



Improving Animal Health with Genomics

Until only a few decades ago, it would not be uncommon for pig farmers to unload a shipment of live hogs and find within it a dead animal. The cause was Porcine Stress Syndrome (PSS), a genetic disorder that affected the ability of the pigs to regulate calcium levels in their muscles. When stressed by hot weather, exercise, confinement or any number of possible scenarios, affected pigs would breathe rapidly, shake, become overheated and within 20 minutes, collapse into a rigid death pose. If they did survive long enough to make it to market, their meat was pale, soft and dry, making it unattractive to consumers¹. Researchers understood that the disorder was genetic, but determining which animals had it was expensive, and determining which were merely carriers - that is, they didn't have the disorder, but could pass it on to their offspring - was almost impossible.



Genetic disorders like PSS are just one example of the ways in which animal health is affected by genetics. credit Thomas Wanhoff, via [Flickr](#)

In 1991, a team of researchers from the University of Toronto and the University of Guelph determined the exact location of the faulty gene that causes PSS². They developed a quick, simple and accurate DNA test that could tell farmers which pigs were susceptible to the disorder, which simply carried the gene, and which pigs were defect-free. This test is now used worldwide, and as a result, PSS is rarely seen.

Genes can also contribute to an animal's susceptibility or resistance to infectious diseases carried by viruses and bacteria. Infectious disease has always had a tremendous economic impact for pork producers. *E. coli* for example brings with it sickness and death. A particular strain, *E. coli* F18, could cause 40% mortality in swine herds infected for the first time^A but it was noticed that some pigs seemed to have a built-in defense. In 1999, researchers identified that protected pigs carried a version of a gene that made their gut harder for the *E. coli* to colonize³. Now *E. coli* F18 resistant strains of pig are commercially available.

Of course, farmers work hard to ensure their production facilities are well designed and clean, and they can use antibiotics to treat sick animals. But even the cleanest environment can't prevent genetic disorders like PSS, and the overuse of antibiotics can produce microbes resistant to the drugs, leading to so-called "superbugs." When all is said and done, one of the best strategies for ensuring animal health is also the one of the oldest: selecting the healthiest and most resilient animals for breeding the next generation.



What's a genome?

An organism's genome is the 'blueprint of life,' the complete set of instructions for making the molecules, cells and tissues that control how an animal can perform throughout its life. Every cell in the body contains the complete genome, encoded in the form of DNA. DNA is a long chain molecule made by combining four possible types of building blocks: organic molecules named adenine (A), cytosine (C), guanine (G) and thymine (T). Thus, the genome can be thought of as a book written in a code that contains four possible letters: A, C, G and T. The study of genomics has enabled scientists to learn some of the words in this code, for example, sequences that describe how to make a particular protein molecule are called genes. These genes influence observed traits, everything from eye and coat colour to disease resistance. Mammals have two copies of every gene; one from each parent. These genes could be the same or different, and some versions could confer improved traits.



Today, genomics allows us to quickly and easily sequence DNA from animals in order to help understand its impact on observed traits. While genomic technology can be applied to change the genome of an organism - including inserting genes from one species into another - this approach is used primarily in plants, not livestock. Instead, genomics helps livestock breeders and researchers better understand the causes of various diseases and design selective breeding programs to ensure that their animals can resist or eliminate the causes of sickness. A healthy herd provides stability for farmers, while making higher quality produce available to consumers.

How it works

A given animal's DNA is more than 99 percent identical to every other member of the same species; it's the tiny differences that all together can help determine why one animal performs better than another. One type of difference is called a single nucleotide polymorphism, or SNP (pronounced 'snip'). A SNP is a location in the genome where some members of the population have one letter (e.g. an A) and other members have a different letter (e.g. a G). By looking at a number of different SNPs and determining which version of each an animal has, it's possible to map out a 'SNP profile' for that particular animal; the process is called genotyping.

Once a SNP profile is created for an animal, it can be matched with information on how that animal performs, including whether or not it is resistant or tolerant to a particular disease. This correlated information can then be fed into a database containing both genetic and performance information on hundreds or thousands of animals. Computer programs can mine this vast amount of data to identify which SNP profiles are associated with top performers. Breeders can then select these animals or ones with similar SNP profiles for breeding the next generation. If the programs are sophisticated enough, they can even identify which genetic differences - i.e. which SNPs - have the strongest influence on particular traits such as disease resistance.

