

ABSTRACT

Intensive genetic selection has led to incredible improvements in pig production traits but has resulted in increasing environmental sensitivity. This drives the need to breed a robust pig— an animal exhibiting high genomic potential in combination with resilience to external stressors allowing it to achieve its maximum potential. Resilience is an animal's ability to be either minimally affected by a stressor or quickly return to its pre-stress state. Weaning is a multifaceted stressor and provides an excellent opportunity to investigate resilience. We conducted two studies characterizing physiological resilience (SR) or vulnerability (SV) to weaning stress using serum cortisol pattern surrounding weaning and investigated lasting impact on production, behavior, and molecular modifications. The first study was conducted on gilts from 26 crossbred litters (PIC 359 x Yorkshire sows) and the second study on gilts from 13 purebred Yorkshire litters. We detected no associations between resilience and post-weaning growth in either study. In crossbred gilts, there were no differences in pork quality measures at slaughter, but resilient gilts had lower live weight and hot carcass weight as well as a smaller loin muscle area. Crossbred SR gilts engaged in more agonistic interactions at 1 d post-mixing, as estimated by skin lesion counts, but this was not observed in purebred SR gilts. We observed differences in behavioral responses during a novel object test at 12 wk-of-age, but results varied between studies. Crossbred SR gilts exhibited greater object touches and fewer vocalizations, whereas purebred SR gilts exhibited less overall activity and fewer escape attempts. In our second study, we additionally performed RNAseq and whole genome bisulfite sequencing on hypothalamus and hippocampus samples from 10 gilts (5 SR, 5 SV) at 13 wk-of-age. We detected 97 differentially expressed genes (DEGs) in hippocampus and 5 DEGs in hypothalamus. Hypothalamic DEGs included down-regulation of *FOS*, *ADCYAP1*, and *HDC* in SR gilts; genes which have been established to be involved in stress regulation. Hippocampal DEGs included *FOS*, *CARTPT*, *NPY2R*, *CHRNA4* and *HTR2A*, and were enriched for GO terms including behavior, neurological system process, and catecholamine secretion. Transcript abundance of DEGs were correlated with pre-weaning cortisol concentration and behavioral measures. We also identified 2,053 differentially methylated regions (DMRs) in hippocampus and 3,314 DMRs in hypothalamus. Hippocampal genes containing DMRs were enriched for processes of neuron differentiation and myelination, while hypothalamic genes containing DMRs were enriched for neuron migration and GTPase activity. Our results indicate that resilience to weaning stress is associated with modified transcriptomic and epigenetic profiles of brain tissues, as well as behavioral differences later in life. Further research is needed to determine if genes indicated in this study are predictive or adaptive in nature, and the biological relevance of the observed molecular modifications.