



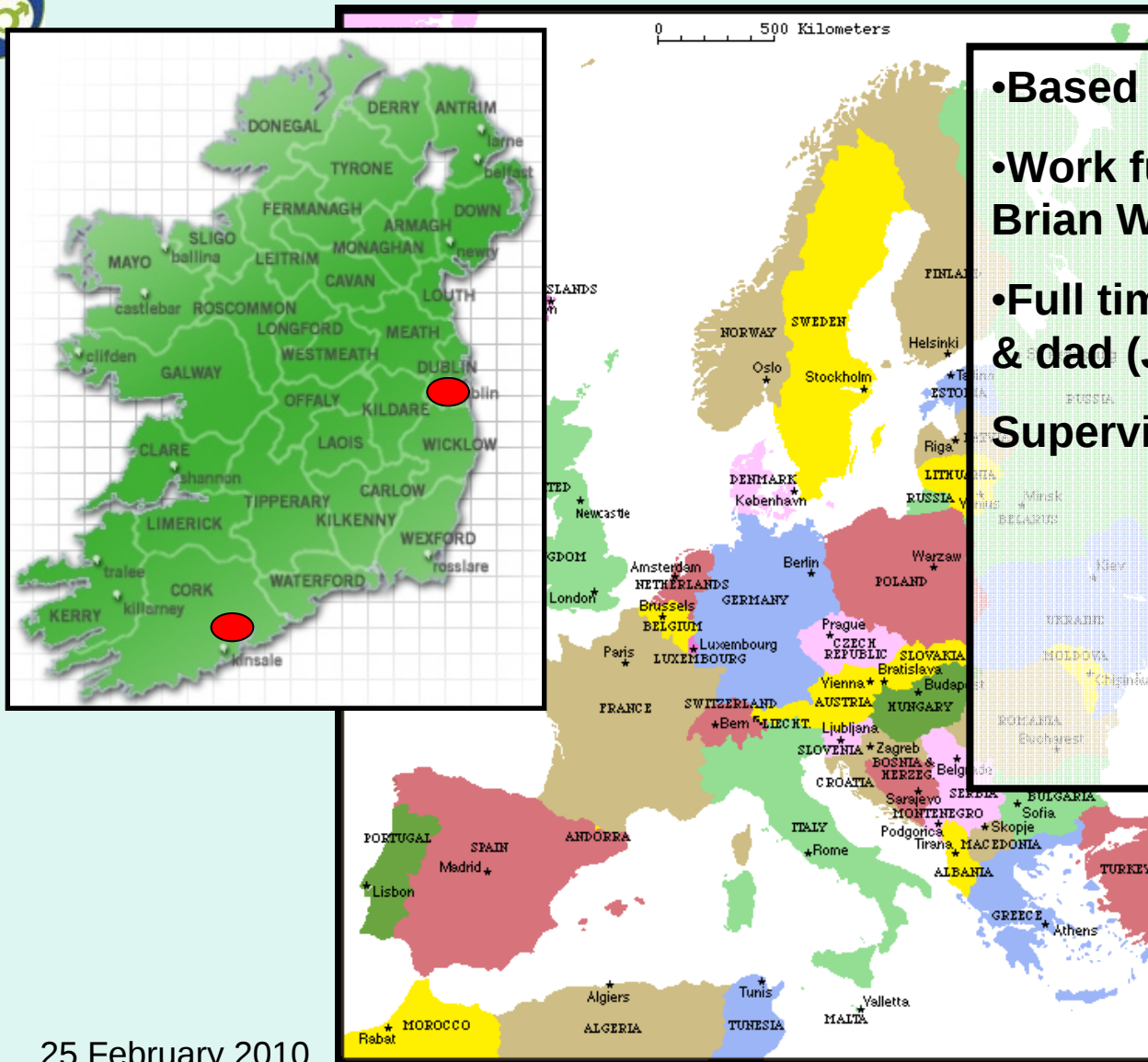
National & International Genetic Evaluation for Irish Beef Cattle

Thierry Pabiou

Half time seminar
25th February 2010
SLU-Hgen



A quick look on the map



- Based in Ireland
- Work full time for ICBF (CEO Brian Wickham)
- Full time husband (Heather) & dad (James, Lily & Eloise)