While a complete genome may contain billions of SNPs, in practice it's only necessary to track a few of these to identify beneficial differences. The technology that makes this possible is the SNP chip which provides a simple, fast and inexpensive way to test a DNA sample from the animal - a few hair follicles would be enough - against many possible SNPs in order to create a SNP profile/genotype that can be correlated to real-life traits. Such chips began to become available in the early 2000s, first for dozens of SNPs, then for hundreds. In 2009, a consortium that included the American biotech company Illumina, and researchers from Britain, the US, and The Netherlands created the Illumina PorcineSNP60K BeadChip⁴ which tracks 64,232 SNPs in the

The fight against PRRS

First reported in 1987 in North Carolina, Iowa and Minnesota, porcine respiratory and reproductive syndrome (PRRS) was originally known as "mystery swine disease." PRRS is spread by a virus with a particular fondness for lung cells. In piglets, it causes difficulty breathing which can lead to a lack of oxygen, giving rise to its other nickname, "blue-ear pig disease." In adult pigs, it is less likely to be fatal, but can still cause difficulties with reproduction, including spontaneous late-term abortions. A 2013 study estimated that if it weren't for PRRS, 8 million more pigs [per year] would survive in the US alone⁵. A major outbreak in China in 2006 resulted in 2.1 million infected pigs, 400,000 of which died^{6,7}.

Vaccines exist for PRRS, however just like the flu virus that affects humans each winter, PRRS mutates rapidly and often moves faster than vaccine formulations⁸. This makes it difficult and very costly to vaccinate the whole herd. A group known as the PRRS Host Genetics Consortium has used SNP chips to test 15 groups of 200 pigs for genetic differences that allow them to resist the disease. Their work has identified a region of the genome on chromosome 4 (pigs' DNA is organized into 19 chromosomes; humans have 23) that do appear to have genes associated with resistance. By mapping these genes, they create an opportunity to produce pigs with reduced susceptibility to PRRS⁹.



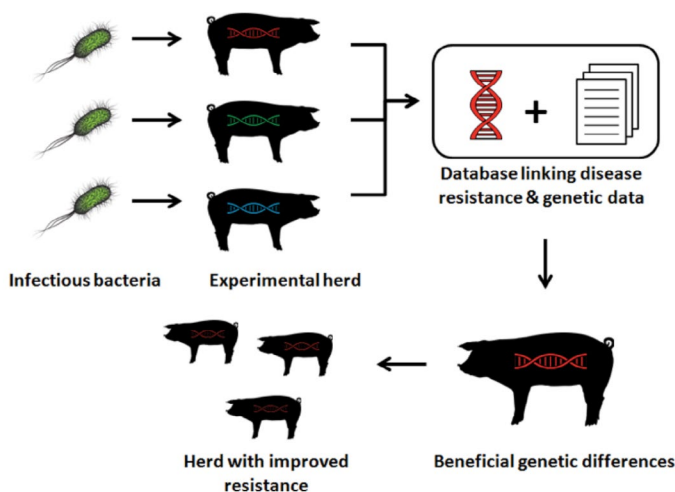
Porcine Respiratory and Reproductive Syndrome (PRRS) is a viral infection that makes it hard for pigs to breathe reducing the amount of oxygen in their blood and turning their ears blue. (Photo credit: [New Zealand Pork](#))

pig genome. It's also possible (but more costly) to sequence the complete genome of an animal. However, given that most SNPs will not be associated with beneficial traits, this level of detail isn't usually required in tackling animal diseases.

Benefits

Controlled experiments

Unlike other traits that farmers might want to optimize (e.g. feed intake) disease resistance is something that can't easily be tracked for every animal. Instead, a 'training set' is used. The training set is a group of experimental animals that can be profiled using a SNP chip and then exposed to a given disease to see which ones have the genetic profiles that confer resistance. Deliberately exposing animals to a disease may seem harsh, but it's the only way to root out the genetic basis of resistance that could help protect future herds.



By mapping the genomes - that is, creating SNP profiles - for animals in an experimental herd, then exposing them to a given infection, researchers can identify which genetic differences are associated with disease resistance. They can then ensure those beneficial genetics are passed on to the next generation.

