Data Article

RNA sequencing data describing transcriptional changes in aorta of ApoE-/mice after alpha 7 nicotinic acetylcholine receptor (α7nAChR) stimulation

Marcus A. Ulleryd, Filip Mjörnstedt, Dimitra Panagaki, Li Jin Yang, Kajsa Engevall, Saray Gutierrez, Yixin Wang, Li-Ming Gan, Holger Nilsson, Erik Michaëlsson, Maria E. Johansson

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A B S T R A C T

This manuscript is a companion paper to Ulleryd M.U. et al., “Stimulation of alpha 7 nicotinic acetylcholine receptor (α7nAChR) inhibits atherosclerosis via immunomodulatory effects on myeloid cells” Atherosclerosis, 2019 [1]. Data shown here include RNA sequencing data from whole aorta of ApoE-/mice fed high fat diet and treated with the alpha 7 nicotinic acetylcholine receptor (α7nAChR) agonist AZ6983 for 8 weeks using subcutaneously implanted osmotic minipumps. Here we present the top gene networks affected by treatment with AZ6983, as well as the up- and down-regulated genes in aorta after treatment. Further, a URL link to the RNA sequencing datasets submitted to GEO is included.
Specifications table

| Subject | Medicine |
|---------|----------|
| Specific subject area | Physiology, Experimental atherosclerosis |
| Type of data | Table |
| Figure |
| How data were acquired | RNA sequencing (Nextseq500) |
| Data format | Raw |
| Analyzed |
| Parameters for data collection | ApoE-/- mice were treated with alpha 7 nicotinic acetylcholine receptor (α7nAChR) agonist AZ6983 or vehicle for 8 weeks using subcutaneously implanted osmotic minipumps. RNA from whole aorta were extracted and used for RNA sequencing analysis. n=6 per group. |
| Description of data collection | Data shown here includes top gene networks affected by treatment with AZ6983, identified with IPA software, and a table with Complete list of up- and down-regulated genes in the aorta after treatment with AZ6983, ranked by q-value. We also supply a URL link to the RNAseq datasets submitted to GEO. GEO accession numbers: GSE131162, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE131162 |
| Data source location | Gothenburg, Sweden |
| Data accessibility | Repository name: NCBI (http://www.ncbi.nlm.nih.gov/geo/) |
| Data identification number: GSE131162 |
| Direct URL to data: | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE131162 |
| Related research article | Ulleryd, M.A., Mjörnstedt, F., Panagaki, D., Yang, L.J., Engevall, K., Gutierrez, S., Wang, Y., Gan, L., Nilsson, H., Michaelsson, E., Johansson, M., E. Stimulation of alpha 7 nicotinic acetylcholine receptor (α7nAChR) inhibits atherosclerosis via immunomodulatory effects on myeloid cells. Atherosclerosis 2019 Aug;287:122–133 PMID: 31260875 DOI: 10.1016/j.atherosclerosis.2019.06.903 |

Value of the data

- These data provide information on the transcriptional effects on whole aorta after treatment with alpha 7 nicotinic acetylcholine receptor (α7nAChR) agonist AZ6983 in the atherosclerosis-prone ApoE-/- mouse.
- Researchers interested in atherosclerosis, as well as, α7nAChR signaling will find these data a valuable resource.
- The information provided here may be used for future studies on how α7nAChR stimulation influence the vascular transcriptome.
- These data can generate hypothesis for new studies investigating the α7nAChR-related transcriptomic profiles, as well as signaling pathways, in other tissues
- The present data on α7nAChR signaling is predominantly available from cell culture experiments, using cell lines, this data set provides additional information on the signaling pathways in tissue from long-term treatment in vivo.