Supervisors

- Anna Näsholm
- Freddy Fikse
- Donagh Berry
- Andrew Cromie



Beef Production in Ireland*

2 million cows

- 1 000 000 beef cows
- 14 cows / herd
- 6 major beef breeds
- Cross breeding:
47 (Her) to 85% (Bbb)

Destination

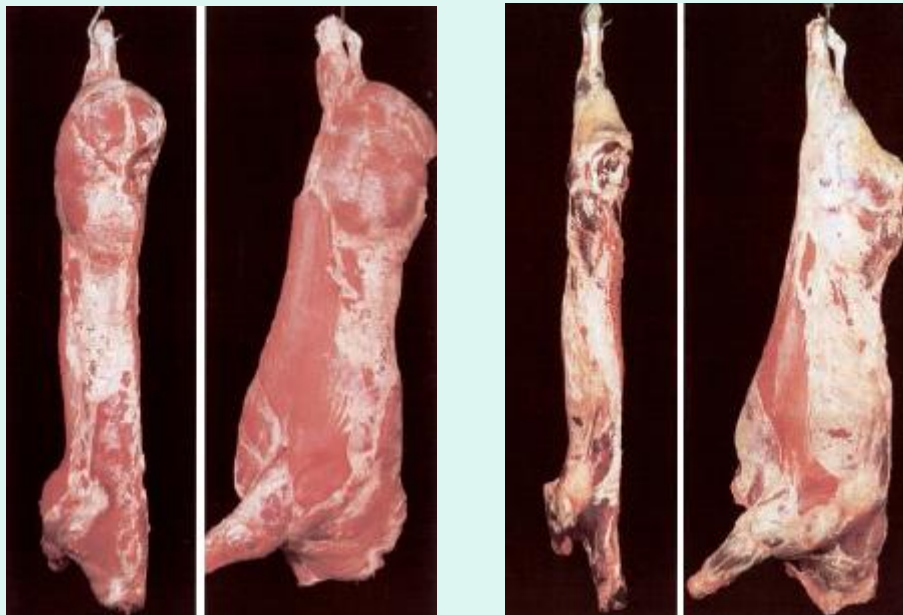
- 22% replacement
- 16% Live export
- 62% Slaughtered
in Ireland





Project Background: on the Farm

- The EUROP carcass classification
 - Assessment of conformation (6 grades) & fat (5 grades) by Experts / machines



Payment on carcass weight, conformation grading & fat grading.



Project Background: on the shelves

- Different cuts, different prices





My PhD Project

- Can selection help Irish farmers produce carcasses that fit more the retailer's demand?
- Can new carcass traits be used and improve breeding programs?
- *What data?*
 - *Is selection possible?*
 - *Integration into current breeding program?*
 - *Benefit for the Irish beef industry?*
 - *...*



The PhD Aims

- Develop equations to predict wholesale meat weight from digital images
- Estimate genetic parameters
- Estimates genetic association with other predictors currently used in Ireland
- Estimates correlations / genetic gains with carcass traits from other countries



Done so far



Paper I

Genetic Parameters for Carcass Cut Yields in Irish Beef Cattle

Pabiou, Fikse, Näsholm, Cromie, Drennan, Keane, & Berry

Submitted JAS September 2008

Published JAS September 2009

Objective: Genetic variability in primal cut weights?



