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A. Canovas, Gonzalo Rincon, Claudia Bevilacqua, Alma Islas- Trejo, Pauline Brenaut, et al.. Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing. Scientific Reports, 2014, 4, np. 10.1038/srep05297 . hal-01193860

HAL Id: hal-01193860

<https://hal.science/hal-01193860>

Submitted on 27 May 2020

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OPEN

SUBJECT AREAS:
RNA SEQUENCING
GENE EXPRESSION

Received
10 October 2013

Accepted
23 April 2014

Published
8 July 2014

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Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing

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The objective of this study was to examine five different sources of RNA, namely mammary gland tissue (MGT), milk somatic cells (SC), laser microdissected mammary epithelial cells (LCMEC), milk fat globules (MFG) and antibody-captured milk mammary epithelial cells (mMEC) to analyze the bovine mammary gland transcriptome using RNA-Sequencing. Our results provide a comparison between different sampling methods (invasive and non-invasive) to define the transcriptome of mammary gland tissue and milk cells. This information will be of value to investigators in choosing the most appropriate sampling method for different research applications to study specific physiological states during lactation. One of the simplest procedures to study the transcriptome associated with milk appears to be the isolation of total RNA directly from SC or MFG released into milk during lactation. Our results indicate that the SC and MFG transcriptome are representative of MGT and LCMEC and can be used as effective and alternative samples to study mammary gland expression without the need to perform a tissue biopsy.

The mammary gland is a secretory skin gland unique to the class Mammalia. Mammary epithelial cells are unique in that they synthesize and secrete milk. They also form part of a complex and heterogeneous tissue along with multiple cell types including myoepithelial, stromal and immune cells, making it difficult to precisely assign gene expression to the different cell types. Thus, it is important to distinguish which cell populations play specific functions, and to obtain relevant expression profile data reflecting the *in vivo* state in order to recognize differences in these cell fractions and to obtain reliable transcriptomic results¹. Mammary epithelial cells are normally subject to turnover and are replaced by new cells². These exfoliated cells are shed into the milk and represent a proportion of the somatic cells found in milk. Separately, a portion of the cytoplasm of the mammary epithelial cells is included within the milk fat globules during the secretion process³.

Total RNA extracted from these different fractions such as milk epithelial cells and milk fat globules has been used to assess the transcriptional activity of the secretory mammary epithelium in livestock⁴. Alternative sampling approaches include isolating RNA directly from biopsies of mammary gland tissue⁵, from somatic cells in milk that are naturally released during lactation^{6,7}, from antibody-captured epithelial cells in milk^{8–10} and from milk fat globules¹¹. Also, laser-capture microdissection has been used to selectively isolate epithelial cells from frozen tissue sections of the mammary gland¹. Some of these sampling procedures were validated in an earlier study using qPCR for specific genes and/or using microarray¹¹. With the advent of Next Generation sequencing, RNA-Sequencing presents the opportunity to examine gene expression on a global basis, thereby providing numerous advantages over microarray analyses because of its wide dynamic range and its ability to quantify all genes present and not only those targets found on the array¹². Only SC have been validated in relation to MGT using RNA-Sequencing⁵. Hence, here we compared the transcriptome for cells isolated by all the above different sampling methods to document the representation of genes and their levels of expression. We collected samples from the same cows and examined the transcriptome of mammary gland tissue (MGT), milk somatic cells (SC), laser



microdissected mammary epithelial cells (LCMEC), milk fat globules (MFG) and antibody-captured mammary epithelial cells from milk (mMEC) using RNA-Sequencing.

Results

RNA preparation and amplification. A total of 14 bovine samples (three MGT, three LCMEC, three MFG, two SC and three mMEC) from two Jersey and one Normande cows were analyzed by RNA-Sequencing. Figure 1 shows the chromatogram traces profiling the quality of the RNA obtained for each fraction. The spectrophotometric absorbance profile for RNA from the MGT (Figure 1A) and LCMEC (Figure 1C) were similar (RIN = 6.5–7.0). The quality of the RNA may be affected by time taken to obtain the tissue biopsy until it is frozen, and the time to cut the sections to freeze in the OCT blocks

used for LCMEC. Comparison between mammary gland epithelial cells before and after laser microdissection was performed (Figure 2). Alveolar (acinar) structures (Figure 2A) lined by mammary epithelial cells (yellow arrows) could be easily distinguished after staining mammary tissue sections with Mayer's hematoxylin (Sigma). The LCMEC were dissected and collected on a cap at 60× (Figure 2B1) and 4× (Figure 2B2) magnifications. The RIN was similar (6.5 to 7.0) between MGT (Figure 2A1) and LCMEC (Figure 2B3), as illustrated in the chromatogram profiles. The total RNA yield for one laser capture cap ranged between 5 to 10 ng. In addition, to assess a possible contamination of microdissected MEC, qPCR systems were carried out to quantify specific markers for mammary myoepithelial cells (KRT14), lymphocytes (CD3e), neutrophils (CD18), macrophages (CD68 and CD18) and MEC (CSN3). In

