Milk exosome-derived miRNAs from water buffalo are implicated in immune response and metabolism process

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Research article

Keywords: buffalo milk, exosomal miRNA, cell-cell communication, immune and metabolism

Posted Date: December 6th, 2019

DOI: <https://doi.org/10.21203/rs.2.18250/v1>

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Abstract

Buffalo milk represents an indispensable source of nourishment, and recently receives increasing research interest and investment in various countries due to its high nutrient content compared with non-buffalo milks. Exosomes are membranous vesicles of endocytic origin that are found in various breast milks, and those can mediate intercellular communication with exosomal miRNAs. In comparison with non-buffalo milks, we therefore hypothesized that buffalo milk exosomes provided novel information on miRNA composition, and highlighted the unrealized physiological importance of exosomes on drinking behaviour. Here, we isolated exosomes from buffalo and cow milk samples that were obtained at mid-lactation period, and the exosomal miRNA profiles were then generated using RNA-seq. As control, miRNA sequencing data of pig, human and panda milk exosomes were downloaded from GEO database. Finally, a total of 27 milk exosomal miRNA profiles that included 4 buffalo, 4 cow, 8 pig, 4 human and 7 panda were analyzed using the miRDeep2 program. For these datasets there were 558 unique miRNA candidates existed across all species, and the top 10 highly expressed miRNA were evolutionarily conserved across multiple species. Functional analysis revealed that these milk enriched miRNAs targeted 400 putative sites to modulate disease resistance, immune responsiveness and basic metabolism events. In addition, a total of 32 miRNAs in buffalo milk were significantly up-regulated compared with non-buffalo milks, while 16 were significantly down-regulated. Of interest, functional analysis showed that up-regulated miRNAs were mainly related to host metabolism processes, while the predicted functions of down-regulated miRNAs were enriched in immune response. In this study, we explored the exosomal miRNAome differences between milks of different animals, expanding the theoretical basis for potential applications of the miRNA-containing vesicles.

Background

Water buffaloes are predominant dairy animals, contributing the most important source of 13% to the milk production worldwide [1]. In recent years, buffalo milk receives increasing research interest and investment in various countries, owing mainly to its attractive nutrient content. Compared with cow milk, buffalo milk is characterized by a rich composition with fat [2], proteins [3], amino acids [4], vitamins and minerals [5, 6], as well much healthier in terms of lower concentration of cholesterol and higher magnitude of unsaturated fatty acids [7]. In addition to nutritional ingredients, increasing evidences have reported that a type of membrane-bound carriers termed as exosomes were identified to present in the breast milk of human [8, 9], cow [10, 11] and pig [12], which have recently been considered as major players in cell-cell communication [13]. Exosomes are 40–100 nm vesicles in diameter that are widely present in almost all biological fluids [14]. And exosomes have been proposed to signal by binding to the recipient cell surface receptors or by internalisation with the cell membrane [15], potentially donating substantial amounts of exosomal miRNAs to the recipient tissue/cells and subsequently playing pivotal roles in the post-transcriptional regulation of gene expression [14]. Previous report showed that human breast milk exosomes with immune modulatory features were important for the development of the infant's immune system [8]. And the roles of bovine milk exosomes have been proved as transporters of

miRNAs for eliciting regulatory functions in the recipient cells [10]. Overall, we therefore hypothesized that buffalo milk exosomes also provided novel information on miRNA composition differing from other types of non-buffalo milks, and highlighted the unrealized physiological importance of exosomes on drinking behaviour.

