Data in Brief

Transcriptome analysis of genetic mechanism of growth curve inflection point using a pig model

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A R T I C L E  I N F O

Article history:
Received 11 August 2015
Received in revised form 20 August 2015
Accepted 25 August 2015
Available online 2 September 2015

A B S T R A C T

Animal growth curves play an important role for animal breeders to optimize feeding and management strategies (De Lange et al., 2001 [1]; Brossard et al., 2009 [2]; Strathe et al., 2010 [3]). However, the genetic mechanism of the phenotypic difference between the inflection point and noninflection points of the growth curve remains unclear. Here, we report the differentially expressed gene pattern in pig *longissimus dorsi* among three typical time points of the growth curve, inflection point (IP), before inflection point (BIP) and after inflection point (AIP). The whole genome RNA-seq data was deposited at GenBank under the accession number PRJNA2284587. The RNA-seq libraries generated 117 million reads of 5.89 gigabases in length. Totals of 21,331, 20,996 and 20,139 expressed transcripts were identified in IP, BIP and AIP, respectively. Furthermore, we identified 757 differentially expressed genes (DEGs) between IP and BIP, and 271 DEGs between AIP and IP. Function enrichment analysis of DEGs found that the highly expressed genes in IP were mainly enriched in energy metabolism, global transcriptional activity and bone development intensity. This study contributes to reveal the genetic mechanism of growth curve inflection point.

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1. Direct link to deposited data

The RNA-seq raw data has been uploaded in GEO database under the accession number GSE69113 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE69113).

The whole project was deposited at GenBank under the accession number PRJNA2284587 (http://www.ncbi.nlm.nih.gov/bioproject/PRJNA2284587).

2. Experimental design, materials and methods

One Chinese native mountain-type pig breed, Liangshan pig, was taken as the animal model in the study (Shen et al., 2014 [4]). A total of 275 female Liangshan pigs were raised from birth to 250 days old to collect the growth traits (feed conversion rate, daily feed intake and average daily gain). The growth curve was fitted by three different non-linear models. The inflection point analysis of the growth curve suggested that the Liangshan pig reached the maximum growth rate at day 193.40. Therefore, we selected other two symmetric non-inflection points (143 days for BIP and 243 days for AIP) to explore the transcriptome diversity of muscle development. The *longissimus dorsi* muscle was harvested from 9 Liangshan pigs (3 pigs for each time point), and used for transcriptome analysis.

For RNA-Seq library preparation, total RNA was extracted from *longissimus dorsi* using TRIzol (Invitrogen, CA, USA) and further purified with RNaseasy column (Qiagen, USA) according to the manufacturer’s protocol. The total RNA was isolated poly (A) mRNA by poly-T oligo attached magnetic beads (Thermo-Fisher). Following purification, the mRNA was fragmented into small pieces using divalent cations under an elevated temperature. Then the cleaved RNA fragments were constructed into the final cDNA library in accordance with the protocol for the Illumina RNA ligation based method (Illumina, San Diego, USA). A reverse transcription followed by PCR was used to create cDNA constructs. The average insert size for the single-end libraries was 300 bp (± 50 bp). Then the single end sequencing (50 bp) was
performed on an Illumina Hiseq2000 platform. For data analysis, the raw data containing adaptor sequences, reads with low quality sequences and unknown nucleotides N were filtered to obtain clean reads with 50 nt in length. Clean reads were then conducted for quality assessment (data shown in Table 1). These include the classification of total and distinct reads and show their percentage in the library, analyze saturation of the library and correlation analysis of biological replicates. All clean reads were mapped to the transcript sequence by bowtie (1.0.0); only 1 bp mismatch was allowed. For monitoring the mapping events on both strands, both the sense and complementary antisense sequences were included in the data collection (data shown in Table 2). The number of perfect clean reads corresponding to each gene was calculated and normalized to the number of Reads Per Kilobase of an exon model per Million mapped reads (RPKM). Based on the expression levels, the significant DEGs (differentially expressed genes) among different samples were identified with p-value ≤0.05 and log₂ fold-change|log 2 FC| ≥ 1. Raw and normalized data of our study were accessible on public database: GEO submission number GSE69113.

