

NSIF Conference and USDA Industry Workshop on QTL Mapping Des Moines, Iowa, Dec. 4-5, 2003

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The 2003 NSIF annual meeting was hosted by the Animal Breeding and Genetics Group of Iowa State University and held in Des Moines, Iowa on December 4 - 5, 2003. The focus for the meeting was on QTL mapping and marker-assisted selection. The first day was a workshop on QTL mapping and marker assisted selection contributed mainly by researchers working on gene mapping from Universities and USDA Meat Animal Research Center, whereas the second day was a session on industry use of marker-assisted selection, in which industry representatives from different companies presented their marker-assisted selection programs and achievements.

Industry Workshop on QTL Mapping and Marker-Assisted Selection

The industry workshop on QTL mapping updated the methods for gene identification and application for economic traits in the swine industry, and presented results from a collaborative Iowa State University – University of Illinois research project on the Detection and Use of QTL for Meat Quality, using the Berkshire, Yorkshire, and Duroc breeds. This research has been sponsored by a USDA-IFAFS grant, along with initial research funding from an industry consortium consisting of the National Pork Producers Council, the Iowa Pork Producers Association, the Iowa Purebred Swine Council, Babcock Swine, Danbred USA, Monsanto Choice Genetics, PIC/Sygen, SeghersNewsham USA, and Shamrock Breeders.

During the workshop, Jack Dekkers from Iowa State University gave several presentations on principles of detecting QTLs and on using marker assisted selection in swine breeding. These presentations presented a simplified overview of these techniques, statistical approaches and QTLs found.

Max Rothschild presented the candidate genes for meat quality traits. His presentation also included an overview of the reasons for different magnitudes of effects of candidate genes in various studies. He illustrated that many of the results obtained from earlier studies were not replicated due to limitation of sample size, random error, poorly used control, failure to detect linkage disequilibrium, failure to attempt study replication, interaction with the genetic background etc.

Jon Beever and Sandra Rodriguez from University of Illinois presented respectively the experimental design for QTL mapping in University of Illinois and the QTLs detected in the gene mapping populations.

In the afternoon, Gary Rohrer, Ron Bates and Rodger Johnson talked about the gene mapping researches and results in US Meat Animal Research Center, Michigan State University and University of Nebraska, respectively.

Industry Use of Marker-Assisted Selection

During the session of Industry Use of Marker-Assisted Selection, six speakers presented their breeding programs of marker-assisted selection, including the presentation from CCSI for Canadian Swine Industry. Many of these companies have been carrying out research in the area for past several years and found very useful results.

Gentec N. V.

Nadine Buys from company Gentec N. V. , Belgium talked about the use of IGF2 gene for marker assisted selection in commercial swine population. An imprinted QTL with major effect on muscle mass and fat deposition was mapped to the IGF2 locus on the distal end of chromosome 2. It explains 15-30% of the variation in muscle mass and 10-20% of the variation in back fat thickness. No influence was found on growth rate, birth weight and meat quality. Recent fine mapping of the QTL at IGF2 led to discovering a causative mutation within the QTL, a single nucleotide polymorphism influencing methylation status and the gene expression of IGF2 in skeleton muscle. The imprinting mechanism is due to methylation of nucleotides in the region. IGF2 mutation has been tested in different breeding programs. Field experiment in USA hogs showed that hogs sired by boars homozygous at IGF2-QTL had 1.98% more lean meat than previous farm average (n=1678). The uniformity of the hogs in leanness was increased. In addition to the previous evidences about this QTL at IGF2 (Nezer et al. 1999 and Jeon et al. 1999), Nadine Buys mentioned two recent publications in Nature (Laere et al. 2003) and in Genetics (Nezer et al. 2003). IGF2 gene was patented by Gentec N. V., and research groups M. George and G. Andersson.

Sygen International

Graham Plastow from Sygen/PIC talked about “Practical application of DNA markers for genetic improvement”. DNA markers have been routinely used in PIC genetic improvement program for selections for coat color, growth and leanness, litter size, reproductive longevity, aspects of meat quality and disease resistance, as well as in quality control and traceability, including 12 genes and 40 markers.

