

Online Supplementary Materials

miR-511-3p Protects Against Cockroach Allergen-Induced Lung Inflammation by Antagonizing CCL2

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METHODS

Flow cytometry analysis

Single-cell suspensions from whole lung tissues were prepared from minced lung tissues following by collagenase D (2 mg/mL) and DNase I (40 U/mL) digestion in DMEM supplemented with 10% v/v FBS for 60 min at 37°C with shaking. The digested lung solution was passed through a sterile 40 µm strainer and centrifuged for 10 min at 400 x g, 4°C. Red blood cells were lysed with 5 mL of ACK buffer (ThermoFisher) and resuspended in cold PBS for antibody staining. To prepare stained cells for flow cytometric analysis, Fc-receptors were blocked with anti-CD16/32 and stained for the macrophage surface antigens F4/80 and CD11c, In a separate sample, the T-cell surface antigens CD4 and CD25 were also stained. Cells were fixed and permeabilized using the Transcription Factor Fixation/Permeabilization Buffer Set (BioLegend) as instructed by the manufacturer and stained for either the intracellular marker iNOS, arginase-1, or FoxP3. In each test, a minimum of 100,000 cells was analyzed using a FACSCalibur (BD) flow cytometer. M1 and M2 macrophages (1), and Tregs are defined as F4/80⁺CD11c⁺iNOS⁺, F4/80⁺CD11c⁺Arg-1⁺, or CD4⁺CD25⁺FoxP3⁺, respectively. Cells collected from the BAL fluids were also stained and analyzed using this method.

miR-511-3p overexpression in macrophages with Lentivirus transduction

Murine bone marrow (BM) cells were obtained from the femurs and tibias of 6-8 week-old mice. The BM cells were cultured at a starting density of 5x10⁶ cells/mL at 37°C in a humidified atmosphere containing 5% CO₂ and differentiated into macrophages (BMDMs) in DMEM containing 10% FBS, 1% penicillin /streptomycin, and 20 ng/mL of recombinant murine M-CSF (BioLegend) for 7 days. BMDMs were seeded onto a 6-well tissue culture plate (CellTreat,

Pepperell MA) at a density of 1×10^5 cells/well 24 h prior to treatment. Over-expression of miR-511-3p in BMDMs were accomplished by LV transduction at a calculated MOI=3 48 h prior to treatment. Classically (M1) or alternatively (M2) activated macrophages were induced with 100 ng/mL of LPS (ThermoFisher) or 20 ng/mL of murine recombinant IL-4 (ThermoFisher). Total RNA was isolated from the cells using the Ribospin™ II kit after 6 or 18 h prior to LPS or IL-4 stimulation, respectively. In some experiments, BMDMs were treated with recombinant murine Ccl2 (BioLenged) at 5, 20, or 50 ng/mL in DMEM containing 10% FBS and 1% penicillin/streptomycin. Total RNA was isolated from the cells ~2 h post-treatment.

Isolation of murine lung macrophages

The isolation of murine lung macrophages from the BAL was accomplished using the method described by Zhang *et al* (2) with minor modifications. In brief, 6-8 weeks old Mrc1^{-/-} mice were terminally anesthetized using a ketamine/xylazine cocktail. Circulating red blood cells were flushed from the lungs with 10mL of phosphate-buffered saline (PBS) through the right ventricle. The lungs were infused with 1 mL of prewarmed (37°C) calcium and magnesium-free PBS supplemented with 0.5 mM EDTA via a tracheal catheter and gently withdrawing the fluid into the syringe. This was repeated 9 more times, the collected volumes were pooled together, and centrifuged for 10 min at 400 x g, 4°C. The cells were resuspended in DMEM/F12 medium supplemented with 10% (v/v) fetal bovine serum, 10 mM L-glutamine, 100 IU/ml penicillin, and 100 µg/ml streptomycin. Macrophage purity was assessed by flow cytometry and defined as CD45⁺F4/80⁺CD11c⁺ cells.

