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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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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.

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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*

Table 1
List of the 94 genes studied.

Gene symbol	Gene name	Selection criteria	Detector
ADAM33	*ADAM metallopeptidase domain 33*	3	ADAM33-Hs00905552_m1
ADRB1	*adrenoceptor beta 1*	2	ADRB1-Hs02330048_s1
AKT1	*v-akt murine thymoma viral oncogene homolog 1*	2	AKT1-Hs00178289_m1
ALOX15	*arachidonate 15-lipoxygenase*	1	ALOX15-Hs00993765_g1
ALOX5	*arachidonate 5-lipoxygenase*	2	ALOX5-Hs01095330_m1
APAF1	*apoptotic peptidase activating factor 1*	2	APAF1-Hs00559441_m1
BAX	*BCL2-associated X protein*	2	BAX-Hs00180269_m1
C3AR1	*complement component 3a receptor 1*	2	C3AR1-Hs00269693
CCL11	*chemokine (C-C motif) ligand 11*	3	CCL11-Hs00237013_m1
CCL-17	*chemokine (C-C motif) ligand 17*	3	CCL17-Hs00171074_m1
CCL5	*chemokine (C-C motif) ligand 5*	3	CCL5-Hs00982282_m1
CD40	*CD40 molecule, TNF receptor superfamily member 5*	2	CD40-Hs01002913_g1
CD48	*CD48 molecule*	2	CD48-Hs00914738_m1
CD86	*CD86 molecule*	2	CD86-Hs01567026_m1
CHI3L1	*chitinase 3-like 1 (cartilage glycoprotein-39)*	1	CHI3L1-Hs00609691_m1
CLCA1	*chloride channel accessory 1*	1	CLCA1-Hs00976287_m1
CPA3	*carboxypeptidase A3 (mast cell)*	1	CPA3-Hs00157019_m1
CRTAP	*cartilage associated protein*	2	CRTAP-Hs00197261_m1
CTSC	*cathepsin C*	1	CTSC-Hs00175188_m1
CTSG	*cathepsin G*	1	CTSG-Hs01113415_g1
CX3CR1	*chemokine (C-X3-C motif) receptor 1*	1	CX3CR1-Hs01922583_s1
DUSP1	*dual specificity phosphatase 1*	1	DUSP1-Hs00610256_g1
RNASE3	*ribonuclease, RNase A family, 3*	3	RNASE3-Hs01923184_s1
EIF5A	*eukaryotic translation initiation factor 5A*	1	EIF5A-Hs00744729_s1
FOXP3	*forkhead box P3*	3	FOXP3-Hs01085834_m1
FPR3	*formyl peptide receptor 3*	2	FPR3-Hs00266666_s1
GADD45B	*growth arrest and DNA-damage-inducible, beta*	1	GADD45B-Hs04188837_g1
GPX3	*glutathione peroxidase 3 (plasma)*	1	GPX3-Hs01078668_m1
GZMH	*granzyme H (cathepsin G-like 2, protein h-CCPX)*	2	GZMH-Hs00277212_m1
HLA-DQB1	*major histocompatibility complex, class II, DQ beta 1*	1, 2	HLA-DQB1-Hs03054971_m1
HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	2	HLA-DRB1-Hs99999917_m1
IFNG	*interferon, gamma*	3	IFNG-Hs00989291_m1
IL-10	*interleukin 10*	2	IL10-Hs00961622_m1
IL13	*interleukin 13*	1	IL13-Hs00174379_m1
IL-17	*interleukin 17A*	3	IL17A-Hs00174383_m1
IL1R1	*interleukin 1 receptor, type I*	1	IL1R1-Hs00991002_m1
IL1R2	*interleukin 1 receptor, type II*	1	IL1R2-Hs01030384_m1
IL-2	*interleukin 2*	3	IL2-Hs00174114_m1
IL-25	*interleukin 25*	3	IL25-Hs03044841_m1
IL2RB	*interleukin 2 receptor, beta*	1	IL2RB-Hs01081697_m1
IL33	*interleukin 33*	1	IL33-Hs00369211_m1
IL-4	*interleukin 4*	3	IL4-Hs00174122_m1
IL4R	*interleukin 4 receptor*	3	IL4R-Hs00166237_m1
IL5	*interleukin 5*	1	IL5-Hs01548712_g1
IL6	*interleukin 6 (interferon, beta 2)*	1, 2	IL6-Hs00985639_m1
IL8	*interleukin 8*	1	IL8-Hs00174103_m1
IL-9	*interleukin 9*	3	IL9-Hs00914237_m1
IRAK3	*interleukin-1 receptor-associated kinase 3*	3	IRAK3-Hs00936103_m1
ITGAL	*integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)*	2	ITGAL-Hs00158218_m1
ITGB7	*integrin, beta 7*	2	ITGB7-Hs01565750_m1
ITGB8	*integrin, beta 8*	2	ITGB8-Hs00174456_m1
LCK	*lymphocyte-specific protein tyrosine kinasep*	2	LCK-Hs00178427_m1
LGALS3	*lectin, galactoside-binding, soluble, 3*	3	LGALS3-Hs00173587_m1
LYN	*v-yes-1 Yamaguchi sarcoma viral related oncogene homolog*	2	LYN-Hs00176719_m1
MAPK13	*mitogen-activated protein kinase 13*	2	MAPK13-Hs00559623_m1
MSR1	*macrophage scavenger receptor 1*	2	MSR1-Hs00234007_m1
MUC2	*mucin 2, oligomeric mucus/gel-forming*	1	MUC2-Hs03005103_g1
MUC5AC	*mucin 5AC, oligomeric mucus/gel-forming*	1	MUC5AC-Hs00873651_Mh