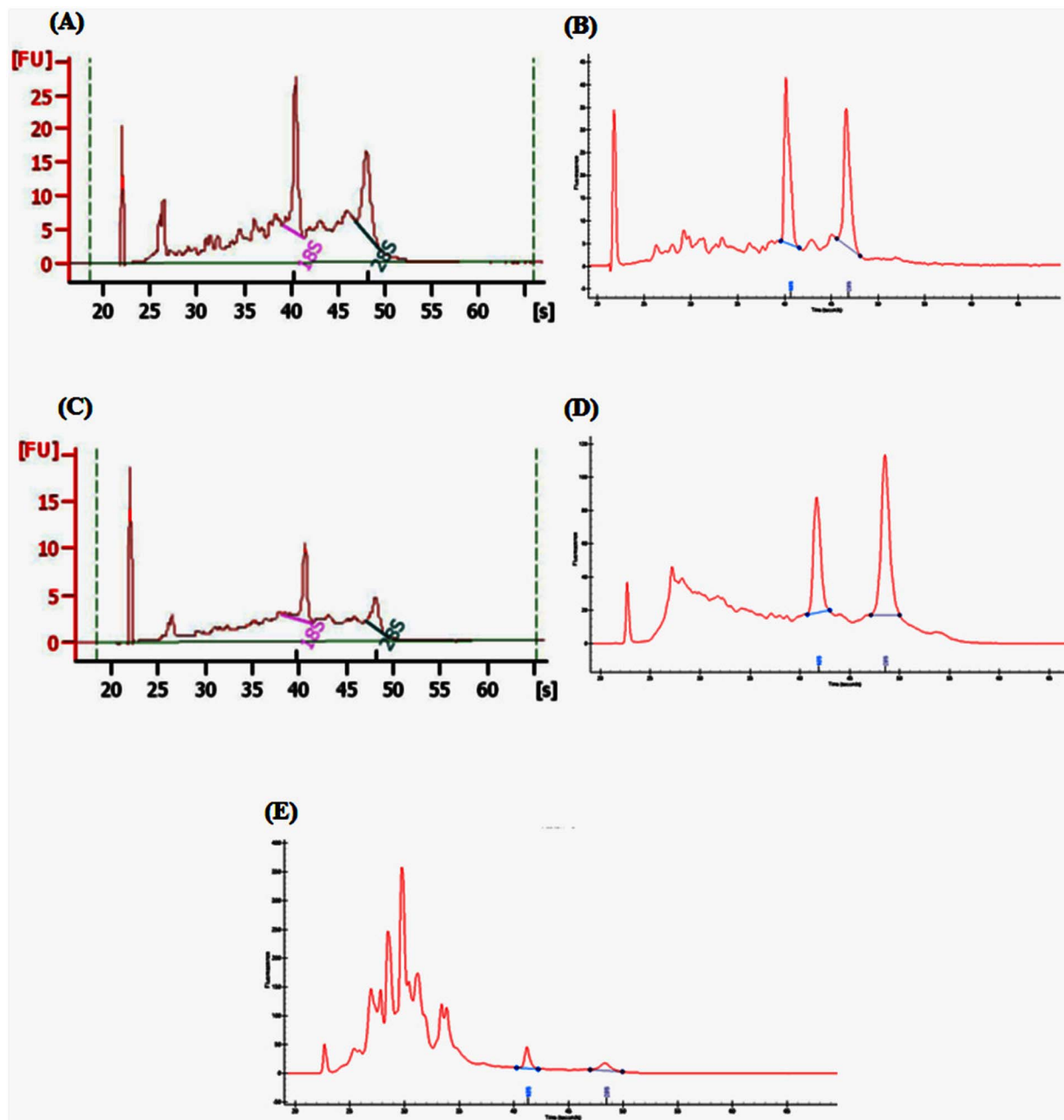


Figure 1 | Total RNA capillary electrophoresis chromatograms from mammary and milk fractions. (A) Mammary tissue (MGT), (B) Somatic cells (SC), (C) Laser capture mammary epithelial cells (LCMEC), (D) Antibody-captured milk mammary epithelial cells (mMEC), (E) Milk fat globule (MFG). Traces (A) and (C) (Agilent Bioanalyzer), traces (B), (D), (E) Experion Analyzer (BioRad). These diagrams show the differences in quality of RNA obtained from the different fractions.