RT-PCR

Total RNA was isolated using RibospinTM II (GeneAll, Seoul Korea) with on-column DNase I digestion as instructed by the manufacture. RNA quality and concentration was assessed by Nanodrop-2000 spectrometer (Agilent Technologies, Santa Clara CA). cDNA templates were synthesized with SuperScript II (Invitrogen, Carlsbad CA) as instructed. qRT-PCR was performed in duplicates using Power SYBR Green Universal 2X qPCR Master Mix (Applied Biosystems, Foster City CA) on an ABI Prism 7300 detection system. mRNA levels were normalized to the internal control gene (β -actin) and data were analyzed using the $2^{-\Delta\Delta CT}$ method (3). Primers sequences are annotated by PrimerBank (4) and provided in the online depository.

Co-immunoprecipitation

Co-immunoprecipitation (IP) was performed as previously described (5). THP-1 cells were treated with 50 ng/mL of recombinant human CCL2 (BioLegend) for 2 h and rinsed with ice-cold 1X PBS. Cells were lysed with Cell Lysing Buffer (Cell Signaling) containing Protease/Phosphatase Inhibitor Cocktail (Cell Signaling). Cell lysate was pre-cleared with Protein A magnetic beads (Cell Signaling) and incubated with anti-CCR2 (clone D14H7, Cell Signaling) or isotype control (clone DA1E, Cell Signaling) overnight at 4°C with rotation. Antibody-protein complexes were enriched using Protein A magnetic beads and washed 5 times with 1X Cell Lysing Buffer. The beads were resuspended in SDS lysing buffer and heated to 95-100°C for 5 min. The pellet beads were separated using magnetic rack and the the supernatant was analyzed by Western Blot.

REFERENCE

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4. Wang X, Spandidos A, Wang H, Seed B. PrimerBank: a PCR primer database for quantitative gene expression analysis, 2012 update. *Nucleic Acids Res* 2012; 40: D1144-1149.
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FIGURE LEGENDS

Figure E1. Confirmation of AAV-miR-511-3p delivery into the mouse lung and infected

major cell populations. (A) Flow cytometry analysis of single cell suspensions from mouse lung on day 35 after AAV-miR-511-3p delivery and AAV-Mock control. Gating was made on GFP with F4/80 and CD11C (macrophages), CD11C, and MHCII (DCs), and MHCII and EpCaM (epithelial cells). (B) Representative images of co-immunostaining for eGFP with F4/80 (macrophages) and EpCaM (epithelial cells) from paraffin embedded lung section of AAV-treated mice. Original magnification x20. (C) Quantitative RT-PCR analyses for miR-511-3p expression in the single cell suspensions from mouse lung on day 35 after AAV-miR-511-3p delivery or AAV-Mock control. n=3/group. Data represent means \pm SEMs, comparisons were made using 2-tailed Student's t test between groups. $**P < 0.01$.

Figure E2. Gating strategies to measure bronchoalveolar lavage fluid cells by flow

cytometry. Eosinophils were gated SSC^{high} SiglecF⁺Mac-3⁻ cells, macrophages on SSC^{high} SiglecF⁺ Mac-3⁺ cells, granulocytes on SSC^{high} Gr-1⁺ cells, and lymphocytes on $FSC^{\text{low}}/SSC^{\text{low}}$ CD3⁺ cells. Flow cytometry was performed on a FACSCalibur cytometer.

Figure E3. Confirmation of purity of macrophages enriched from bronchoalveolar lavage fluids by flow cytometry analysis. Macrophages: CD45⁺F4/80⁺/CD11C⁺.

