

Use of Electronic Identification in the Genetic Pyramid

Tom Long, Jason Pooley, Robert Peffley, Amy Rodriguez and Ryan Hardison
Smithfield Premium Genetics Group, Pampa, TX

Introduction

Accurate and timely collection of phenotypic data is critical to swine genetic improvement programs, whether using quantitative genetics, molecular genetics, advanced genomics or combinations of these. Additionally, processing of these data, genetic analyses and timely return of results to the farm for selection and culling is critical to program success. In the recent past, phenotypic data have been recorded on paper, and manually entered into the system database via keypunch entry (either at the nucleus farm or at a central data processing office). These processes were laborious and time consuming. Additionally, risks of error introduction into the database via transcription errors, legibility of records and keypunch errors were increased. These processes continue to evolve across the US swine industry to take advantage of advancements in other fields, such as electronics, information science and enhanced software/hardware systems. This paper will discuss some of these advancements currently being used in one genetic organization with reference to electronic identification and its implementation in a genetic pyramid.

Nucleus Data Capture

Within our nucleus system, all sows are identified with RFID tags as they enter the herd. This facilitates the electronic data capture of important events in the sow's life such as:

- Initial and subsequent heat cycles
- Breeding events
- Pregnancy checking
- Farrowing events
- Weaning events
- Culling events
- Death

These data are captured in either a TEAM station (Osborne Industries) or by using a PDA by the farm staff on a daily basis. Use of this technology facilitates:

- More timely capture of nucleus production data
- Handling of larger volumes of data
- Avoidance of laborious key punch entry of data, as done in the past
- Reduction of error levels in data due to key punch or transcription errors
- Development of screening software to manage data quality control

Additionally, at the stud all semen tubes are bar-coded with the boar's ID and genetic line. At the time of insemination, the semen barcode label and sow RFID are read

into a PDA to record the service. This eliminates the level of misidentification of matings within the database.

All pigs are processed within 24 hours of birth. Each pig is double-tagged with a barcode tag representing a unique number, unique within the system. These barcode tags facilitate the electronic data capture of a number of events:

- Individual birth weight
- Individual weaning weight
- Data linkage to FIRE (Osborne Industries) station events
- Off test data, such as end weight, backfat, muscle depth, IMF
- Mortality

The use of electronic capture of these data reduces the risk of error introduction via manual data recording and reduces the time needed to get data into the system database.

Commercial Data Capture

As geneticists, it is our mission to improve the genetic merit of the nucleus populations under our supervision. We have a second mission to facilitate the movement of that genetic improvement down into the genetic pyramid (e.g., daughter nucleus herds, multiplier herds, commercial herds and commercial boar studs). Often the second mission is inadequately addressed either through disconnects in information flow in either direction, poor communication between genetic supplier and customer tiers and/or long-term vs. short-term goals/perspectives of the production sector. We often only think of electronic identification as using RFID or barcode tags, but it also tracking animal identification throughout the genetic pyramid. This tracking is key to accomplishing the second mission described above.

We continue to expand the scope of testing nucleus animals through the commercial operations. In this effort, specific commercial herds have been designated, where identification of commercial females has been tracked through the multiplication phase so parentage of the females in these herds is known within the main database. As young terminal line boars enter the nucleus studs, their semen is sent to these commercial herds, as well as to the nucleus farms. Their commercial progeny are barcode tagged at birth, and subsequent carcass data are captured on all pigs at harvest. These data are then used in the genetic evaluation, along with the purebred nucleus data. This facilitates a more accurate genetic assessment of these boars as it incorporates data from high health nucleus herds as well as data from commercial herds with conventional health and environments.

Utilization

To aid with communication across the system, we have web-enabled large components of our information system. This facilitates a number of capabilities to aid in moving genetic improvement throughout the pyramid. It allows:

- Access to genetic results across management levels
- Visibility/accountability of the genetic program across the system
- Real-time posting of indexes to facilitate selection and culling decisions in nucleus units, daughter nucleus herds and all boar studs
- Summary statistics to monitor genetic performance of the system across a number of levels of the genetic pyramid

The most critical components of the use of electronic identification within the genetic pyramid are the people using the technology. From farrowing personnel processing litters with PDAs to middle management personnel using the web-enabled tools, training and education is needed to reap the greatest benefit from these applications. We have programs of continual training and workshops for new personnel and review/updates for people already using the systems. Without adequate training, support, and monitoring of these identification systems, the potential opportunities these technologies offer cannot be fully realized. Finally, we have striven to develop a culture within our system where all levels are continually looking at ways to improve the data and information systems. With users and developers working together, refinements can be made that continue to effectively extend the spread of genetic improvement throughout our business.