

Expression patterns of Rho-associated protein kinase signaling pathway-related genes in mouse submandibular glands

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Salivary glands are exocrine glands that secrete saliva into the oral cavity, and secreted saliva plays essential roles in oral health. Therefore, maintaining the salivary glands in an intact state is required for proper production and secretion of saliva. To investigate a specific signaling pathway that might affect the maintenance of mouse submandibular gland (SMGs), RNA sequencing was performed. In SMGs, downregulated expression patterns of Rho-associated protein kinase (ROCK) signaling pathway-related genes, including *Rhoa*, *Rhob*, *Rhoc*, *Rock1*, and *Rock2*, were observed. Gene expression profiling analyses of these genes indicate that the ROCK signaling pathway is a potential signal for SMG maintenance.

Keywords: Submandibular glands, RNA sequencing, ROCK signaling pathway

Introduction


Salivary glands are exocrine glands composed of three major glands (submandibular, parotid, and sublingual glands) that produce and secrete saliva into the oral cavity. Secreted saliva is essential to oral and intestinal health and functions such as food digestion, speech, taste perception, mastication, swallowing, and protection from bacteria [1,2]. Bicarbonate in saliva maintain pH of saliva at 6.5–7.4 and protect teeth from cariogenic pathogens [3]. Glycoproteins included in saliva bind with bacterial receptors and agglutinate oral microorganisms to eliminate overload of bacteria [4]. Saliva secreted from each of the major glands have distinguished constituent due to differences in secretory cell type [5]. Tenacious saliva from parotid glands by serous acini, mucin-rich saliva from sublingual glands by mucous acini, and mixed saliva from submandibular

glands (SMGs) by both acinar cell types [6].

Xerostomia, a subjective feeling of dry mouth that may or may not be accompanied by hyposalivation, can be caused by radiotherapy for head and neck cancer, Sjögren's syndrome, or aging [1,2]. Irreversible loss of secretory acinar cells is the major cause of dry mouth [7,8]. Therefore, replacement of the acinar cells is a potential treatment method for dry mouth [9].

Activation of Rho-associated protein kinase (ROCK) signaling pathway is related to the development of various diseases such as asthma, erectile dysfunction, glaucoma, cancer, and kidney failure indicating the importance of ROCK signaling pathway in homeostasis of various organs [10–14]. In rat SMGs, small Rho GTPases, including RhoA and RhoB and RhoC, was detected in newly regenerated acinar cells [15]. Inhibition of ROCK using Y-27632 increased proacinar cells in salivary gland organoids [16] and delays senescence of salivary

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gland stem cells [17]. Based on previous studies, we hypothesized that ROCK signaling pathway may affect salivary gland maintenance and investigated the expression pattern of ROCK signaling pathway-related genes using RNA-sequencing (RNA-seq).

Materials and Methods

1. Animals

Five-week-old female mice (C57BL6×DBA2 F1-hybrid) were used. All animal experiments were carried out following the guidelines of the Institutional Animal Care and Use Committee of Seoul National University (Approval number: SNU-180403-4).

2. Isolation of mouse SMGs

Salivary glands isolated from mice were washed twice with phosphate buffered saline (PBS). Using micro forceps, parotid and sublingual glands were removed. SMGs were then dissected by razor blade for total RNA extraction.

3. Primary isolation and culture of mouse skin fibroblasts

Underarm area was used to obtain skin fibroblasts. Incision site was sterilized with 70% ethanol and shaved with a scalpel. Approximately 1 cm² of skin was excised and placed in 60 mm culture dishes with PBS. Remaining subcutaneous fat on skin tissues was removed. Skin tissues were cut into 1 mm² pieces and transferred into 100 mm culture dishes. Cells from skin

