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Franck Thuny, Julien Textoris, Amira Ben Amara, Adil El Filali, Christian Capo, et al.. The Gene Expression Analysis of Blood Reveals S100A11 and AQP9 as Potential Biomarkers of Infective Endocarditis. PLoS ONE, 2012, 7 (2), pp.e31490. 10.1371/journal.pone.0031490 . hal-01772605

HAL Id: hal-01772605
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PLoS one

The Gene Expression Analysis of Blood Reveals *S100A11* and *AQP9* as Potential Biomarkers of Infective Endocarditis

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Abstract

Background: The diagnostic and prognostic assessments of infective endocarditis (IE) are challenging. To investigate the host response during IE and to identify potential biomarkers, we determined the circulating gene expression profile using whole genome microarray analysis.

Methods and Results: A transcriptomic case-control study was performed on blood samples from patients with native valve IE (n = 39), excluded IE after an initial suspicion (n = 10) at patient's admission, and age-matched healthy controls (n = 10). Whole genome microarray analysis showed that patients with IE exhibited a specific transcriptional program with a predominance of gene categories associated with cell activation as well as innate immune and inflammatory responses. Quantitative real-time RT-PCR performed on a selection of highly modulated genes showed that the expression of the gene encoding S100 calcium binding protein A11 (*S100A11*) was significantly increased in patients with IE in comparison with controls ($P<0.001$) and patients with excluded IE ($P<0.05$). Interestingly, the upregulated expression of the *S100A11* gene was more pronounced in staphylococcal IE than in streptococcal IE ($P<0.01$). These results were confirmed by serum concentrations of the S100A11 protein. Finally, we showed that in patients with IE, the upregulation of the aquaporin-9 gene (*AQP9*) was significantly associated with the occurrence of acute heart failure ($P = 0.02$).

Conclusions: Using transcriptional signatures of blood samples, we identified *S100A11* as a potential diagnostic marker of IE, and *AQP9* as a potential prognostic factor.

Citation: Thuny F, Textoris J, Ben Amara A, El Filali A, Capo C, et al. (2012) The Gene Expression Analysis of Blood Reveals *S100A11* and *AQP9* as Potential Biomarkers of Infective Endocarditis. PLoS ONE 7(2): e31490. doi:10.1371/journal.pone.0031490

Editor: Roger Le Grand, Commissariat a l'Energie Atomique(cea), France

Received June 30, 2011; **Accepted** January 9, 2012; **Published** February 3, 2012

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Funding: This work was supported by a grant from the Fédération Française de Cardiologie, to Dr. Franck Thuny. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

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Introduction

Infective endocarditis (IE) is a severe disease with an incidence ranging from 30 to 100 episodes per million person-years [1,2]. Mortality is high, and more than one-third of the patients die within the first year of their diagnosis [3,4,5,6]. Despite the development of microbiological and imaging techniques, the diagnosis of IE remains challenging. Indeed, etiologic diagnoses may not be obtained in 2.5% to 31% of cases [1,7], and echocardiography is negative for approximately 10% of cases [1]. Thus, morbidity and mortality remain high, and strategies fail to detect and predict a substantial number of events, such as heart failure and embolic events. One of the reasons for these issues is the complex pathogenesis of the disease that involves many host-pathogen interactions. Indeed, previous endocardial lesions can lead to the exposure of the underlying extracellular matrix proteins, local inflammation with interleukin-1 release, and then thrombus formation, which is termed "non-bacterial vegetation". In the case of bacteremia, valves with pre-existing sterile vegetations or tissues with minimal lesions can be colonized because of crucial interactions between the bacteria, platelets and endothelial cells via several bacterial surface proteins or plasma-bridging molecules. This process leads to the recruitment of circulating cells, including neutrophils and monocytes, the release of cytokines and procoagulant factors that contribute to the enlargement of vegetations and the protection of bacterial pathogens from host defenses [2].

This complex situation highlights the need for methods that improve the management of IE. Specifically, the identification of new biomarkers for diagnosis and risk stratification will be useful, as well as biological indicators for a rapid surgical management. Molecular signatures of IE represent promising means for addressing these challenges. In particular, microarray-based transcriptomes can identify specific signatures of the disease that might ultimately be translated into clinically useful molecular biomarkers [3]. Recently, we identified a transcriptional signature of IE from valvular tissue [4], but this approach cannot be used by physicians in their daily practice. Peripheral blood is an alternative

to a tissue sample for the molecular profiling of human diseases [3] because it interacts with every tissue in the body and plays a crucial role in many IE pathophysiological processes, such as immunity, inflammation and coagulation.

To investigate the host response during IE and identify potential biomarkers, we determined the circulating gene expression profile through a unique whole genome microarray analysis. We show that patients with IE exhibited a specific transcriptional program with a predominance of gene categories associated with cell activation as well as innate immune and inflammatory responses. We demonstrate that the gene encoding the S100 calcium binding protein A11 (*S100A11*) and the serum concentration of S100A11 protein are both significantly increased in IE patients, especially in the case of staphylococcal etiology. Moreover, in IE patients, the upregulation of the aquaporin-9 gene (*AQP9*) is associated with the occurrence of acute heart failure.

Methods

Study Population

All participants in the study were prospectively enrolled from January 2009 to December 2010 at the Cardiology Department of La Timone Hospital (Marseille, France), which is an adult tertiary care teaching hospital. The patients were eligible for the study if they had a clinical suspicion of native valve IE. The exclusion criteria were age <18 years, pregnancy, history of previous IE, intracardiac material (prosthetic valve, pacemaker or implantable cardioverter defibrillator), failure in the RNA extraction procedure, and an antibiotic treatment for more than one week. Among the 71 patients eligible for the study, 22 were excluded because of the presence of at least one exclusion criterion. Their baseline characteristics are summarized in Table 1.