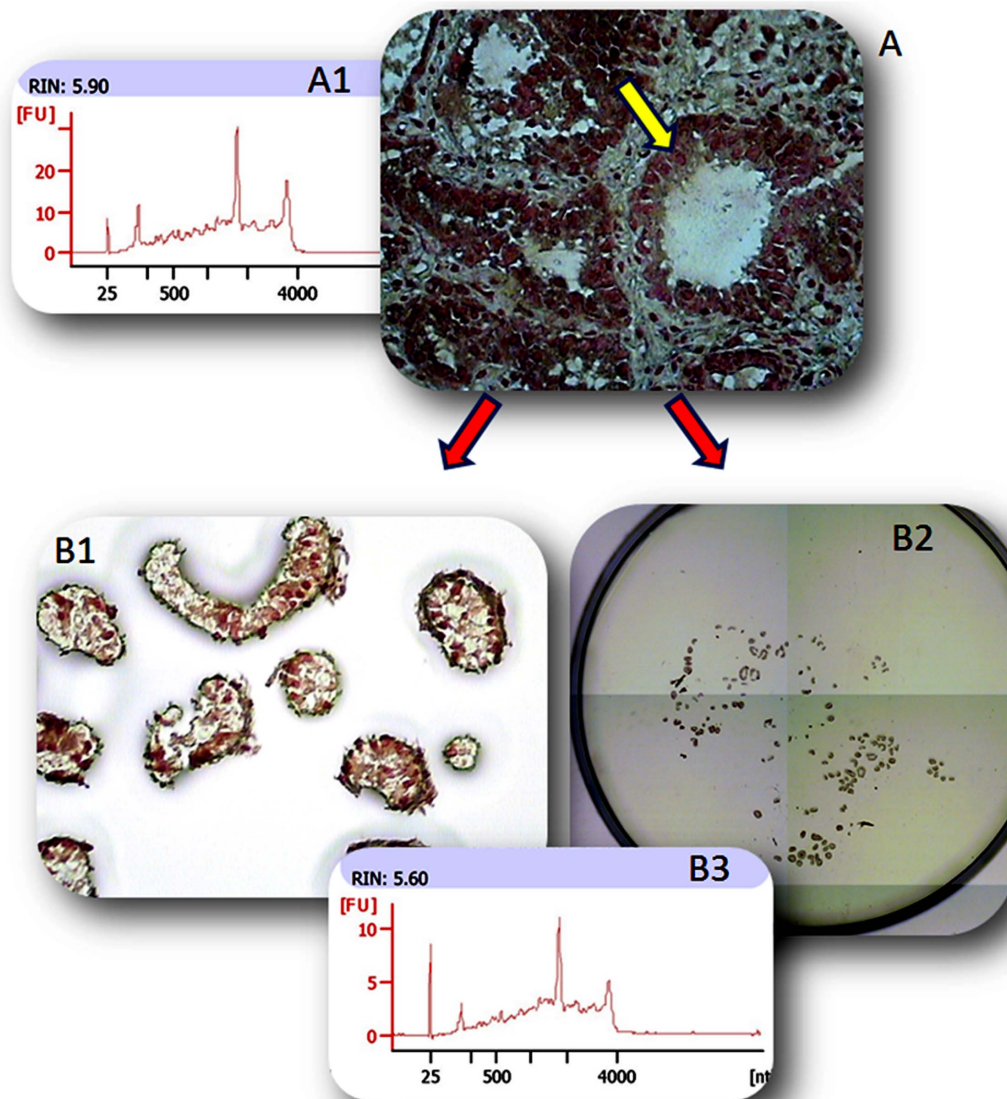


Figure 2 | Mammary gland tissue (MGT) before microdissection (A) and mammary epithelial cells after laser microdissection (LCMEC) (B1 and B2). Chromatograms from total RNA capillary electrophoresis; MGT before microdissection (A1) LCMEC after microdissection (B3).

general, LCMEC showed a similar profile for each sample, with over-expression of MEC specific markers (LALBA and CSN2S2) and under-expression of mammary myoepithelial cells markers (KRT14) and immune cells markers (CD3e and CD68). Also, the same profile was observed in MFG and mMEC fractions with an over-expression of marker CD68, suggesting the presence of macrophages (Supplementary File 2).

High RIN values (around 8.0) were consistently observed for total RNA from SC (Figure 1B) despite the fact that the milk sample was kept on ice for three hour until transported to the laboratory for RNA extraction. The RNA from MFG contains low molecular weight fragments and a very low amount of ribosomal RNA (RIN = 6.0) (Figure 1E).

The membrane of MFG contains specific components such as phospholipids, proteins and glycoproteins that are known to have an affinity for the surface of bacterial cells. By analyzing all the MFG reads not mapping to the bovine genome (~11 million reads), we identified the presence of 618 different bacteria. In contrast, approximately 9 million not mapped reads were found in SC as being associated just with *E. coli*.

The mMEC samples purified with the antibody method presented a pattern similar to the MFG RNA, with a large fraction of low

molecular weight RNA (Figure 1D) significantly impacting the RIN value (RIN = 6.0). The quality of RNA obtained from the mMEC in this study was not representative of the quality generally obtained with this method⁸.