1. Data description

To investigate the effects of alpha 7 nicotinic acetylcholine receptor (α7nAChR) stimulation on atherosclerosis in apolipoprotein E deficient (ApoE-/-) mice, mice were treated with α7nAChR
agonist AZ6983 for 8 weeks. Thoracic aortas were used for RNA sequencing analysis. Fig. 1 describes the top two networks identified with Ingenuity Pathway Analysis (IPA) software for differently expressed genes in aorta of ApoE-/- mice treated with AZ6983 compared with controls. Major functions of the networks are indicated in A and B, followed by the network score. Networks are ranked according to their degree of relevance to the eligible network molecules in the data set and the score is calculated with an algorithm based on p-scores derived from q-values.
Table 1 shows the complete list of up- and down-regulated genes in the aorta after treatment with AZ6983 ranked by q-value.

2. Experimental design, materials, and methods

2.1. Experimental animals

Male apoE/- mice (C57BL/6 background, B6192P2-Apoetm1UncN1, Taconic, Denmark) were kept at the Laboratory for Experimental Biomedicine, Gothenburg, Sweden. At 10 weeks of age, mice were anesthetized using isoflurane and subcutaneously implanted with osmotic minipumps

| Symbol | Entrez Gene Name | Up/down | Expr Log Ratio | Expr p-value | Location | Type(s) |
|--------|-----------------|---------|----------------|--------------|----------|---------|
| IMPDH1 | inosine monophosphate dehydrogenase 1 | Up | 1.427 | 3.24E−07 | Cytoplasm | enzyme |
| SREBF1 | sterol regulatory element binding transcription factor 1 | Up | 1.010 | 6.13E−07 | Nucleus | transcription regulator |
| LPCAT3 | lysophosphatidylcholine acyltransferase 3 | Up | 0.594 | 2.36E−04 | Plasma Membrane | enzyme |
| Scd2 | stearoyl-Coenzyme A desaturase 2 | Up | 0.962 | 1.22E−03 | Cytoplasm | enzyme |
| MBD6 | methyl-CpG binding domain protein 6 | Up | 0.779 | 5.23E−03 | Nucleus | other |
| LTF | lactotransferrin | Up | 1.647 | 6.54E−03 | Extracellular Space | peptidase |
| SLC22A23 | solute carrier family 22 member 23 | Up | 0.674 | 7.01E−03 | Other | transporter |
| Apoc1 | apolipoprotein C-I | Up | 1.295 | 7.78E−03 | Extracellular Space | other |
| PXN | paxillin | Up | 0.240 | 7.78E−03 | Cytoplasm | other |
| UTP14C | UTP14C small subunit processome component | Up | 0.665 | 7.78E−03 | Nucleus | other |
| IGHG1 | immunoglobulin heavy constant gamma 1 (G1m marker) | Up | 3.965 | 8.95E−03 | Extracellular Space | peptidase |
| Cmah | cytidine monophospho-N-acetylmuraminic acid hydroxylase | Up | 0.551 | 1.36E−02 | Cytoplasm | enzyme |
| SPON2 | spondin 2 | Up | 0.979 | 2.09E−02 | Extracellular Space | other |
| Ngp | neutrophil granule protein | Up | 1.934 | 2.68E−02 | Extracellular Space | other |
| PTGES | prostaglandin E synthase | Up | 0.857 | 3.03E−02 | Cytoplasm | enzyme |
| ABCA1 | ATP binding cassette subfamily A member 1 | Up | 0.514 | 3.16E−02 | Plasma Membrane | transporter |
| Scd4 | stearoyl-Coenzyme A desaturase 4 | Up | 0.902 | 3.62E−02 | Cytoplasm | enzyme |
| GP1BA | glycoprotein Ib platelet alpha subunit 3 receptor | Up | 2.025 | 4.58E−02 | Plasma Membrane | transmembrane receptor |
| CSF3R | colony stimulating factor receptor | Up | 1.122 | 4.72E−02 | Plasma Membrane | transmembrane receptor |
| H2-M1/H2-M9 | histocompatibility 2, M region locus 1 adrenocorticotropin | Up | 0.950 | 4.72E−02 | Other | other |
| ADRB2 | adrenocorticotropin | Up | 0.711 | 4.87E−02 | Plasma Membrane | G-protein coupled receptor |

