

10-2008

Pork production improvement expected from the use of new genetic markers

Ken Stalder

Iowa State University, stalder@iastate.edu

Max Rothschild

Iowa State University, mfrothsc@iastate.edu

Follow this and additional works at: https://lib.dr.iastate.edu/ans_pubs

 Part of the [Agriculture Commons](#), [Animal Sciences Commons](#), and the [Genetics and Genomics Commons](#)

The complete bibliographic information for this item can be found at https://lib.dr.iastate.edu/ans_pubs/397. For information on how to cite this item, please visit <http://lib.dr.iastate.edu/howtocite.html>.

This Article is brought to you for free and open access by the Animal Science at Iowa State University Digital Repository. It has been accepted for inclusion in Animal Science Publications by an authorized administrator of Iowa State University Digital Repository. For more information, please contact digirep@iastate.edu.

Pork production improvement expected from the use of new genetic markers

Abstract

Breeders have been using gene markers since the 1990s to remove genes known to negatively impact pork production. Genes like the porcine stress syndrome (HAL) and the NAPOLE gene (RN-) have been identified and are commonly selected against in most breeding herds so the deleterious genes are removed from their herds. In this manner commercial pork producers do not have to address these genes in their breeding herds because their genetic supplier has already managed the genes for them.

Disciplines

Agriculture | Animal Sciences | Genetics and Genomics

Comments

This article is published as Stalder, K., and M. Rothschild. 2008. Pork production improvement expected from the use of new markers. *Western Hog Journal, Alberta Pork*, Edmonton, Alberta, Canada, 30(2):33-35. Posted with permission.



Pork production improvement expected from the use of new genetic markers

By Ken Stalder, Associate Professor and Extension Swine Specialist & Max Rothschild, C.F. Curtis Distinguished Professor Department of Animal Science, Iowa State University, Ames, IA 50011-3150

Background

Breeders have been using gene markers since the 1990s to remove genes known to negatively impact pork production. Genes like the porcine stress syndrome (HAL) and the NAPOLE gene (RN-) have been identified and are commonly selected against in most breeding herds so the deleterious genes are removed from their herds. In this manner commercial pork producers do not have to address these genes in their breeding herds because their genetic supplier has already managed the genes for them.

Today, swine breeders have new gene marker tools commercially available to them at relatively low costs. These new gene markers are for traits that include feed efficiency, growth, backfat and pork quality and litter size.

Two companies, DNA LandMarks, a BASF Plant Sciences company that performs genetic testing located in Quebec, Canada and GeneSeek Inc., a molecular biology company in the US, have purchased the licensing agreements from the researchers who originally developed them. Included in the group of available tests are markers developed in Max Rothschild's lab at Iowa State University, which is responsible for developing tests for litter size, pork quality and feed efficiency, backfat and growth rate. A breeder wanting to screen animals can simply submit a blood or tissue sample (whole blood, blood blotter cards, ear notches, docked tails, or tissue obtained through a new ear tagging system from Typifix are all examples of sources of DNA that can be used to run these tests) and have the marker genotypes determined on as many animals as they desire. The costs for these tests are relatively inexpensive and as technology improves it is likely that more and more tests can be offered and prices for these tests typically decline.

As an example, we discuss the commercially available tests from DNA Landmarks (http://www.dnalandmarks.com/english/livestock_overview.html)

Markers for growth rate, feed efficiency, feed intake, and backfat

Three markers associated with growth rate and feed efficiency are available. These markers are MC4R, HMGA1, and CCKAR. Briefly, the MC4R locus impacts growth and leanness in the pig. The name MC4R is taken from the gene's name Melanocortin-4 receptor. There are two alleles or variants for this marker, A and G. The A allele is associated with fast growth while the G variant is associated with lean and efficient growth. The producer and breeder can decide if they wish to choose the "fast" growth form of the gene or the "lean/efficient growth" form of the gene. Pigs that are homozygous for the fast growth alleles (i.e. AA) have been shown to reach market weight 3 days sooner compared to pigs that are homozygous for the lean allele. If producers chose to select for the MC4R lean alleles (i.e. GG) pigs will have 8% less backfat and eat significantly less feed (improving feed efficiency). In Table 1 research results are shown indicating the effects of MC4R in two different populations of pigs. These results have been well validated and are effective in all breeds except Hampshire.

Table 1: Example effects of the MC4R molecular marker in pigs.