Results And Discussion

In 27 sequencing libraries, there were 558 unique miRNA candidates sequenced across all species, and only 395 miRNAs which were identified at least in four libraries were considered further (Table S1A). Of these, the top 10 highly expressed miRNA in four buffalo libraries, which accounted for $75.45 \pm 1.18\%$ of all aligned reads, were evolutionarily conserved across multiple species. These miRNAs represented four different miRNA families; miR-let-7 (bta-let-7a-5p, bta-let-7b, bta-let-7c, bta-let-7e and bta-let-7f), miR-30 (bta-miR-30a-5p, bta-miR-30d and bta-miR-30e-5p), miR-148 (bta-miR-148a), and miR-26 (bta-miR-26a). In addition, four of these miRNAs (miR-148a, miR-30a-5p, bta-miR-30d, bta-let-7c) shared common ranking as top 10 expressed miRNAs when parsing the sequence data based on different species (buffalo, cow, pig, human and panda milks) (Table S1A), suggesting these miRNAs could be important nutritional components of milk [16]. In details, the most abundant was bta-miR-148a accounting for $38.88 \pm 3.12\%$ in each buffalo library, which was consistent with previous reports in cow [17], pig [12] and human [9] milks. Recent characterizations of the human salivary exosome have also highlighted the miR-148a expression at high levels that expected to modulate oral cavity defence [18]. To date, although the underlying regulatory mechanism of the most predominant miRNA (miR-148a) packaged into milk exosomes was still unclear, it was intriguing to suggest that miR-148a was a potential biomarker for the quality control of mammalian milk [19]. The miR-30a was highly enriched in exosomes from the serum of acute myocardial infarction patients in vivo, and inhibition of miR-30a or exosome release contributed to maintaining of autophagy after hypoxia [20]. In addition to miR-30a, exosome-enriched miR-30d in endometrial fluid was proposed to be taken up by the pre-implantation embryo, thereby resulting in the observed modifications to the transcriptome and embryo adhesion [21]. The enrichment of let-7 miRNA family in the extracellular fractions, particularly, in the exosomes from gastric cancer cells reflected their oncogenic characteristics including tumorigenesis and metastasis [22]. These data implied the roles of highly expressed miRNAs with a specified function in the milk exosomes. To further identify the potential function of the top expressed miRNAs, target prediction was performed using miRanda software. A total of 400 putative target sites for the top 10 expressed miRNAs were identified (Table S1B), and then all of these target candidates were submitted for homology and functional annotation using an online version of the DAVID program. These target genes belonged to 5 KEGG annotated categories that significantly related to a wide variety of disease resistance, immune responsiveness and basic metabolism events, including microRNAs in cancer, lysosome, glycerophospholipid metabolism, proteoglycans in cancer, galactose metabolism and neurotrophin signaling pathway (Table S1C).

For validation and identification of species-specific miRNAs in buffalo milk, we compared the sequencing libraries between buffalo and non-buffalo milks and found that 27 indexed libraries were obviously divided into five groups based on breed differences (Fig. 1). To comparison with miRNA expression in

non-buffalo milks, a total of 32 miRNAs in buffalo milk were significantly up-regulated (Fig. 2A), while 16 were significantly down-regulated (Fig. 2B) using the R Bioconductor package EdgeR analysis with TMM-normalized algorithm. In addition, target prediction revealed a total of 4372 miRNA-target interactions between significantly expressed miRNAs and NCBI RefSeq genes. This resulted in 1759 unique genes targeted by up-regulated miRNAs (Table S1D), 1761 genes targeted by down-regulated miRNAs (Table S1F), and 477 genes targeted by both up and down-regulated miRNAs. Especially, pathway analysis revealed that 39 predicted targets of up-regulated miRNAs were significantly enriched in categories annotated as a role in endocytosis (Table S1E). The endocytosis pathway, for instance, has been highlighted as an important step in the delivery of bovine exosomes and their cargo to human vascular endothelial cells and peripheral tissues by endocytosis [23]. Additionally, we also revealed many of the other pathways which have been previously implicated in series basic metabolism processes in animals. These pathways included metabolic pathways enriched with 127 targets, glycerophospholipid metabolism enriched with 18 targets, protein processing in endoplasmic reticulum enriched with 26 targets, glycosaminoglycan biosynthesis enriched with 6 targets, biosynthesis of amino acids enriched with 13 targets, etc (Table S1E). Taken together, these analyses strongly suggested that up-regulated miRNAs that were differentially expressed between buffalo and non-buffalo milks were key regulators of the host metabolism processes shuttling within exosomes by endocytosis. On the contrary, the targets of down-regulated miRNAs were annotated with a total of 31 significantly KEGG pathways (Table S1G). In addition to metabolic pathways shared with the target annotation of up-regulated miRNAs, computational analysis of the down-regulated miRNA targets has identified the statistical over-representation of several terms previously implicated in response to immunity events, such as T cell receptor signaling pathway, NF-kappa B signaling pathway, AMPK signaling pathway, HTLV-I infection, lysosome, inflammatory mediator regulation of TRP channels, etc. The evidences indicated that the down-expressed miRNAs identified in this study were likely central regulators of the immune response and thus represented potential targets or novel biomarkers of infection and inflammation.

