

Genome-Wide Association Analyses of Biological Responses to Heat Stress in Pigs

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Summary and Implications

With genetic selection for rapid, lean tissue accretion, pigs are becoming increasingly sensitive to heat stress (HS) due to their physiological limitations such as the lack of functional sweat glands to effectively dissipate heat. Increased respiration rate and reduced feed intake are immediate and conserved biological responses to HS in pigs and other livestock species. Genetic differences in how animals respond to high ambient temperatures have been previously reported, but genetic factors contributing to the response variability remain ill-defined. In this study, porcine high density single nucleotide polymorphism (SNP) beadchips were used to genotype 236 female pigs who had been exposed to HS conditions, and analyzed to detect chromosomal regions associated with biological responses measured before and after HS, including rectal temperature, respiration rate, feed intake, and body weight loss. We identified significant gene region associations for rectal temperature on SSC12, respiration rate on SSC14 and SSC16, as well as feed efficiency and weight loss on SSC13. Further analyses of these detected regions will likely reveal potential candidate genes and suggest molecular mechanisms contributing to the variability in the biological response of pigs to environmentally-induced hyperthermia.

Introduction

Heat stress reduces feed intake, growth, feed efficiency, and increases mortality and health care costs. Heat-stressed pigs have increased rectal temperatures and respiration rates and these are highly conserved biological responses. It would be desirable to select pigs that are both resistant to HS and highly productive during thermal neutral conditions.

The objective of this study was to identify chromosomal regions responsible for differences in biological responses during HS. The detected chromosomal regions would be useful to identify important genetic factor(s) regulating physiological processes for constant

body temperature under HS. Thus it could be possible to use the identified genetic factor(s) as management/selection tools in the pig breeding and production under HS susceptible environments.

Materials and Methods

A total of 236 crossbred female pigs were used to measure biological responses between thermal neutral (TN; ~21.0°C) and HS (~30.0°C) conditions; each exposed for 24 h. The biological responses recorded during HS were rectal and skin temperatures and respiration rates. Body weight (BW) was collected at the beginning of the acclimation period (at least 3 days in TN condition) and at the end of the TN and HS periods. Feed intake was calculated daily for each pig during the entire experiment period. HS tolerance (or susceptibility) was determined by the difference in the average of collected measurements between TN and HS days. These animals were genotyped using GGP porcine HD beadchips (GeneSeek) and the genome-wide association analysis was performed to identify the chromosomal region associated with the variation in the biological parameter. The statistical model accounted for the effects of chamber (or room), replication, and initial body weight (Golden Helix SVS7 software).

Results and Discussion

Significant SNPs for increased rectal temperature were discovered on SSC12 (29M-33M) and SSC7 (111M-119Mb). However, these regions did not have significant association with other measurements. Significant SNPs for the difference in skin temperature were identified on SSC15 (127.8Mb-129.2Mb). Significant SNPs for increased respiration rate were determined on SSC16 (27Mb) and SSC14 (137.7Mb). Significant SNPs for weight loss during HS were localized to SSC13 (153Mb-203Mb) and for feed intake (196Mb-203Mb).

These chromosomal regions were identified with individual SNP analysis, which could be noisy through false association. Therefore, further study is required using several adjacent 3-5 SNP windows which results in more precise locations of significant chromosomal regions and validation of individual SNP analysis, with the aim to eventually suggest candidate genetic factors associated with HS tolerance in pigs.

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