

12. Gene expression profiling of the parous mouse oviduct. Possible implications in ovarian cancer

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Background

Ovarian cancer (OC) is among the major lethal gynecological cancers worldwide. The facts that prophylactic salpingectomy reduces OC risk plus recent genomic analyses uncovering an oviductal epithelium signature in the most frequent OC variant, led to the notion that OC would actually originate from oviductal cells. In addition, periods of interrupted ovulation such as pregnancy and oral contraception have largely known to decrease OC risk through a protective hormonal effect. As the oviduct might also be responsive to pregnancy hormones, the aim of this study was to obtain transcriptional profiles of multiparous C57BL6 female mice compared to age-matched virgin animals aiming to detect altered expression of genes implicated in OC protection by pregnancy and pre-neoplastic transformation by repetitive ovulation.

Description

Gene expression profiling was conducted in one-channel Illumina MouseRef-8 v2 beadchips (Illumina, Inc., San Diego, CA) for two divergent reproductive conditions (multiparous vs virgins; n=4/group). Regarding the multiparous/virgin comparison, 159 genes were upregulated and 336 genes were downregulated. Importantly, 26 of these genes were described as tumor suppressors in TSG database, in particular 4 upregulated (Dido1, Igfbp5, Eif2ak2 and Isg15) and 22 downregulated. Functional enrichment analyses (GO, KEGG and WikiPathways) of upregulated genes showed heat shock protein binding (e.g. Cdc37, Pdxp, innate immune response (e.g. Irf9, Stat), cholesterol

biosynthesis (e.g Mvd) and mRNA processing, for instance Rbm4. In contrast, major downregulated genes functions included vascular morphogenesis, negative regulation of inflammatory response, tight junctions and focal adhesions (eg ITGB, TGFBR1), regulation of actin cytoskeleton, cell cycle, signaling of the Wnt, MAPK and insulin pathways and mRNA processing.

Conclusion

Parity promotes oviductal expression of genes related to immunological response and cell stability suggesting a preparation to stress. In addition, the repression of those genes that promote cell migration, anti-apoptosis and proliferation suggests that pregnancy condition inhibiting or decrease likelihood of pre-neoplastic lesions or cell migration toward ovary reducing the risk of ovarian cancer. This event may drive by progesterone and estradiol, the same pregnancy hormones that may protect the ovary. The possible mechanism would be to subject the oviduct to a constant and mild stress that it will be prepared for a worse one, for instance, neoplastic process.

GENETIC VARIATION ANALYSIS

13. Selecting potential functional candidate genes for temperament of Guzera cattle in a region of chromosome 1

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Background

The Guzera cattle presents heat tolerance and resistance; and the ability to survive under limited food resources during dry periods of the year, due to it, Guzera cattle is one of the most common zebu breeds in northwest semi-arid region of Brazil. Zebu breeds was known popularly as "brave" breeds, due to having more aggressive temperament. When compared with calm animals, the angry ones produce meat of poorer quality, are more susceptible to

diseases, have lower weight gains, lower reproductive efficiency and lower milk production. Genome-Wide Association Studies (GWAS) use genotyping technologies for analyzing several single-nucleotide polymorphisms (SNPs) and relate them to clinical conditions and measurable traits. This kind of study usually identify SNPs in linkage disequilibrium with the real variant that contributes to the phenotype measured. A region around SNPs found to be associated with reactivity in a previous GWAS performed by our research group was delimited and investigated by a literature data-mining in the present study. The region was delimited by the rising of p-values around the associated marker found in chromosome 1. A list with all the genes located inside the region previously delimited, was constructed. The software Gene Relationships Across Implicated Loci (GRAIL) was used to perform the data-mining. This software uses our text-based definition of relatedness to identify a subset of genes, and it is based on two key methods: a text-based similarity measure that scores two genes for relatedness to each other based on text in PubMed abstracts and a novel statistical framework that assesses the significance of relatedness between genes in disease regions. The input file for GRAIL analyzes was made using the Gene name and the Gene ID of the homologous gene in Human genome.

Results

Initially, the input file consisted for 39 genes. After the analyses we were able reduce considerable the number of genes that can be associated with temperament in Guzerá cattle. The keywords related to the phenotype evaluated were temperament, behavioural and stress. These results show the genes in chromosome 1 that may be associated with behavioural traits and temperament in Guzerá cattle.

Conclusions

The bovine temperament is an important characteristic in the animal's well-being, and it affects the animals productivity. Given these facts, and the importance of this study for the breeding selection, the results shown in the

present work are very important for the temperament genetics from Guzerá and milk production in Brazil.

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14. SNP clustering on DBSCAN and sensitivity analysis

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The aims of this work are the knowledge acquisition from genotype data of 56K single nucleotide polymorphism (SNP) chip in genome of three cattle breeds through the algorithm DBSCAN (Density-Based Spatial Clustering of Applications with Noises) and its sensitivity analysis with respect to changes on its initial conditions in this database. The database used has 2467 samples distributed in three cattle breeds. Two breeds are taurine cattle and have 56947 markers: Holstein (577) and Jersey (1024); and one breed is zebu cattle and have 54000 markers: Nellore (866). Through this work was possible to find markers that do not discriminate samples of these breeds, since they remain constant independently of their breeds. In addition, it was possible to analyze the algorithm's sensibility and show that it presents relative stability in this scenario, since the clustering results converged with no difficulty. Finally, this work demonstrates the possibility to build a model able to generalize and predict the unknown breed samples of cattle efficiently.

GENOME ASSEMBLY AND ANNOTATION

15. CGIIS: an automated tool to Close Gaps Inter and Intra Scaffolds

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Background

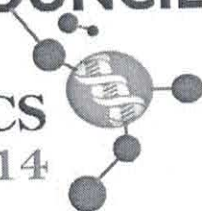
One of the main issues in whole genome sequencing is to fill the gaps on the final assembled genomic sequence, linking the different

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