The transcriptomic case-control study was performed in:

i. 39 consecutive patients with native valve IE (IE group) diagnosed by a multidisciplinary team who applied the modified Duke criteria [5] (two major criteria in 37 patients and 1 major with 3 minor criteria in 2 patients),
ii. 10 patients with a previous valvular heart disease (VHD) admitted for a suspicion of IE because of persistent fever or new abnormalities detected by echocardiography, but with a final excluded IE diagnosis (excluded IE group). Of these, the final diagnosis was an acute degenerative mitral chordae rupture (n = 4), a respiratory tract infection (n = 2), an urinary tract infection (n = 1), and no diagnosis after a 3-month follow-up (n = 3). Among these 3 patients, fever disappeared spontaneously without antibiotics.
iii. 10 age-matched healthy volunteers (control group).

Initially, 10 IE patients and 5 controls were arbitrarily selected, and their samples were analyzed with microarrays; however, samples from all of the patients were eventually analyzed by quantitative real-time reverse transcriptase-polymerase chain reaction (qRT-PCR).

For each case, the following data were collected: age, sex, comorbidity [6], signs and symptoms, duration of symptoms, biological results, history of antimicrobial therapy for the current illness that prompted the patient to seek medical attention, antecedent disease, predisposing factors for IE including systemic disease, intravenous drug use, treatment received during the course of hospitalization and complications (acute heart failure, embolic event, and cardiac abscess). Echocardiography was performed by a systematic transthoracic and trans-esophageal approach [5]. For the microbiological diagnosis, a diagnostic kit, including blood cultures and serologies, was used as previously described [7]. When cardiac surgery was required, valvular surgical samples were analyzed using cultures and PCR amplification.

Table 1. Characteristics of the patients according to the final diagnosis.

	IE group (N = 39)	Excluded IE group (N = 10)	*P* Value
Age, mean ±SD, years	58±18	63±15	0.42
Sex ratio (M/F)	30/9	7/3	0.65
Intravenous drug user	5 (13%)	0 (0%)	0.57
Cancer	3 (8%)	1 (10%)	1.0
Diabetes	5 (13%)	1 (10%)	1.0
Comorbidity index >2	15 (38%)	3 (30%)	0.72
Fever, temperature >38°C	38 (97%)	7 (70%)	0.02
Vascular phenomena*	14 (36%)	1 (10%)	0.15
Immunologic phenomena†	0 (0%)	0 (0%)	NA
Heart failure	16 (41%)	5 (50%)	0.72
Serum creatinine >20 mg/L	3 (8%)	1 (10%)	1.0
Valve localization of abnormality			1.0
Aortic	17 (44%)	4 (40%)	
Mitral	23 (59%)	6 (60%)	
Right valves	3 (8%)	0 (0%)	
Severe valvular regurgitation	32 (82%)	7 (70%)	0.41
Vegetation	32 (82%)	0 (0%)	<0.001
Abscess	10 (26%)	0 (0%)	<0.001
Blood cultures			<0.001
Streptococci‡	27 (69%)	0 (0%)	
Staphylococci§	12 (31%)	1 (10%)	
Negative	0 (0%)	9 (90%)	

NA = not applicable.
*Including arterial emboli, septic pulmonary infarcts, mycotic aneurysms, intracranial hemorrhages, conjunctival hemorrhages, and Janeway's lesions.
†Including glomerulonephritis, Osler's nodes, Roth's spots, and rheumatoid factor.
‡Including three enterococci.
§Including nine *Staphylococcus aureus*.
doi:10.1371/journal.pone.0031490.t001

The study was performed according to the principles of the Declaration of Helsinki. Informed and written consent was obtained from each subject, and the Ethics Committee of the Université de la Méditerranée approved the study.

RNA Preparation and Microarrays

At the admission of patients, peripheral blood was drawn into PAXgene tubes (Qiagen). The RNA was extracted according to the manufacturer's recommendations, which included a DNase step. The quality and quantity of isolated RNAs were assessed using the Nanodrop (Thermo Scientific) and 2100 Bioanalyzer (Agilent Technologies), and the RNAs were eluted in 80 µL of water and stored at −20°C. Subsequently, the RNAs were analyzed using microarray chips (Agilent Technologies), including 45,000 probes (4×44 K Whole Human Genome, Agilent Technologies) and one-color microarray-based gene expression analysis, as recently described [8]. Briefly, 400 ng of RNA was labeled with cyanine-3 CTP using a commercial kit (Low RNA

Input Fluorescent Amplification Kit, Perkin Elmer). The samples were deposited on a slide, and hybridization was performed at 65°C using the In situ Hybridization Plus kit (Agilent Technologies) for 17 hours. The arrays were scanned with a pixel size of five microns using the DNA Microarray Scanner G2505B (Agilent Technologies). The image analysis and correction of intra-array signals were performed with the Feature Extraction Software A.9.1.3 (Agilent Technologies). Microarray data analysis was performed using the R and the Bioconductor software suite. Raw data were filtered and normalized using the *Agi4x44PreProcess* library. Unsupervised and supervised analysis were done using hierarchical clustering, principal component analysis (*made4* library) [9], and Significance Analysis of Microarray (SAM) algorithm (*siggenes* library). Genes were considered to be differentially expressed if False Discovery Rate (FDR, Benjamini-Hochberg [10]) was below 1% and absolute fold change was above 1.5. Functional enrichment analysis was performed on selected genes with DAVID Tools [11], using the following ontologies: Gene Ontology (GO) [12], INTERPRO [13] and KEGG pathways [14]. The figures were designed using Cytoscape [15] and Inkscape softwares. The data were generated according to the Minimum Information About a Microarray Experiment guidelines and were deposited in the National Center for Biotechnology Information's Gene Expression Omnibus [16]. The data are accessible using the following accession number: GSE29161.

qRT-PCR Analyses

Reverse transcription of 150 ng of total RNA per reaction was performed with the MMLV-RT kit (Invitrogen), as previously described [8]. Quantitative real-time PCR was performed using gene-specific primers designed using Primer3 [17]. The list of primers with their sequences is provided in the Table S1. The transcriptional profiles of the selected genes were screened in homemade 384-well plates using the 7900HT Fast Real Time PCR System, and the qRT-PCR data were extracted using the SDS 2.2 software (Applied Biosystems). The results were normalized using the housekeeping gene β-actin and are expressed as $FC = 2^{-\Delta\Delta Ct}$, where $\Delta\Delta Ct = (CtTarget - CtActin)_{assay} - (CtTarget - CtActin)_{control}$, as previously described [8].