RNA-Seq expression analyses. An average of 32 million short-sequence reads was obtained for each individual sample; these were assembled and mapped to the annotated UMD3.1 bovine genome assembly (27,368 genes). In all the samples, 60–75% of the reads were categorized as mapped to the bovine reference sequence (Table 1).

RPKM values¹³ were used to establish the total number of genes expressed in the MGT, SC, LCMEC, MFG and mMEC transcriptome. In this context, approximately 90% of the total annotated genes in the UMD3.1 bovine genome assembly were expressed in the samples under study (24,616 genes out of a total of 27,368).

Correlations between RPKM expression levels for the MGT, SC, LCMEC, MFG and mMEC transcriptomes. The different sampling methods were compared by calculating a Pearson correlation between the RPKM expression levels of the ~24,616 expressed genes in samples of MGT, SC, LCMEC, MFG and mMEC. Our results indicate that gene expression is highly correlated among



Table 1 | Total reads and mapped reads obtained in each sample analyzed

RNA Fraction	Sample number	Breed	Reads (n)	*Mapped reads (n)	% mapped reads
MGT	653	Jersey	40,147,740	24,732,197	61.6
	671	Jersey	38,508,068	23,163,085	60.2
	1816	Normande	26,480,391	19,732,280	74.5
SC	653	Jersey	40,209,699	28,036,287	69.7
	671	Jersey	39,507,994	26,136,100	66.2
LCMEC	653	Jersey	27,335,082	17,121,159	62.6
	671	Jersey	24,355,141	14,345,582	58.9
	1816	Normande	23,173,807	16,973,772	73.3
MFG	653	Jersey	23,918,861	14,588,022	60.9
	671	Jersey	24,334,219	14,475,382	59.5
	1816	Normande	34,023,717	22,407,126	65.9
mMEC	653	Jersey	38,899,626	29,284,686	75.3
	671	Jersey	38,495,029	28,292,867	73.5
	1816	Normande	29,191,918	22,056,958	75.6
Average			32,041,521	21,524,679	66.9

*Reads categorized as mapped to the annotated UMD3.1 bovine genome assembly (27,368 genes). MGT: mammary gland tissue; SC: milk somatic cells; LCMEC: laser microdissected mammary epithelial cells; MFG: milk fat globules; mMEC: antibody- captured milk mammary epithelial cells.

LCMEC, MGT, SC and MFG. These sampling methods showed the highest correlation values in gene expression with LCMEC, ranging from $r = 0.80$ to $r = 0.99$ (MGT), from $r = 0.80$ to $r = 0.95$ (SC) and from $r = 0.81$ to $r = 0.93$ (MFG) in Jersey and Normande cows, respectively (Table 2). Interestingly, gene expression in SC was significantly correlated with that in MGT in Jersey and Normande cows ($r = 0.98$ and $r = 0.92$, respectively). By contrast, a low correlation existed between mMEC and LCMEC in both Jersey and Normande cows (correlation ranged from $r = 0.15$ to $r = 0.39$, Table 2). In addition, independent correlation analysis were performed using the list of highly expressed (≥ 500 RPKM), normally/medium expressed (ranged from 500 to 10 RPKM) and lowly expressed (< 10 RPKM) genes¹⁴. A homogeneous distribution of expressed genes was obtained across LCMEC, MGT, SC, MFG and mMEC. All fractions had a higher number of lowly expressed genes. The high correlation among LCMEC, MGT, SC and MFG persist in highly-expressed, normally/medium-expressed and lowly-expressed genes (Additional files 3, 4 and 5).

A correlation was also calculated using the ranking/position of the RPKM gene expression values. The ranking/position stretched from the most highly expressed to the lowest expressed gene for each sample analyzed. Consistently, the highest correlated values were between LCMEC and MGT, MFG and SC samples in both breeds (correlation ranged from $r = 0.90$ to $r = 0.94$; $p < 0.0001$). In this analysis, relatively high correlations (ranging from $r = 0.79$ to $r = 0.90$) were observed between LCMEC and mMEC (Supplementary File 6).

Most highly expressed genes in MGT, SC, LCMEC, MFG and MEC. We also compared the genes having the greatest expression

in MGT, SC, LCMEC, MFG and mMEC (Table 3). As reported by Wickramasinghe et al.¹⁴ for milk SC, the genes having the greatest expression in all MGT, SC, LCMEC and MFG transcriptomes were the caseins (i.e. CSN2, CSN3, CSN1S1 and CSN1S2), the main two whey proteins (BLG and LALBA) and GLYCAM1 (glycosylation-dependent cell adhesion molecule 1). Among these, CSN2 and CSN3 showed the highest RPKM values ranging from 207,305 to 1,877 depending on the sample (Table 3). BLG, LALBA and GLYCAM1 were abundantly expressed in MGT, SC, LCMEC and MFG. Surprisingly BLG, LALBA and GLYCAM1 were not highly expressed in mMEC. In general the overall transcriptome expression level in mMEC was several orders of magnitude lower than in the other samples. In cattle, mMEC only account for no more than 5% of the somatic cells¹⁵. Also, the additional step in the purification of mMEC from SC may explain the observed different expression profile.

