

IFAFS project



Mapping and use of QTL for marker-assisted improvement of meat quality in pigs

Jack Dekkers, Max Rothschild, Rohan Fernando Iowa State University

Sandra Rodrigues-saz, Jonathan Beever University of Illinois - Urbana Champaign



Pork Quality



- Consumer demands pork that is:
 - reasonably priced
 - wholesome
 - palatable
 - attractive
- Pork quality has important genetic basis
- Difficult to improve by conventional selection
- Improvement possible if genes are known







Carcass traits

Marbling, color, firmness scores



- Ultimate pH
- Light reflectance
- Water holding capacity
- Glycolytic potential
- Lipid and cholesterol content
- Fiber type

Sensory panel traits

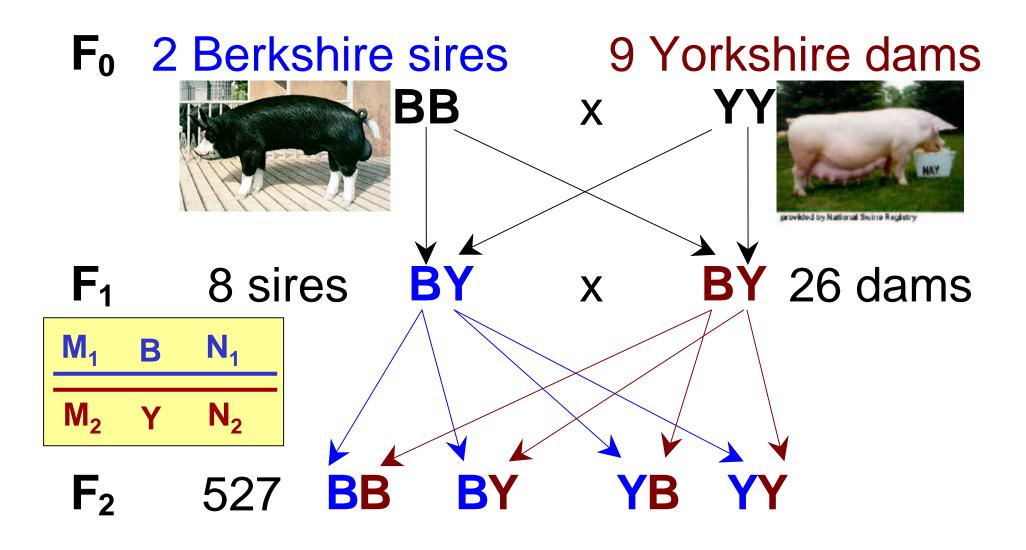


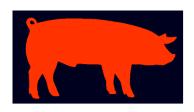
- Tenderness
- Chewiness
- Juiciness
- Flavor
- Off flavor

Cooking traits

- Star probe tenderness
- % Cooking loss

Genome Scan for Meat Quality





Traits measured



Growth traits

- Birth weight
- 16d weight
- ADG to 16 d.
- ADG to slaughter

Sensory panel traits

- Tenderness
- Chewiness
- Juiciness
- Flavor
- Off flavor

Carcass traits

- Carcass weight
- marbling, color, firmness scores
- Ultimate pH
- Minolta reflectance, Hunter L color
- Water holding capacity
- Drip loss (72 hrs)
- Lipid and cholesterol content
- Fiber type I (%) Fiber type Ia/Ib (%)

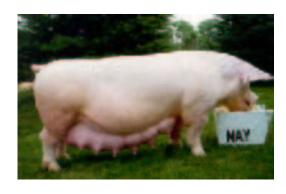
Cooking traits

- Star probe tenderness
- % Cooking loss

Second phase research







- Positional Candidate Gene analyses
- Further statistical analyses
- Use of QTL findings in selection programs