S100A11 Assay

The serum concentrations of S100A11 protein were assessed by enzyme-linked immuno-sorbent assay kit (USCN, Life Science Inc.) according to the manufacturer's protocol. The sensitivity of the test is 0.37 ng/mL.

Statistical Analysis

The categorical data were reported as frequencies and percentages and were compared using the Fischer exact two-tailed test. The continuous data are expressed as the mean ± SEM or the median and interquartile range. Comparisons between two groups were performed using the Mann-Whitney *U* test, and comparisons between the three groups of individuals were performed using the Kruskal-Wallis test with post-hoc Dunn's multiple comparison test. This statistical analysis was conducted using SPSS for Windows, version 16.0 (SPSS Inc., Chicago, Illinois). Values of $P<0.05$ were considered statistically significant.

Results

Microarray Analysis of Patients with IE

A whole-genome microarray approach was used to define the peripheral transcriptional signature of IE. For that purpose, we

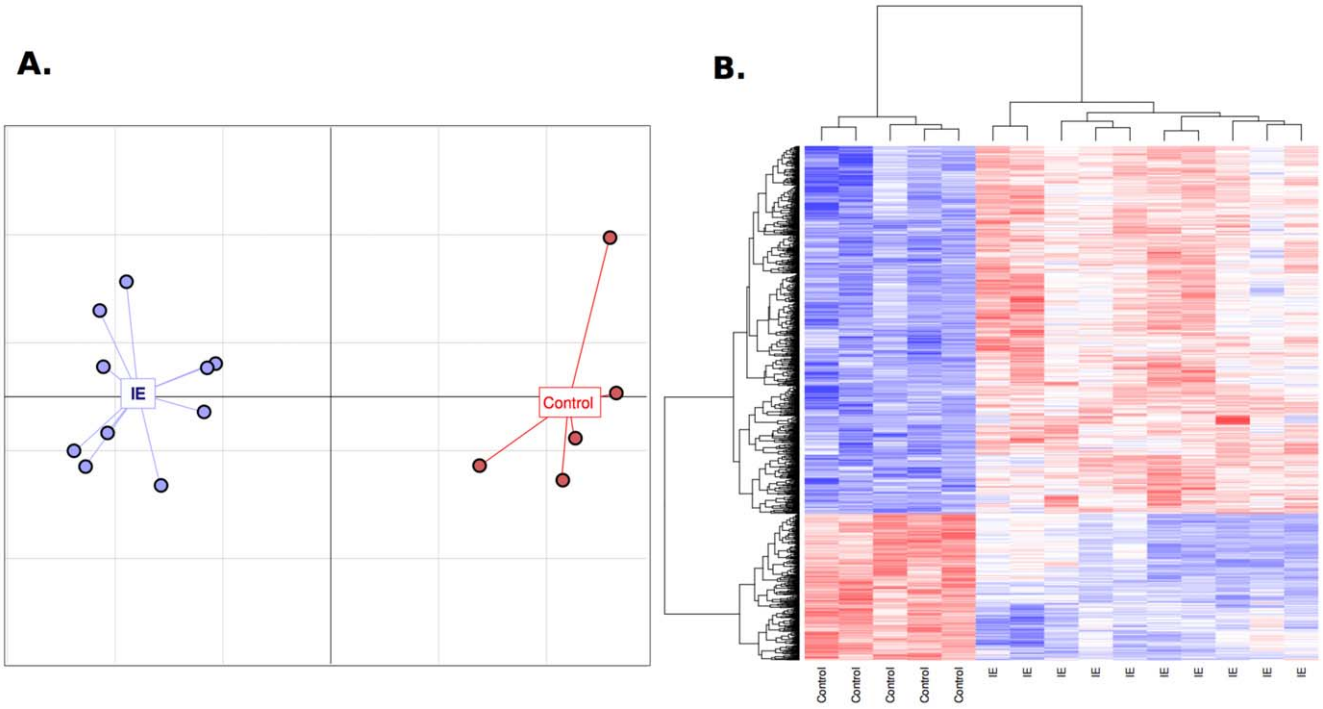


Figure 1. Gene expression signature between endocarditis and control patients. Differential gene expression between infective endocarditis (IE) and control patients was analyzed by Principal Component Analysis (A) and Hierarchical clustering (B). In panel A, IE patients (red) are clearly separated from control patients (blue) on the first component (x-axis) of the PCA. In panel B, selected genes with FDR<1% and absolute fold change above 1.5 were represented as a heatmap, with genes in rows and samples in columns. Gene expression level was color-coded from blue to red.
doi:10.1371/journal.pone.0031490.g001

arbitrarily selected ten IE patients and five controls. The principal components for the analysis of the overall gene expression showed that the IE patients and controls were organized in two different groups (Figure 1, Panel A). Supervised analysis using the SAM algorithm identified 1,782 probes differentially expressed with an absolute fold change above 1.5, and a FDR<1% (Figure 1, Panel B). Modulated genes in the IE patients and controls were distributed in two different clusters. Finally, we found that 1,274 probes (912 genes) were upregulated and 508 probes (339 genes) were downregulated in IE patients compared with controls. Taken together, these different analyses of the gene expression demonstrated that the patients with IE exhibited a specific transcriptional program.

