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Data in Brief

Data Article

Data from a proteomic analysis of colonic fibroblasts secretomes

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A R T I C L E   I N F O

A B S T R A C T

The tumor cell proliferation, migration and invasion were influenced by the interaction between the cancer cells and their microenvironment. In current study, we established two pairs of the primary fibroblast cultures from colorectal adenocarcinoma tissues and the normal counterparts and identified 227 proteins in the colonic fibroblast secretomes; half of these proteins were novel. The mass spectrometry data and analyzed results presented here provide novel insights into the molecular characteristics and modulatory role of colon cancer associated fibroblasts. The data is related to "Identification of colonic fibroblast secretomes reveals secretory factors regulating colon cancer cell proliferation" by Chen et al. [1].
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Specifications table

Subject area	*Biology*
More specific subject area	*Cancer microenvironment*
Type of data	*Excel tables*
How data was acquired	*Mass spectrometry, data acquired using Synapt G1 mass spectrometer*
Data format	*Analyzed*
Experimental factors	*Conditioned media were collected, proteins were concentrated using filters*
Experimental features	*The proteins were separated using SDS-PAGE, in-gel tryptic digested and analyzed using LC-MS*
Data source location	*Shanghai, China*
Data accessibility	*The data is available with this article and is related to* [1]

Value of the data

- 227 colonic fibroblast secretome proteins are identified at a false discovery rate of 1.3%.
- 125 proteins (55.1%) are novel identified secretome proteins of colonic fibroblasts.
- These proteins are enriched for functional categories of extracellular matrix, adhesion, cell motion, inflammatory response, redox homeostasis and peptidase inhibitor.
- The data are valuable for understanding of the molecular feature of colonic fibroblasts and are ripe for further exploration and data mining.
- The data are useful for comparing purpose when addressing the heterogeneities of the fibroblast expressions from different isolation.

1. Data, experimental design, materials and methods

Secreted proteins were extracted from the conditioned medium of one pair of the fibroblast cultures. We performed a proteomic analysis of the proteins using a Synapt G1 mass spectrometer. The mass data interpretation was performed using ProteinLynx Global Server, X! Tandem and Scaffold softwares. The proteomic data presented here include the protein and spectrum identification results, as well as the cellular component annotation and functional analyzing results. 227 proteins were identified with a false discovery rate of 1.3% based on 15,000 assigned spectra. Half of the proteins were novel identifications in the secretome of colonic fibroblasts comparing with the known report. The subcellular localization of the identified proteins were annotated using UniProt database, DAVID, SignalP, SecretomeP, Phobius, WoLF PSORT and exosome databases. The occurrence of the fibroblast secretome proteins in the colon cancer cell proteomes was also analyzed. The functional enrichment of the identified proteins was performed using DAVID.

2. Establishment of fibroblast cultures from fresh surgical specimen

We established two pairs of colon cancer-associated fibroblast (CAF) and normal fibroblast (NF) cultures. The fresh colorectal cancer tissues and adjacent normal colonic tissues (at least 5 cm away from the loci of cancerous tissue) from two patients with colon ulcerated adenocarcinoma were collected during surgery at the Zhongshan Hospital of Fudan University according to the procedure described in the Journal of Proteomics paper [1]. The clinic and pathological data of the two patients are available in Supplementary Table 1.

3. Proteomic analysis of the colonic CAF and NF secreted proteins (SPs)

Fifty micro gram of the SP extracted from the 1031_NF and 1031_CAF conditioned medium (CM) were separated using 10% SDS-PAGE. Equal amount of sample was loaded in triplicate. Two gel lanes