Table 1 (*continued*)

Gene symbol	Gene name	Selection criteria	Detector
MUC5B	*mucin 5B, oligomeric mucus/gel-forming*	1	MUC5B-Hs00861595_m1
NCF2	*neutrophil cytosolic factor 2*	1	NCF2-Hs01084940_m1
NFATC1	*nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1*	2	NFATC1-Hs00542678_m1
NFKBIZ	*nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta*	1	NFKBIZ-Hs00230071_m1
NLRP3	*NLR family, pyrin domain containing 3*	2	NLRP3-Hs00918082_m1
NOS2A	*nitric oxide synthase 2, inducible*	1	NOS2-Hs01075529_m1
ORMDL3	*ORM1-like 3 (S. cerevisiae)*	1	ORMDL3-Hs00918021_m1
PHLDA1	*pleckstrin homology-like domain, family A, member 1*	1	PHLDA1-Hs00705810_s1
PI3	*peptidase inhibitor 3, skin-derived*	1	PI3-Hs00160066_m1
POSTN	*periostin, osteoblast specific factor*	1	POSTN-Hs01566734_m1
PRKACA	*protein kinase, cAMP-dependent, catalytic, alpha*	2	PRKACA-Hs00427274_m1
PRKACB	*protein kinase, cAMP-dependent, catalytic, beta*	2	PRKACB-Hs01086757_m1
PTGER2	*prostaglandin E receptor 2 (subtype EP2)*, 53 *kDa*	2	PTGER2-Hs04183523_m1
PTPRC	*protein tyrosine phosphatase, receptor type, C*	3	PTPRC-Hs04189704_m1
S100A9	*S100 calcium binding protein A9*	1	S100A9-Hs00610058_m1
S1PR5	*sphingosine-1-phosphate receptor 5*	2	S1PR5-Hs00928195_s1
SCD	*stearoyl-CoA desaturase (delta-9-desaturase)*	1	SCD-Hs01682761_m1
SELL	*selectin L*	2	SELL-Hs00174151_m1
SERPINB2	*serpin peptidase inhibitor, clade B (ovalbumin), member 2*	1, 2	SERPINB2-Hs01010736_m1
SERPINB4	*serpin peptidase inhibitor, clade B (ovalbumin), member 4*	1	SERPINB4-Hs01691258_g1
SMURF1	*SMAD specific E3 ubiquitin protein ligase 1*	2	SMURF1-Hs00905759_m1
SOS1	*son of sevenless homolog 1 (Drosophila)*	2	SOS1-Hs00362308_m1
SPN	*sialophorin*	2	SPN-Hs01872322_s1
SPP1	*secreted phosphoprotein 1*	3	SPP1-Hs00959010_m1
STAT1	*signal transducer and activator of transcription* 1.91 *kDa*	3	STAT1-Hs01013996_m1
SVIL	*supervillin*	1	SVIL-Hs00931028_m1
TAGAP	*T-cell activation RhoGTPase activating protein*	2	TAGAP-Hs00299284_m1
TCF21	*transcription factor 21*	1	TCF21-Hs00162646_m1
TGFB1	*transforming growth factor, beta 1*	2	TGFB1-Hs00998133_m1
TLR4	*toll-like receptor 4*	2	TLR4-Hs00152939_m1
TNFA	*tumor necrosis factor*	3	TNF-Hs01113624_g1
TNFAIP3	*tumor necrosis factor, alpha-induced protein 3*	1	TNFAIP3-Hs00234713_m1
TRIM37	*tripartite motif containing 37*	2	TRIM37-Hs00248701_m1
TSLP	*thymic stromal lymphopoietin*	1	TSLP-Hs00263639_m1
VCAN	*versican*	2	VCAN-Hs00171642_m1
ZAP70	*zeta-chain (TCR) associated protein kinase* 70 *kDa*	2	ZAP70-Hs00896347_m1

Selection criteria were: 1. Relevant genes by differential expression or SNP studies in asthma/allergy, which were found in more than one independent work following a literature search; 2. Genes with differential expression found in results of previous studies from our laboratory; 3. Genes of interest because of their role in cellular plasticity, inflammation and/or regulation that could have been excluded by the other criteria. The detector refers to the specific primer of each gene used to carry out qRT-PCR.