A comparison of the list of the most highly expressed genes revealed that approximately 15 out of the 17 genes with greatest levels of expression in LCMEC were also expressed abundantly in both MGT and SC. In contrast, only 9 out of these 17 were abundantly expressed in mMEC (Table 3). The transcriptome for MGT, SC, LCMEC and MFG had a very similar expression pattern. Both SC and MFG showed highly expressed genes, such as SPP1 (secreted phosphoprotein 1 or osteopontin), RPS17 (ribosomal protein S17), TCTP (translationally controlled tumor protein) and PTMA (prothymosin alpha). Among these, SPP1 cooperates with other pro-inflammatory cytokines such as TNF α to participate in the overall inhibition of mammary epithelial cell viability that is required for tissue remodeling in the bovine mammary gland during the course of

Table 2 | Correlations between RPKM expression levels of MGT, SC, LCMEC, MFG and mMEC transcriptome in Jersey and Normande cows

		MGT		SC	LCMEC		MFG		mMEC	
		Jersey	Normande	Jersey	Jersey	Normande	Jersey	Normande	Jersey	Normande
MGT	Jersey	1.00	-	-	-	-	-	-	-	-
	Normande	0.97	1.00	-	-	-	-	-	-	-
SC	Jersey	0.98	0.92	1.00	-	-	-	-	-	-
LCMEC	Jersey	0.80	0.90	0.79	1.00	-	-	-	-	-
	Normande	0.90	0.99	0.95	0.80	1.00	-	-	-	-
MFG	Jersey	0.90	0.88	0.93	0.81	0.85	1.00	-	-	-
	Normande	0.88	0.92	0.95	0.85	0.93	0.93	1.00	-	-
mMEC	Jersey	0.18	0.15	0.26	0.39	0.23	0.50	0.37	1.00	-
	Normande	0.15	0.16	0.22	0.23	0.15	0.37	0.32	0.67	1.00

MGT: mammary gland tissue; SC: milk somatic cells; LCMEC: laser microdissected mammary epithelial cells; MFG: milk fat globules; mMEC: antibody- captured milk mammary epithelial cells.



Table 3 | Most highly expressed genes in MGT, SC, LCMEC, MFG and mMEC transcriptome in Jersey and Normande cows expressed in RPKM values (reads per kilo base per million mapped reads). Green color represents the most highly expressed genes, red color represents the lowest expressed genes and the different color tones are intermediate values

Gene	MGT		SC	LCMEC		MFG		mMEC	
	Jersey	Normande	Jersey	Jersey	Normande	Jersey	Normande	Jersey	Normande
CSN2	207305	145263	156130	105065	179820	76891	45571	13651	2591
CSN3	72233	87335	30208	51838	84031	15602	18689	1877	1991
CSN1S1	39736	45340	24903	25982	50297	11528	7652	956	710
CSN1S2	12056	32973	4010	9093	29740	2156	4592	206	551
LALBA	5619	6537	3056	2706	11139	2693	1719	43	42
GLYCAM1	4035	8346	3579	2668	10633	1758	2995	119	90
BLG	3231	2407	6835	2697	5925	3854	707	121	84
SPP1	1406	1036	6975	845	1301	927	6250	10680	992
RPS17	1374	366	3164	120	90	2183	916	118	69
TCTP	937	1098	2724	974	917	2451	2656	1320	42
PTMA	893	123	2876	401	104	1843	392	3345	28
MFG8	705	186	576	75	84	95	49	177	2
CD36	486	691	264	322	673	56	112	65	27
SCD	265	459	44	222	570	39	98	4	6
FABP4	171	527	138	182	103	90	123	5	4
FRIH	127	134	1898	121	87	779	3400	2165	53
RL19	519	358	1351	348	405	1142	717	255	16
RS12	412	152	1172	516	186	66	66	1379	84
CD68	3	3	1108	7	4	84	62	1755	46
RS17	157	117	117	1577	433	87	119	1499	33
B2MG	171	156	766	482	265	97	1055	84	21
PLIN2	57	65	77	75	73	994	8195	38	23
TUBA1B	46	39	38	35	37	59	46	1625	53
HMOX1	4	0.2	1	0.09	0.04	7	3	1073	54
S100A11	33	4	2	10	5	51	10	936	57
RL10	36	4	34	32	35	45	33	668	53

