Use of Genomic Information in Canadian Swine Improvement

Yuefu Liu
Canadian Centre for Swine Improvement Inc.

Molecular Genetics Research Project

In 2002, CCSI launched a research project supported by swine industry and AAFC

- Main objectives:
  - What genes and markers are available?
  - What are the most promising ones for the Canadian swine industry?
  - How best can we use them in selection programs?
- Pramod Mathur; Bill Muir

Mapped Genes and QTLs

- **Candidate genes:**
  - **Meat Quality**: Hal, RN, HFABP, CAST, Calpain, FOS, AFABP, LETR, MC5R, PPAR, GLUT4, ADD1, …
  - **Reproduction**: ESR, PRLP, RBP4, OPN, LIF, …
  - **Carcass and Growth**: IGF2, MCR4, Myostatin, GH, IGF1, HDAC1, HDAC3, …
  - **Disease resistance**: PUT1, PUT2, SLA, NRAMP, K88AB
  - **Coat Color**: c-Kit, MC1R, …
- **QTLs:** A large number of QTLs mapped. For each trait category, QTLs were found almost on all chromosomes.

How to use these genomic information?

- Strategy:
  - Begin with the most useful ones
  - Stepwise priority
- Handle each gene individually
  - Independent culling
  - Combining genomic information with phenotypes in index

Independent culling

- **Selection focuses on the targeted gene**
- **Quick fixation of the favorable allele or quick elimination of undesired alleles**
- **Less total genetic gain of the trait than selection on aggregate EBV (Muir & Stick 1998)**
- **It is often needed**

Where independent culling needed

- **Quick elimination of undesirable genes with low frequency such as Hal, RN, will increase the reputation of a swine population and can facilitate management.**
- **Some genes can explain a large proportion of a trait. Quick fixation of these genes can increase uniformity of animals.**
- **Reputation and uniformity may have significant economic value that is usually not considered in estimating economic weights.**

Genes used and to be used in CCSI

- Selected: Hal, RN
- To be used
  - IGF2 gene for carcass leanness and uniformity
  - HFABP for Intramuscular fat
- A research program for these two genes is proposed as research project by CCSI for Canadian Swine Industry and might be started in October, 2004

IGF2 gene

- In Canada, there are more and more concerns about the extreme leanness of hog carcass. Market survey: About 20% of hog carcasses have lean yield percentage higher than the demanded upper threshold of 63%.
- Really too lean? Maybe not ! The average lean yield in Canada is 60-61% whereas the most desired (best paid) grid is between 61% and 63% (with an average of 62%). The problem actually is due to the low uniformity of carcass leanness .
- Swine Carcass needs to be 2% leaner and more uniform
- IGF2 gene is very promising to meet these requirements

IGF2 gene

- Location: The distal end of SSC2p
- Imprinting gene, only paternal gene expressed
- Phenotypic effect:
- Lare et al (2003): A (G-A) SNP in IGF2 adds 3-4% more lean meat
- A field experiment by Gentec:
  - Hogs more uniform: CV reduces 25%
  - Hogs leaner

Backfat	-2.3 mm
Lean yield %	1.98 %

HFABP gene

- Marbling and intramuscular fat are positive correlated with eating attributes such as tenderness, juiciness and flavor.
- Minimum acceptance threshold for IMF : 2%
- There is a large proportion of pork loin contain less than 2% of IMF. According to a study, 25% pork loin contains less than 2% intramuscular fat.
- HFABP gene is very promising for increasing IMF

HFABP gene

- Effect on IMF
  - Gerben et al. (1999): 0.40%
  - Gerben et al. (2000): 0.36%
  - Meadus (2001): 0.30%
- IMF can be improved by selecting HFABP, independently from back fat thickness.

Combining genomic information and phenotypic data in MAS

CCSI did some work on methods for MAS

- Simulation studies on MAS
- Statistical method for MAS in CCSI
- Developed a mixture approach

Method for MA genetic evaluation

- Combining information on
  - candidate genes
  - markers linked to QTLs
  - phenotypic data
- Non-additive effects
- Computing simplification

Mixture model equations

- Mixture model method for marker-assisted genetic evaluation is developed
- Henderson's mixed model equations (MME) have been extended to a mixed effect mixture model equations (MEMME)
- MEMME is a statistical tool for linear models with uncertain design matrices, It is useful for marker-assisted breeding value estimation

Concluding remarks

- Swine gene mapping has advanced rapidly during the last decade
- Molecular genetics have reached the stage where genomic information should be selectively applied to swine improvement.
- For many decades, animal breeders wish to be able to select economic traits according to genotypes. Molecular genetics is going to make it possible to measure genotypes directly and use the genotypic information for swine improvement.