



IRISH CATTLE BREEDING FEDERATION

# Carcass Video Images in Genetic Evaluation and Breeding Program in Ireland

Thierry Pabiou

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# Beef production in Ireland

## 2 million cows

- 1,000,000 beef cows
- 14 cows / herd
- 6 major beef breeds
  - CH LM AA SI HE BB
- Large uses of cross breeding

## Destination

15% replacement



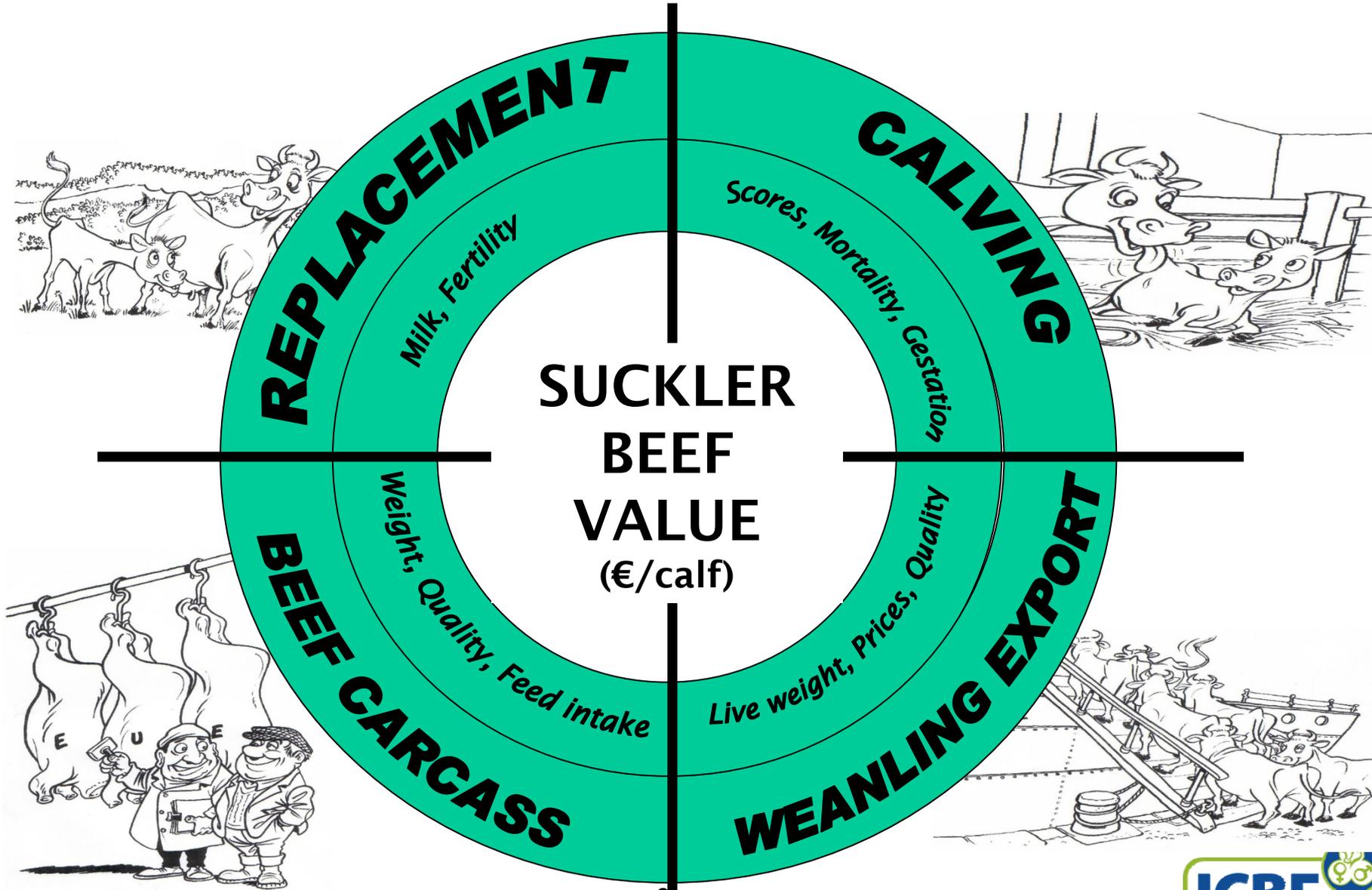
16% Live export



69% Slaughtered in Ireland



# Beef breeding objective



# Current assessment of carcass quality

- The EUROP carcass classification
  - Assessment of conformation & fat grades by experts/machines