Data Used

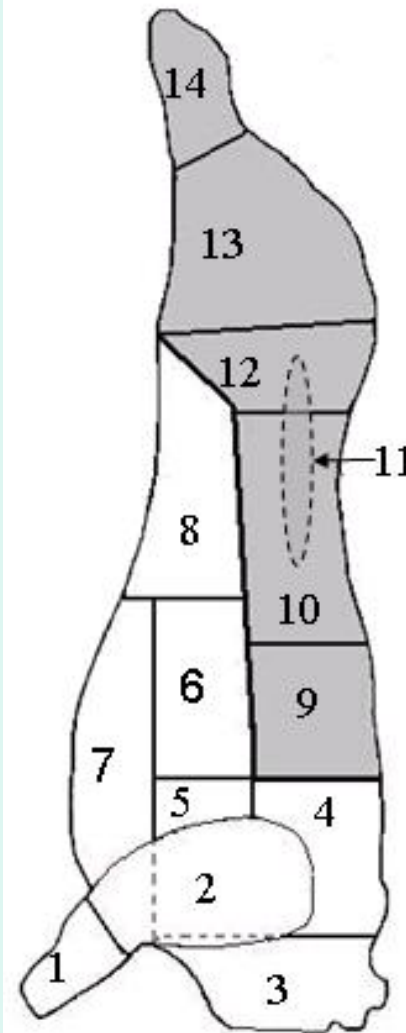
Carcass dissections: 2 datasets

- Experimental dataset Teagasc (n=579)
 - Collected 2005 – 2008
 - 1 carcass broken into 23 cuts (kg)
- Commercial dataset (n=10,845)
 - Collected 1999 – 2005
 - 1 carcass broken into 16 cuts (kg)



Example of cuts

- Experimental dissection
 - ↳ 23 cuts
 - ↳ 14 groups of cuts



Forequarter

1. Front shin
2. Shoulder
3. Neck
4. Chuck
5. Ribs 1 to 5
6. Ribs 6 to 13
7. Brisket
8. Flank

Hindquarter

9. Rib Roast
10. Strip-loin
11. Fillet (inside)
12. Sirloin
13. Round
14. Back shin

Heritability of primal cuts

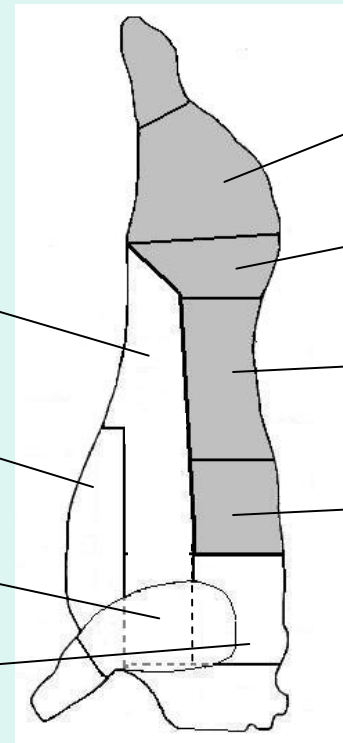
- h^2 calculated on 346 steers
- $0.15 < \text{Standard error} < 0.23$

