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Data in Brief

Distinct microRNA expression profiles in follicle-associated epithelium and villous epithelium

Gaku Nakato [a,1], Koji Hase [a,2], Hiroshi Ohno [a,b,*]

[a] Laboratory for Intestinal Ecosystem, RIKEN Center for Integrative Medical Sciences (IMS), Kanagawa, Japan
[b] AMED-CREST, Japan Agency for Medical Research and Development, Tokyo, Japan

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ABSTRACT

M cells in follicle-associated epithelium (FAE) covering intestinal lymphoid follicles serve as a portal of entry for particulate antigens (Kanaya and Ohno, 2014 [1]). Despite their biological significance, molecular mechanisms that govern M-cell differentiation and function have not been fully elucidated. MicroRNAs (miRNAs) have a role to control host gene expression profiles that modulate cellular physiology and characteristic. Many studies have shown that miRNAs regulate diverse biological processes including developmental timing, differentiation and growth control of cells and tissues (Ivey and Srivastava, 2010 [2]). miRNAs are also relevant to differentiation and function of intestinal epithelium (McKenna et al., 2010 [3]; Runtsch et al., 2014 [4]). Expression profiles and functions of miRNAs in the intestinal epithelium have been examined in jejunal and colonic mucosa [3]. In contrast, those in FAE remain uncharacterized. To address this deficiency, we isolated Peyer's Patch (PP) FAE and villous epithelium (VE) surrounding the FAE, and compared the miRNA expression profiles of FAE and VE by microarray analysis. This revealed that 43 miRNAs were up-regulated, whereas 9 miRNAs were down-regulated, in FAE compared to VE. A unique pattern of miRNA expression by FAE may reflect important diversity in cellular phenotypes and/or functional features of FAE. All microarray data has been deposited at GEO under accession number GSE46264.

Specifications	
Organism/cell line/tissue	*Mus musculus*
Sex	Female
Sequencer or array type	Agilent Scanner (G2505B)
Data format	Analyzed
Experimental factors	Healthy mice in SPF facility
Experimental features	Conducted miRNA expression profiling of intestinal epithelium in BALB/cA mice
Consent	N/A
Sample source location	Yokohama, Japan

1. Direct link to deposited data

http://www.dtd.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46264.

2. Experimental design, materials and methods

PP FAE and VE were isolated from 10 week old SPF BALB/cA mice. Briefly, intestinal tissue was soaked in Hank's balanced salt solution containing 30 mM EDTA for 20 min at 4 °C. After incubation, FAE and VE were isolated by dissection with 26G needles using stereomicroscopic monitoring, as shown in Fig. 1 (Hase et al., 2005 [5]). Isolated epithelial cell sheets were maintained in ice-cold HBSS before RNA extraction. Total RNA was extracted from isolated FAE and VE using mirVana kit (Ambion) according to the manufacturer's instructions. miRNA expression profile was assessed by using Mouse miRNA Microarray Release 12.0 (Agilent Technologies). A hundred nanograms of total RNA was labeled with Agilent miRNA Complete Labeling Reagent and Hyb Kits (Agilent) according to the manufacturer's instructions. The labeled RNA was used to probe the array plates via hybridization for 20 h at 55 °C. Array plates were subsequently washed and then scanned with an Agilent G2565CA Microarray Scanner (Agilent Technologies). Data analysis was performed with Genespring software version 11.0 (Agilent Technologies). Two-fold expression difference between FAE and VE were considered to be significant.

Scatter plot of normalized miRNA expression profiles showed that 43 miRNAs were up-regulated, and nine miRNAs were down-regulated, in FAE compared with VE by at least two-fold (Fig. 2). To efficiently promote particulate antigen uptake, the cellular

* Corresponding author at: Laboratory for Intestinal Ecosystem, RIKEN Center for Integrative Medical Sciences (IMS), 1-7-22 Suehiro, Tsurumi, Kanagawa 230-0045, Japan.
E-mail address: hiroshi.ohno@riken.jp (H. Ohno).
[1] Present address: Dermatology Branch, Center for Cancer Research, National Cancer Institute, NIH, Bethesda, MD, USA.
[2] Present address: Division of Biochemistry, Faculty of Pharmacy, Keio University, Tokyo, Japan.

