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Supplemental Information

PPARa Inhibition Overcomes

Tumor-Derived Exosomal Lipid-Induced

Dendritic Cell Dysfunction

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 PKH67-4 DC MFI 29.6 GFP-TDE-DC MFI 82.2 DC MFI 367 PKH67⁺% in tumor 20000 GFP-TDE-DC MFI 691 Count Count 10000 ٨ 4 0-0 100 "' "² " GFP-TDE GER* GER TID TAM ONE DON' ➤ Lipid TIDC TAM Н MHC II 39.8 SSC-A **CD45** CD1 100K 150K 200 FSC-A 10³ 19⁴ CD11c PKH67 "³ Ly6C 10 MHC II 10 108 F4/80 М Κ L Ν **** **** 10001 80-0.25 2500-Divided CD8+T (%) LipidTOX Deep Red (MFI) **** *** **** *** 800-IFN-y (ng/ml) 0.20 2000-PKH67⁺% in LN 600-0.15-1500-◆ Count 400 0.10-1000-200 0.05-500-L'COLLENNA L'COLLENNA 0r cell CLN)+T cell TDENER N^N ic^R e^{gh} f^{gh} J^O to^R to^R DC (LN)+T cell 0.00 0-TOFFai TDENear 100 102 Vehicle TOFFat Vehicle CFSE *

Figure S1 (related to Figure 1). TDEs induce lipid laden DC

(A) Intracellular lipid level of CD45⁺MHC II⁺CD11c⁺ F4/80⁻ DCs in spleen (sDC) and tumor (TIDC) from various tumor models was measured by Bodipy 493/503 staining (n=3 per group).

(B) Western blot reveals exosome markers in both cell lysate and TDE.

(C) Intracellular lipid levels in BMDCs treated with 4T1 or B16/F10 tumor cells derived exosomes (400 µg/ml)

for 24 h. Representative of two independent experiments.

(D) Flow cytometry and gating strategy of tumor infiltrating DCs in GFP-CD9-tumor or CTR-tumor.

(E) Intracellular lipid levels in GFP⁺ or GFP⁻ TAMs were analyzed by flow cytometry, related to Figure 1I-K. Each dot represents an individual mouse.

(F) Representative confocal images showing the intracellular lipid level of DCs treated with 100 μ g/ml GFP-TDE for 8 h. Scale bar = 15 μ m.

(G) GFP-TDE uptake and lipid level of DCs treated with 400 $\mu g/ml$ GFP-TDE for 24 h.

(H) MC38 tumors (on day 10) were harvested 48 h after 1000 µg PKH67 labeled TDEs injection. Flow cytometry and gating strategy of tumor infiltrating myeloid cells.

(I and J) Relative proportions of tumor infiltrating myeloid cells as a percentage of total PKH67⁺ cells (I). TIDC (CD45⁺Ly6C⁻MHC II⁺CD11c⁺F4/80⁻), TAM (CD45⁺Ly6C⁻MHC II⁺F4/80⁺), Monocytes (CD45⁺CD11b⁺Ly6C^{hi}), Neutrophils (CD45⁺CD11b⁺Ly6C^{mid}). Lipid content in PKH67⁺ or PKH67⁻ TIDC and TAM were analyzed by flow cytometry (n=4) (J). Each dot represents an individual mouse.

(K-N) 1000 μ g PKH67 labeled TDEs were injected into the footpad of wild type C57BL/6 mice and measured the phenotype change of DCs in popliteal lymph nodes (LN)(near) and inguinal lymph nodes (far) at 48 h post injection. Frequency of DC populations as a percentage of total PKH67⁺ cells (K). Lipid content was analyzed by flow cytometry (L). The isolated DCs (CD45⁺Ly6C⁻MHC II⁺CD11c⁺F4/80⁻) from lymph nodes were treated with 2 mg/ml OVA overnight, then co-cultured with OT I CD8⁺ T cells for 3 days. Proliferation of CD8⁺ T was analyzed by CFSE dilution (M) and the production of IFN- γ of CD8⁺ T cells was analyzed by ELISA (N). T: undivided OT-I cells as a negative control. PMA: OT-I T cells primed by PMA and ionomycin as a qualification control. Each dot represents an individual mouse.

