Gene Database

Of all livestock genetic traits, Randy Prather knows the one that puts the most money in a producer's pocket is reproductive efficiency. The University of Missouri (MU) animal scientist also knows that breeding such efficiency into a herd isn't an exact science, even with today's most advanced predictors.

"We have expected progeny differences (EPDs), but they're just what their name implies, expected, not absolute," he says. "We don't know which genes at which reproductive stages control whether a cow calves reliably or whether a sow births a large litter."

The effort to identify those critical genes in cattle and swine has been bolstered by two new livestock gene libraries developed by MU researchers. Scientists worldwide using the libraries could one day help producers put more money in the bank. Interdisciplinary teams of MU researchers from animal sciences, computer science and the MU DNA Core Facility have worked together on the MU Swine Genome and MU Bovine Genome projects since 2000 and 2003, respectively. The goal of both projects is to identify all genes that play a role in regulating reproduction.

"The female reproductive system undergoes tremendous remodeling during pregnancy," Prather says. "During the first week of swine embryonic development alone, thousands of genes change. Some turn on, some turn off, and some change their level of expression."

To catalog these changes, the researchers collected reproductive tissues at each stage of reproductive development and sequenced the genes that were turned on, creating expression sequence tag libraries. Scientists use these libraries to see how genes of interest change throughout the reproductive cycle.

"In swine, we identified about 15,000 genes that are involved in reproduction, and about 30% of them weren't in any database before," Prather says. "While the bovine project is not yet complete, we're expecting a similar number."

On average, about 30% of mammalian embryos or eggs with the potential to be fertilized never reach maturity, he says. Using the genome libraries, scientists hope to identify what genes are responsible for the losses and select against them.

"We slaughter about 100 million hogs a year in the United States," Prather says. "Even improving reproduction by a few percent means millions more animals can be produced."

He says that libraries such as these take gene science to an entirely new scale. "Instead of researchers studying 10 genes at a time, they can now study all 15,000."

In addition to improving efficiency, the libraries also may improve other reproduction-related science.

"When we work with embryos invitro, or when we clone embryos, there is a high percentage of loss, and we don't know exactly why," Prather says. "By studying the gene expression in those embryos, we can see what's being perturbed and adjust our cultures accordingly to improve our techniques."

The two libraries already are being used by the international research community, he says. "Every time we announce an update to the database, the server gets very busy. The last update tripled the number of daily page requests."

Prather adds that Jonathan Green, assistant professor of animal sciences, is seeking funding for a proposal to conduct a similar genome project for sheep.

Editor's Note: This article was written by Jason Jenkins, senior information specialist, MU Extension & Ag Information, which supplied this article.