S > E > U > R > O > P  
15 > > > > > > > > > 1

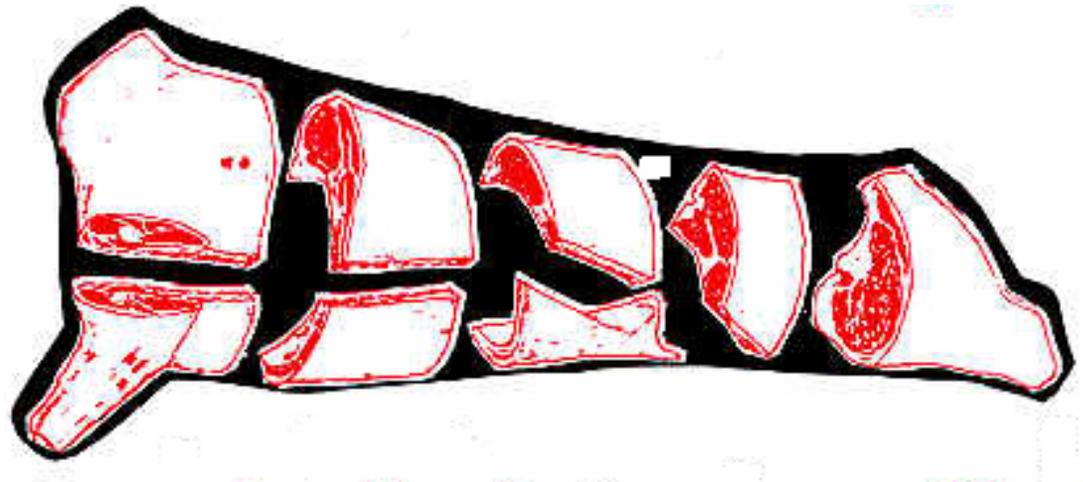


1 < 2 < 3 < 4 < 5  
1 > > > > > > > > 15

=> Current selection tool for carcass quality

# Motivations

- Improving carcass quality



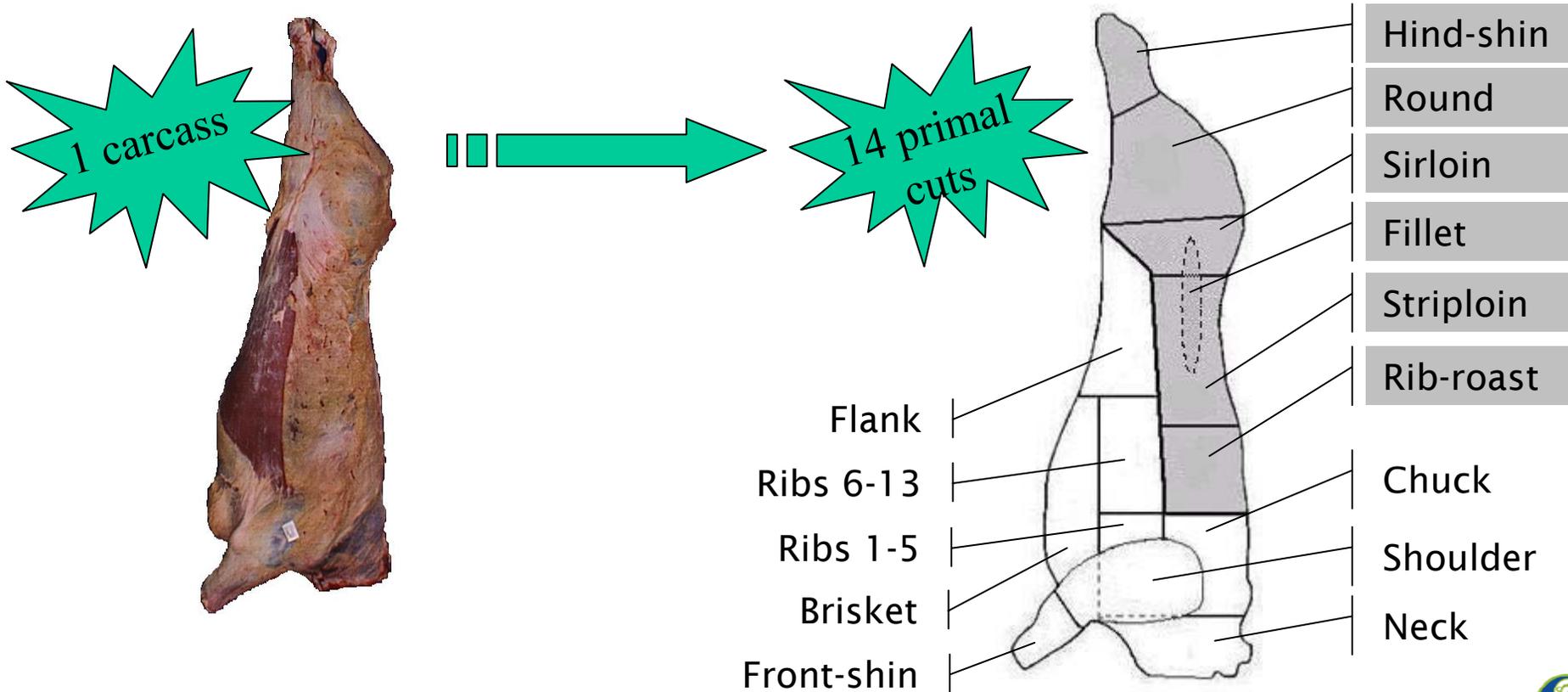
Going deeper in the carcass => new selection tools for carcass quality?