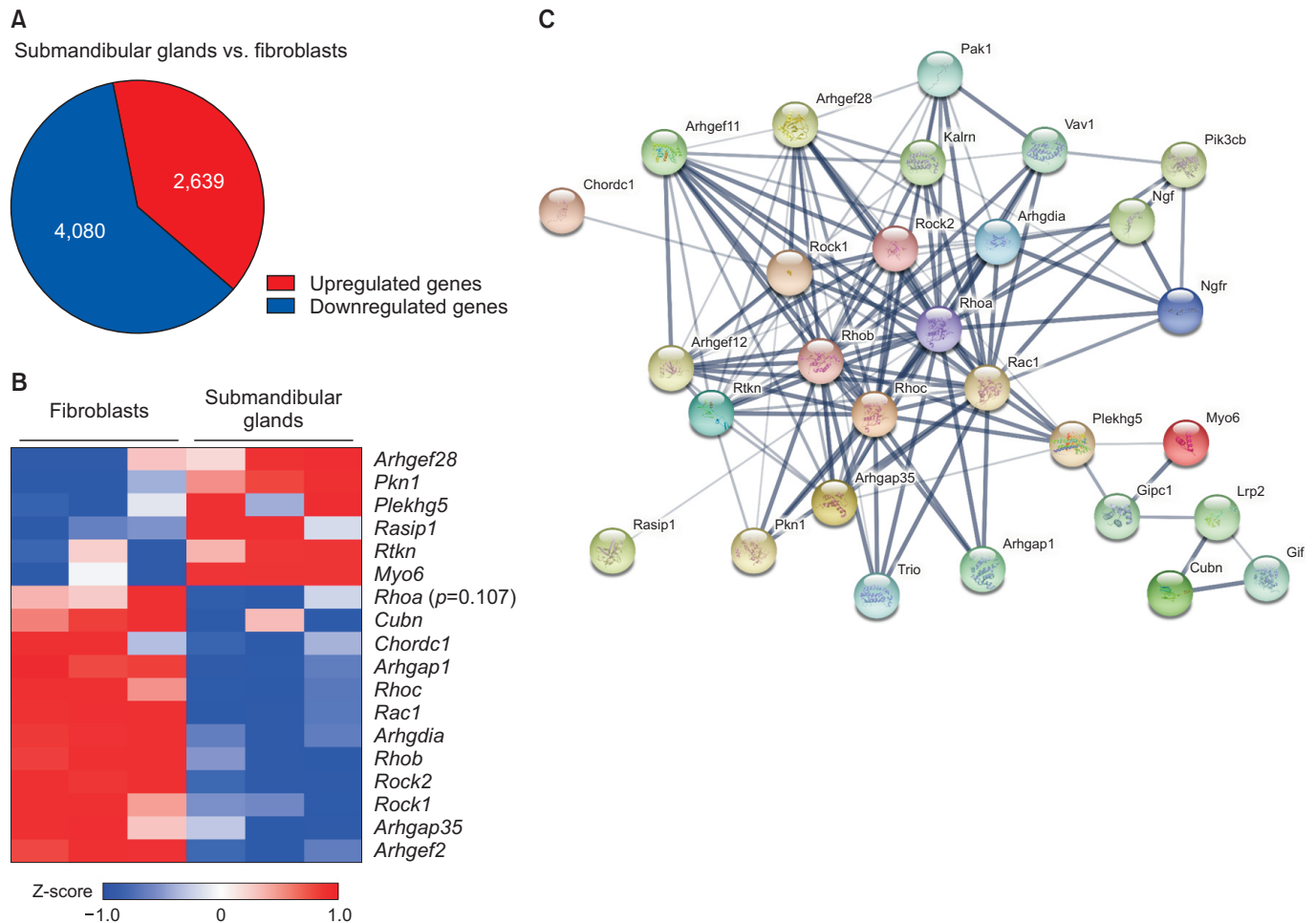


Fig. 1. Comparison of gene expression between mouse submandibular glands (SMGs) and skin fibroblasts. (A) Venn diagram indicating the up-regulated and down-regulated genes in mouse SMGs compared with mouse skin fibroblasts. (B) The expression data of 18 genes in fibroblasts and SMGs that satisfying the criteria are presented as heat map. (C) Extended protein-protein interaction network derived from genes of (B) was visualized using STRING (<https://string-db.org/>).

tissues were then grown in Dulbecco's modified Eagle's medium (Hyclone Laboratories, Logan, UT, USA) containing 10% fetal bovine serum (Hyclone Laboratories) and 1% penicillin-streptomycin (Sigma-Aldrich, St. Louis, MO, USA).