Genotype	Number of Pigs	Backfat (mm)	Shoulder Fat (mm)	Loin Depth (mm)	Average Daily Gain (g/d)	Feed Intake (kg/d)
GG vs. AA						
2 Commercial genotypes ^a	679	-1.3	-1.4	+1.4	-26.0	-0.15
P value		<.05	<.05	<.10	<.10	<.05
GG vs. AA						
Pure Line Data	2,366	-1.1	n/d	n/d	-28.0	-0.17
P value		<.0001			<.0001	<.01

continued on page 34

TOLL FREE: 1 888 553 4844

count

your money saved using AI

with

Magnum Force



www.magnumpress.com

The second marker available is HMGA1. The abbreviation HMGA1 is taken from the gene's name, High-mobility group A. This gene marker is highly associated with backfat and lean growth. HMGA1 variants are consistently associated with fat deposition, growth rate, and lean mass percentage traits across several pig populations. With this particular marker, producers need to remember that the T allele is the beneficial allele and the one that should be selected for to reduce backfat and thereby improve lean percentage. Producers can test and select animals which are likely to be leaner and produce offspring that are leaner. Thus, selection of the beneficial alleles will reduce backfat and improve percentage lean in terminal market animals that are from breeders that have incorporated the beneficial alleles into their breeding program. Improvement in feed efficiency should also occur when selecting for the beneficial allele of this marker because a reduction in the amount of fat deposited reduces the

amount of feed needed to add weight to the animal.

The last gene marker in this group is CCKAR. CCKAR is an abbreviation for cholecystokinin type A receptor. This marker is associated with the control of feed intake, hunger control, and obesity. There are two genetic alleles or variants, G and A, for this marker. In this case the G allele is dominant to the A allele. Pigs that have at least one copy of the G allele (i.e. can be GG or GA) for this marker have, on average, about 5% higher daily feed intake, 3% higher daily gain, and 3% fewer days to reach market weight, when compared to homozygotes (i.e. AA) for the A allele.

Markers for meat quality

Production of high quality pork to meet both domestic and export market demand has been a selection goal of most swine breeders in recent years. Many niche market programs are in place to meet white tablecloth and export demand for quality pork. In the past several years, markers have been identified which improve pork quality.

Two genetic marker tests that impact pork quality have been licensed to DNA Landmarks from ISU. The two markers associated with meat quality offered in this package include PRKAG3 and CAST.

The PRKAG3 is an abbreviation for protein kinase, AMP activated, gamma 3 subunit. This marker is associated with muscle glycogen content and meat quality. Producers and breeders can select for animals that have the higher pH and better meat color from of the gene. Other variations of this gene have been referred to as the Rendement Napole (RN) gene marker. The RN gene marker has been shown to cause low ultimate pH and reduced water holding capacity in pork. This gene marker has been largely observed in pure bred Hampshire or crossbred animals involving Hampshire. Hence, this gene was also known as the Hampshire effect. Another variation of this gene has been identified and is what DNA Landmarks is offering in the PRKAG3 gene, which determines the presence of the 1991le, A-nucleotide variant, which is the one that is preferred.

This marker is also associated with lower glycogen, higher ultimate pH (about 0.1) and favorable color in loin and ham

tissues. Animals possessing this beneficial genotype have a pH of nearly 0.1 higher in their loin and ham samples than those that are homozygous for the non-beneficial allele. Thus, producers should select animals that have at least one copy of the A allele with the ultimate goal of having the genotype of all animals be AA. The effects of this marker have been observed in all major pig breeds and this test would be very useful in breeds like the Berkshire and Duroc to remove the unwanted forms of the gene.

The second meat quality genetic marker is called CAST, which is an abbreviation for Calpastatin. Calpastatin is responsible for inhibiting enzymes called proteases that affect meat tenderness after harvest. Two variants have been identified within the CAST gene area. This gene impacts firmness, juiciness, Instron force, cooking loss, chewiness, and tenderness scores. Breeders should select for the favorable CAST A allele.

ESR marker for litter size

Increasing litter size is one way to improve production efficiency of a pork operation using fewer sows and less feed. Selection for increased litter size is responsible for the large gains breeders have made in this trait in the last 20 years.

