Data in Brief 12 (2017) 632–643

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data on expression of genes involved in estrogen and progesterone action, inflammation and differentiation according to demographic, histopathological and clinical characteristics of endometrial cancer patients

Maša Sinreih [a], Saša Štupar [b,1], Luka Čemažar [b,2], Ivan Verdenik [c], Snježana Frković Grazio [d], Špela Smrkolj [b,c], Tea Lanišnik Rižner [a,*]

[a] Institute of Biochemistry, Faculty of Medicine, University of Ljubljana, Ljubljana, Slovenia
[b] Faculty of Medicine, University of Ljubljana, Ljubljana, Slovenia
[c] Division of Gynaecology and Obstetrics, University Medical Centre Ljubljana, Ljubljana, Slovenia
[d] Department of Pathology, Division of Gynaecology and Obstetrics, University Medical Centre Ljubljana, Ljubljana, Slovenia

ARTICLE INFO

Article history:
Received 20 February 2017
Received in revised form
16 March 2017
Accepted 27 April 2017
Available online 4 May 2017

Keywords:
Gene expression
Endometrial cancer
Estrogens
Progesterone
Inflammation
Differentiation

ABSTRACT

Endometrial cancer is the sixth most common cancer in women worldwide. It is associated with aberrant actions of steroid hormones, estrogens and progesterone, but also with enhanced inflammation and reduced cellular differentiation. Here, we show data on demographic and histopathological characteristics of 51 patients with endometrial cancer, together with data on correlations between the expression of 38 genes involved in estrogen and progesterone actions, inflammation and differentiation, and demographic characteristics. We also show data on changes in gene expression of these 38 genes according to histopathological and clinical characteristics of these patients. This article includes data referenced in the manuscript entitled »STAR and AKR1B10 are down-regulated in high-grade endometrial cancer by Sinreih et al. (in press) [1].

DOI of original article: http://dx.doi.org/10.1016/j.jsbmb.2017.02.015
* Corresponding author.
E-mail address: Tea.Lanisnik-Rizner@mf.uni-lj.si (T. Lanišnik Rižner).
[1] Current address: Department of Gastroenterology, General Hospital Celje, Celje, Slovenia.
[2] Current address: Department of Haematology, University Medical Centre Ljubljana, Ljubljana, Slovenia.

http://dx.doi.org/10.1016/j.dib.2017.04.050
2352-3409/© 2017 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

© 2017 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

Specifications Table

Subject area	Biochemistry, Molecular biology
More specific subject area	Molecular endocrinology, Gynecological endocrinology
Type of data	Tables
How data was acquired	Clinical and histopathological data was obtained from the patients' medical and histopathological records, respectively. The gene expression data obtained by quantitative real-time PCR was statistically analyzed.
Data format	Analyzed
Experimental factors	
Experimental features	Ratios for expression of 38 genes in samples of endometrial cancer *versus* adjacent control endometrium were calculated and this data was statistically analyzed.
Data source location	Ljubljana, Slovenia
Data accessibility	The statistically analyzed data is available within this article and the raw expression data may be provided upon request.

Value of the data

- Data on correlations between the expression ratios of these 38 genes and demographic characteristics may be helpful for explanation of different etiological factors identified in epidemiological studies.
- Data on changes in the expression ratios of these 38 genes according to histopathological and clinical data may lay foundation for further investigations of individual players of the individual pathophysiological processes.

1. Data

We provide data on demographic, histopathological and clinical characteristic of 51 endometrial cancer patients treated at the University Medical Centre Ljubljana, at the Division of Gynaecology and Obstetrics. Demographic (age, body mass, BMI, menopausal status, parity), histopathological and clinical data (histological type and grade of tumor, depth of myometrial invasion, presence of lymphovascular invasion, FIGO stage) (Table 1) together with data on statistical analysis of gene expression ratios (Tables 2–11) are included. The study was approved by the National Medical Ethics Committee of the Republic of Slovenia.

1.1. Demographic, histopathological and clinical data

The demographic, histopathological and clinical characteristics are given in Table 1. For the 51 patients, the mean age was 63.16 years (SD, 13.33 years; range, 26.72–83.58 years), the mean body weight was 81.24 kg (SD, 17.25 kg; range, 51–130 kg), and the mean BMI was 30.63 kg/m^2 (SD,

Download English Version:

https://daneshyari.com/en/article/4765228

Download Persian Version:

https://daneshyari.com/article/4765228

Daneshyari.com