MGT: mammary gland tissue; SC: milk somatic cells; LCMEC: laser microdissected mammary epithelial cells; MFG: milk fat globules; mMEC: antibody-captured milk mammary epithelial cells. Jersey data provided correspond to mean values of the two analyzed Jersey cows.

involution¹⁶. Furthermore, MFG showed high levels of gene expression for perilipin 2 (PLIN2) that is related to lipid accumulation and secretion¹⁷. In contrast, mMEC showed a different profile for all caseins and major whey proteins, and also uniquely expressed high levels of the TUBA1B (tubulin alpha 1B), HMOX1 (heme oxygenase (decycling) 1), S100A11 (S100 calcium binding protein A11) and RL10 (ribosomal protein L10) genes in Jersey cows. These genes represent markers of cell development and immunity. Also, expression of CD68 (CD68 molecule), a specific marker for macrophages, was elevated in the SC and mMEC transcriptomes in Jersey cows, perhaps due to the presence of a higher proportion of macrophages.

Discussion

The transcriptome for mammary gland was studied using five different sampling methods. Total RNA from MGT, SC, LCMEC, MFG and mMEC were compared using RNA-Sequencing to examine the representation of genes and their levels of expression.

The integrity and type of the RNA varied considerably between samples depending on the sampling method, which in turn had a bearing on the RNA-Sequencing results (Table 1). The RNA from the MGT, LCMEC and SC showed similar electrophoresis chromatograms profiles. The RNA from MFG contained low molecular weight fragments and a very low amount of ribosomal RNA due to the presence of small amounts of cytoplasmic material in the bovine milk fat globules during the MFG secretory process³. This likely explains the lower RIN value (RIN = 6.0) of this tissue. The low MW RNA may be due to the presence of bacteria and also very small RNAs that are abundant in this fat fraction¹⁸. The MFG membrane contains specific components such as phospholipids, proteins and glycopospholipids that are unique in this cell fraction. Interestingly, these components are known to have an affinity for the cell surface of

bacteria¹⁹. Considering this, we analyzed all the MFG reads not mapping to the bovine genome (~11 million reads) for the presence of bacterial genes. From this analysis we found that 618 different kinds of bacteria were identified with MFG. Comparatively, approximately 9 million reads were found in SC as being associated just with *E. coli*. The mMEC samples purified with the antibody method presented a pattern similar to the MFG RNA, with a large fraction of low molecular weight RNA significantly impacting the RIN value (RIN = 6.0).

The transcriptome for bovine LCMEC was highly correlated with that for MGT, SC and MFG, and showed a high correlation with MGT in Jersey ($r = 0.80$) and Normande ($r = 0.99$) cows ($p < 0.0001$). A significant correlation was found between MGT and SC in Jersey ($r = 0.98$) and Normande ($r = 0.92$) cows. By contrast, a low correlation existed between mMEC and LCMEC in both Jersey and Normande cows (correlation ranged from $r = 0.15$ to $r = 0.39$). The MGT is complex and heterogeneous, with multiple cell types including myoepithelial, stromal and immune cells. In terms of immune cells, SC is more similar to MGT than mMEC due to the high proportion of immune cells such as neutrophils, lymphocytes and macrophages which account for *ca.* 95% of SC in milk from healthy cows¹⁵. It is important to note that the isolation of mMEC utilized the binding of bovine MEC to a monoclonal antibody recognizing cyto-keratins⁸. Different antibody reactions both with not much high RNA quality level can alter and affect the final product, which may explain why these samples had a low correlation with all the cellular fractions analyzed (range from $r = 0.13$ to $r = 0.50$).

In general, the highly expressed genes such as caseins (CSN1S1, CSN1S2, CSN2, CSN3) and whey proteins (BLG, LALBA) showed a similar expression profile in MGT, LCMEC, SC and MFG. However, MFG had a unique abundant expression of the PLIN2 gene that is implicated in lipid accumulation.



The majority of the lipid produced during lactation is secreted into milk by a process of membrane envelopment of cytoplasmic lipid droplets (CLDs). Others have hypothesized that PLIN2 plays a pivotal role in both formation and secretion of milk lipids, where it functions as an adaptor to couple CLDs to the cytoplasmic leaflet of the apical plasma membrane of MEC²⁰. This gene may also be involved in development and maintenance of adipose tissue. Furthermore, PLIN2 is expressed by a wide range of cultured cell lines, including fibroblasts, endothelial and epithelial cells, and tissues, suggesting that it may serve as a marker of lipid accumulation in diverse cell types and diseases²¹.

Expression of CD68 (CD68 molecule), a specific marker for macrophages, was elevated in the SC and mMEC transcriptomes in Jersey cows, perhaps due to the presence of a higher proportion of macrophages. This finding would suggest that mMEC purification was not totally effective. Although the antibody-directed mMEC purification method allowed the specific selection of epithelial cells, which account for less than 5% of total milk cells (SC), the mMEC transcriptome was different from the rest of the transcriptomes analyzed. In our results, immunomagnetic mMEC purification method showed that a conjoint of reactions was affecting the proportion and/or the function of white cells present in milk, showing a unique set of highly expressed genes such as TUBA1B, HMOX1, S100A11 and RL10 involved in anti-inflammatory processes, cell death or apoptosis, specifically in Jersey mMEC samples.