Functional Analysis of Modulated Genes in Patients with IE

The genes that were differentially expressed in IE patients were classified into different categories based on GO, SP_PIR keywords, Interpro and KEGG ontologies (Table 2). In the upregulated genes, there was an enrichment of the biological processes related to cell activation, post-translational modification of proteins, intra-cellular transport and localization, phagocytosis and immune response. Post-translational modification of proteins was supported by the following terms: ''acetylation'', ''ubiquitin conjugation pathway'' and ''modification-dependant protein catabolic process''. Intra-cellular transport and localization, as well as phagocytosis were supported by the following terms: ''establishment of protein localization'', ''protein transport'', ''vesicle mediated transport'', ''golgi apparatus'', ''lysosome'', ''endosome'' and FC-γ receptor mediated phagocytosis''. These latter terms, together with the terms ''host-virus interaction'', ''regulation of I-kappaB kinase/NF-kappaB cascade'', ''Zing finger, RING-type'' and ''defense response'' support the involvement of the up-regulated genes in the immune response. In the downregulated genes, the GO terms corresponding to cation binding, extracellular matrix and regulation of vesicle-mediated transport were enriched. Two KEGG pathway linked to the immune response were enriched in the upregulated signature: ''lysosome'' and ''FC-γ receptor mediated phagocytosis''.

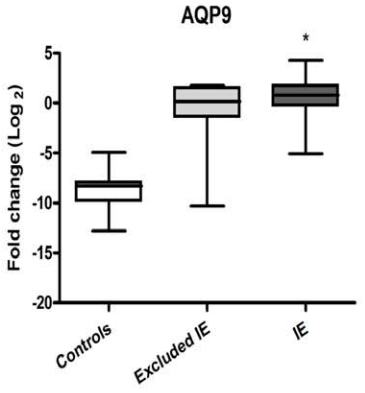
Validation of Modulated Genes in Patients with IE

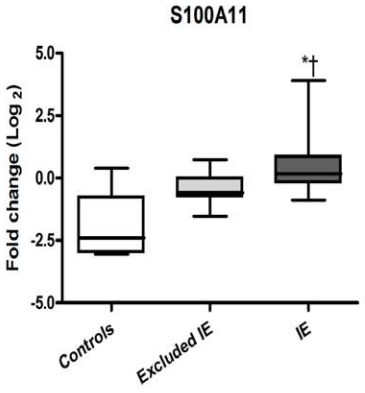
Because of the large number of modulated genes and the density of transcriptomic networks, the following procedure was used to validate the microarray data. Seven upregulated genes were selected from a list of the 300 most modulated genes according to their putative role in IE pathophysiology. Their expression was determined by qRT-PCR in an enlarged cohort of IE patients (n = 39) and controls (n = 10). The genes encoding aquaporin-9

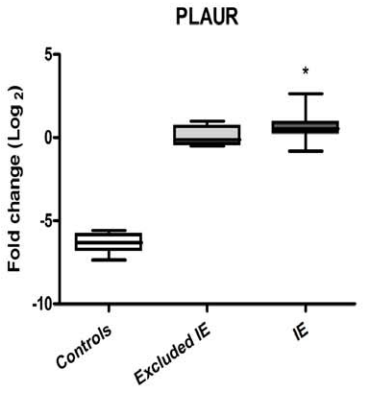
Table 2. Ontology enrichement analysis.

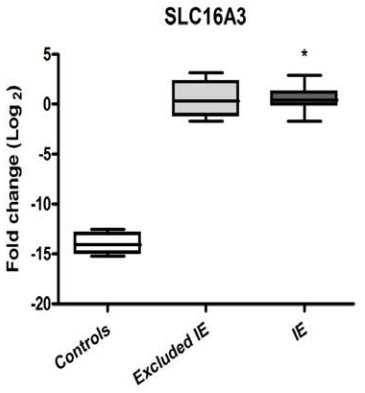
	Ontology	ID	Count	P-value	Term
Up-regulated					
	SP_PIR	-	287	$1.1_{\times}10^{-14}$	Acetylation
	SP_PIR	-	75	$2.7_{\times}10^{-10}$	Protein transport
	SP_PIR	-	75	$2.4_{\times}10^{-9}$	Ubiquitin conjugaison pathway
	GO_BP	0045184	101	$6.1_{\times}10^{-8}$	Establishment of protein localization
	GO_BP	0019941	81	$7.7_{\times}10^{-8}$	Modification-dependent protein catabolic process
	GO_MF	0032555	199	$8.9_{\times}10^{-8}$	Purine ribonucleotide binding
	GO_BP	0016192	81	$9.0_{\times}10^{-8}$	Vesicle mediated transport
	GO_BP	0044257	83	$1.5_{\times}10^{-8}$	Cellular protein catabolic process
	GO_CC	0005794	102	$6.5_{\times}10^{-7}$	Golgi apparatus
	GO_CC	0005764	35	$6.4_{\times}10^{-6}$	Lysosome
	SP_PIR	-	41	$2.6_{\times}10^{-5}$	Host-virus interaction
	GO_CC	0005768	44	$3.1_{\times}10^{-5}$	Endosome
	KEGG	hsa04142	24	$7.4_{\times}10^{-5}$	Lysosome
	GO_BP	0007242	132	$8.5_{\times}10^{-5}$	Intra-cellular signalling cascade
	KEGG	hsa04666	20	$2.5_{\times}10^{-4}$	FC-g receptor mediated phagocytosis
	GO_BP	0043122	20	$4.2_{\times}10^{-4}$	Regulation of I-kappaB kinase/NF-kappaB cascade
	Interpro	0017907	37	$8.4_{\times}10^{-4}$	Zinc-finger, RING-type
	GO_BP	0006952	68	$1.8_{\times}10^{-3}$	Defense response
Down-regulated					
	GO_MF	0046872	133	$7.1_{\times}10^{-4}$	Metal ion binding
	GO_MF	0043169	134	$8.2_{\times}10^{-4}$	Cation binding
	Interpro	019787	9	$1.1_{\times}10^{-3}$	Zinc-finger, PHD finger
	GO_CC	0031012	19	$1.3_{\times}10^{-3}$	Extracellular matrix
	GO_BP	0042127	82	$1.9_{\times}10^{-3}$	Regulation of cell proliferation
	GO_BP	0060627	9	$2.3_{\times}10^{-3}$	Regulation of vesicle mediated transport
	Interpro	013098	11	$2.7_{\times}10^{-3}$	Immunoglobulin I-set

