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Data in Brief

Data Article

Data set on a study of gene expression in peripheral samples to identify biomarkers of severity of allergic and nonallergic asthma

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ARTICLE INFO

ABSTRACT

This article contains information related to the research article entitled "Biomarkers associated with disease severity in allergic and nonallergic asthma" (S. Baos, D. Calzada, L. Cremades, J. Sastre, J. Quiralte, F. Florido, C. Lahoz, B. Cárdaba, In press). Specifically, the clinical criteria stablished for selecting the study population ($n=104$ subjects) are described. Moreover, this article describes the criteria for selecting the 94 genes to be analyzed in PBMCs (peripheral blood mononuclear cells), it is provided a description of these genes and a Table with the genes most differentially expressed by clinical phenotypes and, finally it is detailed the experimental methodology followed for studying the protein expression of MSR1 (macrophage scavenger receptor 1), one of the genes evaluated in the research.

Specifications Table

Subject area	Biology
More specific subject area	Immunology, biomarkers, asthma, allergy.
Type of data	Table, text file.
How data was acquired	Bibliographic search, qRT-PCR, Western Blot.
Data format	Raw
Experimental factors	Subjects´ diagnosis was done according to the GEMA (Spanish Guide for Asthma Management) classification. PBMCs were extracted from peripheral blood through gradient separation. RNA and protein from PBMCs were extracted with TRIzol´s method.
Experimental features	Genes selected were according to the 3 criteria stated. Through qRT-qPCR, gene expression differences among clinical groups were studied. The highest statistically significant data among the three clinical phenotypes are showed. Western blot was done to determine the protein expression of one of the genes studied.
Data source location	Madrid, Spain; Seville, Spain; Granada, Spain.
Data accessibility	Data is with this article.

Value of the data

- Data presented here shows the selection and clinical criteria [1] of the study population.
- Gene selection criteria of interesting candidates to be asthma´ biomarkers are provided in order to understand the validity of genes studied.
- A gene list of candidate biomarkers of asthma and allergy diseases is suggested for studying.
- A summary of the most differential genes among clinical phenotypes is showed. These data could be important for future biomarkers analyses.
- Western-blot method for MSR1 expression on protein extracted from PBMCs could be useful for future research.

1. Data

The data shown in the article give information on the criteria of patients´ selection and the criteria for choosing genes to be studied as candidate biomarkers for these diseases in peripheral samples. The specific western-blot method for the analysis of MSR1 expression on protein extracted from PBMCs is provided. Table 1 provides a list of candidate genes to be validated as relevant biomarkers and Table 2 summarize the possible biomarkers that differentiate asthmatic and allergic phenotypes.

2. Experimental design, materials and methods

2.1. Subjects

The study population comprised 104 unrelated subjects, 30 healthy control (HC) subjects, 30 patients with nonallergic asthma (NA), 30 with allergic asthma (AA), and 14 nonasthmatic allergic (AR) subjects. The samples of the groups with asthma came from the asthma biobank of the CIBERES (IIS-Fundación Jiménez Díaz-UAM, Madrid). A biorepository in which were included samples from clinically well-characterized subjects, from 5 Spanish Hospitals participant of this network (*Fundación*