Up to this point, the majority of gene expression analyses related to bovine lactation have been developed using tissues obtained by biopsy^{22,23}. This biopsy approach is invasive during a stage when vascularization of the gland is at a maximum, which presents significant technical challenges and management issues in the recovery of the animals.

An alternative sampling procedure has been proposed via isolating mRNA directly from mMEC^{8,9}, MFG¹¹ and SC^{6,7} that are released into milk during lactation. Using RNA extracted from mMEC, MFG or SC represents a more accessible method for assessing gene expression in the mammary epithelium⁴, particularly when dynamic studies require the repeated analysis of samples from the same animal. Considering the cost and labor involved to obtain a sample of mammary parenchyma for RNA extraction, analyzing milk SC and MFG appears to be an alternative, direct and simple approach that provides a high correlation with gene expression in MGT and LCMEC without the need to perform a biopsy of the mammary gland tissue. Our results present the similarities between different sampling methods by examining the transcriptome of mammary gland tissue and different RNA sources from milk. This information can guide investigators in choosing the most appropriate sampling method to examine specific physiological states from different sources of RNA during lactation for different research applications. One of the simplest procedures to examine the transcriptome associated with milk appears to be to isolate mRNA directly from MFG and SC that are released into milk during lactation. Our analyses suggest that the SC and MFG transcriptome are the most representative of MGT and LCMEC and can be used as an effective and easy way to study gene expression using RNA-Sequencing, without the need to perform a mammary gland biopsy.

Methods

Animal material. Mammary gland tissue and milk samples were obtained from two Jerseys and one Normande cow at the University of California – Davis (UCD) and the Institut National de la Recherche Agronomique (INRA) herd (Le Pin-au-Haras, France), respectively. Jersey cows were in their 3rd and 4th lactation around 100 days in milk whereas Normande cow was in its 2nd lactation around 180 days in milk. Mammary tissue biopsies were performed using a 9-gauge, 12-cm probe with a 12-mm aperture as described by VanKlompenberg et al.²³ in Jersey cows and 70 × 4 mm rotating stainless steel cannula in Normande cow²⁴. A 5-mm incision was made through the skin and connective tissue approximately half-way up the rear udder quarter using a scalpel blade before the parenchyma was penetrated with a Hologic ATEC Biopsy Console Handpiece for excision of a tissue core (Hologic Inc., Bedford,

MA) and Farr's Instrument. Triplicate milk samples were collected before performing tissue biopsies and were held on ice. Sample collections and procedures were performed in accordance with the approved guidelines of the UC Davis Institutional Animal Care and Use Committee (IACUC).

RNA extraction. Biopsied mammary gland tissue (MGT) was divided in two: one part was immediately put in a cryomold with OCT compound and frozen with a mix of dry ice and isopropanol for future microdissection. The other portion was frozen in liquid nitrogen for subsequent extraction of RNA. Total RNA from MGT was extracted using Trizol (Invitrogen).

Laser capture microdissection of epithelial cells (LCMEC) from the mammary tissue was performed using an Arcturus Veritas Microdissection system and software (Applied Biosystems). Cryosectioning, staining, dehydration and harvesting of microdissected cells was performed as described Bevilacqua et al.¹. Total RNA was extracted from captured cells using the PicoPure® RNA Isolation Kit (Arcturus, Applied Biosystems) according to the manufacturer's instructions, including an on-column DNase I treatment (Qiagen). An aliquot of RNA was reverse transcribed to validate the selectivity and specificity of laser capture microdissection by qPCR for markers of myoepithelial cells, MEC and immune cells. To assess a possible contamination of microdissected MEC, qPCR systems designed to quantify specific markers for mammary myoepithelial cells (Krt14), lymphocytes (CD3e), neutrophils (CD18), macrophages (CD68 and CD18) and MEC (CSN3) were implemented. Sequences were from GenBank (Supplementary File 1).

Milk was centrifuged at 2,000 g for 10 min to pellet somatic cells (SC) and to separate the upper milk fat globule (MFG) fraction. The MFG fraction was mixed with Trizol LS and heated briefly at 30°C while shaking to emulsify the fat. Total RNA was extracted from milk somatic cells (SC) and from milk fat using Trizol (Invitrogen) following the protocol from the manufacturer as described in Cánovas et al.²⁵ and Brenaut et al.¹¹, respectively. In addition, MEC from milk (mMEC) were obtained according to the procedure described by Boutinaud et al.⁸ using a protocol based on the binding of mMEC to a monoclonal antibody recognizing cytokeratin 8 (clone 34BE12, Sigma-Aldrich), except that milk was kept on ice for approximately 3 h until it was transported to the laboratory. In all cases the purified total RNA was treated with Turbo DNase (Invitrogen, Carlsbad, CA). Quality of the total RNA was evaluated using the RNA Integrity Number (RIN) value in the Agilent Bioanalyzer 2100 or in the Experion Analyzer (BioRad).

