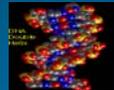# Developments in Molecular Genetics of Swine

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Outline:

- NSIF meeting
  Industry uses of genomic information

- Advancement of molecular genetics research

2003 NSIF meeting

Day 1: Workshop on
   QTL mapping and MAS

Day 2: NSIF meeting
   Industry uses of genomic information

Monsanto MAS program

- Gene and QTL mapping for many generations, used SNPs since F4.

- MAS in 3 nucleus lines, since 2002, routinely
- 78 SNPs and 26 QTLs
- Performance, body composition, feed intake meat quality and health traits
- Software: MA-BLUP

PIC MAS Program

- MAS routinely used in genetic improvement program
- Included 12 genes and 40 QTLs
- Growth, leanness, litter size, reproduction longevity, meat quality, disease resistance, coat color and birth defect

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PIC: QTLs for Scrotal Hernia

PIC: Two QTLs
- SH markers used together with other PICmark™ (BLUP) for selection
- Effectively controlled the hernia condition:

Period	Incidence (%)
Jan 2000 - June 2000	1.87
July 2000 - June 2001	1.80
July 2001 - June 2002	0.58
July 2002 - June 2003	0.75

- Monsanto: 5 chromosome regions for SH

Babcock

- Found 5 microsatellite markers for lean growth
- Recently found 2 SNPs for meat quality
- MAS program now includes disease resistance, tenderness and juiciness, and reproduction

US National Swine Registry

- Introduced Hal and RN gene tests, parentage test, Hampshire purity test

  NSR requirements:
- Jan 2000, HAL gene status documented for all AI sires
- Jan 2001, database of a set markers established for all AI sires, serving as reference for research, parentage test and purity test
- July 2002, DNA samples for all AI sires saved in DNA bank

US National Swine Registry

- NSR is planning to expand the purity test from Hampshire to all breeds
- NSR entered into a research agreement with MARC and NCSU to identify SNPs in Landrace, Yorkshire, Duroc and Hampshire breeds. The objective of the research is to develop DNA chips eventually.

Advancement of molecular genetics research
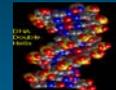
Advancement of gene mapping

- Genetic linkage map: New genes and markers continue to be added: In total, nearly 3000 loci including over 900 genes and nearly 2000 markers.
- Effort to locate causative mutations within candidate genes, e.g. IGF2
- Effort for Fine-scale mapping of QTLs

Advancement in sequence effort

- 120,000 EST sequences in GenBank, 700,000 EST by Sino-Danish Pig Genome Project.
- Very useful for
  - Causative mutation discovery within candidate genes
  - SNP searching and genotyping

Functional Genomics

cDNA Microarray for swine improvement:
- PathoChip for immune response in EU
- QualityPorkGENES, cDNA array for pork quality in EU
- Univ. of Nebraska: gene expression pattern for litter size selection

Microarray

Why use Microarray?
- A very powerful tool
- A DNA arrays can test all useful genes in the genome of an organism

	Routine use	Current limit
Spotted array:	10,000	
Affymetrix genechip	12,000	40,000

SNP

- Can be within genes
- Suitable for high throughput genotyping (Siler 2003: 70,000 genotypes a day), low cost.
- Bridging the gap from QTLs to specific genes
- Genome wide selection