His presentation mainly focused on gene mapping for scrotal hernias. PIC discovered two markers in two different genome regions that have a strong association with scrotal hernia EBV in one of the PIC lines. PIC launched the study because PIC began to receive reports of elevated incidence of hernias among cross-bred progeny of a new parent boar line since 1998. These two markers have been incorporated into the genetic improvement program as part of the EBV calculation for susceptibility to scrotal hernias. The marker information together with implementation of BLUP analysis provides a very robust estimate of susceptibility for hernias according to Graham Plastow’s presentation.

According to Plastow, the combination of the qualitative and molecular approaches has solved the problem to the extent that they no longer see an elevated incidence of hernias among cross-bred progeny of the parent boar line. The combined effects of family selection and scrotal hernia EBV have resulted in a significant reduction in the incidence of scrotal hernias in one of the affected lines.

Monsanto Company

Michael Lohuis talked about the MAS program in Monsanto Company. Monsanto's MAS program carried out routinely in 3 genetic lines. 26 QTLs and 78 SNPs have been used. The traits include performance, body composition, feed intake, meat quality and health traits. Monsanto developed software for marker-assisted genetic evaluation, named as MA-BLUP and have been improving constantly by People in Monsanto and Iowa State University. Right now, they are developing more efficient PDQ algorithm, where PDQ is the probability for a QTL allele decent from parents to progeny. The calculation of this probability is complicated due to incomplete marker information such as missing marker, unknown parental origins of marker alleles and unknown linkage phases among markers. He emphasized the importance of accurate animal identification and complete phenotypic data for routine swine breeding, gene mapping and marker-assisted selection. For that, Monsanto Company developed a quality control (QC) protocols and standard operating procedures (SOP) for animal identification and sample handling. The bar coding and scanning technology have been used in Monsanto Company to minimize error opportunity.

An intercross experiment for QTL discovery and validation has been run for many years in Monsanto. Since F4 generation, only SNPs have been used. Recently, Monsanto discovered 5 loci on two chromosomes responsible for the incidence of scrotal hernias. Ten markers have been identified to flank these 5 regions. Lohuis also talked about strategy of fine-mapping for QTLs using SNP markers. This step-wise fine-mapping strategy is allowed to end up with positional candidate gene mapping.

Babcock Genetics Inc.

J. F. Schneider described the marker-assisted selection used in Babcock Genetics Inc. Babcock began the MAS program with Halothane gene and RN gene in 1992. Five microsatellite markers have been found to be associated with lean growth in their gene mapping project since 1999. Currently, they are looking for useful SNPs for MAS. Two SNP markers for meat quality, named as maker 19 and marker 27, were discovered in Babcock. The traits considered in MAS program of Babcock are disease resistance, tenderness and juiciness, and reproduction.

National Swine Registry

Rick Pfortmiller from National Swine Registry talked about the missions of NSR, implementation of DNA technology and future research plans in NSR. NSR was formed in 1994. It introduced Halothane test, RN gene test, parentage test and Hampshire breed-purity test.

NSR has taken up a number of effective steps in the area of molecular genetics:

- ✚ Effective January 2000, all AI sires are required to document PSS gene status
- ✚ Beginning January 2001, a sire database was established to serve as a bank for research and as a future reference for parentage testing and breed purity testing
- ✚ Since July 1, 2002, NSR required that DNA samples of all sires be banked using a blotter card technology.
- ✚ NSR is planning to expand the breed-purity test from Hampshire to other breeds.

Recently, NSR entered into a research agreement with USDA MARC and North Carolina State University to identify SNPs in Landrace, Yorkshire, Duroc and Hampshire breeds of pigs. This SNP searching effort will eventually lead to developing “DNA chips” for high throughput genotyping. NSR aims to build a world nucleus foundation in USA by using the advancement and latest innovation of molecular genetics.

Genetics of pork quality

In the afternoon of the session of Industry Use of Marker-Assisted Selection, a graduate student of Iowa State University, D. W. Newcom, who received the NSIF award, presented his research on genetics of pork quality including intramuscular fat measurement on living animals using ultrasound machine (Aloka 500V). The study also included genetic evaluation and selection. The study concludes that IMF can be estimated using real-time ultrasound technology. After one generation of selection the average EBV of selection line was 0.50% greater than the control line.

Genetic improvement of immune response

Bonnie Mallard from University of Guelph made a special presentation about genetic improvement of immune response and disease resistance.