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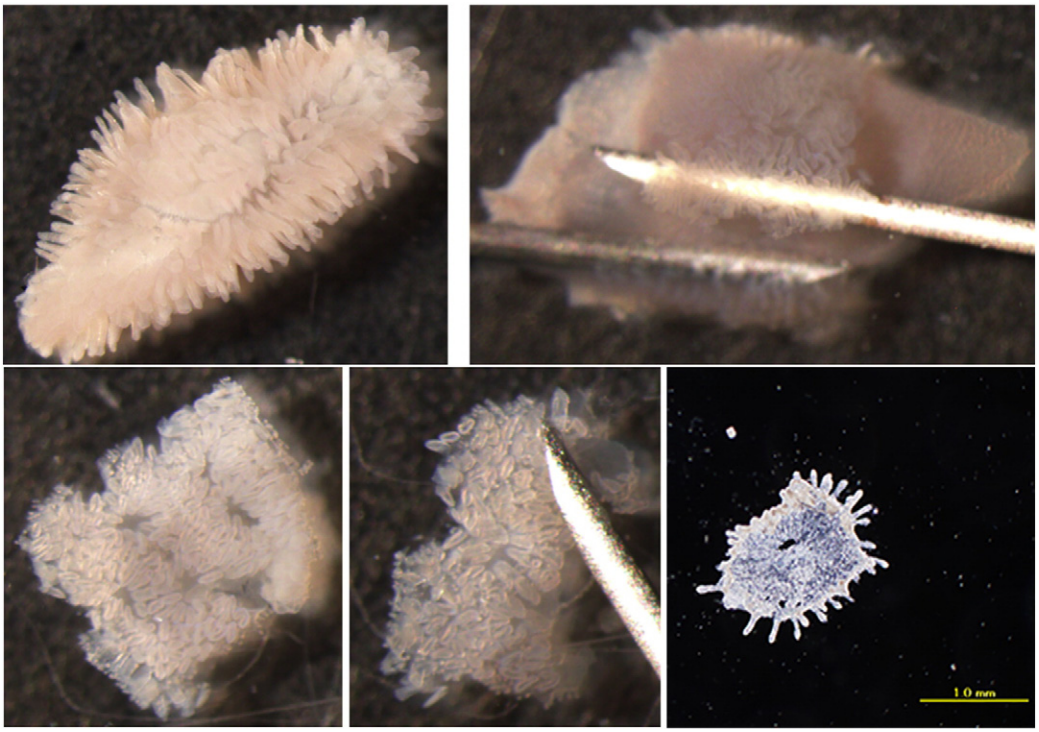

Fig. 1. Procedure of FAE and VE isolation from Peyer's patch.

composition and functions of FAE differ dramatically from VE. VE is dominated by absorptive enterocytes, with scattered goblet cells and enteroendocrine cells. By contrast, FAE contains few goblet or enteroendocrine cells and instead is characterized by the presence of antigen-sampling M cells [1]. Reflecting the difference in epithelial cell compositions, gene expression is differently regulated between FAE and VE [5]. Consistent with this, our microarray data showed that miRNA profiles between FAE and VE were different (See Tables 1 and 2). A unique pattern of miRNA expression for FAE may reflect important cellular phenotypes as well as functional features in FAE. We believe that detailed analysis of FAE/M cell-specific miRNAs will likely provide new insights related to mechanisms of M-cell development and function.

