Abstract

Sow productive life, also called sow longevity, has been a major concern for commercial swine operations. The average sow in U.S. commercial operations is averaging 3.4 litters before she leaves the herd. A sow must produce on average three litters before she recovers her investment cost. This small differential between when the average sow leaves the herd and when a sow has paid for herself leaves a large burden on relatively small proportion of the sow population. Even a small increase in the average number of parities that a sow produces such as one tenth of a parity could increase the revenue of commercial operation by over $15 million in the U.S. alone. While there are many different contributing factors to sow productive life, research in model organisms has showed a clear and consistent association with genes involved in growth pathways and the lifespan of these animals. Most notably are the genes involved in the insulin pathway that either reduce caloric intake or mimic the response of calorie restriction. Our hypothesis was that these same genes would also prove to be important to sow productive life, though we realize that the lifespan of simple model organisms would not be completely correlated with sow productive life, especially with the enormous demands that sows are under to continuously farrow large healthy litters. We also expanded our research to include genes that are included in nutrition, disease resistance, and reproduction. Our research on 2,000 commercial sows showed that CPT1A, CCR7, IGFBP1, WARS2, and MBL2 all proved to be significantly associated with sow survival, either to a certain parity or day, when tested using extremely stringent analysis. The genes IGFBP1, MBL2, CPT1A, CCR7, SLC22A5, and ACE all were significant with at least one reproductive trait.