# Objective

- Is it possible to create new carcass traits from digital images?
- Is that interesting/useful for farmers and the industry?

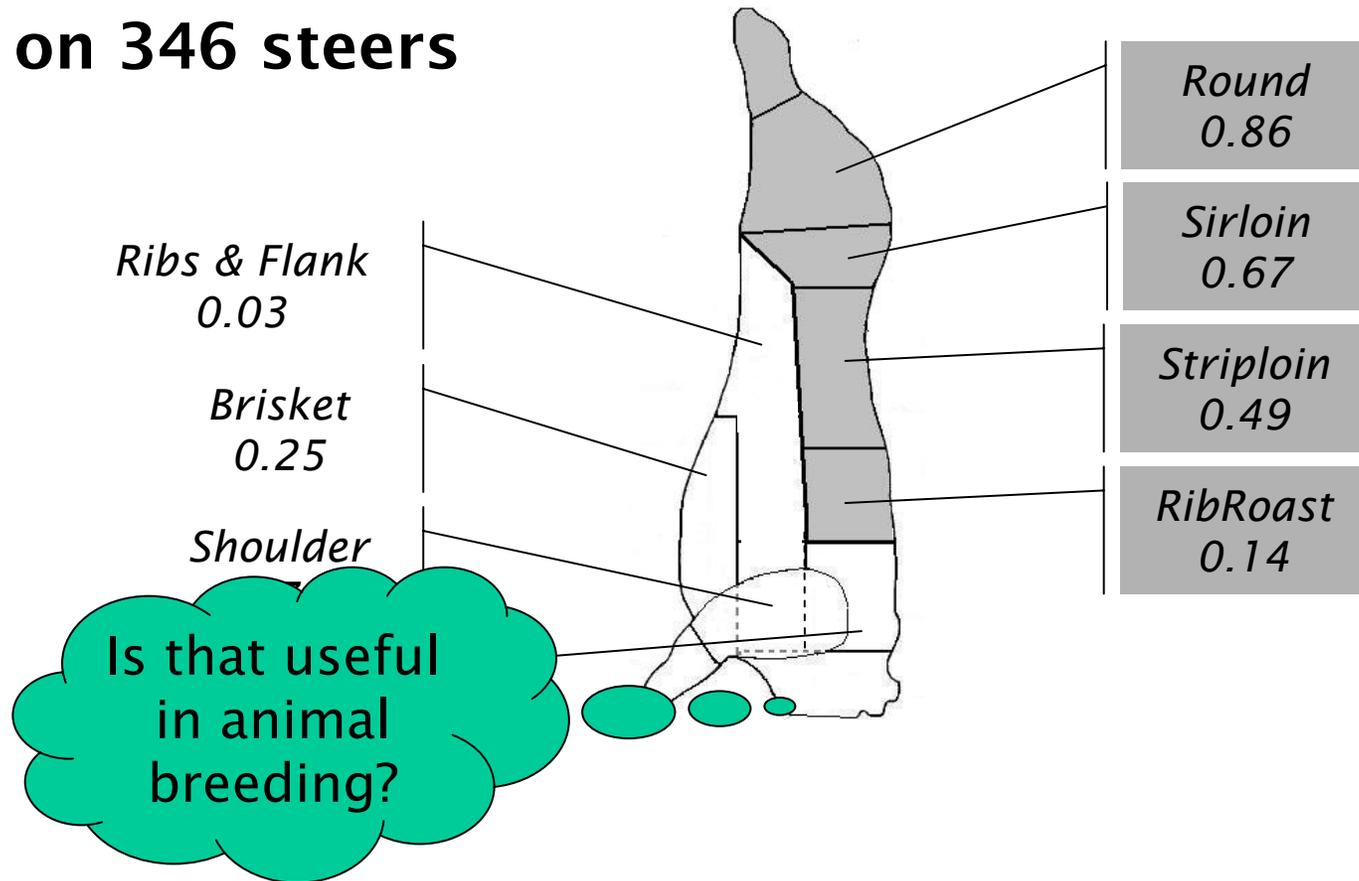
# Data used: Primal cuts

- Research center: n = 413 (mostly) steers
- Commercial partner: n = 615 (mostly) heifers



