Data in Brief

Gene expression profiling of human calcific aortic valve disease

Jaana Rysä

School of Pharmacy, University of Eastern Finland, Kuopio, Finland

ARTICLE INFO

ABSTRACT

Calcific aortic valve disease is a slowly progressive disorder that ranges from mild valve thickening (i.e. aortic sclerosis) to severe calcification of valves (i.e. aortic stenosis). Gene expression profiling analysis of non-calcified controls, sclerotic, and calcified aortic valves was performed to better understand the progression of calcific aortic valve disease. The complementary information related to processing and statistical analysis of the DNA microarray data is provided in this article. Interpretation of this data can be found in a research article entitled "MicroRNA-125b and chemokine CCL4 expression are associated with calcific aortic valve disease" [1]. The microarray data complies with MIAME guidelines and is deposited in the Gene Expression Omnibus (GEO) database under accession number GSE51472.

Specifications

Organism/cell line/tissue	Human aortic valve tissue samples
Sex	Males
Sequencer or array type	Affymetrix GeneChip® Human Genome U133 Plus 2.0 Arrays
Data format	Raw
Experimental factors	Samples are from 3 groups: non-calcified control, fibro(sclero)tic and stenotic valves, n = 5 in each group
Experimental features	RNA was extracted from valvular cups, converted to cDNA and hybridized to Affymetrix arrays
Consent	Not applicable
Sample source location	Aortic valves were removed from patients undergoing valve or aortic root surgery at Oulu University Hospital, Oulu Finland

1. Direct link to deposited data

All samples are separately available in GEO database under accession number GSE51472 http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE51472.

2. Experimental design, materials and methods

2.1. Materials

Aortic valves for this study were removed from patients undergoing valve or aortic root surgery [1]. The study protocol complied with the principles outlined in the Declaration of Helsinki, and it was approved by the Research Ethics Committee of Oulu University Hospital, Oulu, Finland. All operations were made following normal surgical procedures. After removal, aortic valve cusps were placed immediately in liquid nitrogen and stored at −70 °C until analyzed [1–2].

Total RNA from five samples from each group (non-calcified control, fibro(sclero)tic and stenotic valves) was extracted with the guanidine thiocyanate-CsCl method [3–4] and further purified by RNeasy Midi Kit (Qiagen) according to manufacturer's instructions. The quality and integrity of the isolated total RNA were monitored by gel electrophoresis.

2.2. DNA microarray analysis

The biotinylated cRNA probes were prepared and hybridized according to the Affymetrix GeneChip Expression Analysis Technical Manual. First, cDNA was reverse-transcribed from 5 μg of total RNA with a T7-(dT)24-primer by using the One-cycle cDNA synthesis kit (Affymetrix). The DNA was purified using GeneChip Sample Cleanup Module (Qiagen). The cRNA was prepared and biotin-labeled by in vitro transcription by using an IVT-labeling kit (Affymetrix), biotinylated cRNA was cleaned with a GeneChip Sample Cleanup Module (Qiagen), followed by fragmentation from 35 to 200 nt. Then, 10 μg of cRNA was hybridized on Affymetrix GeneChip® Human Genome U133 Plus 2.0 Arrays for 16 h at 45 °C. After hybridization GeneChips were washed and stained with streptavidin–phycoerythrin (Molecular Probes) in the Affymetrix Fluidics Station 400. Staining signal was amplified by biotinylated anti-streptavidin (Vector Laboratories) and second staining with streptavidin–phycoerythrin by using Affymetrix Fluidics station according to the standard protocol. GeneChip Scanner 3000 (Affymetrix) with GeneChip Operating Software (GCOS) v. 1.2 (Affymetrix) was used in scanning. Scanned images were processed using Affymetrix Microarray Suite 5.0. The probe quality was evaluated by the 3′/5′ hybridization ratio for the set of housekeeping genes on the

Affymetrix chip. The obtained ratio was <2 and comparable among all hybridized samples.

2.3. Statistical analysis

The Affymetrix software GCOS was used to generate cell intensity data files (CEL). The software program GeneSpring version 7.2 (Agilent) was used for normalization, clustering, filtering, and statistical analyses. CEL files (from GCOS 1.2) were imported into GeneSpring using the Robust Multi-Array Average normalization. All the samples were then normalized to the median of the controls. Genes were defined as differentially expressed if the change was at least 2.0-fold and statistically significant (P < 0.05, one-way ANOVA and Benjamini and Hochberg false discovery rate).

Acknowledgments

References

[1] P. Ohukainen, S. Syväranta, J. Näpänkangas, K. Rajamäki, P. Taskinen, T. Peltonen, S. Helske-Suihko, P.T. Kovanen, H. Ruskoaho, J. Rysä, MicroRNA-125b and chemokine CCL4 expression are associated with calcific aortic valve disease. Ann. Med. 47 (5) (2015) 423–429, http://dx.doi.org/10.3109/07853890.2015.1059955.

[2] T.O. Peltonen, P. Taskinen, Y. Soini, J. Rysä, J. Ronkainen, P. Ohtonen, J. Satta, T. Juvonen, H. Ruskoaho, H. Leskinen, Distinct down-regulation of C-type natriuretic peptide system in human aortic valve stenosis. Circulation 116 (11) (2007) 1283–1289.

[3] J.M. Chirgwin, A.E. Przybyla, R.J. MacDonald, W.J. Rutter, Isolation of biologically active ribonucleic acid from sources enriched in ribonuclease. Biochemistry 18 (1979) 5294–5299.

[4] J. Rysä, H. Leskinen, M. Ilves, H. Ruskoaho, Distinct upregulation of extracellular matrix genes in transition from hypertrophy to hypertensive heart failure. Hypertension 45 (2005) 927–933.