



LncRNAs Variability in Porcine Skeletal Muscle

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Objectivnes

- to investigate the variability of IncRNAs among pigs in context of their number, length, expression
- to investigate the **impact of IncRNA on the expression** of their potential target genes



- RNA-seq data sequenced with the Illumina NovaSeq 6000
- 6 Polish Landrace boars
- muscle tissue (*longissimus dorsi*)

Methods



Bioinformatics pipeline

- Quality control (FastQC and MultiQC)
- Alignment to Sscrofa11.1 reference genome (HISAT2)
- Post-aligment processing (Samtools)
- Quantification of gene expression (StringTie)
- LncRNA filtration

Statistical analysis

- Descriptive statistics
- Statistical tests
 - χ^2 test
 - Kolmogorov Lilliefors test
 - Kruskall Walis test
 - Dunn test
 - Quade test
 - Wilcoxon signed rank of test
- log fold change
- Pearson correlation
- Fisher Exact test



- 241, 605, 646 337, 017, 230 raw reads/individual
- 87.21 to 91.51% of reads remained after editing

Results - numbers





- interindyvidual differences in numbers IncRNA
- 341 812 known transcripts

Results - numbers





- interindyvidual differences in numbers IncRNA
- 341 812 known transcripts
- 949 2,689 novel transcripts

Results - 232 common IncRNA

















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Results - length and expression





no linear correlation between the lncRNAs length and their expression level \Longrightarrow the expression was not biased by some extraordinary long/short lncRNAs



significant inter-individual variability in the expression level (FPKM) of IncRNA common for all boars - $P = 4.52 \cdot 10^{-15}$ (Quade test for dependent pairs)

Results - expression





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Results - log fold change





co-expression (605 IncRNA related protein-coding genes)

- regulation of cellular metabolic process
- regulation of apoptotic signalling pathway
- positive regulation of apoptotic process
- mitochondrial electron transport
- mitochondrial respiratory chain complex I assembly
- translation
- rRNA processing
- cellular response to lipopolysaccharide

- ribosome assembly
- ribosomal large subunit biogenesis
- ribosomal small, subunit biogenesis
- protein-RNA complex assembly
- protein-DNA complex disassembly
- negative regulation of protein modification process
- mRNA splicing, via spliceosome
- nucleocytoplasmic transport



co-localization (1585 IncRNA related protein-coding genes)

- protein modification by small protein conjugation or removal
- RNA metabolic process
- response to stress
- underrepresentation of G protein-coupled receptor signalling pathway
- detection of chemical stimulus involved in sensory perception of smell

Conclusions

- Individuals significantly varied in IncRNA number, length, and expression
- No consistent pattern has been found between pairs of half-brothers
- The co-expression analysis revealed 605 and co-localization 1,585 related protein-coding genes
- shared IncRNA target genes determined a variety of biological processes that play fundamental roles in cell biology and they were mostly related to whole-body homeostasis maintenance, energy and protein synthesis as well as dynamics of multiple nucleoprotein complexes.

THANK YOU FOR YOUR ATTENTION!

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