

Comparison of microarray mRNA profiles expressed in longissimus dorsi in
porcine of different ages

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Abstract

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We use mRNA microarrays to study possible differential expressed genes responsible for growth of porcine longissimus dorsi muscle. Six sibling pigs of the most commonly reared hybrid species in Taiwan were collected at three stages: the birth period (at one week), the growing period (at three months), and the finishing period (at eight months). Total RNA samples were obtained and hybridized with the human cDNA probes from Agilent commercial microarrays. The experiment data were normalized, ruled out the unreasonable blank outliers, filtered out with the conflicting data. We set the threshold of the log₂ value of the Cy3/Cy5 ratio (M value) greater than 1 or less than -1 for a selection standard. The results showed that (1) the same individuals had good correlation coefficients; and (2) there are 1106 up-regulated genes and 360 down-regulated genes from birth to growing term. There are 596 up-regulated genes and 229 down-regulated genes from growing to finishing term. A total of 218 genes showed changes at all three periods, of which 143 genes up-regulated, 75 down-regulated. We provide the developmental gene expression profile of longissimus muscle from hybrid porcine commonly used in Taiwan.

Keyword : mRNA growth performance, cDNA microarray, porcine longissimus