Fewer interventions (antibiotics, vaccines, castration)

If farmers can use genomics to select and breed animals with stronger disease tolerance, it means they will have to use fewer interventions over the animal's lifetime. According to the US Food and Drug Administration, in 2010 more than 13 million kilograms of antibiotics were sold for use in agriculture¹⁰. Reducing this amount would not only save costs for farmers but could also reduce the selection pressure on disease agents - e.g. bacteria - to develop resistance.

There are other interventions that can be avoided; a good example is castration to avoid 'boar taint.' Upon reaching sexual maturity, a small percentage of male pigs

begin to accumulate foul-smelling compounds - called skatole and androstenone - in their fat; this gives their meat a bad taste and odour. A common way to eliminate this problem is to castrate male pigs when they are a few weeks old. Researchers at the University of Guelph are using SNP profiles to determine which genetic differences are responsible for boar taint in the small number of animals that have it¹¹. By selecting for pigs that don't develop boar taint, the requirement for castration will decrease, reducing stress on the animals. This improves both animal welfare but also lean growth performance, so it is 'win-win'.

Faster disease detection

Examining the genomes of livestock can help them develop resistance, but improvements can also be made by looking at the genomes of the disease-causing organisms themselves - viruses and bacteria. For example, tests have been developed that can test for a DNA sequence from a specific strain of virus or bacteria in a sample of blood from an animal, allowing animal health researchers to track the spread of various strains of PRRS or other infectious diseases.

Researchers in Canadian universities are looking into ways to use genomics to increase the efficiency of diagnostics. DNA microarrays are tools that can quickly test a single sample for the presence of multiple sequences from various bacterial or viral strains. Rather than just confirming or denying the presence of a particular strain, they could test against many strains and quickly identify the one that is present, allowing farmers and veterinarians to choose the best antibiotics or treatment. Researchers from the Canadian Food Inspection Agency are looking to develop such a tool¹².

Climate-resilient animals

Researchers believe genomics could also help farm animals deal more effectively with environmental factors. In dairy cattle for example, heat stress caused by hot and humid weather compromises milk production, fertility, and the health of cows. Some cows seem better able to deal with it than others. Last year, American researchers found SNPs that were linked to the physiological response of cows to heat stress¹³. This could be useful to breeders who could select cattle to produce milk in hot climatic conditions that are a struggle for many herds.

In an effort to find animals who can cope with a hot desert climate, American researchers teamed up with Egyptian scientists to study sheep and goats. In March 2014, they announced that they had found regions in both sheep and goat genomes that control responses to heat stress and drought tolerance¹⁴.



Genes aren't everything, but with the tools of genomics, researchers can discover new ways to improve animal health. (Photo credit: Mark Forman, via HAAP Media Ltd.)

Conclusion

Genes aren't everything; environment, nutrition, and treatment of disease are still important. Nevertheless, by breeding livestock that is more resistant to infectious disease, eliminating genetic disorders like PSS, and reducing the need for interventions, genomics can not only keep animals healthy but save farmers money while ensuring that the best products are available to consumers.

About

Science Media Centre of Canada

The Science Media Centre of Canada is an independent, not-for-profit organization that exists to raise the level of public discourse on science in Canada by helping journalists access the experts and evidence-based research they need in order to cover science in the news.

The SMCC is supported by our Gold Patron, MaRS Discovery District and Engineers Canada, 132 Charter Members and ongoing support from our patron organizations. Backgrounder prepared for Genome Alberta, May 2014.