# Heritability of primal cuts

• Calculated on 346 steers



*Pabiou et al. (2009) J. Anim. Sci.*

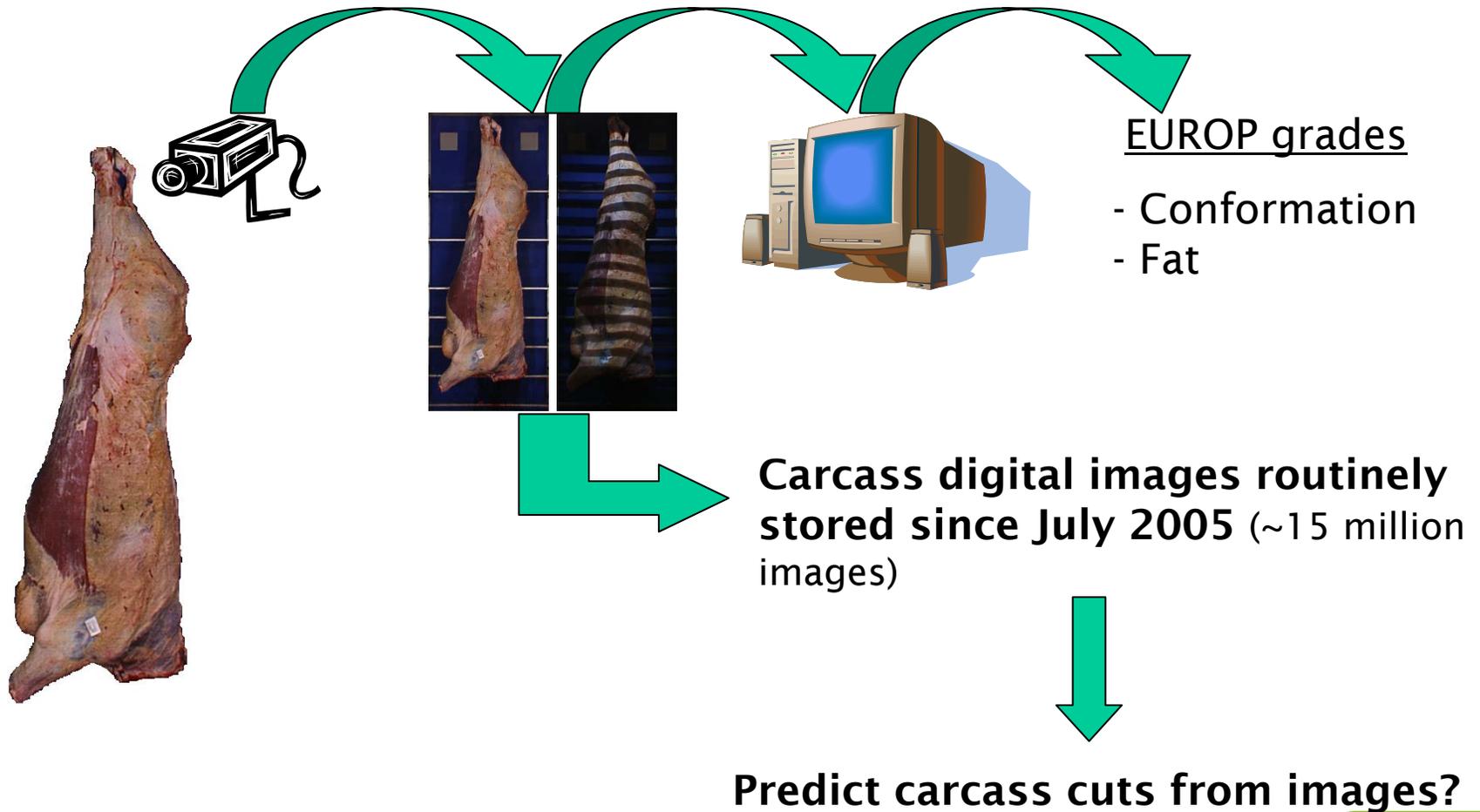


# Why creating new traits?