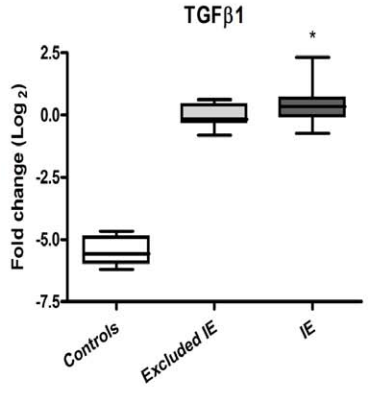
doi:10.1371/journal.pone.0031490.t002

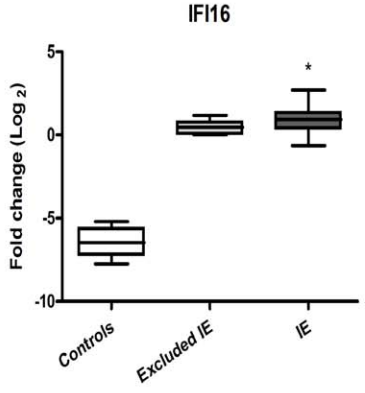

AQP9
Fold change (Log 2)
5
0
-5
-10
-15
-20
*
Controls
Excluded IE
IE


S100A11
Fold change (Log 2)
5.0
2.5
0.0
-2.5
-5.0
*†
Controls
Excluded IE
IE


PLAUR
Fold change (Log 2)
5
0
-5
-10
*
Controls
Excluded IE
IE


SLC16A3
Fold change (Log 2)
5
0
-5
-10
-15
-20
*
Controls
Excluded IE
IE


TGFβ1
Fold change (Log 2)
2.5
0.0
-2.5
-5.0
-7.5
*
Controls
Excluded IE
IE


IFI16
Fold change (Log 2)
5
0
-5
-10
*
Controls
Excluded IE
IE

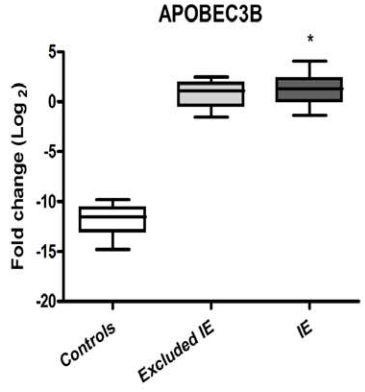

APOBEC3B
Fold change (Log 2)
5
0
-5
-10
-15
-20
*
Controls
Excluded IE
IE

Figure 2. Analysis of genes modulation using qRT-PCR. Blood samples from 39 patients with IE, 10 patients with excluded IE after an initial suspicion, and 10 controls were analyzed by qRT-PCR for the expression of seven genes that were found to be upregulated by microarray. The results were normalized with the β-actin gene. *$P<0.001$ for the comparison between IE patients and controls. †$P<0.05$ for the comparison between IE patients and patients with excluded IE.
doi:10.1371/journal.pone.0031490.g002

(AQP9), S100A11, plasminogen activator urokinase receptor (PLAUR), solute carrier family 16, member 3 (SLC16A3), transforming growth factor beta 1 (TGFβ1), interferon gamma-inducible protein 16 (IFI16), apolipoprotein B mRNA editing enzyme, and catalytic polypeptide-like 3B (APOBEC3B) were significantly upregulated in IE patients ($P<0.001$ for all, Figure 2).

Because these results may be due to the underlying valvular abnormality or the global inflammatory response, they were compared with those obtained in the group of patients with excluded IE after an initial suspicion (n = 10). The *S100A11* gene was significantly upregulated in the IE patients as compared with the patients with excluded IE ($P<0.05$, Figure 2). The upregulated expression of the *S100A11* gene had functional consequences. Indeed, the serum concentration of S100A11 protein was higher in patients with IE than in patients with excluded IE (5.0±1.0 versus 2.1±0.5 ng/mL, $P<0.05$).

Finally, we tested whether the bacterial etiology of IE plays a role in the modulated expression of the *S100A11* gene. In our series, 23 patients were infected with staphylococci (*Staphylococcus aureus* in nine patients) and 16 patients with streptococci. The expression of the *S100A11* gene was significantly higher in staphylococcal IE than in streptococcal IE and patients with excluded IE ($P<0.01$ and $P<0.001$, respectively) (Figure 3, Panel A). Similarly, the serum concentration of S100A11 protein was slightly increased in staphylococcal IE when compared with streptococcal IE and was significantly ($P<0.05$) increased when compared with patients with excluded IE (Figure 3, Panel B). Taken together, these results suggested that the determination of S100A11 at both the transcriptional and the protein levels was potentially predictive of IE. The S100A11 determination also discriminated between staphylococcal and streptococcal IE.

IE Transcriptional Signature and Major IE-Related Complications

Finally, we analyzed the modulation of the seven genes by qRT-PCR at admission according to IE-related complications, including acute heart failure (n = 17), embolic events (n = 14), and cardiac abscess (n = 10). The expression of the *AQP9* gene was increased only in patients who experienced acute heart failure ($P<0.05$). The expression of the *S100A11*, *PLAUR*, *SLC16A3*, *TGFβ1*, *IFI16*, and *APOBEC3B* genes was not related to acute heart failure, embolic events, or abscess (Figure 4). Taken together, these results suggested that the *AQP9* gene might be a marker of prognosis in IE.