Ribs & Flank
0.03

Brisket
0.25

Shoulder
0.79

Chuck
0.83



Round
0.86

Sirloin
0.67

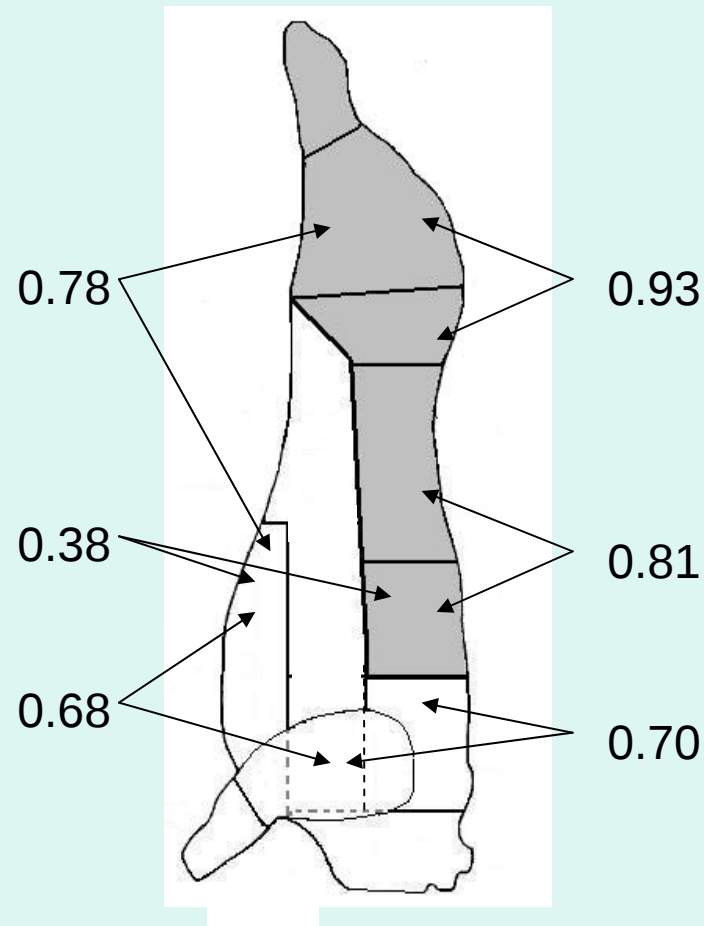
Striploin
0.49

RibRoast
0.14



Genetic correlations between primal cuts

- r_g calculated on 346 steers
- $0.05 < \text{Standard error} < 0.58$





Conclusion Paper I

- Selection on meat cuts possible
- Can meat cut data be collected on a routine basis?



Paper II

Use of Digital Images to Predict Carcass Cut Yields in Cattle

*Pabiou, Fikse, Kreuchwig, Keane, Drennan, Näsholm,
Cromie, & Berry*

Submitted Livestock Sciences February 2010

Objective: Assess feasibility of predicting wholesale meat
weight from digital images



Data Used

1. Carcass dissections from experiment in Paper I

+

2. Digital images from factory used to derive the EUROP grades

=

436 Steers 281 Heifers 73 Bulls

Example of Images

- Mechanical grading machine VBS2000 (EplusV, Germany)
 - Approved since 2001 for grading beef carcasses
 - 2 images / carcass (2D & 3D)
 - Fed into Irish database on a routine basis since 2005





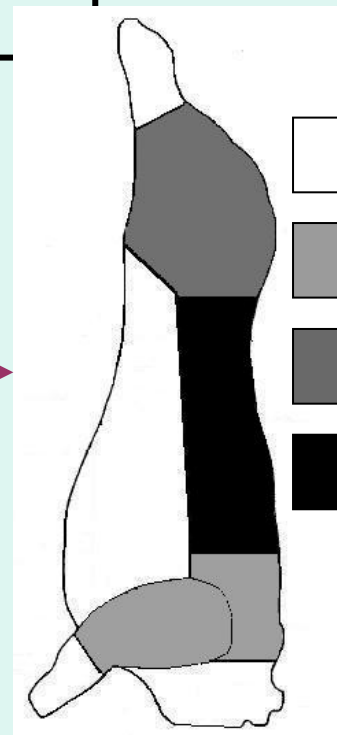
Prediction of 4 Wholesale €cuts



428
variables

Conf.	Fat
E	1
U	2
R	3
O	4
P	

Multiple
Regression
Methods



-  Lower value cuts
-  Medium value cuts
-  High value cuts
-  Very high value cuts



Calibration / Validation

For each wholesale cuts

- **Calibration file** (67%) : to built up the regressions equations
- **Validation file** (33%) : to assess regression accuracy & fit



Model / Methods Tested

- Model 1
Wholesale Cut = Carcass weight
- Model 2
Wholesale Cut = Carcass weight + EUROP conf. + EUROP fat
- Model 3
Wholesale Cut = Carcass weight + 428 VIA variables
 - Method a: Stepwise regression
 - Method b: Stepwise LASSO
 - Method c: Partial least square regression
 - Method d: Principal components analysis
 - Method e: Canonical correlations



Results Models / Methods

- Models (based on R^2 , RMSE, Bias, & residual correlations)

Model 1 << Model 2 < Model 3

- Methods (based on Nb predictor used, R^2 , RMSE, Bias, & residual correlations)





Results Regression R²

Stepwise regression / Carcass weight + VIA variables

Weight (kg)	Commercial (Heifer)	Experimental (Steer)
Total meat	0.84	0.98
Total fat	-	0.77
Total bone	-	0.81
Lower value cuts	0.65	0.92
Medium value cuts	0.70	0.86
High value cuts	0.85	0.93
Very high value cuts	0.72	0.84



Conclusion Paper II

- Wholesale meat cut weight can successfully be predicted from digital images.
- More dissections needed on bulls and COWS.