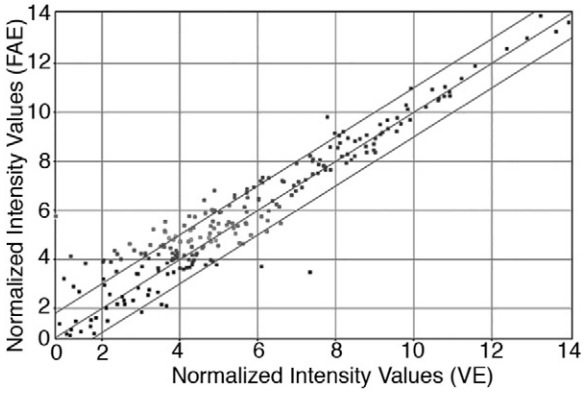

Fig. 2. Comparison of miRNA expression level between FAE and VE. Lines indicate the threshold of two-Fold change.

Table 1
miRNAs upregulated more than 2-fold in the FAE as compared to VE.

miRNA name	miRBase accession number	Fold change
mmu-miR-15a*	MIMAT0004624	7.28
mmu-miR-511	MIMAT0004940	5.69
mmu-miR-872*	MIMAT0004935	5.16
mmu-miR-582-3p	MIMAT0005292	4.51
mmu-miR-193	MIMAT0000223	4.23
mmu-miR-466d-3p	MIMAT0004931	3.95
mmu-miR-365	MIMAT0000711	3.66
mmu-miR-204	MIMAT0000237	3.47
mmu-miR-149	MIMAT0000159	3.32
mmu-miR-335-5p	MIMAT0000766	3.29
mmu-miR-210	MIMAT0000658	3.22
mmu-miR-18a*	MIMAT0004626	3.21
mmu-miR-485*	MIMAT0003129	3.08
mmu-miR-466 h	MIMAT0004884	3.01
mmu-miR-452	MIMAT0001637	2.97
mmu-miR-191*	MIMAT0004542	2.87
mmu-miR-290-5p	MIMAT0000366	2.84
mmu-miR-1224	MIMAT0005460	2.70
mmu-miR-34a	MIMAT0000542	2.69
mmu-miR-466a-3p	MIMAT0002107	2.69
mmu-miR-335-3p	MIMAT0004704	2.68
mmu-miR-1894-5p	MIMAT0007877	2.67
mmu-miR-150	MIMAT0000160	2.62
mmu-miR-297a*	MIMAT0004864	2.61
mmu-miR-203*	MIMAT0004547	2.54
mmu-miR-764-5p	MIMAT0003894	2.50
mmu-miR-328	MIMAT0000565	2.43
mmu-miR-296-5p	MIMAT0000374	2.42
mmu-miR-669a	MIMAT0003477	2.42
mmu-miR-206	MIMAT0000239	2.37
mmu-miR-326	MIMAT0000559	2.36
mmu-miR-346	MIMAT0000597	2.33
mmu-miR-207	MIMAT0000240	2.29
mmu-miR-211	MIMAT0000668	2.25
mmu-miR-1196	MIMAT0005857	2.22
mmu-miR-467 g	MIMAT0005854	2.20
mmu-miR-467e*	MIMAT0005294	2.18
mmu-miR-376b	MIMAT0001092	2.17

Table 1 (*continued*)

miRNA name	miRBase accession number	Fold change
mmu-miR-376a	MIMAT0000740	2.16
mmu-miR-669 h-3p	MIMAT0005842	2.13
mmu-miR-294	MIMAT0000372	2.09
mmu-miR-672	MIMAT0003735	2.07
mmu-miR-34b-3p	MIMAT0004581	2.06

Table 2
miRNAs upregulated more than twice in the VE compared to the FAE.

miRNA name	miRBase accession number	Fold change
mmu-miR-143	MIMAT0000247	16.31
mmu-miR-451	MIMAT0001632	5.79
mmu-miR-654-3p	MIMAT0004898	5.76
mmu-miR-224	MIMAT0000671	2.92
mmu-miR-10a	MIMAT0000648	2.34
mmu-miR-219	MIMAT0000664	2.17
mmu-miR-101a	MIMAT0000133	2.17
mmu-miR-494	MIMAT0003182	2.07
mmu-let-7e	MIMAT0000524	2.06

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