Discussion

The aim of the present study was to characterize the peripheral transcriptional profile of patients with IE and to identify potential biomarkers. The clinical history of IE is dependent on the causative microorganism, the presence or absence of pre-existing cardiac disease, and the mode of presentation. The modified Duke criteria for IE diagnosis have been validated [5]; but they have clear limitations, especially when blood cultures and/or echocardiography are negative. Other parameters have been proposed to increase the yield of the diagnostic process, but none have been definitely implemented into the diagnostic criteria. A small study suggested that serum procalcitonin may be a valuable diagnostic marker in patients with suspected IE [18]. New imaging techniques, such as computed tomography (CT) [19], positron emission tomography/CT scan [20], three-dimensional echocardiography [21], or systematic cerebral MRI [22], are emerging to improve IE diagnosis; their final place has yet to be defined. The transcriptional analysis of a disease is a promising method to identify novel candidate biomarkers that might ultimately be translated into clinical practice [3]. In the present study, we found that blood transcriptomics may be used to characterize IE. We

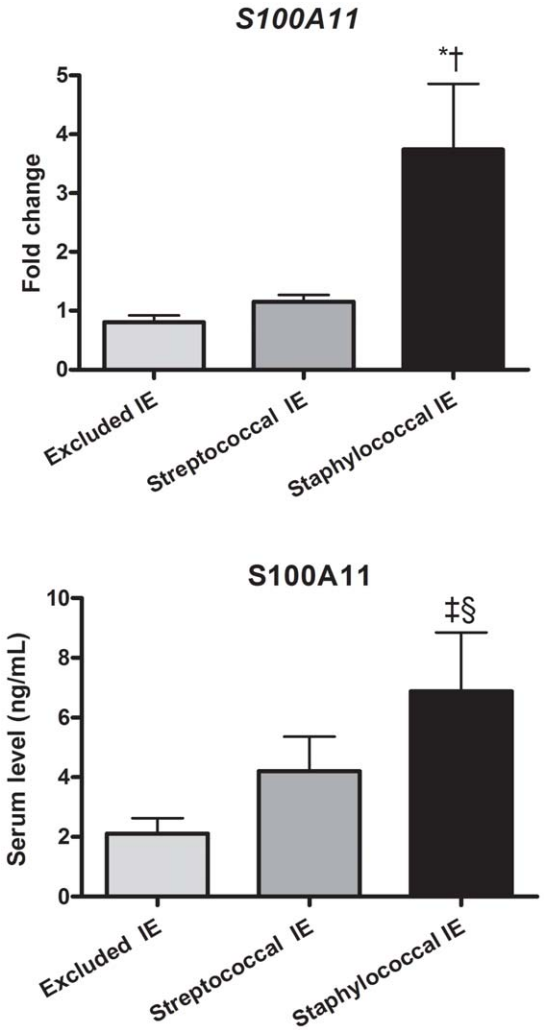


Figure 3. Expression of *S100A11* gene and S100A11 protein. A, The *S100A11* gene was significantly overexpressed in IE patients as compared with excluded IE patients ($P<0.05$). *$P<0.001$ for the comparison between staphylococcal IE and excluded IE. †$P<0.01$ for the comparison between staphylococcal IE and streptococcal IE. **B,** The S100A11 serum level was higher in staphylococcal IE (6.9±2.0 ng/mL) than in excluded IE (2.1±0.5 μg/mL) and staphylococcal IE (4.2±1.2 ng/mL). ‡$P<0.05$ for the comparison between staphylococcal IE and excluded IE. §$P = 0.17$ for the comparison between staphylococcal IE and streptococcal IE.
doi:10.1371/journal.pone.0031490.g003