RNA-Sequencing. RNA-Sequencing was used to measure gene expression in the MGT, SC, LCMEC, MFG and mMEC transcriptome. Total RNA (DNase-treated) was used to synthesize amplified cDNA following the protocol in the Ovation RNA-seq system and the Encore NGS library system (NuGEN, San Carlos, CA). Total RNA (100 ng DNase treated) was subjected to an RNA amplification process using the Ribo-SPIA technology from the Ovation RNA-seq System (NuGEN, San Carlos, CA). The amplified cDNA (200 ng) was fragmented using the Bioruptor sonicator (Diagenode) 30 sec ON, 30 sec OFF cycles for 10 min to produce fragments with 150–200 bp size distribution. Adaptor molecules were ligated to the ends of each fragment and amplified by PCR to produce the final library using the Encore NGS library system (NuGEN, San Carlos, CA). A single library was made for each sample.

Fragmented DNA was sequenced on a GAII sequencer analyzer (Illumina, San Diego, CA).

Quality control (QC) analysis was performed using the application NGS quality control tool of CLC Genomics workbench software (CLC Bio, Aarhus, Denmark). This tool assess sequence quality indicators based on the FastQC-project (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). Quality was measured taking into account sequence-read lengths and base-coverage, nucleotide contributions and base ambiguities, quality scores as emitted by the base caller and over-represented sequences. All the samples analyzed passed all the QC parameters having the same length (36 bp), 100% coverage in all bases, 25% of A, T, G and C nucleotide contributions, 50% GC on base content and less than 0.1% over-represented sequences, indicating a very good quality.

Short sequence single reads (36 bp) were mapped to the annotated UMD3.1 bovine reference genome (<http://www.ncbi.nlm.nih.gov/genome/?term=bos+taurus>). Analysis of RNA-Seq expression data was performed using the transcriptomics analysis tool of CLC Genomics workbench software. Data were normalized by calculating the 'reads per kilobase per million mapped reads' (RPKM) for each gene¹³. To select expressed genes a threshold of RPKM ≥ 0.2 was used¹⁴.

Large gap mapping analysis was performed to identify those reads not mapping to the bovine genome. Then, de novo assembly analysis was performed from unmapped reads to generate contigs using CLC Genomics workbench software (CLC Bio, Aarhus, Denmark). Blast2GO software (<http://www.blast2go.com>) was used for contig annotation and bacteria identification (Gotz et al., 2008). Blast2Go performs the Blast step by communicating directly to NCBI (National Center for Biotechnology Information) blast service. The Blastn algorithm was used to compare a nucleotide query sequence against all the nucleotide sequence database. A statistical significance threshold of 1.0 E-3 (e-value) was established for reporting matches against the database sequences. Also a minimal length (30 bp) of a blast hit and 90% of similarity was used to exclude hits with only small local alignments from the blast results.

Statistical analysis. To examine the similarities between the different sampling procedures a correlation between the RPKM expression levels of MGT, SC, LCMEC, MFG and mMEC transcriptomes was performed using the CORR procedure of SAS (SAS Institute Inc.).



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Acknowledgments

The authors would like to thank Doug Gisi from U.C. Davis Dairy Facility and S. Leurent and Y. Gallard from INRA Experimental Farm of Le Pin-au-Haras, France and S. Marion from UMR PEGASE for their technical help. We gratefully acknowledge the support for this collaborative project from the France-Berkeley Fund.

Author contributions

A.C. analyzed the data and wrote the manuscript, **G.R.** design, analysis and sample collection, **C.B.** laser capture experiments and sample collection, **A.I.T.** sample collection and construction of sequencing libraries, **P.B.** study design and sample collection, **R.C.H.** sample collection, **M.B.** sample collection and processing, **C.M.** sample collection, **M.K.V.** sample collection, **P.M.** and **J.F.M.** conceived, designed and funded the study. All authors reviewed and contributed to the final manuscript.

Additional information

Supplementary information accompanies this paper at <http://www.nature.com/scientificreports>

Competing financial interests: This project was partially funded by the France Berkeley Fund (<http://fbf.berkeley.edu/>), collaboration between JFM and PM and by Incentive credits from the Animal Genetics Department of INRA. Angela Cánovas received a contractual Postdoctoral grant from ME/Fulbright.

How to cite this article: Cánovas, A. *et al.* Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing. *Sci. Rep.* **4**, 5297; DOI:10.1038/srep05297 (2014).



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