Jiménez Díaz Hospital and *Doce de Octubre* Hospital from Madrid, Doctor Negrín Hospital from Las Palmas de Gran Canaria, *Clinic* Hospital and *Sant* Pau Hospital both from Barcelona). These patients fulfilled the following criteria: severe, mild, or moderate asthma diagnosis assigned according to the GEMA [1]; no treatment was given before or during the collection of the samples. Pulmonary function test was determined by percentage of forced vital capacity (FVC) and forced vital volume in one second (FVE_1). Patients with allergic asthma showed a positive skin prick test result for some of the airborne allergens from a battery of common allergens.

HCs were healthy subjects with no history of respiratory diseases. HCs and patients with allergy (rhinitis) without asthma were recruited and diagnosed at the Allergy Service of two hospitals in

Table 2
Differential genes among clinical phenotypes.

Comparison	Number of genes with significant differential expression*	Number of genes upregulated	Number of genes downregulated	Genes statistically significant with a RQ > 10
NA*vs* AA	74	74 in NA	–	*CCL5, CHI3L1, CTSG, GMH, IL1-R2*
NA*vs* AR	66	64 in NA	2 in NA	*CCL5, CRTAP, GPX3, HLA-DQB1, IL-10, IL2RB, MSR1, NLRP3, PHLDA1, SERPINB2,* ***PI3***
AA*vs* AR	14	4 in AA	10 in AA	***CHI3L1, CPA3, CTSG, PI3***

NA: Nonallergic asthma group; AA: allergic asthma group; AR: nonasthmatic allergy (rhinitic) group; RQ: relative quantification.

* Significance established at an adjusted $p < 0.05$ and a RQ < -2 or > 2. All genes mentioned in the last column are overexpressed except the ones marked in bold which are underexpressed.

Andalusia (Spain), *Vírgen del Rocío* University Hospital from Seville, and *San Cecilio* University Hospital from Granada, Spain. AR patients fulfilled the following criteria: seasonal rhinitis without asthma, positive skin prick test for some of the airborne allergens from a battery of common allergens, and no previous immunotherapy.

HC and AR biological samples that were not used in this work were stored in the FJD Biobank, IIS-Fundación Jiménez Díaz Madrid.

Informed consent was obtained from each subject. Ethical approval for the study was obtained from the Ethical and Research Committee of the participating hospitals.

2.2. Gene selection criteria

Ninety-four genes (Table 1) were chosen following three main criteria for a gene expression analysis [2] through quantitative real time PCR with RNA of the study population described before:

a. Relevant genes associated with asthma and allergic diseases in more than one independent work, selected after a Pubmed literature search of analyses of differential gene expression, or polymorphic variants (SNPs) related to the disease.
b. Relevant genes previously described by our group [3].
c. Genes excluded by the other two criteria but that could be interesting due to their implication in cellular plasticity, inflammation, and/or regulation of the disease.

2.3. Gene expression analysis

Gene expression analysis between the 3 clinical groups is summarized in Table 2. The statistical analysis for testing differential gene expression was performed by using the StatMiner program (http://www.integromics.com/StatMiner). This program follows a simple, step-by-step analysis workflow guide that includes parametric, non-parametric, and paired tests for relative quantification of gene expression, as well as 2-way ANOVA for two-factor differential expression analysis. Significance was defined by RQ (relative quantification) < -2 or > 2 and corrected P value (< 0.05) adjusting the P value with the Benjamini–Hochberg FDR method.

2.4. MSR1 protein analysis by Western Blot

The protein expression of MSR1 was analyzed [2]. Specific protein was extracted from PBMCs (10^6 cells) using the TRIzol method (Invitrogen, Carlsbad, CA, USA) and quantified by the BCA method (Thermo Scientific, Rockford, IL USA). Western blot used was the Invitrogen WesternBreeze® Chemiluminescent Western Blot Immunodetection Kit (Life Technologies) following the

manufacturer's instructions with minor modifications. Briefly, 40 µg of proteins from each subject were running in a 12% SDS-PAGE Novex Bolt™ Mini gels (Life Technologies) and transferred using the Invitrogen Blot® Dry Blotting System to nitrocellulose membranes. After 30 min of incubation with blocking solution, were incubated overnight at 4 °C with rabbit anti-human polyclonal CD204/Macrophage Scavenger Receptor I antibody (dilution 1:2500) (Thermo Scientific) as specific antibody and, with a rabbit anti-human monoclonal β-Actin antibody (dilution 1:1000) (Cell Signalling Technology, Danvers, MA, USA) as control. The result was visualized by chemiluminiscence using a luminescent image analyzer: ImageQuant LAS 4000 (GE Healthcare Life Science, Little Chalfont, Buckinghamshire, UK). Data of MSR1 results were relativize to β-Actin expression.

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Transparency document. Supporting information

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