Outline

QTL results with new markers in ISU population

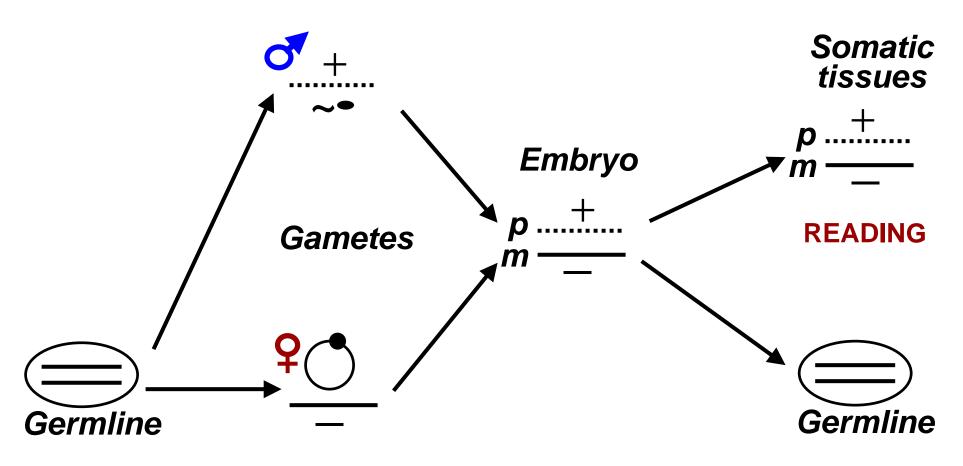
Detection of QTL with non-Mendelian expression

Use of identified QTL in introgression programs

Gametic imprinting

DNA methylation

Constancia et al. Genome Research, 1998



ERASURE ESTABLISHMENT

Generation one

MAINTENANCE

ERASURE

Generation two

Gametic imprinting

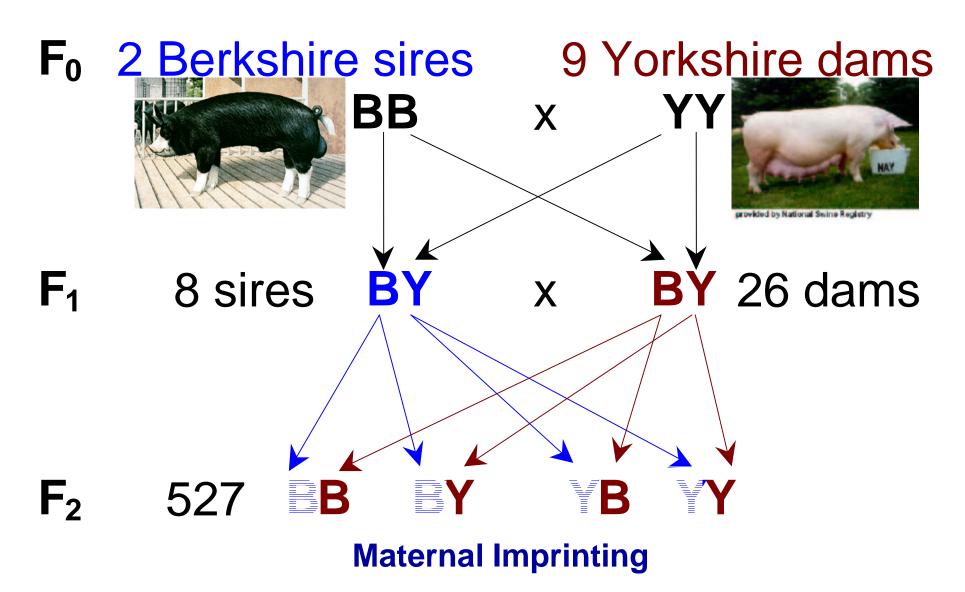
Gene expression depends on parental origin

