The Potential of Genomics for Swine Genetic Improvement

Project submitted to CDAQ
Summary

Background

For many years, swine selection has been based on reproductive and production performances of purebred animals. These performances along with pedigrees are analyzed using statistical methods in order to estimate the genetic potential of animals. The Canadian Centre for Swine Improvement (CCSI) is responsible for genetic evaluations of purebred swine on the Canadian Swine Improvement Program.

These traditional quantitative genetics methods have been proven and have allowed substantial genetic improvement on numerous traits of economic interest such as litter size, rate of growth and lean yield of carcasses.

An amazing revolution is happening in the genetic improvement sector. Indeed, the swine genome is almost completely sequenced and new tools are being made available which allow the identification of DNA sequences at numerous loci and chromosomes. SNP chips allow thousands of sites to be tested. These chips are already available in other species such as poultry and cattle and are in the process of being included in the main selection programs. For instance, the Canadian Dairy Network is planning to publish the first 'genomic indices' for dairy bulls in the spring of 2009. Validation studies carried out for dairy cattle showed that using genomics could almost double the genetic gain on some low heritable traits.
In pigs, the very first SNP panels will be available in December 2008 and will be tested right away in all countries and all breeding companies. The Canadian swine breeders, together with the Canadian Centre for Swine Improvement, feel it is critical to work together and put resources and expertise in common in order to assess these new tools and confirm their role of leaders in swine breeding.

Project objectives

The general objective of this project is to evaluate the value of genomic selection for the Canadian swine industry, more specifically for paternal traits such as meat quality.

Specific objectives are:

- Use new genomic technologies available (SNP chips, 'Single Nucleotide Polymorphism') for genotyping station-tested pigs;
- Estimate the effects of SNPs in relation to pig performance in different breeds and lines;
- Develop methodologies to include genomics in swine genetic evaluations;

- Estimate pilot genomic breeding values for several sire line traits recorded in test stations;
- Develop a DNA repository in relation with a database for traits recorded in test stations;
- Provide guidelines regarding the use of SNP chips for the Canadian swine breeding sector.

Innovative aspects of the project

The main innovative aspect of this project will be the very first use of SNP chips in pigs, So far, specific genes and markers have been used (Halothane, RN, IGF2, etc.) but with SNP chips, thousands of genes (50,000 loci) can be tested along the genome.

This technology started to be sued in species which genome was sequenced before the pig genome, such as chicken and cattle. In both cases, genomic selection offers huge opportunities for new selection potential, on traits already selected (ie milk yield and milk components) and on new traits (ie resistance to mastitis, calving ease). In addition, accessing DNA sequence allows better evaluation and management of genetic variability, more efficiently than by minimizing inbreeding. Genetic diversity is very important for future genetic gains.

Expected deliverables

- References on SNP frequencies in Canadian swine breeds;
- Detailed results on SNP chips and their association with numerous traits such as growth, carcass, feed efficiency, carcass and meat quality and disease resistance;
- Recommendations for the Canadian swine industry regarding the value of SNP chips ad their optimal use in swine breeding.