## Primal cuts

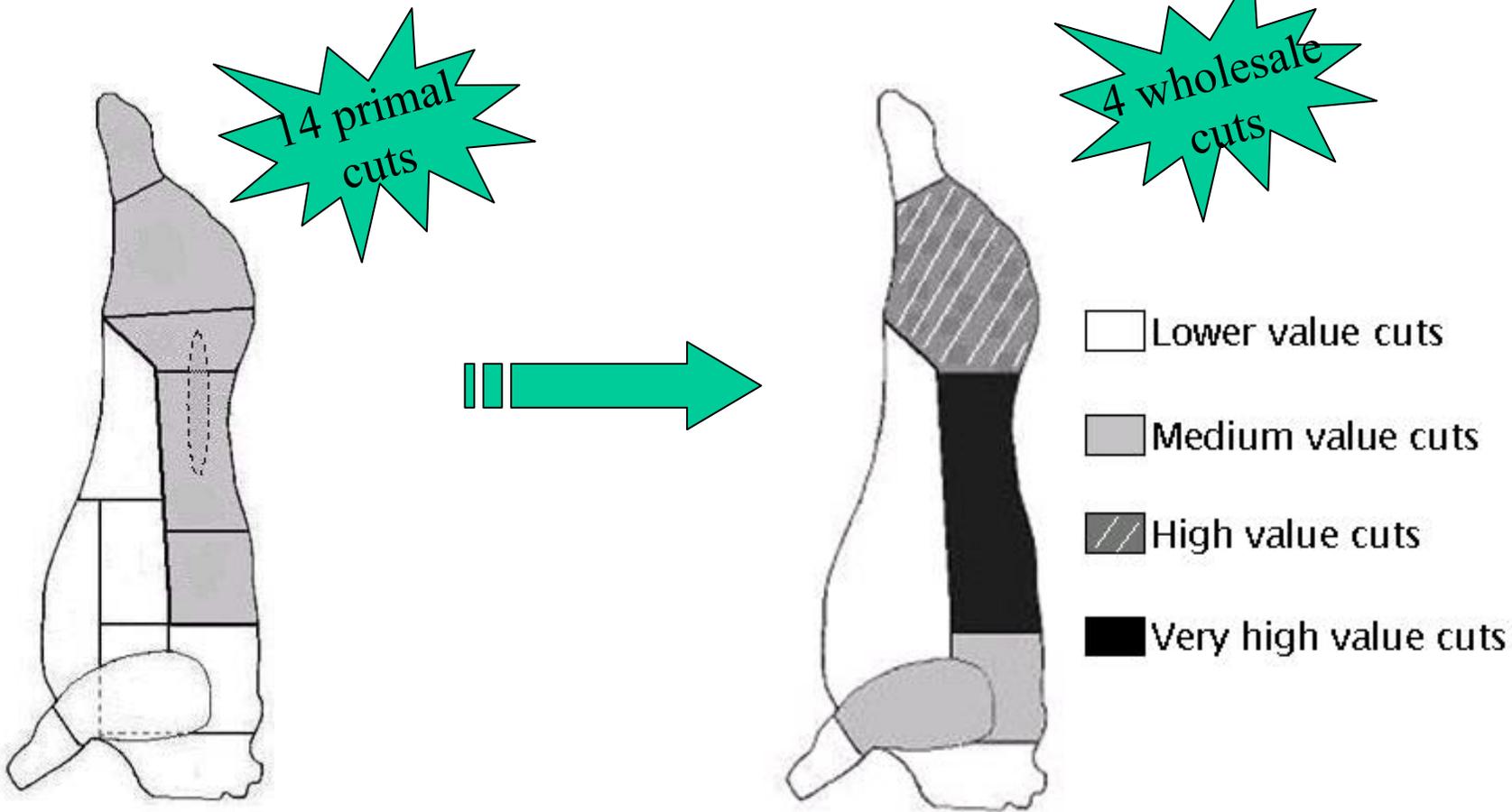
- Interest for farmers / industry... **Yes!**
- Genetic variability..... **Yes!**
- Availability..... **No**