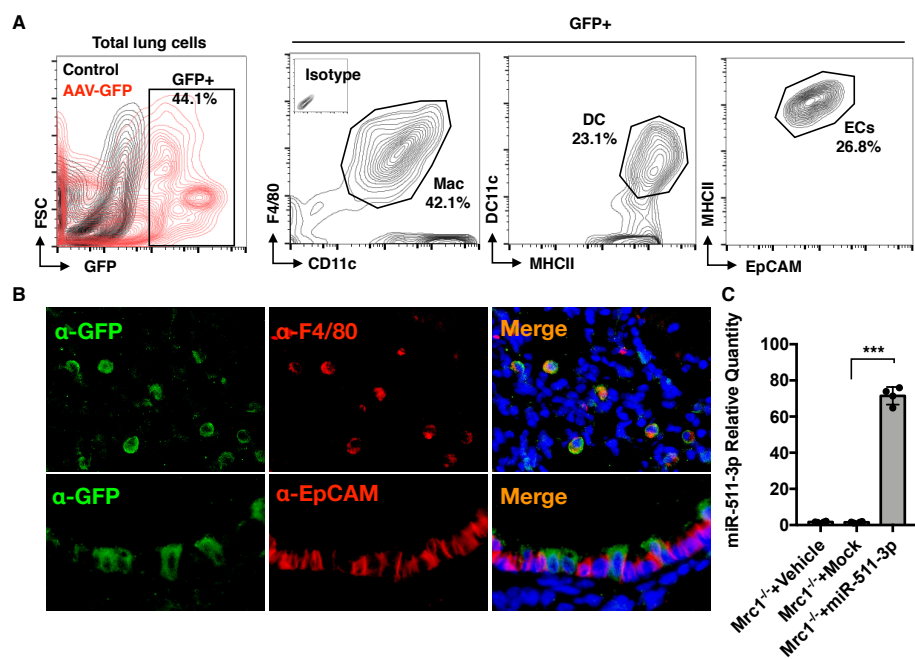
Figure E4. Expression of miR-511-3p in different cells. The figure was generated based on data provided online by Geome.ucsc.edu.

Figure E5. Flow cytometry analyses of T regulatory cells (Tregs) in the lung tissues and bronchoalveolar lavage fluids of mice treated with or without AAV-miR-511-3p. (A)

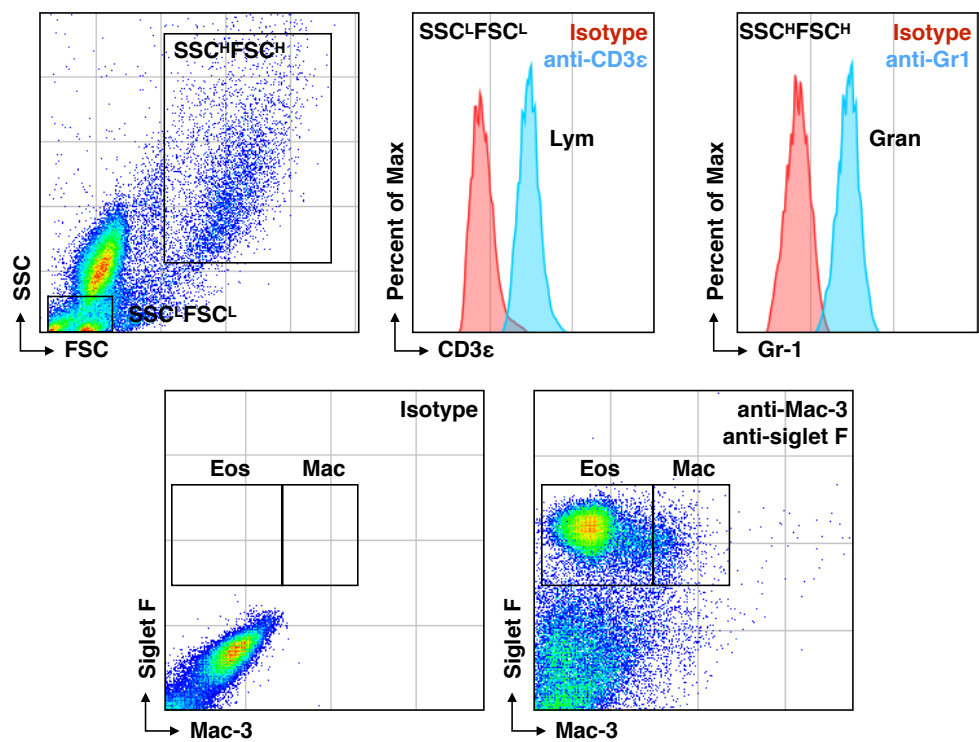
Representative flow cytometric gating of Tregs from the single cell suspension of whole lung tissue and BALs of mice treated with AAV-miR-511-3p (top panel) and AAV-Mock control