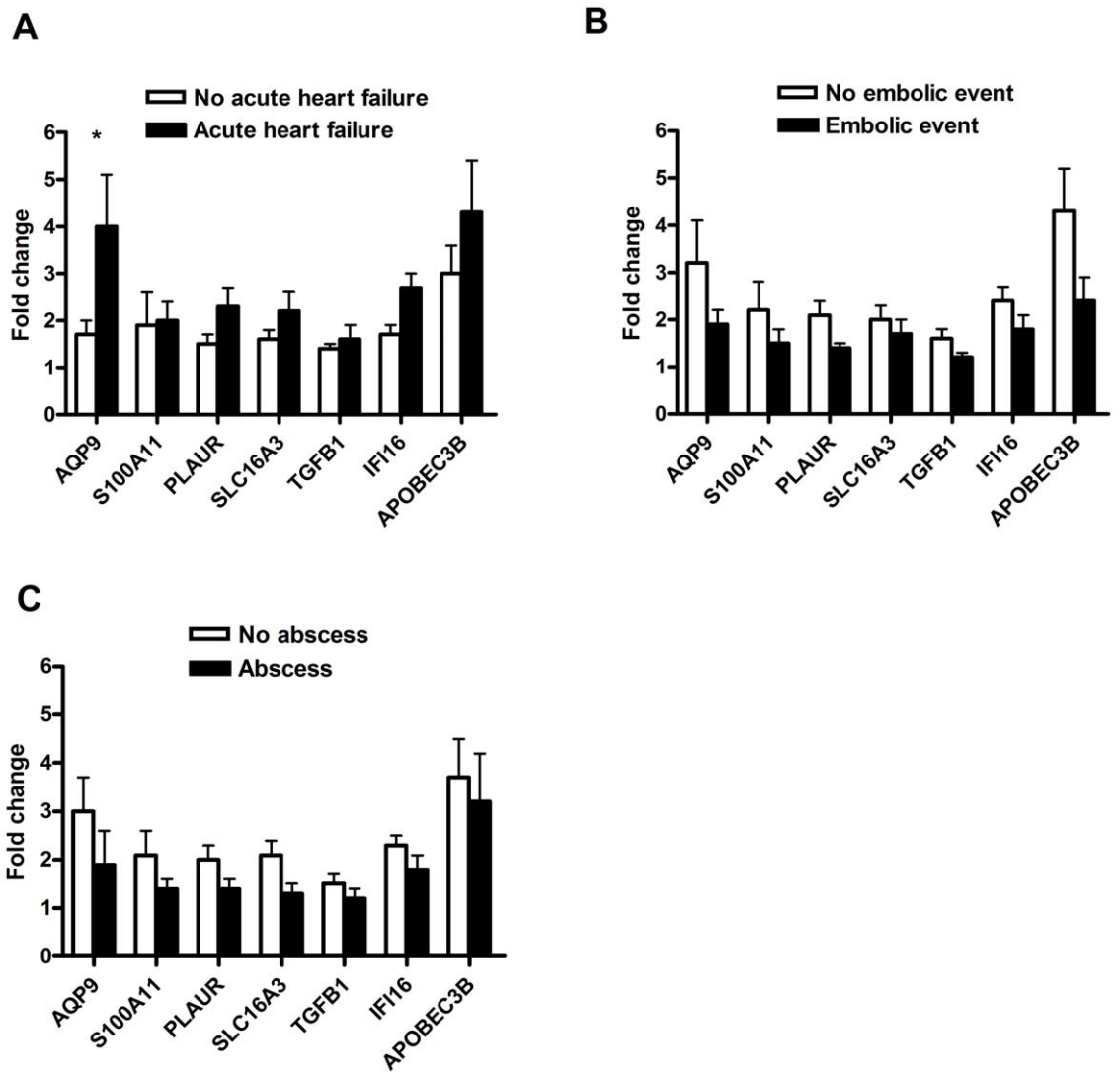


Figure 4. Gene expression according to the major IE-related complications. A, The expression of the *AQP9* gene was significantly increased only in patients who experienced acute heart failure. **B and C,** The expression of the *S100A11*, *PLAUR*, *SLC16A3*, *TGFβ1*, *IFI16*, and *APOBEC3B* genes was not related to acute heart failure, embolic events, or abscess. *$P<0.05$.
doi:10.1371/journal.pone.0031490.g004

have recently described the valvular transcriptional signature of IE [4]; to our knowledge, this is the first time that the host response in IE was studied at the blood level, which is more accessible and relevant than valvular tissue in the clinical practice.

The present analysis of the peripheral signature of IE allowed the identification of potential candidates for the diagnostic and prognostic assessment of IE. We showed that the expression of the *S100A11* gene was increased in patients with a final diagnosis of IE as compared with patients with an excluded IE diagnosis after an initial suspicion. The increased expression of the *S100A11* gene was essentially related to *Staphylococcus* infection. These transcriptional results were consistent with higher serum concentrations of the S100A11 protein in IE patients. S100A11 is a member of the family of S100 proteins that are localized in the cytoplasm and/or nucleus of a wide range of cells. S100A11 proteins are involved in endocytosis and exocytosis [23], regulation of enzyme activity, cell growth regulation, apoptosis and inflammation [24]. Note that endocytosis and inflammation were two hallmarks of the peripheral signature of IE determined in this study. Regarding the role of S100A11 in the pathophysiology of IE, our analysis extracted from the litterature a pathway that involves receptor for advanced glycation end-products (RAGE) and S100A11, which is one of its ligand. RAGE ligation causes cellular activation via signalling cascades including nuclear factor NF-kB, MAP kinases leading to induction of inflammatory cytokines, proteases ans oxydative stress [25]. NF-kB and the presence of RAGE ligand also up-regulates RAGE expression, ensuiring maintenance and amplification of the initial signal (Figure 5). RAGE and their ligands are strongly involved in the pathogenesis of systemic inflammation and represent a potential therapeutic target in sepsis and several acute infectious diseases [26]. Although S100A protein family can be associated with several human diseases, such as neurological diseases, cardiomyopathy, cancers, and inflammatory diseases, only few data exist on the specific implication of the S100A11 in pathology. In our microarray analysis, we compared IE patients with healthy subjects in order to bring out great significant differences with a small sample size. Thereafter, we analyzed *S100A11* gene expression in a population of patients with