# Mechanical grading of carcasses



# Data used : Wholesale cuts

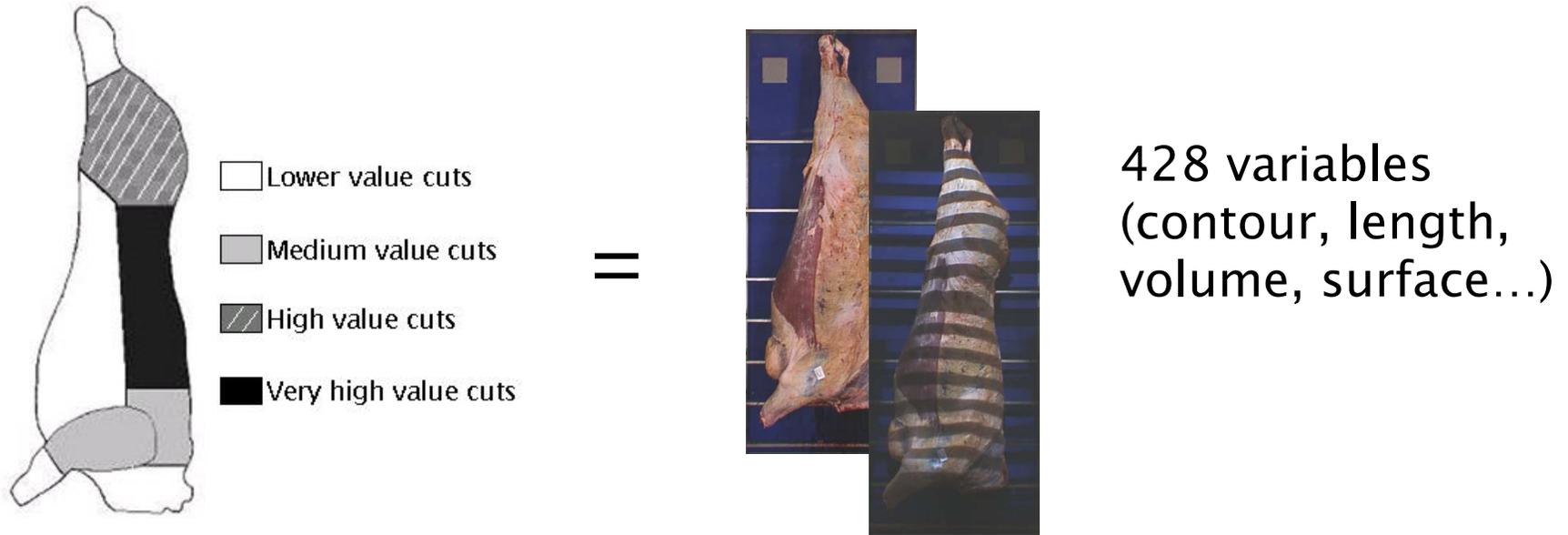
• Primal cuts grouped by retail value (steers & heifers)



# Predicting weights from images

- **Building prediction equations**

- Using multivariate analysis



- Calibration (2/3 data) / validation (1/3 data)
- Built on 346 steers & 281 heifers

*Pabiou et al. (2010) Livestock Sci.*

# Accuracy of prediction

## R<sup>2</sup> of prediction in validation datasets

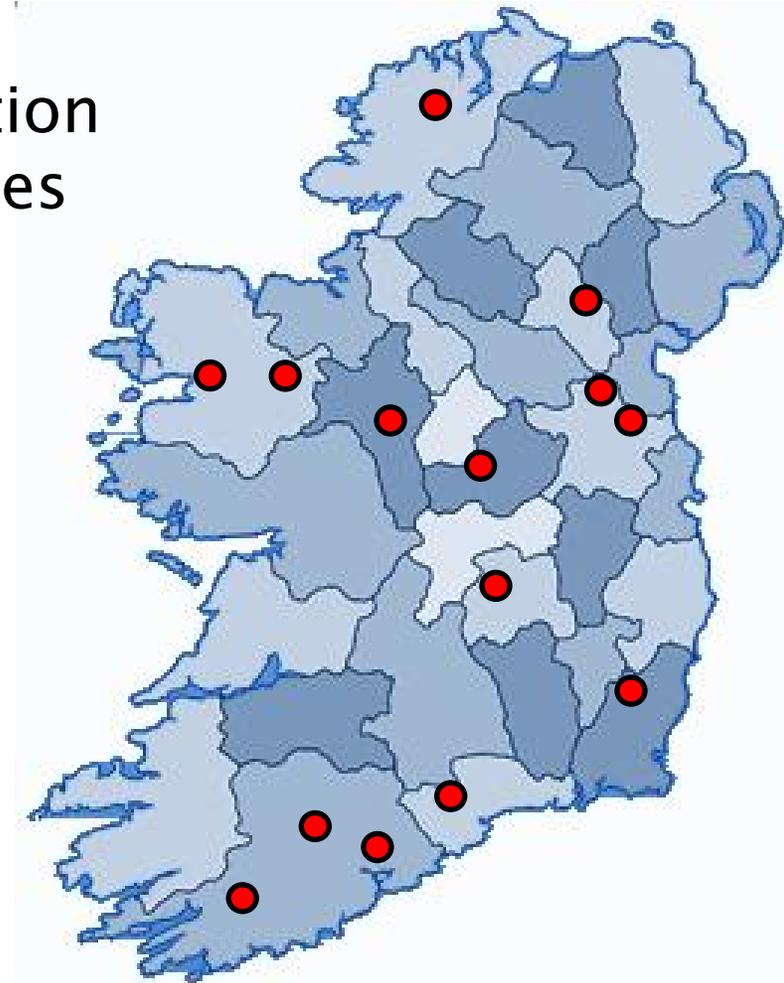
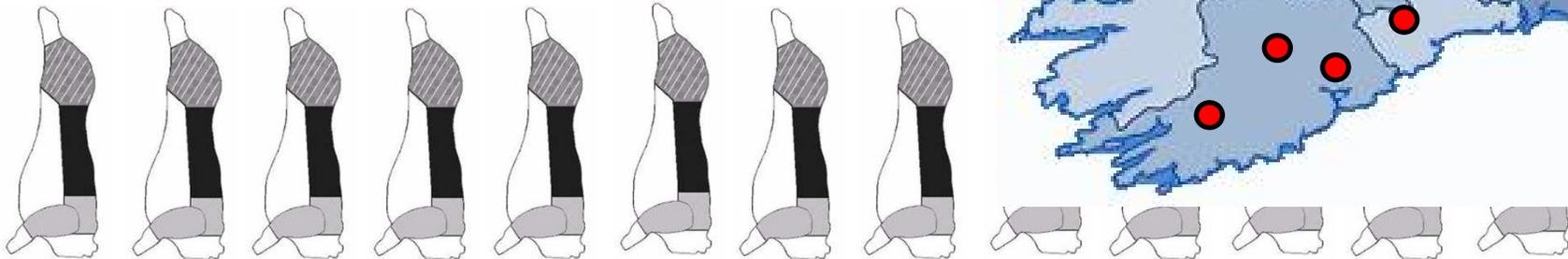
|                      | STEER | HEIFER     |
|----------------------|-------|------------|
| Total meat           | 0.97  | 0.84       |
| Total fat            | 0.77  | <i>n/a</i> |
| Total bone           | 0.81  | <i>n/a</i> |
| Lower Value Cuts     | 0.92  | 0.65       |
| Medium Value Cuts    | 0.86  | 0.70       |
| High Value Cuts      | 0.93  | 0.85       |
| Very High Value Cuts | 0.84  | 0.72       |