(continued on next page)
| Symbol   | Entrez Gene Name                                      | Up/down | Expr Ratio | Log p-value | Location       | Type(s)                                |
|----------|------------------------------------------------------|---------|------------|-------------|----------------|----------------------------------------|
| MXD1     | MAX dimerization protein 1                           | Up      | 0.314      | 5.85E−02    | Nucleus        | transcription regulator                |
| NPAS2    | neuronal PAS domain protein 2                        | Up      | 0.780      | 5.89E−02    | Nucleus        | transcription regulator                |
| SYTL1    | synaptotagmin like 1                                 | Up      | 1.214      | 5.89E−02    | Cytoplasm      | enzyme                                 |
| LENG     | leukocyte receptor cluster member 8                  | Up      | 0.365      | 6.06E−02    | Other          | other                                  |
| WNT2     | Wnt family member 2                                  | Up      | 0.656      | 6.66E−02    | Extracellular  | cytokine                               |
| NAV2     | neuron navigator 2                                   | Up      | 0.667      | 6.73E−02    | Nucleus        | other                                  |
| STIL     | STIL centriolar assembly protein                      | Up      | 1.388      | 6.73E−02    | Nucleus        | other                                  |
| ESM1     | endothelial cell specific molecule 1                 | Up      | 0.560      | 6.86E−02    | Extracellular  | growth factor                          |
| CD177    | CD177 molecule                                       | Up      | 1.525      | 6.94E−02    | Cytoplasm      | other                                  |
| CLK1     | CDC like kinase 1                                    | Up      | 0.297      | 6.94E−02    | Nucleus        | kinase                                 |
| PABPC1   | poly(A) binding protein cytoplasmic 1                | Up      | 0.345      | 6.94E−02    | Cytoplasm      | translation regulator                  |
| PITPNM1  | phosphatidylinositol transfer protein membrane        | Up      | 0.187      | 7.12E−02    | Cytoplasm      | transporter                             |
| MGAM     | maltase-glucoamylase                                 | Up      | 1.396      | 7.24E−02    | Plasma Membrane| enzyme                                 |
| PGLYRP1  | peptidoglycan recognition protein 1                  | Up      | 1.271      | 7.24E−02    | Plasma Membrane| transmembrane receptor                |
| DENND1A  | DENN domain containing 1A                            | Up      | 0.330      | 7.26E−02    | Plasma Membrane| other                                  |
| Stfa2/Stfa2I | stefin A2                                        | Up      | 2.402      | 7.26E−02    | Cytoplasm      | other                                  |
| BLVRB    | biliverdin reductase B paired box 1                   | Up      | 0.183      | 7.67E−02    | Cytoplasm      | enzyme                                 |
| PAX1     | interferon induced transmembrane protein 6           | Up      | 0.593      | 7.74E−02    | Nucleus        | transcription regulator                |
| PC       | pyruvate carboxylase                                 | Up      | 0.601      | 7.85E−02    | Cytoplasm      | enzyme                                 |
| CYP26B1  | cytochrome P450 family 26 subfamily B member 1       | Up      | 0.482      | 8.03E−02    | Cytoplasm      | enzyme                                 |
| Acaa1b   | acetyl-Coenzyme A acyltransferase 1B                 | Up      | 0.708      | 8.11E−02    | Other          | enzyme                                 |
| CAMP     | cathelicidin antimicrobial peptide                   | Up      | 2.056      | 8.11E−02    | Cytoplasm      | other                                  |
| SCARB1   | scavenger receptor class B member 1                  | Up      | 0.573      | 8.11E−02    | Plasma Membrane| transporter                             |
| Ifitm6   | interferon induced transmembrane protein 6           | Up      | 0.923      | 8.27E−02    | Other          | other                                  |
| VWF      | von Willebrand factor                                | Up      | 0.369      | 8.27E−02    | Extracellular  | other                                  |
| PACS1    | phosphofurin acidic cluster sorting protein 1        | Up      | 0.382      | 8.34E−02    | Cytoplasm      | other                                  |
| SLC12A7  | solute carrier family 12 member 7                    | Up      | 0.386      | 8.34E−02    | Plasma Membrane| transporter                             |
| KLHL4    | kelch like family member 4                           | Up      | 0.442      | 9.12E−02    | Cytoplasm      | other                                  |
| GIGYF1   | GRB10 interacting GYF protein 1                      | Up      | 0.392      | 9.62E−02    | Extracellular  | other                                  |
| DENND2D  | DENN domain containing 2D                            | Up      | 0.819      | 9.78E−02    | Cytoplasm      | other                                  |
| PRKDC    | protein kinase. DNA-activated. catalytic polypeptide | Up      | 0.259      | 9.92E−02    | Nucleus        | kinase                                 |
Table 1 (continued)