Conclusions

Milk exosomal miRNA profiles that included 4 buffalo, 4 cow, 8 pig, 4 human and 7 panda were analyzed, and milk enriched miRNA candidates across all species were annotated to modulate disease resistance, immune responsiveness and basic metabolism events. In addition, a total of 32 miRNAs in buffalo milk were significantly up-regulated and 16 miRNAs were significantly down-regulated. Functional analysis showed that up-regulated miRNAs were mainly related to host metabolism processes, while the predicted functions of down-regulated miRNAs were enriched in immune response. Our data highlights the biological role of milk exosomes which contain a rich plethora of miRNAs that are not only involved in immune regulation, but also in the growth, repair and development events.

Methods

Milk exosomes collection and sequencing analysis

Buffalo (*Murrah* breed) and cow (*Friesian* breed) milk samples were obtained respectively from 4 healthy mid-lactating animals in a local farm (Panyu town, Guangzhou city, Guangdong province, China), and crude exosomes were purified following our previous method [23]. Then, exosomal RNAs from each milk sample were used for library construction and subjected to single-end sequencing in the length of 40 nt with an Illumina Genome Analyzer (Biomarker Technologies, Beijing city, China). All procedures were conducted under protocols approved by the Institutional Animal Care and Use Committee of South China Agricultural University, China.

MiRNA analysis

In addition to the indexed sequencing data of buffalos and cows, we downloaded the exosomal small RNA data of pig, human and panda with the experiment series accession number GSE36590, GSE32253 and GSE89755 in the GEO database (<https://www.ncbi.nlm.nih.gov/gds/>), respectively. Using the miRDeep2 program [17], a total of 27 sequencing libraries that included 4 buffalo, 4 cow, 8 pig, 4 human and 7 panda were further analyzed by blasting against bovine miRBase miRNA annotation (<http://www.mirbase.org/>) to identify conserved candidates between different species. The read count of each identified miRNA was firstly normalized with TMM-normalized algorithm, and the R Bioconductor package EdgeR analysis (<http://bioconductor.org/packages/edgeR/>) was applied to identify differentially expressed (DE) miRNAs with P value < 0.05 and fold change ≥ 2 between different groups.

Target predictions and annotation

The 3'UTR sequences of the bovine RefSeq genes were downloaded from the University of California Santa Cruz (UCSC) table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>). The targets of highly and differentially expressed miRNAs were successfully predicted using miRanda software (<http://34.236.212.39/microna/home.do>), and the biological KEGG pathway analysis of the predicted targets were further performed by an online version of the DAVID program (<https://david.ncifcrf.gov/>).

Declarations

Abbreviations

GEO: NCBI Gene Expression Omnibus; DAVID: The Database for Annotation, Visualization and Integrated Discovery; KEGG: Kyoto Encyclopedia of Genes and Genomes; TMM: the trimmed mean of M-values; AMPK: Adenosine 5'-monophosphate-activated protein kinase.

Ethics approval and consent to participate

All procedures were conducted under protocols approved by the Institutional Animal Care and Use Committee of South China Agricultural University, China.

Consent for publication

Not applicable.

Availability of data and material

The datasets supporting the conclusions of this article are included within the article and its additional files.

Competing interests

The authors declare that they have no competing interests.

Funding

This research was supported by the projects of Guangdong Provincial Promotion Project on Preservation and Utilization of Local Breed of Livestock and Poultry, the major scientific projects in general colleges and Universities of Guangdong Province [2017KTSCX023], and the Opening Foundation of The State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources [OSKL201502].

Authors' contributions

YQX and JJS collected data, perform analysis and also drafted the manuscript. ZJC contributed to data analysis. JYL, TC, QYX and YLZ conceived this study and revised the manuscript. All authors read and proved the final manuscript.

Acknowledgements

We thank the High Performance Computing center of South China Agricultural University for providing computational resources in this work.

Permission to collect

The exosomal small RNA datas of pig, human and panda were free downloaded from the publicly accessible NCBI GEO database, and this is an open escience data sharing platform and allowed to shared the datas for scientific research.

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