### Conflicts of interest

The authors declare no conflicts of interest.

### Acknowledgments

The study was supported by the Sichuan Sci & Tech Support Program (No. 2013NZ0041, and No. 2013NZ0056), the earmarked fund for China Agriculture Research System (No. CARS-36-05B), the Chinese National Sci & Tech Support Program (No. 2013BAD20B07), and International Science & Technology Cooperation Program of China (2014DFA31260).

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### Table 1

Overview of sequencing data (total reads). BIP: before inflection point; IP: under inflection point; AIP: after inflection point. CopyNum: copy number of reads.

| Items         | BIP-1     | BIP-2     | BIP-3     | IP-1      | IP-2      | IP-3      | AIP-1     | AIP-2     | AIP-3     |
|---------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Raw data      | 13339799  | 10330457  | 17695127  | 11864291  | 12318028  | 13499142  | 13119946  | 12619451  | 12905984  |
| After adaptor cut | 13275704  | 10285839  | 17684488  | 11856882  | 12319119  | 13456169  | 13105441  | 12614571  | 12900101  |
| After junk filter | 13244525  | 10263834  | 17662944  | 11834152  | 12297883  | 13430696  | 13085474  | 12601514  | 12886097  |
| Valid data    | 13244525  | 10263834  | 17662944  | 11834152  | 12297883  | 13430696  | 13085474  | 12601514  | 12886097  |
| CopyNum 1     | 13244525  | 10263834  | 17662944  | 11834152  | 12297883  | 13430696  | 13085474  | 12601514  | 12886097  |
| CopyNum ≥ 5   | 7460500   | 5454381   | 1042294   | 6570150   | 6978726   | 7925320   | 8018356   | 7371137   | 7704734   |
| CopyNum ≥ 10  | 6562426   | 4736476   | 9820014   | 608702    | 6946867   | 7129213   | 6504642   | 6847125   | 6055181   |
| CopyNum ≥ 20  | 5749527   | 4094905   | 8738767   | 496257    | 5089506   | 6089260   | 6347582   | 5696676   | 6055181   |
| CopyNum ≥ 50  | 4646376   | 3149458   | 7274146   | 3871935   | 3862539   | 4702611   | 5229975   | 4552111   | 4894318   |
| CopyNum ≥ 100 | 353075    | 2230578   | 5927035   | 2875443   | 2864061   | 3641747   | 4091514   | 3569003   | 3817406   |

### Table 2

Overview of mapped reference gene on sequencing valid data. BIP: before inflection point; IP: under inflection point; AIP: after inflection point.

| Items         | BIP-1     | BIP-2     | BIP-3     | IP-1      | IP-2      | IP-3      | AIP-1     | AIP-2     | AIP-3     |
|---------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Mapped gene   | 20690     | 19907     | 20904     | 19907     | 19823     | 19599     | 19514     | 19263     | 19599     |
| Match (unique sense) ≤ 1 mismatch | 1 gene –– mapped by 1 unique sequence | 1262 | 1342 | 1160 | 1414 | 1338 | 1376 | 1389 | 1362 | 1361 |
| Match (unique antisense) ≤ 1 mismatch | 1 gene –– mapped by 1 unique sequence | 16256 | 15888 | 16689 | 15552 | 15827 | 15382 | 15460 | 15238 | 15535 |
| Match (unique sense and antisense) ≤ 1 mismatch | 1 gene –– mapped by 1 unique sequence | 114 | 106 | 107 | 164 | 114 | 104 | 110 | 106 | 126 |
| Match (unique sense and antisense) ≤ 1 mismatch | 1 gene –– mapped by n unique sequence | 105 | 136 | 132 | 118 | 108 | 132 | 105 | 143 | 134 |