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2nd International Conference on

Transcriptomics

September 12-14, 2016 Philadelphia, USA

Analysis of parent-of-origin allelic expression in Korean cattle (Hanwoo)

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S ome genes are expressed exclusively or differntially from one of the two parental alleles, resulting in allelic imbalance (AI) in gene expression. Genomic imprinting is a type of AI and determined allele specific expression (ASE) depending on the parent-of-origin. High-throughput transcriptome sequencing strategy can identify ASE through the use of expressed SNPs that have the capacity to detect cis-regulatory variation and imprinted genes by aligning sequence reads to individual alleles. Here, we used RNA-Seq data along with high-resolution to analyze ASE profiles and imprinted genes based on trio data. First, whole-genome resequencing data (average 10X per sample) of one family trio (sire, dam and offspring) was generated by illumina HiSeq 2500 platform. RNA-Seq data (4Gb per tissue) was also produced from twenty three tissues such as backfat, intramuscular fat. Exome SNPs of all individuals were assigned from GATK and SnpEff tools. For each heterozygous SNP, the number of maternal and paternal reads were counted. The deviation between the read numbers was analyzed with the binomial test in R software. To test inactivation of maternal or paternal SNP, we compared parental alleles and offspring's allele between SNPs from resequencing and RNA-Seq as an additional filtering step. Then, candidate imprinted genes were checked for expression patterns in different tissues to have the tissue-specific imprinting signatures. Finally, we confirmed the expression of SNPs and tissue-specificity within imprintig gene by experimental validation.

Biography

Dajeong Lim has completed his PhD from Seoul National University. She is a Researcher in National Institute of Animal Science (NIAS), Rural Development Administration in Korea. She has published more than 30 papers in academic journals.

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