# Generating new phenotypes

- Obtained by applying prediction equations to the digital images historically stored
- Across 14 slaughter houses



**Access to large supply of carcass cuts**



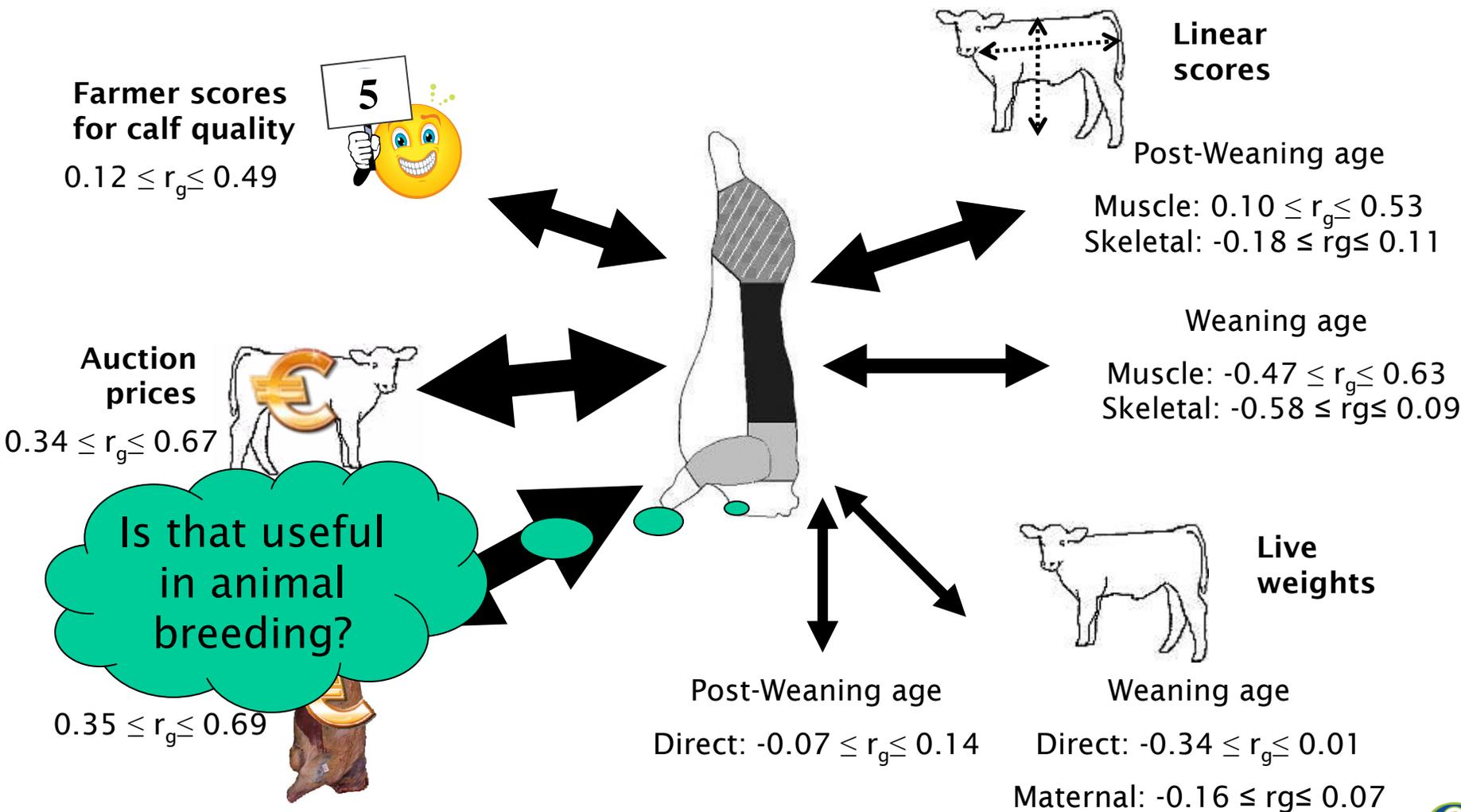
# Genetics of predicted weights

- Heritability on diagonal
- Genetic correlations off diagonal : **HEIFERS** & **STEERS**

| $\begin{matrix} r_g \\ \text{STEERS} \\ \hline h^2 r_g \\ \text{HEIFERS} \end{matrix}$ | Total meat  | Total fat   | Total bone  | LVC         | MVC         | HVC         | VHVC        |
|--|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| Total meat   | <b>0.44</b> | -0.61       | -0.24       | 0.71        | 0.78        | 0.93        | 0.80        |
| Total fat  | <i>n/a</i>  | <b>0.14</b> | 0.13        | -0.50       | -0.56       | -0.58       | -0.54       |
| Total bone   | <i>n/a</i>  | <i>n/a</i>  | <b>0.49</b> | -0.22       | -0.23       | -0.35       | -0.62       |
| LVC  | 0.87        | <i>n/a</i>  | <i>n/a</i>  | <b>0.18</b> | 0.45        | 0.66        | 0.57        |
| MVC  | 0.75        | <i>n/a</i>  | <i>n/a</i>  | 0.47        | <b>0.27</b> | 0.79        | 0.86        |
| HVC  | 0.89        | <i>n/a</i>  | <i>n/a</i>  | 0.80        | 0.82        | <b>0.40</b> | 0.89        |
| VHVC   | 0.82        | <i>n/a</i>  | <i>n/a</i>  | 0.69        | 0.82        | 0.82        | <b>0.17</b> |

*Pabiou et al. (2011a) Animals*

# Relationship with pre-slaughter traits





# Are we there yet?

## Predicted wholesale cuts

- Interest for farmers / industry... **Yes!**
- Availability..... **Yes!**
- Genetic variability..... **Yes!**
- Correlations with other traits.... **Yes!**
- Potential benefit for industry **?**



# Objective & Indexes

Breeding goal = **Suckler Beef Value**

Calving

Weaning

Carcass  
*Built with  
predicted cut*

Replacement

Index 1  
Live traits

Index 2  
Live traits  
Carcass weight

Index 3  
Live traits  
Carcass weight  
EUROP grades  
(=*current index*)

Index 4  