| Symbol | Entrez Gene Name                                      | Up/down | Expr Log Ratio | Expr p-value | Location        | Type(s)          |
|--------|-------------------------------------------------------|---------|----------------|--------------|-----------------|------------------|
| GGACT  | gamma-glutamylamine cyclotransferase neuronatin       | Down    | -0.361         | 2.36E-04     | Cytoplasm       | enzyme           |
| NNAT   |                                                       | Down    | -1.894         | 2.36E-04     | Plasma Membrane | transporter      |
| ATP6V1C1 | ATPhase H+ transporting V1 subunit C1               | Down    | -0.248         | 1.33E-03     | Cytoplasm       | transporter      |
| COL2A1 | collagen type II alpha 1 chain                       | Down    | -4.419         | 6.54E-03     | Extracellular Space | other        |
| 2210407C18Rik | RIKEN cDNA 2210407C18 gene               | Down    | -0.642         | 9.13E-03     | Other            | other            |
| IBSF   | integrin binding sialoprotein                        | Down    | -3.005         | 2.01E-02     | Extracellular Space | other        |
| OTUD6B | OTU domain containing 6B                             | Down    | -0.266         | 2.68E-02     | Other            | Other            |
| PDE1C  | phosphodiesterase 1C                                 | Down    | -0.464         | 4.62E-02     | Cytoplasm       | enzyme           |
| CAP    | titin-cap                                             | Down    | -0.747         | 4.65E-02     | Cytoplasm       | Other            |
| HEPHL1 | hephaestin like 1                                     | Down    | -1.625         | 5.07E-02     | Other            | enzyme           |
| NUDT4  | nudix hydrolase 4                                     | Down    | -0.301         | 5.07E-02     | Cytoplasm       | phosphatase      |
| CRISPLD1 | cyssteine rich secretory protein LCCL domain containing 1 | Down    | -0.570         | 6.07E-02     | Cytoplasm       | Other            |
| CLEC3A | C-type lectin domain family 3 member A              | Down    | -3.948         | 6.41E-02     | Other            | Other            |
| S100B  | S100 calcium binding protein B                        | Down    | -0.853         | 6.41E-02     | Cytoplasm       | Other            |
| LAPT4B | lysosomal protein transmembrane 4 beta               | Down    | -0.233         | 6.66E-02     | Cytoplasm       | Other            |
| CTSZ   | cathepsin Z                                           | Down    | -0.475         | 6.81E-02     | Cytoplasm       | peptidase        |
| EFR3A  | EFR3 homolog A                                       | Down    | -0.265         | 6.84E-02     | Cytoplasm Membrane | Other        |
| GLDN   | gliomedin                                             | Down    | -0.553         | 6.86E-02     | Cytoplasm       | Other            |
| ATP6V1A | ATPhase H+ transporting V1 subunit A               | Down    | -0.228         | 6.94E-02     | Cytoplasm Membrane | Other        |
| MED10  | mediator complex subunit 10                          | Down    | -0.234         | 6.94E-02     | Nucleus          | Other            |
| PON1   | paraoxonase 1                                         | Down    | -0.775         | 6.94E-02     | Extracellular Space | phosphatase |
| HFC1R1 | host cell factor C1 regulator 1                     | Down    | -0.196         | 8.11E-02     | Nucleus          | Other            |
| MSI2   | musashi RNA binding protein 2                       | Down    | -0.154         | 8.25E-02     | Cytoplasm       | Other            |
| AK4    | adenylyl kinase 4                                     | Down    | -0.559         | 9.69E-02     | Cytoplasm       | kinase            |
| DPP10  | dipeptidyl peptidase like 10                         | Down    | -0.750         | 9.92E-02     | Extracellular Space | peptidase |

All differentially expressed genes, after p-value adjustment (q-values) using Benjamini Hochberg [2] and a FDR-q of 10%, in the aorta of AZ6983 treated mice compared with controls. Genes are sorted by up or down regulation, followed by the adjusted p-value.