(bottom panel). **(B-C)** Quantitation of Tregs as indicated by the percentage of CD4⁺CD25⁺FoxP3⁺ cells among total lung single cells from lung tissues **(B)** and BALs **(C)**. n=5/group. Data represent means \pm SEMs, comparisons were made using 2-tailed Student's t test between groups. $**P < 0.05$, $**P < 0.01$, and $**P < 0.001$.

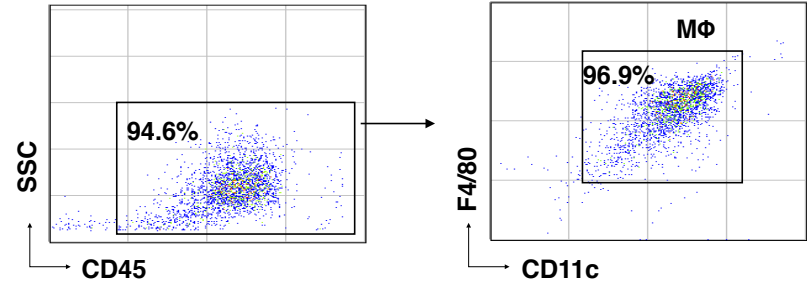
Supl Figure 1



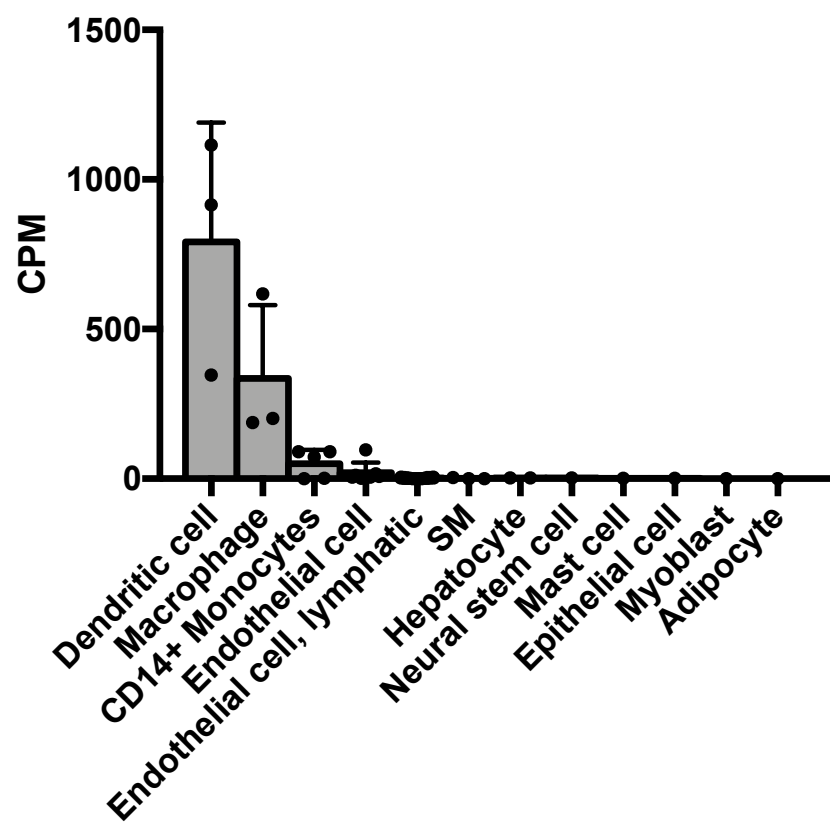
Supl Figure 2



Supl Figure 3



Supl Figure 4



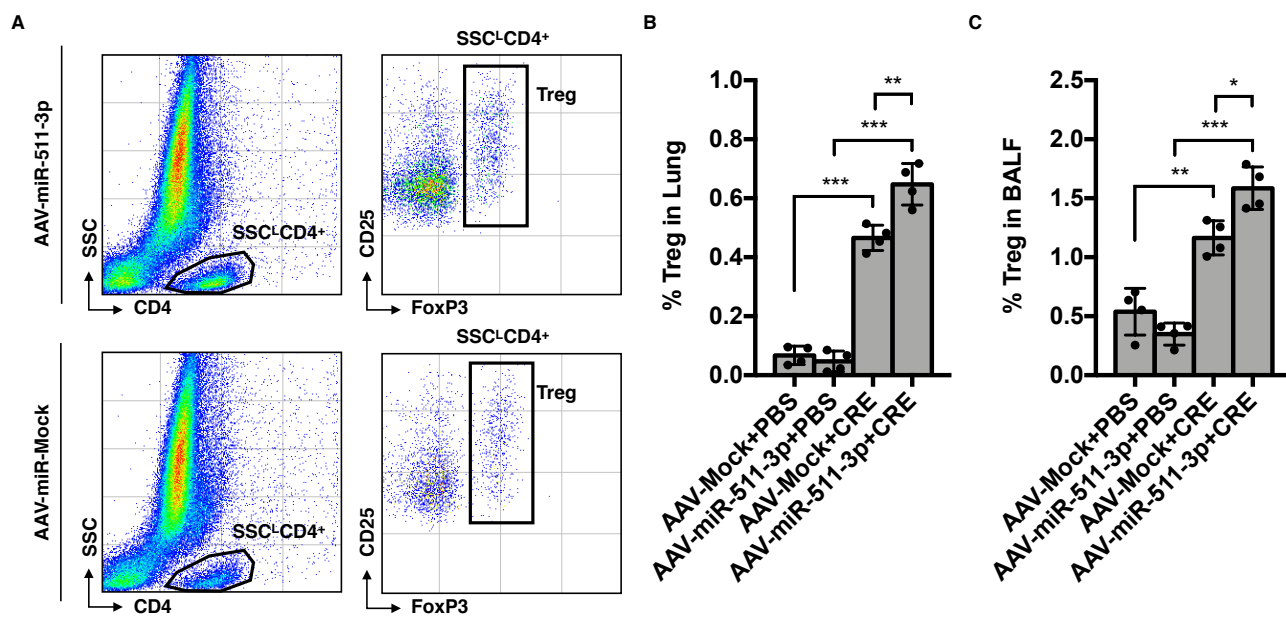


Table E1: mRNA-miR-511-3p Target Region		
Target region (top) miRNA (bottom)	Location	Predicted consequential pairing
Position 872-894 of Ak2 mmu-miR-511-3p	3'UTR	5' CCCUGCUCUUAGGUGCUGGGCAG : : 3' UAGGAC AGAAA ACGAUGUGUAA
Position 5067-5097 of Clcn3 mmu-miR-511-3p	3'UTR	5' UAUCUGAUGUGUCUUACUGCUGAAACACAUG : 3' UAGG ACAGAAA ACGA UGUGUAA
Position 3735-3761 of Plek mmu-miR-511-3p	3'UTR	5' UGUUCUGUUACUGUGAAAAUGCACGUA : : : : : 3' UAGGACAGAAA ACG AUGUGUAA
Position 693-722 of Srgn mmu-miR-511-3p	3'UTR	5' UAUCUUGUUGUUCUGGAAAAUGCCUGCAUU : : : : : 3' UAGGACAGAAA AC GAUGUGUAA