Live traits  
Carcass weight  
EUROP grades  
Predicted cuts

Index 5  
More accurate  
predictions

Selection indexes

# Benefits of adding predicted cuts to the carcass index

## Expected benefit for the Irish industry (million of Euros)

| Scenari tested            | Using carcass weight                   | Using EUROP grades                     | Using predicted carcass cuts           | Using more accurate prediction of carcass cuts |
|---------------------------|--|--|--|--|
| <i>Comparison of with</i> | <i>Scenario 1</i><br><i>Scenario 2</i> | <i>Scenario 2</i><br><i>Scenario 3</i> | <i>Scenario 3</i><br><i>Scenario 4</i> | <i>Scenario 4</i><br><i>Scenario 5</i>         |
| 10 years                  | + € 7.3                                | + € 0.6                                | + € 2.4                                | + € 0.6  |

# Conclusions

- Using phenotypes predicted from VIA for selection purpose is feasible
  - Accurate regressions equations for steers and heifers
  - Routinely available supply of predicted carcass weights
- and beneficial for the Irish industry
  - Exploitable genetic variations
  - Strong genetic associations with early predictors
    - Auction price at weaning and post-weaning
  - New selection index including predicted cuts:
    - increased responses on Carcass sub-index and Suckler Beef Value
  - Potentially the next Quality Payment System?

# In other words

- Is it possible to create new carcass traits from digital images?
  - YES
  
- Is that interesting/useful for farmers and the industry?
  - YES

# Future research

- Strengthen current prediction equations
  - Heifers
  - Bulls & cows
- Investigate meat quality & other technologies
  - Tenderness
- Beef genomic selection will include in time carcass cuts traits
  - In progress
- Expand knowledge to sheep
  - Build on UK research
- Explore ways of collecting more phenotypes
  - Collective organisation

# In other words

- This is only a beginning

**Thank you.**