One gene called ESR, the Estrogen Receptor, is associated with litter size in pigs and has been used for many years by a large pig breeding company. It was first discovered in Meishan pigs (Figure 1). Estrogen is a key female hormone that plays a key role in many reproductive functions in the sow including embryo survival, fetal development, fertility, maintenance of fertility, and secondary sexual characteristics. Based on all of the fertility traits that have been shown to be impacted by estrogen, it is easy to believe that this gene for the hormone receptor is associated with litter size in swine. Animals that carry one copy of the favorable variation of the gene will, on average, have 0.4 more pigs per litter. Sows that are homozygotes (2 copies) for this marker would on average have 0.8 pigs per litter. This test has been shown to be effective in breeds or lines involving Large White or Yorkshire breeds and crossbred sows that have this breed involved in them.

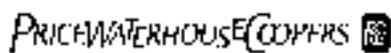
**GREAT PLAINS FARMS LTD.
- IN INTERIM RECEIVERSHIP
("GREAT PLAINS FARMS")**

On December 20, 2007, PrairieProduceCoop, Inc. was appointed as Interim Receiver of Great Plains Farms by the Court of Queen's Bench of Alberta. In its capacity as Interim Receiver of Great Plains Farms, PrairieProduceCoop, Inc. has established a Bid Process to sell the land, buildings and equipment which was used in the hog production operations.

The assets include 158.87 acres of land, three hog barns built in 2002 which have a 2,000 head cow time capacity per barn (6,000 total head) and equipment generally associated with a finishing hog operation. The barns are constructed with concrete panel construction with a metal clad roof on wood frame truss rafters. As well there is an office building with furniture and fixtures.

Bids are to be submitted no later than 3:00 pm Calgary time Friday, October 24, 2008.

For further information including a copy of the Court Order, an Information Memorandum, Bid Letter, Terms and Conditions, and details for arranging site visits please visit our website at www.pwc.com/can-pradplainsfarms or telephone Donald J. Roberts, Senior Vice President at 403-648-7317 for further information.



Where do breeders begin when considering the use of the molecular markers?

Our advice to producers is to begin testing their herd boars and/or boars in the boar studs they use to make pure matings. For boars used in the development of terminal sire lines, the best approach would be to determine the status of all herd boars and boars in the boar stud for the markers impacting growth, backfat, and feed efficiency including MC4R, HMGA1 and CCKAR. Additionally, the same approach could be used to examine the status of herd boars or boars in the boar stud for the markers used to improve meat quality including PRKAG3 and CAST. Similarly, all boars used to make maternal purebred matings should be tested using the ESR marker used to improve litter size.

Once the results are obtained, breeders can determine what the frequency of the alleles, both good and bad, are for the breeds or lines of sires in the boar stud. This information can be used to determine if further testing of females from each breed or line is necessary. Breeders can determine which alleles they would like to fix or be sure that all animals have two copies of in a given breed or line of animals. Selection of the preferred animals and culling of those without the desirable alleles can then be done.

How can the marker information be used to develop breeding programs?

Many of these markers or genes are best used in combination. Use of all five, MC4R, PRKAG3, CAST, CCKAR and HMGA1, would be beneficial for overall terminal line development to improve growth, leanness and meat quality. Using MC4R (growth allele) and HMGA1 could be used for to develop a line that grows fast and has some backfat improvement. Similarly, selecting animals that have the MC4R (lean allele) and HMGA1 could be used together for make even faster progress in improving leanness and efficiency in breeding stock. The PRKAG3 and CAST could be used in combination to improve meat quality. Furthermore, some breeders may choose to select animals for all of the growth and meat quality markers to develop lines of pure breed animals that excel in the production of lean, high quality pork. Maternal lines should be developed that have the favorable alleles for the ESR gene marker. This will enhance the chances of the lines having large litters, which are extremely important to production efficiency and overall profitability of any pork operation.

Breeders and producers should work to develop the best multi-gene combination for their lines that meets customer needs for both maternal and terminal lines.

Marker test costs

The cost for the marker tests varies depending on how many tests are done. Check the DNA Landmarks web site for more information on the market tests and cost information http://www.dnalandmarks.com/english/livestock_overview.html.

While testing is not inexpensive, especially if attempting whole herd tests, useful information can be obtained by testing sub populations of animals at a much lower cost. This allows a strategy to be put in place before entire whole herd testing programs are required to determine status for all of the markers available.

Combined or used in thoughtful combinations these gene markers offer real benefits for future genetic and economic improvement for swine breeders and commercial pork producers.

Figure 1. The Meishan breed of pigs which originated in China and is known for their outstanding litter size, longevity and other reproductive traits. This breed has made significant contributions to the discovery of molecular markers for a variety of economically important reproduction traits in swine.



WHL

simplify
your day to day operations

with

Magnum Force

TOLL FREE: 1 888 553 4844



www.msg.com