Man at work



Paper III

Genetics of Wholesale Carcass Cuts in Beef Cattle Predicted from Digital Images of Carcasses at Slaughter

Pabiou, Fikse, Amer, Näsholm, Cromie, & Berry

Potential journal: Animal

Objective: Genetic parameters for predicted wholesale meat weight



Data Used

- Digital Image stock
 - From mid-2005 to present
 - 5 million 2x images = 2.5 million carcasses
 - Around 50% match the genetic database
- Converting images into meat cuts
 - 1st tests Aug. 2009
 - New version of E+V software Oct. 2009 – Tests
 - ‘Routine’ conversions started end Dec. 2009



Converting Images : Principles

Image file + Daily calibration files + Input file



Carcass ID	Sex	CC W
0801252D0001	C	300
...	...	...



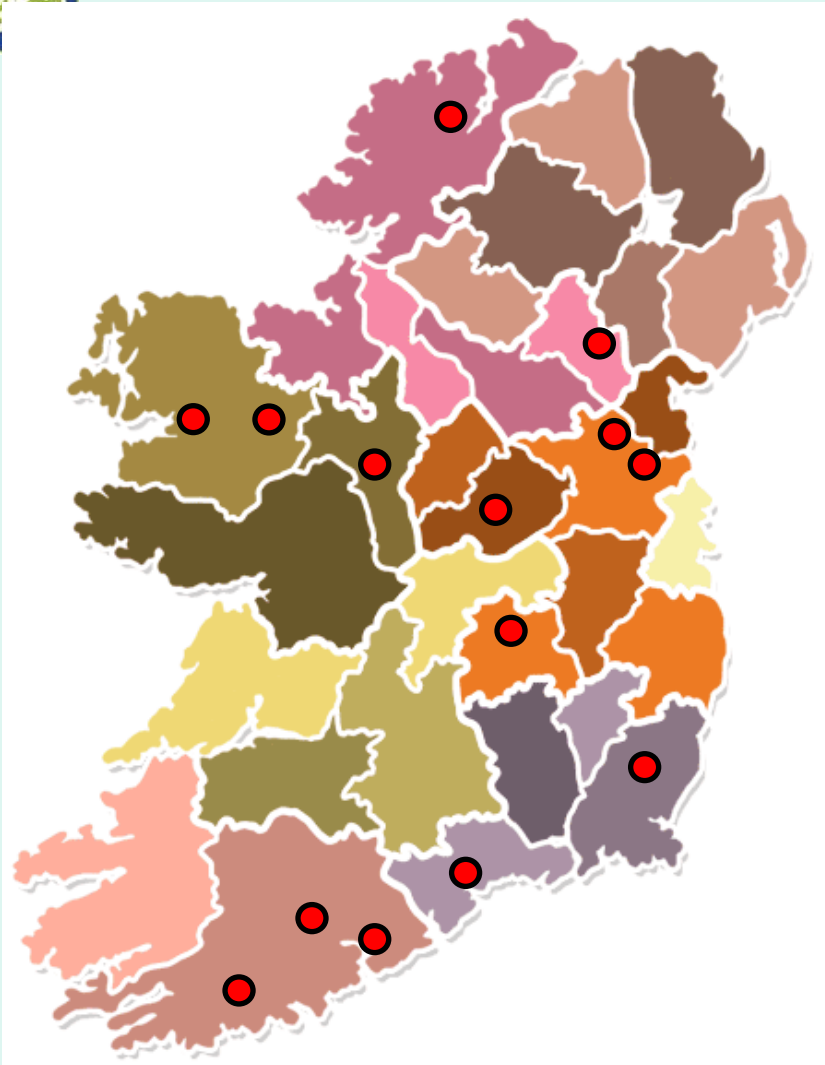
Within
factory

Carcass ID	Sex	CCW	LVC	MVC	HVC	VHVC
0801252D0001	C	300	95	40	60	25
...	...	...	...	...	...	...



