



Swine Innovation Porc

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Building Better Bacon: Genomics Tools for Pork Quality

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Even better bacon? Some might ask how that is even possible for something so good. Well, believe it or not, recent developments in genomics have opened the door to this possibility and much more. Application of new genomics tools will be especially important for traits like pork quality which are difficult or expensive to measure and which can't be measured directly on animals that will be kept for breeding. This paper will focus on new genomics tools to improve the prediction of pork quality, and I've used bacon to get your attention, but it is important to be aware that the same technology can and will be applied to predict any heritable trait. This will include other pork quality traits, carcass quality, feed efficiency, sow productivity and swine health to name a few.



Application of Genomics for Swine Genetic Improvement

Classical genetic evaluation approaches have had huge impact on efficiency of pork production and on carcass quality. Although there are very sophisticated methods for classical genetic evaluation, the approach is essentially based on the principle of "breed the best and cull the rest". If you can measure the trait on the selection candidates and the trait is heritable, you can make genetic progress. This has been very effective for growth rate, carcass lean and litter size along with several other traits which can be measured directly or are correlated with measurable traits. Genomics can help with all of these traits by increasing accuracy and by providing relatively accurate evaluations earlier in life. This is particularly valuable for sow productivity traits which tend to have low heritability and which are only expressed in the mature females. It could also be very useful for feed efficiency due to the economic importance of feed cost and the difficulty to measure feed intake on the individual animal. However, where genomics will be most valuable for pork production is for traits which we know are influenced by genetic variability but for which we haven't been able to evaluate breeding animals. Pork quality falls into this category and is currently the focus of significant genomics research here in Canada and globally.

Genomics and Pork Quality

Pork quality traits tend to be moderately to highly heritable. However, in most cases the traits of interest can only be measured on the carcass. This is difficult, expensive and the animals being measured are no longer available for breeding. As a result, there has been very limited genetic improvement for pork quality traits. Genomic evaluations, however, will allow breeding stock suppliers to evaluate these traits from a simple DNA test as soon as an animal is born. The early research is showing that these evaluations can be as accurate as evaluations based on carcass measurements. In other words, with genomics, the best breeding animals for pork quality traits of interest can be identified shortly after birth. Genomics provides the tools to "breed the best and cull the rest" for pork quality traits. Therefore, if you want pork with a certain level of marbling, genomics will tell you which boars to use. If you want pork with a certain colour, genomics will tell you which boars to use. If you want a certain level of firmness, lower drip loss or more tenderness, genomics will be your guide. And, most importantly for this paper, if you want better bacon, genomics will tell you which boars to use.

What is Required for Genomic Evaluations?

A genomic evaluation is an estimation of the contribution of all the genes across the entire genome of an individual to the expression of a specific trait. In pigs we have available a DNA test for over 60,000 genetic markers known as Single Nucleotide Polymorphisms, or SNPs (60K SNP panel). Each of these markers or SNPs has two possible variants. If pigs with one of the genetic variants for a particular SNP tend to be different for a trait of interest than pigs with the other genetic type, this marker will contribute to

Genetic Sources of Variability in Pork Production

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North American Consumer Want Fat They Can't See

<http://www.prairieswine.com/north-american-consumers-want-fat-they-cant-see/>

Development of New Genomic Tools to Improve Meat Quality Traits and Production Efficiency in Pigs

<http://www.prairieswine.com/poster-development-of-new-genomic-tools-to-improve-meat-quality-traits-and-production-efficiency-in-pigs/>



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the genomic evaluation for the trait. To do a genomic evaluation, each of the 60,000 SNPs is evaluated to see if, and by how much, pigs with one of the genetic types differ from pigs with the other genetic type. This gives an estimate for each marker which can be used to evaluate new pigs based on their own DNA test results. To estimate the effect of each of the 60,000 markers, a large sample of pigs must be measured for the trait and genotyped



with the 60K SNP panel. From this historical data, it can then be determined which markers are related to the trait and how much each marker contributes to the evaluation of that trait. The larger the sample of pigs, the more accurate the marker estimates will be and therefore the more accurate the genomic evaluations on young selection candidates. This is a relatively expensive process because of the need for large numbers of animals and the costs for both measuring pork quality traits and genotyping. Note that the measurement of traits is more of a limitation since an animal only has to be genotyped once no matter how many traits are measured. Collaboration among groups in both research and industry is important in order to accumulate large numbers of historical meat quality data. It is also critical to collaborate on use of standardized procedures for the measurement of meat quality data so that data from different sources is comparable.

Development of New Genomic Tools to Improve Meat Quality Traits

The Canadian Centre for Swine Improvement (CCSI) has led a three year genomics project which was initiated in 2010 in collaboration with Centre de développement du porc du Québec (CDPQ), researchers at Agriculture and Agri-Food Canada and researchers at the University of Guelph. The objective was to develop new genomic tools to improve pork quality traits and production efficiency in pigs. The project investigated the development of genomics tools using porcine 60K SNP panel genotypes along with extensive phenotypic measurements on about 700 purebred Duroc, Yorkshire and Landrace pigs. These pigs were submitted by breeding stock suppliers across Canada to a central test station operated by the CDPQ at Deschambault, Quebec. About 700 parents and littermates of the tested pigs were also genotyped to explore the efficiency of genomic evaluation on traits routinely evaluated at CCSI. At the end of test, all pigs were slaughtered and fresh meat quality was assessed for standard quality measurements such as pH, colour, marbling and drip loss, as well as meat tenderness, chemical composition, enzymatic activities and muscle fibre type determination. The project estimated marker effects for meat quality traits as well as other traits related to production efficiency and carcass quality. The project has positioned the industry to produce genomic evaluations for various meat quality and production traits on young pigs such as candidate boars for artificial insemination. The results are very encouraging from a relatively small dataset of 700 pigs and will only improve as more pigs are genotyped and evaluated for traits of interest. The project also established a database which can be combined with more data in future to increase the accuracy of genomic evaluations and for further genomics research.

Conclusions

Genomics tools are now available that can help make our bacon even better! More generally, genomics provides new tools for predicting the genetic influence on pork quality and any other heritable trait. This is especially valuable for traits that are difficult to improve by conventional genetic evaluation approaches, including pork quality traits. Recently completed genomics research has provided estimates for 60,000 genetic markers for several pork quality and production efficiency traits which can be used by the Canadian industry to apply genomic evaluations on young selection candidates to improve efficiency as well as differentiate pork products.

One of the challenges for application of genomics is the relatively expensive price of the 60K SNP panel (currently about \$100 per animal). However, a 10K SNP panel has recently become available with a price of about \$40 per animal. Using information from animals previously genotyped with the 60K panel, it is possible to use some statistical procedures to genotype with the lower cost 10K SNP panel and impute the other 50K SNPs. This estimation of the 60K SNP panel from a 10K panel can have a similar accuracy as the 60K SNP panel for genomic evaluation. Application of genomic evaluations routinely by breeding stock suppliers will contribute more data to monitor the effectiveness of genomic evaluations and increase the accuracy of future evaluations. Additional research trials, particularly for more difficult traits such as pork quality will be required periodically to increase the accuracy, monitor progress and evaluate more traits, especially bacon quality!

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