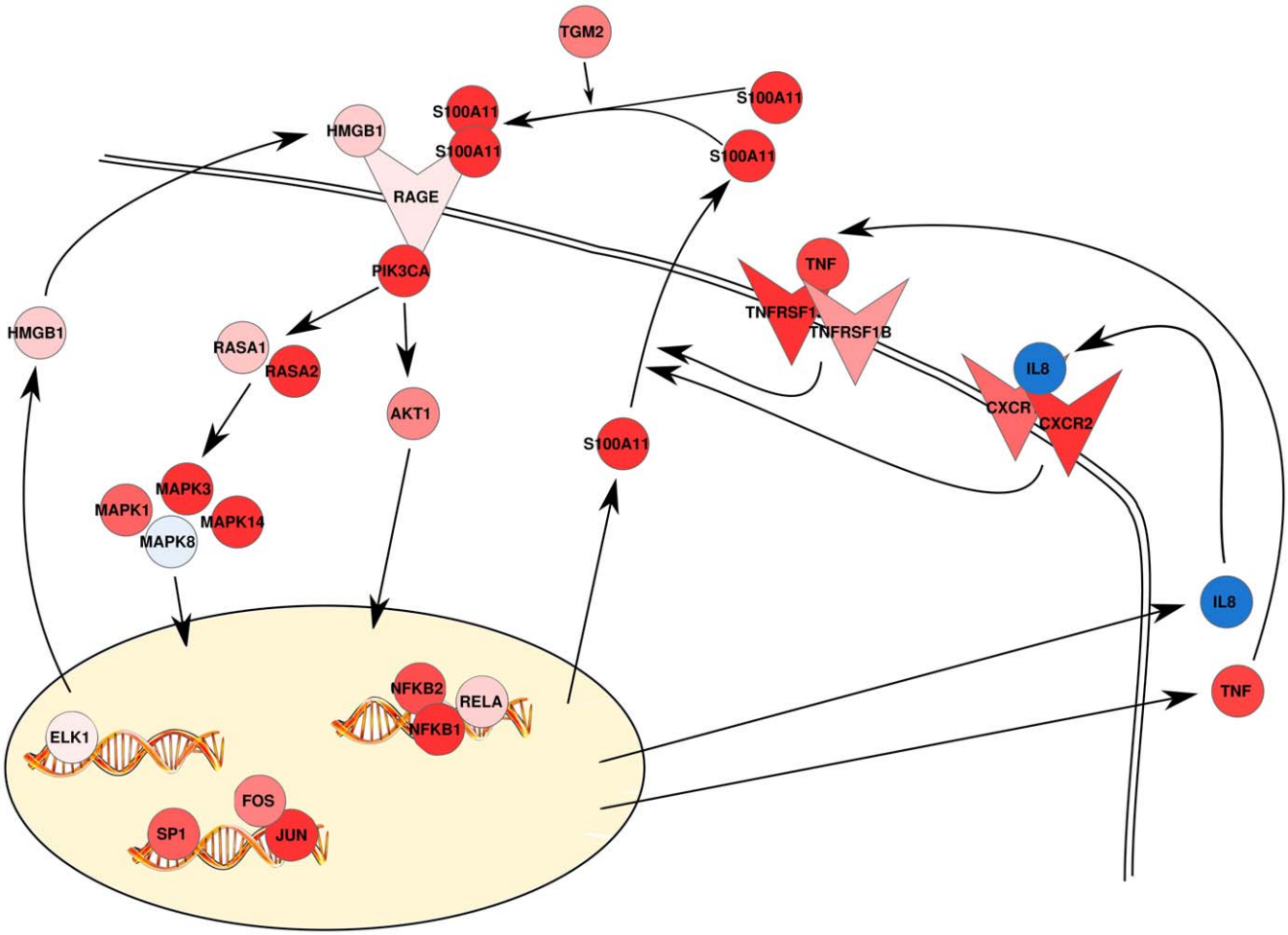


Figure 5. S100A11 relationship with RAGE pathway. RAGE pathway and its relationship with S100A11 were extracted from the literature and shematically represented on top of a virtual cells. Activation of inflammatory molecules induce the release of S100A11. S100A11 can homodimerize by interacting with its ''EF-hand'' domains. Transglutaminase TGM2 creates covalent bounds and a stable S100A11 homodimer. This S100A11 dimer interact with RAGE receptor, which in turn activates the MAP kinase pathway, and transduce membrane signals to the nucleus. The key transcription factors NF-kB, SP1, FOS and JUN, and ELK1 then up-regulate the transcription of their target genes.
doi:10.1371/journal.pone.0031490.g005

a suspicion of IE, i.e. in the setting of the clinical practice. Obviously, our study did not demonstrate that a single dosage of S100A11 is appropriate for the definite diagnosis of IE whatever the situation. Indeed, it does not make sense to use S100A11 without a specific clinical context. Our study showed that, in the case of a clinical suspicion of IE (i.e. a specific population of patients), S100A11 might be a marker of the IE diagnosis in association with other parameters. Moreover, the primers used for RT-PCR were specific and did not amplify the other S100A proteins. Finally, our results were significant both by RT-PCR (*S100A11* gene expression) and enzyme-linked immuno-sorbent assay (S100A11 protein in the serum). Thus, our results are probably not due to chance. Since our work was an exploratory study (first step to determine new candidate biomarkers for IE), we cannot definitely consider S100A11 as a biomarker for the diagnosis of IE, but this investigation open new perspectives for future studies that will test its sensibility and specificity in larger populations of patients with a clinical suspicion of IE.

In addition, the expression of the *AQP9* gene was clearly increased in IE patients who experienced acute heart failure, suggesting that its determination may be useful to the prognosis of IE. The detection of predictors of acute heart failure is of crucial importance because it can indicate the need for valvular surgery at an early stage of the disease [27]. Despite the identification by echocardiography and biological factors that are associated with acute heart failure [2], this complication remains the first cause of death during IE [5]. This fact highlights the need for additional markers. The AQPs are cell membrane-embedded proteins that facilitate water movements by increasing membrane water permeability and water flux in response to osmotic gradients [28]. The AQPs are involved in multiple different pathological processes, including abnormalities of renal function [28], myocardial [29], and brain [30] edema. Interestingly, we previously reported that the *AQP9* gene is overexpressed in the valvular tissue of IE patients and that the AQP9 protein is expressed in endothelial cells lining the lumen of neo-vessels [4]. The association between the modulation of the expression of the *AQP9* gene and acute heart failure may be due to the upregulation of the *AQP9* gene in patients with the most severe valvular damages. Patients with fluid retention may also differently express the *AQP9* gene in organs, such as the lungs and kidneys. These hypotheses offer new perspectives in the prognostic assessment of patients with IE and could have therapeutic implications because patients at high risk for hemodynamic instability are candidates for

an early surgical management [27]. We are aware that the relative small sample size restricts the statistical power of our study, for exemple, confounding factors other than age have not been addressed in the analysis. Thus, it may be useful to extend our results to a larger cohort of patients to confirm the clinical relevance of the use of both biomarkers for the diagnosis and prognosis of IE.

In summary, we are the first to report the circulating gene expression profile of IE patients. This peripheral signature enabled us to address, at least in part, the complex pathogenesis of IE. Our analyses revealed an enrichment of processes related to cell activation and the inflammatory and immune responses. The identification of novel candidates, such as S100A11 and AQP9, for diagnostic and prognostic assessment has likely provided new perspectives for future clinical studies.

Supporting Information

Table S1 List of primers.
(DOC)

Author Contributions

Conceived and designed the experiments: JLM DR CC. Performed the experiments: FT ABA AEF. Analyzed the data: FT JT AEF. Contributed reagents/materials/analysis tools: FT JT ABA AEF CC GH JLM DR. Wrote the paper: FT CC JLM.

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