P < 0.01; *P < 0.001; ****P < 0.0001. (A) and (J) were analyzed with two-way ANOVA. (E) was analyzed with 2-tailed *t* test. Other data were analyzed with one-way ANOVA. Error bars represent SEM. The error bars of (N) represents SD.



Figure S2 (related to Figure 2). TDEs interfere DC immune function

(A) BMDCs were treated with TDEs (400 μ g/ml) for 24 h. The expression of surface markers for BMDCs maturation were analyzed. Representative of two independent experiments.

(B) Cytotoxicity analysis of TDEs in BMDCs with 24 h. Representative of two independent experiments.

(C) BMDCs were treated with 10 μg/ml OVA₂₅₇₋₂₆₄ or OVA₂₅₀₋₂₆₄ in the presence or absence of TDEs (200 μg/ml) for 24 h. Antigen presentation of BMDCs was assessed by staining with H-2Kb-SIINFEKL antibody. Representative of two independent experiments.

(D) BMDCs were treated with 10 μ g/ml OVA₂₅₇₋₂₆₄ or OVA₂₅₀₋₂₆₄ in the presence or absence of TDEs (200 μ g/ml) for 48 h, which were subsequently washed off the antigen and co-cultured with OT I CD8⁺ T cells for 3 days. Proliferation of OT I CD8⁺ T cells was analyzed by CFSE dilution. Representative of two independent experiments.

****P < 0.0001. Data were analyzed with two-way ANOVA. Error bars represent SEM.



Figure S3 (related to Figure 3). The mechanism of TDEs uptake by DCs

(A and B) BMDCs were treated with 100 µg/ml or 200 µg/ml PKH67-labeled TDEs for different periods. 12, 24, 48 and 72 hours later, BMDCs were collected and the fluorescence intensity of Bodipy 493/503 (A) and PKH67 (B) were analyzed by flow cytometry respectively.

(C) Effects of endocytic inhibitors on internalization of PKH67-labeled TDEs. BMDCs were pre-treated with various inhibitors for different lengths of time (see Table 1), and then incubated with 100 μ g/ml PKH67-labeled exosomes for 8 h. Internalized exosomes were detected by flow cytometry. Representative of two independent experiments.

(D) Expression of the indicated transcripts were assessed by RNA-Seq.

(E) Flow cytometry analyzed the effect of CD36 antibody or Msr1 antibody on internalization of PKH67 labeled TDEs. BMDCs were pre-treated with CD36 antibody or Msr1 antibody for 15 min and then incubated with 50 µg/ml PKH67 labeled TDEs for 8 h. CPZ, Chlorpromazine.

*P < 0.05; **P < 0.01; ****P < 0.001; ****P < 0.0001; ns, not significant. (C) and (E) were analyzed with one-way ANOVA. Other data were analyzed with two-way ANOVA. Error bars represent SEM.

Figure S4



Figure S4 (related to Figure 4). Proteomics analysis of BMDC

(A) Upregulation of genes involved in the metabolism of BMDCs cultured with or without TDEs were analyzed by proteomics.

(B) Expression of the indicated transcripts were assessed by qRT-PCR.

(C) 1000 µg PKH67 labeled TDEs were injected into the footpad of wild type C57BL/6 mice and isolated

PKH67+ or PKH67- DCs in popliteal lymph nodes (LN). Expression of the indicated transcripts were assessed by qRT-PCR.

(D) BMDCs were incubated with or without TDEs (400 μ g/ml) in the presence or absence of GSK3787 (1 μ M) for 48 h. Intracellular lipid content was assessed 24 h later via Bodipy 493/503 staining.

