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Discovery and validation of genetic markers for sow longevity

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Introduction and Background. Sow longevity has become a very hot topic in the swine industry over the last several years. The involuntary culling of sows due to death, lameness, health, or reproductive failure has recently been on a upwards trend in swine operations across the U.S. A sow's longevity or more precisely called sow productive life (SPL), is very critical to the financial success of a swine operation. An increase of one tenth in the average parity of sows on a farm will increase profits of a farrow to finish operation by $0.23 for every market hog sold by the operation. Taken as a whole, this would increase the net profit of the U.S. swine industry by 15 million dollars a year. Previously no studies have been conducted that have focused on the genes controlling SPL. Researchers using model organisms such as the mouse, nematode, and yeast have identified genes and gene pathways that are involved in the longevity of those species. These results have also held true in human longevity studies. We report the use of comparative genomics and candidate genes to isolate genes affecting both the number of parities a sow produces and also the number of pigs she produces during her productive life.

Materials and Methods. There have been three populations of sows used to test the association of the genetic markers with SPL. The first data set was comprised of ~200 sires that had complete production records on at least 10 daughters. The second population contained 1100 females that had complete reproduction information. Tissue samples were acquired in the fall of 2005on a third population (P3) consisting of 2,000 commercial females from 3 farms within a 120,000 sow production system. Half of P3 were gilts and the remaining half were sows that had produced at least 5 parities, which served to represent our "ideal" female. Sows from P3 represented two different genetic lines. PigChamp™ records were acquired in June of 2006 for the reproduction and culling information. Genetic markers were developed for the genes *insulin-like growth factor binding protein 1 (IGFBP1), insulin-like growth factor binding protein 3 (IGFBP3), carnitine O-palmitoyltransferase I (CPT1A), organic cation/carnitine transporter 2* (*Solute carrier family 22 member 5*; *SLC22A5*), and *cyclooxygenase-2* (*COX2*). The genetic markers were tested for association with the sows ability to survive to parity 5, the number of pigs born alive, stillborn pigs, and the number of mummies.

Results and Discussion The genetic markers were screened in populations 1 and 2 with only those showing at least a tendency for association with a component of SPL being validated in P3. The gene marker for *IGFBP1*, *IGFBP3*, *SLC22A5*, and *CPT1A* were all significantly associated ($P < 0.05$) for remaining in the herd until 5 parities. Additionally for *IGFBP1*, the same genotype favored for greater SPL showed a tendency ($P < 0.1$) for the number of pigs born alive throughout a sow's productive life. Therefore a sow with the beneficial genotype for *IGFBP*1 will not only have a greater probability of staying in the herd until parity 5, but will also produce an additional 1.5 pigs while doing so. *SLC22A5* was associated with the number of mummies during the sow's lifetime. CPT1A was significantly associated ($P < .05$) with the number of pigs born alive in parities three on with effects as large as 0.7 of a live pig per litter. These results are evidence that there are genes causing variation in sow productive life and give promise to the use of marker assisted selection to improve sow productive life.