GenomeAlberta

*For more information please write to us at:
info@sciencemedia.ca*



Bibliography

- [1] Stalder, K., and Conatser, G. (1999?) Porcine Stress Syndrome and Its Effects on Maternal, Feedlot and Carcass Quantitative and Qualitative Traits. Agricultural Extension Service, University of Tennessee. URL: <https://utextension.tennessee.edu/publications/Documents/PB1606.pdf>
- [2] Fujii, J. et al. (1991). Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia. *Science* 253(5018): 448-451. URL: <http://www.ncbi.nlm.nih.gov/pubmed/1862346>
- [A] Van der Steen, H. A. M., Prall, G. F. W., & Plastow, G. S. (2005). Application of genomics to the pork industry. *Journal of animal science*, 83(13 suppl), E1-E8. URL: http://www.journalofanimalscience.org/content/83/13_suppl/E1.full.pdf+html
- [3] Meijerink, E., S. Neuenschwander, R. Fries, A. Dinter, H. U. Bertschinger, G. Stranzinger, and P. Voegeli. 2000. A DNA polymorphism influencing $\alpha(1,2)$ fucosyltransferase activity of the pig FUT1 enzyme determines susceptibility of small intestinal epithelium to *Escherichia coli* F18 adhesion. *Immunogenetics* 52:129–36.
- [4] Ramos AM, Crooijmans RPMA, Affara NA, Amaral AJ, Archibald AL, et al. (2009) Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. *PLOS ONE* 4(8): e6524. doi:10.1371/journal.pone.0006524
- [5] Holtkamp DJ, Kliebenstein JB, Neumann EJ, et al. (2013). Assessment of the economic impact of porcine reproductive and respiratory syndrome virus on United States pork producers. *Journal of Swine Health and Production* 21(2):72-84. URL: <https://www.aasv.org/shap/issues/v21n2/v21n2p72.html>
- [6] Dietze, K., Pinto, J., Wainwright, S., Hamilton, C., Khomenko, S. (2011). Porcine reproductive and respiratory syndrome (PRRS) virulence jumps and persistent circulation in Southeast Asia. United Nations Food and Agriculture Organization, Emergency Prevention System (EMPRES) URL: <http://www.fao.org/docrep/013/al849e/al849e00.pdf>
- [7] Beltran-Alcrudo, et al. (2007). Porcine reproductive and respiratory syndrome (PRRS) regional awareness. United Nations Food and Agriculture Organization, Emergency Prevention System (EMPRES) URL: <ftp://ftp.fao.org/docrep/fao/011/ai340e/ai340e00.pdf>
- [8] Delisle, B., Gagnon, C. A., Lambert, M., D'Allaire, S. (2012). Porcine reproductive and respiratory syndrome virus diversity of Eastern Canada swine herds in a large sequence dataset reveals two hypervariable regions under positive selection. *Infection, Genetics and Evolution* 12: 1111–1119. URL: http://www.medvet.umontreal.ca/lemp/publications_pdf/Delisle2012_InfGenEvol_QcPRRSV_diversity.pdf
- [9] Roland, R.R.R., Lunney, J., Dekkers, J. (2012). Control of porcine reproductive and respiratory syndrome (PRRS) through genetic improvements in disease resistance and tolerance. *Frontiers in Genetics* 3: 260. URL: <http://journal.frontiersin.org/Journal/10.3389/fgene.2012.00260/abstract>
- [10] Food and Drug Administration. (2010). 2010 Summary Report on Antimicrobials Sold or Distributed for Use in Food-Producing Animals. URL: <http://www.fda.gov/downloads/ForIndustry/UserFees/AnimalDrugUserFeeActADUFA/ucm277657.pdf>
- [11] Leung, M.C., Bowley, K.L., Squires, E. J., (2010). Examination of testicular gene expression patterns in Yorkshire pigs with high and low levels of boar taint. *Animal Biotechnology* 21(2): 77-87. URL: <http://www.ncbi.nlm.nih.gov/pubmed/20379884>
- [12] Ambagala, A. and Lung, O. (2013) Developing efficient, multi-pathogen tests for common cattle diseases. Research project factsheet published by the Beef Cattle Research Council. URL: <http://www.beefresearch.ca/factsheet.cfm/developing-efficient-multi-pathogen-tests-for-common-cattle-diseases-128>
- [13] Dikmen S, Cole JB, Null DJ, Hansen PJ. (2013). Genome-Wide Association Mapping for Identification of Quantitative Trait Loci for Rectal Temperature during Heat Stress in Holstein Cattle. *PLoS ONE* 8(7): e69202. doi:10.1371/journal.pone.0069202.
- [14] http://res.illumina.com/documents/icomunity/article_2014_03_greatergood_isu.pdf

Further reading

Iowa State University, College of Veterinary Medicine. (2013). Porcine Reproductive and Respiratory Syndrome (PRRS). URL: <http://vetmed.iastate.edu/vdpam/new-vdpam-employees/food-supply-veterinary-medicine/swine/swine-diseases/porcine-reproductive->