

The search for SNPs and genes associated with the feed conversion ratio using entropy analysis

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The aim of this study was to detect the chromosomal regions connected with feed conversion ratio and point out the respective genes in meat-type chicken. Analysis covered 862 genotyped commercial line of broiler using 60K Illumina iSelect chicken array and obtained information about 57636 SNPs. Feed conversion ratio between 39–46 days were registered. Finally, 42770 SNPs were analysed. The information theory is employed to detect the association between SNPs and recorded traits. The following parameters were estimated: entropy coefficient, conditional entropy, portion of information and mutual information. Important regions at chromosomes 1 and Z were identified. They are mainly located within genes determining the nervous system and expressed also in gastrointestinal tract.

Keywords: entropy analysis, feed conversion ratio, chicken, SNP

1 Introduction

Feed conversion ratio is one of the most important traits in the broiler industry. Nutrition accounts for about 70% of the total costs of broiler production. Feed conversion ratio (FCR) is expressed as feed intake per body weight gain (Aggrey et al., 2010). It is well known that FCR is considerably correlated with other performance traits. However, a routine registration of this trait is relatively expensive. Hence, from practical perspective, identification of genome regions determining feed efficiency is very desirable. Recently, an information theory has been more and more applied to study the associations between SNPs and traits, mainly categorical ones (Borowska et al., 2014). Based on this approach the interactions between SNPs can be investigated. The aim of this study was to detect the chromosomal regions connected with FCR and point out genes which are connected with FCR in meat-type chicken.

2 Material and methods

Analysis covered 862 commercial broiler chickens genotyped using the 60 K Illumina iSelect chicken array. The genotyping revealed information about 57636 SNPs. Feed conversion ratio between 39–46 days was recorded for all genotyped individuals. More details of the experiment are given by Reyer et al. (2015). After data

editing, 855 individuals and 28 chromosomes (except chromosomes 16 and W) were analysed. The trait values were classified according to quartiles and ranged from 1–4.

The data editing based on the following criteria: minor allele frequency >5% and call rate >95%. Finally, 42770 SNPs were included.

Entropy analysis was employed to study important genome regions contributing to FCR. The following parameters were estimated (Borowska et al., 2014): entropy coefficient, conditional entropy, portion of information and mutual information.

Chromosomal regions were indicated based on the highest mutual information. Higher mutual information between two SNPs means that one SNP is associated with the other. SNPs located in intragenic regions were preferred for the last part of the analysis. The location of SNPs and genes were verified using the *Ensembl* genome database (EMBL-EBI, 2016) and the National Center for Biotechnology Information (NCBI) databases – db SNP and Gene (NCBI, 2016a, b).

3 Results and discussion

Two main regions on chromosomes 1 and Z were detected for FCR by entropy analyses, depend on the

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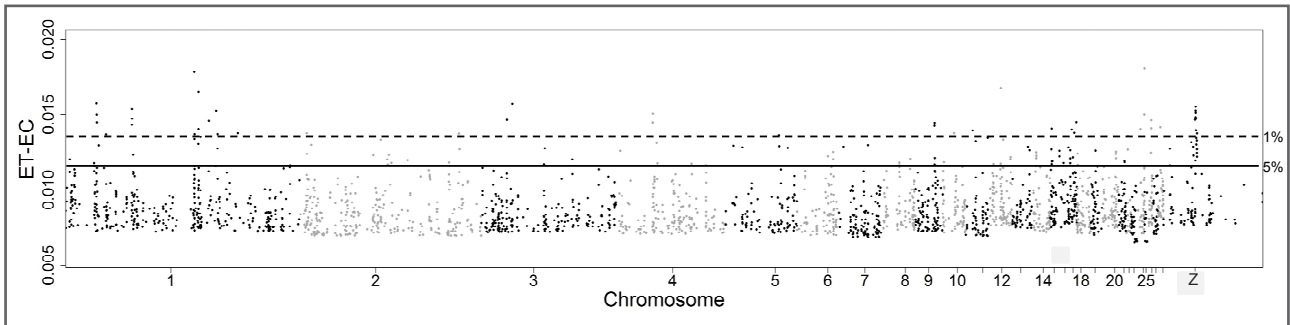


Figure 1 Location of 1% and 5% the most informative SNPs for feed conversion ratio

highest portion on information assigned (entropy of the trait – conditional entropy; ET-EC) and highest mutual information (Figure 1).

Based on the *Ensembl* database, the region on chromosome 1 harbours nine candidate genes with ‘known status’ (i.e. the gene was previously reported in other external databases in the same specie): **CACNA2D1**, **CD36**, **GNAI1**, **GNAT3**, **HGF/SF**, **SEMA3A**, **SEMA3C**, **SEMA3D**, **SEMA3E**. Additionally, four genes had annotations based on homologous genes in well-studied genomes (‘known status by projection’): **GRM3**, **KIAA1324L**, **LOC768552**, **PCLO**. The identified genomic window on chromosome Z includes 33 genes, of which eight had ‘known status’: **ANKRA2**, **CBWD1**, **DMRT1**, **FOXD1**, **JAK2**, **RFLB**, **UTP15**, **VLDL**. Moreover, 25 genes were classified as ‘known status by projection’: **AK3**, **ARHGFE28**, **CD274**, **CDC37L1**, **DMRT2**, **DMRT3**, **DOCK8**, **FCHO2**, **GLIS3**, **KANK1**, **KCNV2**, **MAP1B**, **MRPS27**, **PGM5**, **PUM3**, **RCL1**, **RFX3**, **RIC1**, **SLC1A1**, **SMARCA2**, **TMEM171**, **TMEM174**, **TMEM252**, **TNPO1**, **ZNF366**. Furthermore, two miRNA (gga-mir-101-1, gga-mir-6669), ncRNA (**LOC101749131**, **LOC101750946**), and novel genes (**LOC427201**, **LOC770771**) mapped in this region. For FCR, 51.28% of the informative SNPs in both chromosomal regions were situated inside genes (bolded). These genes may play a role in the development of the trait.

Based on the assumption of ‘known status’ in chicken and with SNP located inside the gene, five genes were pointed out: **CACNA2D1**, **GNAI1**, **JAK2**, **SEMA3A**, **SEMA3D**. **CACNA2D1** is involved in the development of the skin epithelium in chicken embryos (Chang et al., 2015). **GNAI1** is connected with many signalling pathways. The influence of **JAK2** gene on growth and reproduction trait was confirmed in meat-type chicken (Liu et al., 2010). The expression of **SEMA3A** was observed in central nervous system, typically in gray matter of spinal cord in chicken embryos (Fu et al. 2000). **SEMA3D** is also connected with the development of nervous system e.g. in brain. Moreover, it is participating in the development of lens and nasal placodes, the heart, and in the ectoderm of limbs (Bao and Jin, 2006; Jin et al. 2006). Additionally,

the expressed proteins of **GNAI1**, **JAK2** and **SEMA3A** were detected in the gastrointestinal tract (liver, gall bladder, stomach, small intestine etc.) in humans (Pontén et al., 2008).

4 Conclusions

The entropy analysis allows to search for associations between SNPs (in the context of some functional genes) and feed efficiency. These genes (including important SNPs) are connected with nervous system and expressed also in gastrointestinal tract. Hence, their considerable role in chicken feed conversion is suggested.

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