Converted for the analysis

- Images from 14 factories
- Period Feb. 07 – May 09
- 521,605 carcasses



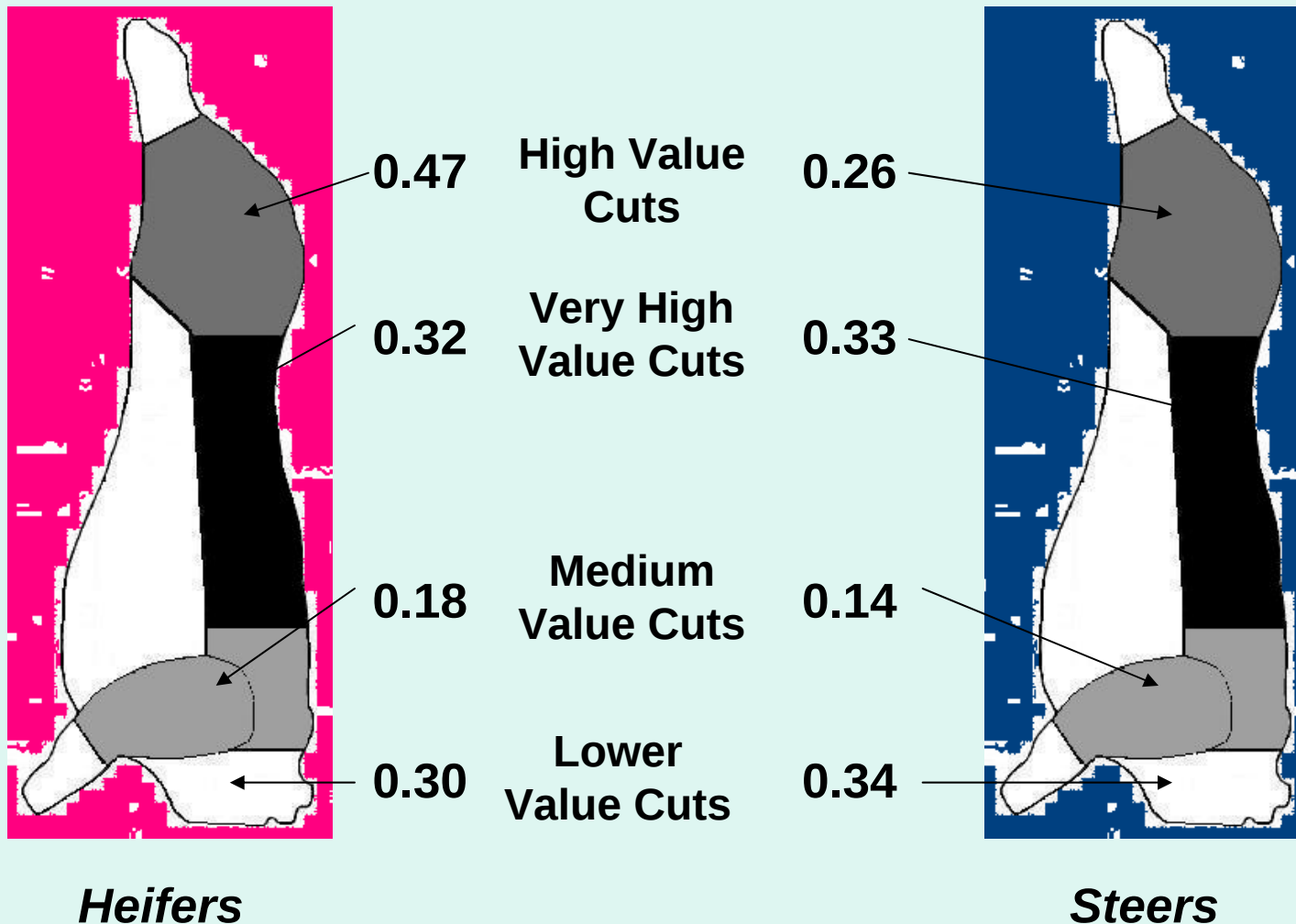


Data Editing / Model

- Major loss of data : missing sire (-369,782 obs)
- Model developed on 41,604 steers and 17,041 heifers
- Fixed effects: birth type, age of dam, contemporary group, calibration
- Fixed regression: age at slaughter, carcass weight, heterosis, recombination, breed type
- Random effect: animal or sire of animal
- Software used: ASreml & DMU



(First) Results on Heritability



s.e. < 0.050



Current work Paper III

- Refine some edits
- Work out correlations between
 - Predicted traits
 - Carcass weight, conf., fat, & predicted traits
 - Predicted and true traits



Blueprints



More Papers?

- Paper IV: Work out the genetic associations between predicted cuts & linear scores at weaning, & price data
- Paper V:
Genetic correlations between predicted cuts and carcass traits recorded in other countries (InterBeef)

Or

Simulation of genetic gains when across country collaboration is installed



Thanks!



25 Februar