4. RNA extraction

Total RNA was extracted using a PureLink™ RNA Mini Kit (Invitrogen, Camarillo, CA, USA) following manufacturer's protocol.

5. RNA-seq expression profiling and analysis

Total RNA of mouse SMGs and skin fibroblasts was prepared and submitted to ebiogen (Seoul, Korea) for the construction of the library. RNA-seq data were analyzed using ExDEGA software ver. 1.6.5 (ebiogen). A heat map was generated with normalized gene expression data of salivary glands and mouse fibroblasts using MeV software ver. 4.9.0 (<http://mev.tm4.org>). ROCK signaling pathway-related gene candidates were obtained and used to visualize the protein-protein interaction network (PPIN) with STRING ver. 11 [18].

Results

1. Downregulated expression patterns of ROCK signaling pathway-related genes in the SMGs

To analyze the epithelial tissue-specific gene expression patterns of SMGs, RNA-seq was conducted and compared with the pattern of mouse skin fibroblasts which have mesenchymal characteristics. Genes with a 1.3-fold difference in expression and a *p*-value of less than 0.1 were selected. A total of 6,719 genes were selected based on these criteria as differentially expressed genes. Among these genes, 2,639 genes were upregulated and 4,080 genes were downregulated in SMGs (Fig. 1A). Expression profiling was conducted for genes that are directly or indirectly associated with the ROCK signaling pathway. The gene expression profile was clearly different in SMGs compared with fibroblasts. Specifically, expression levels of ROCK signaling pathway-related genes such as *Rhoa*, *Rhob*, *Rhoc*, *Rock1*, and *Rock2* were downregulated in SMGs compared with their counterparts in mouse skin fibroblasts (Fig. 1B). Extended PPIN derived from 18 genes analyzed in expression profiling (Fig. 1B) was visualized using STRING (Fig. 1C). *Rhoa*, *Rhob*, *Rhoc*, *Rock1*, and *Rock2* were placed in the

center of the protein network.

Discussion

ROCK signaling pathway regulates several cellular functions including contractility, proliferation, and apoptosis [19,20]. Rho GTPases (RhoA, RhoB, and RhoC) and Rho kinases (ROCK1 and ROCK2) are the main regulators of the ROCK signaling pathway. Previously, as a potential therapeutic target of a variety of pathological conditions, studies on ROCK signaling pathway and ROCK inhibitors were reported [21]. Increased activity of RhoA was observed in human pulmonary artery smooth muscle cells from patients with pulmonary hypertension (PH) and this indicates that RhoA is a promising therapeutic target for PH [22]. In kidney, ROCK2 mediates the development of diabetic kidney disease by regulating TGF- β -induced expression of profibrotic genes [23]. In this report, the expression pattern of ROCK signaling pathway-related genes of mouse SMGs and skin fibroblasts was confirmed using RNA-seq. *Rhoa* was included in profiling analyses as a main regulator of ROCK signaling pathway although its *p*-value (0.107) was statistically out of range. Downregulated expression of *Rhoa*, *Rhob*, *Rhoc*, *Rock1*, and *Rock2* was observed in mouse SMGs and these proteins were placed in the center of the PPIN. These results indicate that downregulated expression of ROCK signaling pathway-related genes might be required for SMG maintenance and used as a therapeutic target of salivary gland diseases accompanied by the activation of Rho GTPases or Rho kinases.

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Conflicts of Interest

No potential conflict of interest relevant to this article was reported.

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