(E and F) BMDCs were treated as in (D) with the addition of 2 mg/ml OVA, which were subsequently washed off the antigen and co-cultured with OT I CD8⁺ T cells for another 3 days. Proliferation of OT I CD8⁺ T cells was analyzed by CFSE dilution (E). The production of IFN- γ by CD8⁺ T cells was assessed by ELISA (F). *P < 0.05; ***P < 0.001; ****P < 0.0001; ns, not significant. (B) and (C) were analyzed with two-way ANOVA. Other data were analyzed with one-way ANOVA. Error bars represent SEM. The error bars of (F) represents SD.

Figure S5



Figure S5 (related to Figure 5). Lipid accumulation and TDE uptake of BMDC

BMDCs were treated with or without TDEs (400 μ g/ml) in the presence or absence of GW6471 (15 μ M) for 8 h, the intracellular lipid content and TDE uptake were detected by Bodipy493/503 or PKH67, and recorded by Opera PhenixTM High Content Screening System. Each dot represents a biological repeat. ****P < 0.0001; ns, not significant. Data were analyzed with one-way ANOVA. Error bars represent SEM.





Figure S6 (related to Figure 1 and 6). Macrophages are dispensable for the combination therapy

(A) B16/F10 bearing C57BL/6 mice were treated with PD-1 mAb (200 μg/dose per mouse on day 3,6,9) and GW6471 (10 mg/kg, from day 6, once every other day). Tumor growth curve was shown (*n*=5 per group).
(B) MC38-OT I bearing C57BL/6 mice were treated with PD-L1 mAb (200 μg/dose per mouse on day 7,10,17) and GW6471 (10 mg/kg, from day 11, once every other day). CSF1R mAb 200 ug/mice was injected intraperitoneally on day 7, 10 and 17. 24 h after the third CSF1R mAb injection, CD45⁺MHC II⁺CD11b^{mid}F4/80⁺ cells were measured by flow cytometry. Each dot represents an individual mouse.

(C) Tumor growth curve was shown (n=5 per group).

(D and E) The isolated TAM (CD45⁺MHC II⁺F4/80⁺) were treated with 2 mg/ml OVA overnight, then co-cultured with OT I CD8⁺ T cells for 3 days. Proliferation of CD8⁺ T was analyzed by CFSE dilution (D) and the production of IFN- γ of CD8⁺ T cells was analyzed by ELISA (E).

(F) BMDMs were differentiated by M-CSF for 7 days, and lipid level in BMDMs treated with TDEs (400 μ g/ml) for 24 h in the presence or absence of GW6471.

(G) BMDMs were treated with 2 mg/ml OVA in the presence or absence of TDEs (400 μ g/ml) for 48 h, which were subsequently washed off the antigen and co-cultured with OT I CD8⁺ T cells for 3 days. The production of IFN- γ by CD8⁺ T cells was analyzed by ELISA.

*P < 0.05; ****P < 0.0001; ns, not significant. Data were analyzed with 2-tailed *t* test. Error bars represent SEM. The error bar of (G) represents SD.

Table S1

Endocytosis inhibitor	Mechanism	Concentration and incubation time
chlorpromazine	interacts with clathrin	25 uM, 30 min
filipin III	binds to 3' β-hydroxysterol	8 uM, 30 min
wortmannin	blocks PI-3 kinase	100 nM, 60 min
chloroquine	increases endosomal pH	100 uM, 30 min
bafilomycin A	blocks v(H+)ATPase	100 nM, 60 min
nocodazole	depolymerizes microtubules	20 uM, 30 min
N-ethylmaleimide	alkylates sulfhydryl	2 mM, 30 min
FCCP	an uncoupling agent	10 uM, 15 min
NaN₃	depletes cellular ATP	10 mM, 15 min

 Table S1 (related to Figure 3). The inhibitors used to block TDEs endocytosis.