CCSI's Contribution to 2003 NSIF Meeting

Molecular Genetics

Pramod Mathur gave a presentation on “Marker-assisted selection for the Canadian swine industry”. The related full paper by Pramod Mathur and Yuefu Liu was included in 2003 NSIF proceedings.

He first talked about the components of Canadian Swine Industry, and the current status and achievements of Canadian swine genetics. He summarized the tools used for genetic evaluation and selection in Canadian swine industry and rapid genetic gain in the past five years that provided a genetic base for solid reputations of the Canadian Swine Industry world wide for superior quality and health status of Canadian swine.

Then, he presented the results from the project supported by CARD program of AAFC. This is a research initiative to evaluate and incorporate the important discoveries into industry breeding programs. This includes evaluating the current advancements in molecular genetics and the economic benefits from their application to the swine

industry, and developing a strategy and methods for integrating molecular genetic advancement into Canadian swine breeding programs.

The project will open up opportunities for further research and innovation in this area by providing a strategic plan for swine molecular genetic research in Canada. He presented the promising genes identified for MAS application and discussed how to use these promising genes in swine breeding. The strategy of stepwise priorities for MAS application of identified genes and QTLs was introduced.

He talked about the identified areas where DNA information is especially useful. These are the traits not measurable on living animals, such as meat quality traits; traits of low heritability, such as sow reproduction; sex-limited traits; disease resistance and early stage selection. For most of candidate genes (or SNPs) and QTLs, the best strategy is to evaluate them together with phenotypic information under optimal selection principle.

The method to incorporate candidate genes and QTLs into a current genetic evaluation system was also presented. The breeding objective is to maximize the accumulative genetic response for a given period to avoid long-term disadvantage of marker-assisted selection. To keep the current framework of genetic evaluation as much as possible and incorporate molecular information into the current system, a simplified genetic model will be proposed and eventually incorporated into current evaluation system.

Genetic defects

Yuefu Liu also presented a poster entitled “Are ridgling and scrotal rupture caused by abnormal size of inguinal canal”, which focused on the genetic causation of the two birth defects. This issue has also received increasing attention from Sygen (PIC) and Monsanto Company who have also invested into search for molecular markers that were reported at the NSIF meeting as well.

Networking

NSIF

Gordon Jones, President of NSIF asked Pramod to participate on their board meeting and thanked us for the contributions from CCSI. Pramod also took an opportunity to extend the possibility of closer co-operation with CCSI and member organizations. This was received very positively. The NSIF meeting in 2005 will be hosted by CCSI in Canada.

Iowa State University

We also had very positive response from Dr. Ken Stalder, the newly elected president of NSIF and from Dr. Jack Dekkers and Dr. Max Rothschild from Iowa state university for further co-operation in various research areas. Pramod has been invited for a seminar on Connectedness at the Iowa State University and to talk about CCSI’s research activities to the faculty members next year.

Yuefu discussed with Jack Dekkers about the issue of long-term disadvantage by using major genes, reported first by John Gibson. The discussion comes to the conclusion that the disadvantage can be remedied to some extent by using BLUP EBV for polygenic

effects. The constant weight over generation can not be very different from variable weight. It is, therefore, acceptable.

Max Rothschild's research group patented 5 genes, RSR, PRLR, RBP4, MC4R and Myostatin. He suggested to Yuefu that his laboratory can provide help in setting up the methods for these tests and that CCSI can be permitted to use the patented genes.

Sygen/PIC

Pramod had a meeting with Marnie Mellencamp, Sygen to discuss about the possibilities of research collaboration in the area of disease resistance, Pramod also had brief conversation with Graham Plastow, Sygen International, regarding the use of candidate genes and markers developed by Sygen (PIC) for the Canadian Swine Industry. Graham indicated the possibility making them available for the Canadian swine industry and that the details could be discussed.

Gentec N. V.

Nadine Buys from Gentec N. V. expressed interest in licensing the use of IGF2 gene for the Canadian swine industry through CCSI. She will send more details for follow up

IPG, Holland

Pramod met with Egbert Knol from the Institute of Pig Genetics (IPG) in Holland. Their institute works closely with Dalland in Holland and ITP in France. His group is interested in the estimation of connectedness. There might also be more opportunities for collaboration in areas of common interest to IPG and CCSI.