Table E2: Antibody Characteristics				
Antibody	Clone	Species	Application	Source
Arg-1	D4E3M IC5868P	Rabbit Sheep	IF (1:100) FC (1:200)	Cell Signaling R&D
β-Actin	2F1-1	Mouse	WB (1:1000)	BioLegend
CCR2	D14H7 3G7	Rabbit Mouse	IP (1:100) WB (1:1000)	Cell Signaling Novus
CD11c	HL3	Hamster	FC (1:100)	BD
CD25	PC61	Rat	FC (1:200)	BioLegend
CD3ε	145-2C11	Hamster	FC (1:100)	BioLegend
CD4	RM4-5	Rat	FC (1:200)	BioLegend
CD45	30-F11	Rat	FC (1:50)	BioLegend
EpCAM	G8.8	Rat	FC (1:200)	BioLegend
F4/80	BM8	Rat	IF (1:100) FC (1:50)	BioLegend
FoxP3	FJK-16s	Rat	FC (1:200)	ThermoFisher
Gr-1	RB6-8C5	Rat	FC (1:100)	BioLegend
iNOS	NB300-605 CXNFT	Rabbit Rat	IF (1:50) FC (1:200)	Novus ThermoFisher
Mac-3	M3/84	Rat	FC (1:100)	BioLegend
RhoA	1A11-4G10	Mouse	WB (1:500)	Novus
RhoA-GTP	26904	Mouse	IF (1:100)	NewEast
SiglecF	1RNM44N	Rat	FC (1:100)	ThermoFisher

Table E3: Primer Sequences

Gene	NCBI GeneID	Primer Sequence	Amplicon size	PrimerBank ID
Ak2	11637	Fwd: 5'GGCTTCGGAACCGGAGATTC Rev: 5'CAGACACAAAAGTTTTAGCCAG	108	34328230a1
Arg-1	11846	Fwd: 5'CATTGGCTTGGAGACGTAGAC Rev: 5'GCTGAAGGTCTCTCCATCACC	124	NA
Actb	11461	Fwd: 5'GGCTGTATCCCTCCATCG Rev: 5'CCAGTTGGTAACAATGCCATGT	154	6671509a1
Col2	20296	Fwd: 5'TTAAAAACCTGGATCGGAACCAA Rev: 5'GCATTAGCTTCAGATTACGGGT	121	6755430a1
Ccr2	12772	Fwd: 5'ATCCACGGCATACTATCAACATC Rev: 5'CAAGGCTCACCATCATCGTAG	104	6753466a1
Chi3l3	12655	Fwd: 5'TACTCACTTCCACAGGAGCAGG Rev: 5'CTCCAGTGTAGCCATCCTTAGG	135	NA
Clcn3	12725	Fwd: 5'AGCTACAACAGCATAACCAGC Rev: 5'GTCCCCGTCTAACAATTGTCAT	108	2599550a1
Fizz1	57262	Fwd: 5'CAAGGAACCTTCTTGCCAATCCAG Rev: 5'CCAAGATCCACAGGCAAGCCA	151	NA
IL-1 β	16176	Fwd: 5'TGGACCTTCCAGGATGAGGACA Rev: 5'GTTTCATCTCGGAGCCTGTAGTG	148	NA
IL-6	16193	Fwd: 5'TAGTCCTTCTACCCCAATTTC Rev: 5'TTGGTCCTTAGCCACTCCTTC	76	13624311a1
iNOS	18126	Fwd: 5'GAGACAGGGAAGTCTGAAGCAC Rev: 5'CCAGCAGTAGTTGCTCCTCTTC	179	NA
Plek	56193	Fwd: 5'CAAAGCGGATCAGGGAGGG Rev: 5'TTGACAAGGGCTAGTGAGAGT	173	11464971a1
Rhoa	11848	Fwd: 5'AGCTTGTGGTAAGACATGCTTG Rev: 5'GTGTCCCATAAAGCCAACCTCTAC	138	31542143a1
Srgn	19073	Fwd: 5'CTCGCCTTCGTCCTGGTTT Rev: 5'CCTCGATGCAGTTCGCAAAA	112	6997243a1