(Alzet model 2004, DURECT Corporation, ALZET Osmotic Pumps, Cupertino, CA, USA) delivering vehicle (28% cyclodextrin in saline), or α7nAChR agonist AZ6983 (50μmol kg-1 per day) for 8 weeks. Due to the duration of the minipumps, they were replaced after 4 weeks. From 10 weeks of age and throughout the experiment, mice were fed a high fat, cholesterol enriched diet (21% fat, 0.15% cholesterol; R638, Lantmännen, Sweden). All animals were housed at 21–24 °C in a room with 12 h light/ 12 h dark cycle. Water and food were available ad libitum. All procedures involving mice were approved by the Regional Animal Ethics Committee at the University of Gothenburg, in accordance with the European Communities Council Directives of 22 September 2010 (2010/63/EU).
2.2. RNA isolation, RNA sequencing and ingenuity pathway analysis

RNA of thoracic aorta was extracted by using the RNAeasy® Fibrous Tissue Mini Kit (Qiagen GmbH, Hilden, Germany) according to the manufacturer’s protocol. Concentration and quality was analyzed using a NanoDrop (NanoDrop Products, DE, US) and electrophoresis (Experion, Bio-Rad Laboratories, CA, USA).

Aortic RNA from mice treated with AZ6983 (n=6) or controls (n=6) was isolated as described above and Stranded Total RNA Sample preparations were performed using the Illumina TrueSeq Stranded Total RNA Sample Preparation Kit with Ribo Sero Gold according to the TruSeq Stranded Total RNA Sample Preparation Guide (15031048 Rev. E). Sequencing of the enriched libraries was performed on Illumina Nextseq500 (2x75bp). The quality of the data was analyzed with FastQC and reads with an average quality score of >30 were included in the sequencing. Differentially expressed genes (DEGs) were identified using the DESeq2-method with Benjamini Hochberg adjusted p-values (q-values) [2] and a FDR-q of 10%.

QIAGEN’s Ingenuity® Pathway Analysis (IPA®, QIAGEN Redwood City, content version 42012434) was used to study potential functions of AZ6983 treatment in the aorta [3–5]. Network analysis was generated by overlaying the eligible network molecules in the data set with the global gene network contained in the Ingenuity® Knowledge Base. Networks are ranked according to their degree of relevance to the genes in the data set. Functional analysis identified the top ranked biological functions and diseases that were enriched in the dataset by calculating the number of molecules that cohere to a functional category and was estimated by Fisher’s exact test (q<0.05). Activation Z-score predicts if a specific function is activated (≥2) or inhibited (≤−2) and is supported by one or more references from Ingenuity® Knowledge Base.

Top two networks identified with Ingenuity Pathway Analysis (IPA) software for genes that were differently expressed in aorta of ApoE−/− mice treated with AZ6983 compared with controls. Major functions of the networks are indicated in A and B, followed by the network score. Networks are ranked according to their degree of relevance to the eligible network molecules in the data set and the score is calculated with an algorithm based on p-scores derived from q-values. The up- (red) or down- (green) regulation of genes are indicated by the intensity of node color, and the functional class of the gene product is indicated by different symbols. Relationship between genes are supported by one or more references and illustrated with a connecting line.

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Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships which have, or could be perceived to have, influenced the work reported in this article.

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**Supplementary materials**

Supplementary material associated with this article can be found, in the online version, at doi: [10.1016/j.dib.2020.105415](https://doi.org/10.1016/j.dib.2020.105415).

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