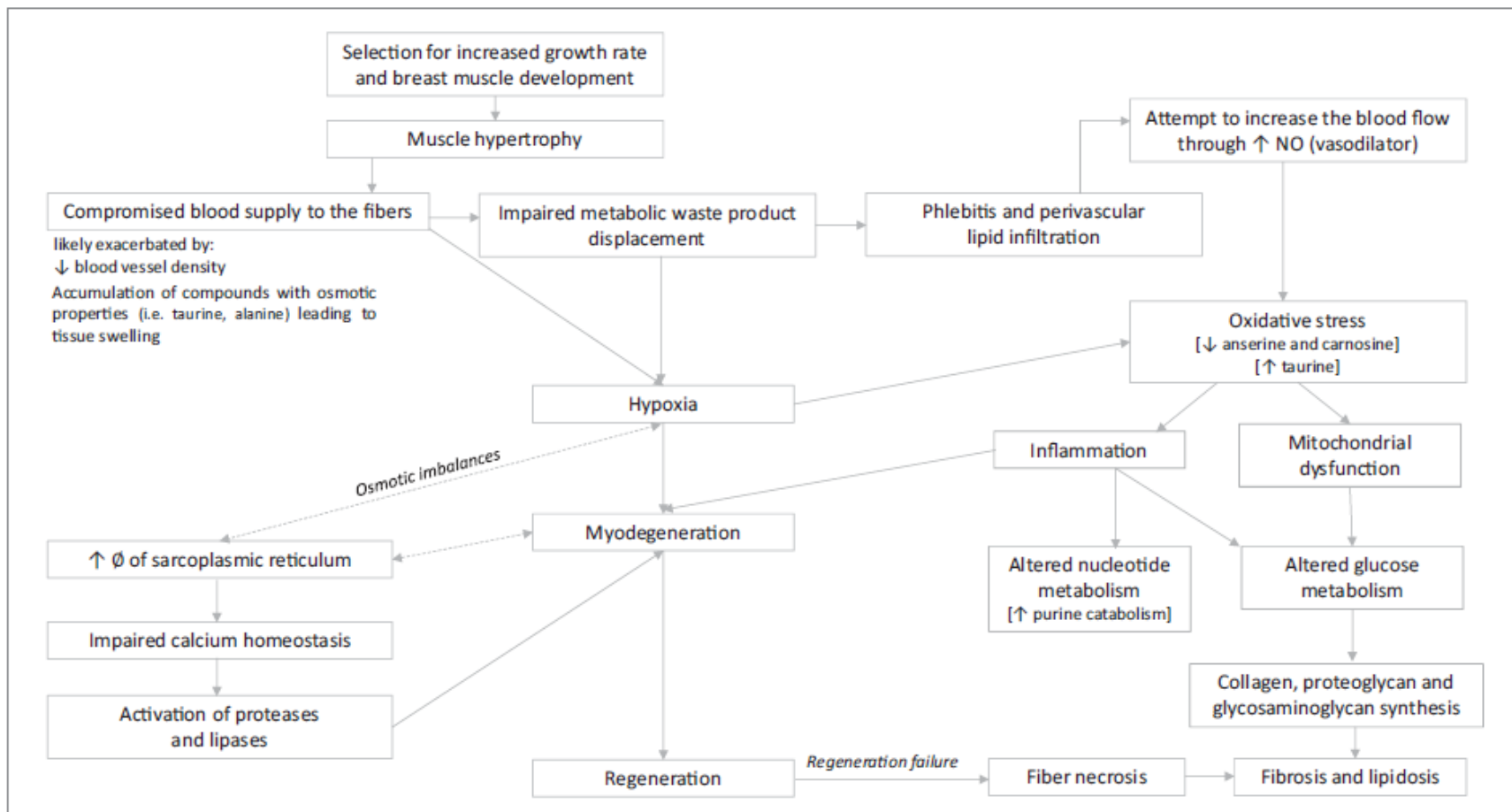


Figure 2–Schematic representation of the possible etiologies and mechanisms leading to the development of white striping (WS), wooden breast (WB), and spaghetti meat (SM) abnormalities.

# Special thanks



Alberto Navarro Villa



Theo van Kempen



Adriano Pérez Bonilla

# Thank you