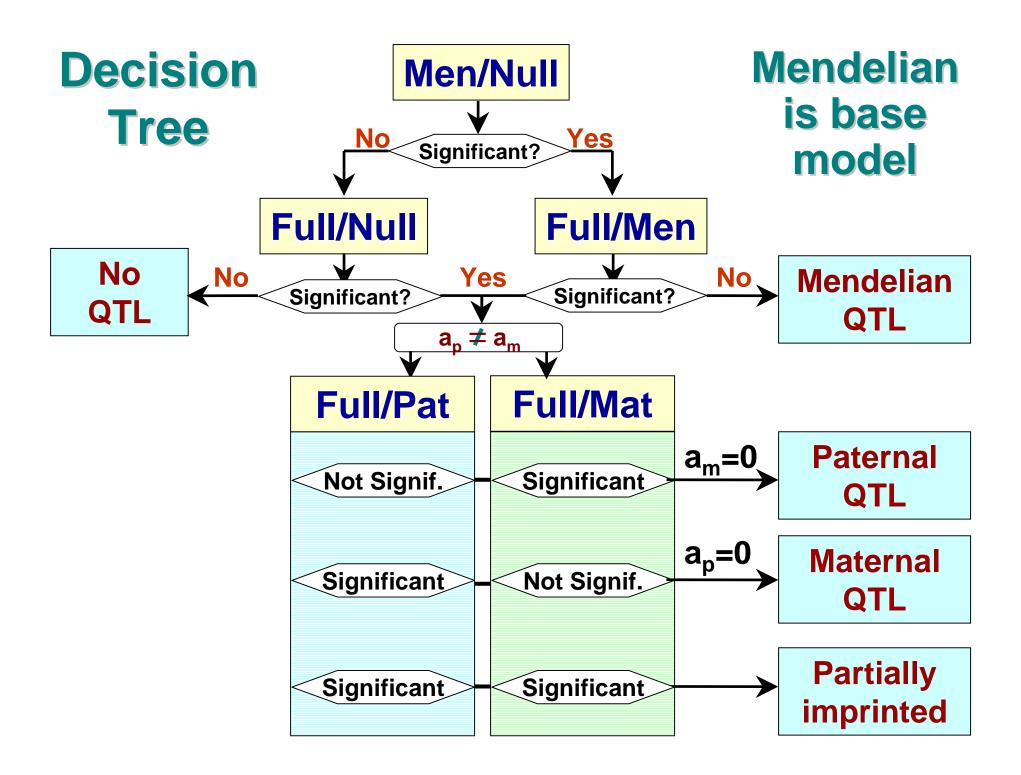
- Human
- Mouse
- Swine IGF-2 region on SSC2
 - muscle mass and fat deposition

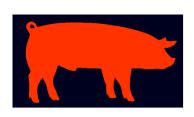
(Nezer et al., '99 and Jeon et al., '99)

Gametic imprinting

Gene expression depends on parental origin



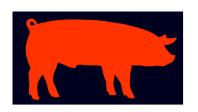






- 1) Develop and apply methods for combined analysis of the ISU and UIUC populations
 - Complete phenotyping and genotyping of the UIUC F₂ population
 - Fill gaps in the ISU population map by 30 additional markers
 - Develop statistical methods for QTL detection for application to the individual and joint data
 - Multiple QTL models
 - Gametic imprinting models
 - Epistatic models
 - Between and within-breed segregation models
 - Multiple trait models
 - Categorical trait models
 - Non-parametric methods

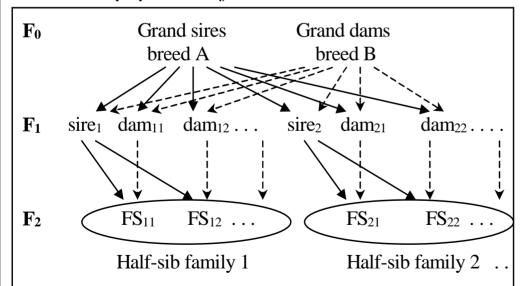
Hypothesis testing procedures



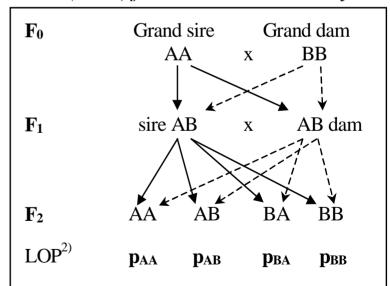


1) Develop and apply methods for combined analysis of the ISU and UIUC populations

Figure 1a. Hierarchical structure of an F_2 resource population from outbred lines¹⁾



1b. Structure and line-of-origin probabilities (LOP) for a breed-cross analysis 1)



Solid lines represent paternal transmission, dashed lines maternal transmission. FS represents full sib family.

²⁾ n_{AB} is the probability that the paternal allele (1st index) originated from breed A and the maternal allele from B

2) Develop strategies for the use of QTL for meat quality in genetic improvement programs





Both breeds had favorable alleles at alternate QTL

- Marker-assisted development of optimal synthetics
- Marker-assisted introgression of multiple QTL

Cont'd

3) Facilitate implementation of results by industry

- Dissemination of information through
 - Scientific articles
 - Industry articles
 - Pig Genome Update Newletter
 - Direct contacts with breeders
- Industry workshop