

Activity-regulated cytoskeleton-associated protein/activity-regulated gene 3.1 (Arc/Arg3.1) enhances dendritic cell vaccination in experimental melanoma

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ABSTRACT

Dendritic cell (DC) vaccination has proven to be an effective and safe adjuvant for cancer immunotherapies. As the presence of DCs within the tumor microenvironment promotes adaptive antitumor immunity, enhancement of DC migration toward the tumor microenvironment following DC vaccination might represent one possible approach to increase its therapeutic efficacy. While recent findings suggest the activity-regulated cytoskeleton-associated protein/activity-regulated gene 3.1 (Arc/Arg3.1) as critical regulator of DC migration in the context of autoimmune diseases, we aimed to investigate the impact of Arc/Arg3.1 expression for DC-based cancer vaccines.

To this end, DC migration capacity as well as the induction of T cell-mediated antitumor immunity was assessed in an experimental B16 melanoma model with *Arc/Arg3.1*^{-/-} and *Arc/Arg3.1*-expressing BMDCs applied as a subcutaneous vaccine.

While antigen presentation on DCs was critical for unleashing effective T cell mediated antitumor immune responses, *Arc/Arg3.1* expression enhanced DC migration toward the tumor and secondary lymphoid organs. Moreover, *Arc/Arg3.1*-expressing BMDCs shape the tumor immune microenvironment by facilitating tumor recruitment of antigen-specific effector T cells.

Thus, *Arc/Arg3.1* may represent a novel therapeutic target in DCs in order to increase the therapeutic efficacy of DC vaccination.

ARTICLE HISTORY

Received 17 December 2020

Revised 1 April 2021

Accepted 16 April 2021

KEYWORDS

Adoptive immunotherapy; CD8-positive T-lymphocytes; dendritic cells; melanoma; tumor microenvironment

Introduction

Dendritic cells (DC) are key mediators at the interface between host and adaptive immunity.¹ Localized in peripheral tissues, immature DCs patrol for invading pathogens. After capturing and processing antigens, DCs undergo maturation and migrate through lymphatic vessels to the site of antigen presentation and immune cell stimulation in the lymphoid organs. There, DCs present the captured antigens as processed MHC-bound peptides to effector T cells for the induction of T cell activation in order to initiate a T cell-based immune response against invading pathogens.²

Preclinical proof-of-principle studies have shown that *ex vivo* generated and antigen-loaded DCs used as antitumor vaccines mount an antigen-specific T cell mediated immune response.^{3,4} Consistently, DC-based cancer vaccines also demonstrated therapeutic efficacy and a robust safety profile in clinical studies on different tumor entities.^{5–8} However, DC vaccines as monotherapy could only hardly engender durable immune responses, pointing to the need for further approaches to enhance its therapeutic efficacy.⁹

The current state of research implicates the application of DC vaccination in combination with other antitumor therapies.^{10,11} In this context, the combination of DC vaccination with adoptive T cell therapies¹² lead to durable tumor control in preclinical¹³ and clinical studies.^{14,15}

Further studies investigated important functions of distinct DC subpopulations in the tumor microenvironment.^{16,17} The murine classical DC1 (cDC1) subpopulation is characterized by CD8a and CD103 expression and depends on the transcription factors BATF3 and IRF8 during development.^{18–20} CD103⁺ DCs take up tumor antigens and subsequently transport them CCR7-dependent to lymph nodes for further T cell priming.²¹ CD8a⁺ DCs prime and activate CD8⁺ T cells by cross-presentation.²² Recent investigations propose a crucial function of cDC1s in the tumor microenvironment for the induction of an effective T cell-based antitumor immune response.^{23–25}

The therapeutic efficacy of DC vaccination is critically dependent on the migration of subcutaneously injected DCs to their effector sites for T cell activation.^{26–28} One possible approach to improve DC vaccination efficacy is to apply DCs with superior migratory capability for vaccination.²⁹ However,

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so far defined surrogate markers for DC migration are not exclusively expressed on migratory DCs and their expression levels vary between steady state and inflamed settings, hence cannot be widely used to select DCs with superior migratory capacity.^{30,31}

Notably, we recently found that DCs with migratory capacity exclusively express the cytoskeleton-associated protein Arc/Arg3.1 and initiate T cell responses in inflammatory models.³² Further ontogeny study showed that Arc/Arg3.1-expressing DCs are distributed among different DC subsets, including skin Langerhan cells (LC), cDC1 (CD103⁺) and cDC2 (CD11b⁺). Arc/Arg3.1 is expressed in 1–2% of *in vitro* generated, GM-CSF cultured BMDCs and in 10–40% of migratory DC subsets *in vivo*. The differentiation of Arc/Arg3.1-expressing DCs *in vivo* was found to be independent of specific transcription factors, suggesting Arc/Arg3.1 as an unequivocal functional marker for DCs with migratory capacity across all DC subsets.³³

These results directed us to the question whether the effect of Arc/Arg3.1 on DC migration may be translatable to immunotherapy for cancer treatment. In this study, we investigated the role of Arc/Arg3.1-dependent DC migration following DC vaccination for its therapeutic efficacy and capability to induce an antigen-specific T cell response in murine experimental melanoma.

Materials and methods

Mice

For *in vivo* tumor experiments, we used 7–9 weeks old male C57BL/6J Ly5.1 mice bred at the animal facility of the German Cancer Research Center Heidelberg or purchased from The Jackson Laboratory. Arc/Arg3.1^{-/-} mice³⁴ were bred at the University Medical Center Hamburg-Eppendorf. Pmel-1 TCR transgenic mice [B6.Cg-Thy1a/Cy Tg(TcraTcrb)8Rest/J] specific for the mouse homologue of human melanoma antigen hgp100₂₅₋₃₃³⁵ were purchased from The Jackson Laboratory. Pmel-1/luc-mcherry mice were generated by crossing pmel-1 mice as above with luc-mcherry mice. Luc-mCherry mice, full name B6-Tg(Actb-Luc,mCherry)#Platt, express luciferase and mCherry under the Actb promoter and were generated in the Transgenic Service of the Center for Preclinical Research, DKFZ. All mice were bred under specific pathogen-free conditions. Animal experimental procedures were carried out according to institutional laboratory animal research guidelines and approved by the governmental authorities.

Cell culture

B16 wild type (WT) melanoma tumor cells were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin and 100 µg/ml streptomycin (all Sigma-Aldrich) at 37 °C, 5% CO₂.

For tumor inoculation, cells were harvested with StemPro Accutase (Thermo Fischer, A1110501) and diluted in PBS (Sigma Aldrich) for injection.

Generation of murine CD8⁺ CTL

To obtain murine CD8⁺ CTL, spleens and lymph nodes of 6–10 weeks old pmel-1 or pmel-luc-mcherry mice were excised and meshed through a 70 µm cell strainer. After lysis of erythrocytes with ACK lysis buffer (150 mM NH₄Cl, 10 mM KHCO₃ and 100 µM Na₂EDTA), the isolated immune cells were cultured in murine T cell proliferation medium consisting of RPMI-1640 (Sigma-Aldrich) supplemented with 10% FBS, 100 U ml⁻¹ penicillin, 100 µg ml⁻¹ streptomycin, 25 mM Hepes pH 7.4, 1 mM sodium pyruvate, 5 × 10⁻⁵ M 2-mercaptoethanol (all Sigma-Aldrich) and 2 mM L-glutamine (Thermo-Fisher) under stimulation with 30 IU/ml IL-2 (Proleukin, Novartis) and 2 µg/ml hgp100₂₅₋₃₃ (custom-made; Research Group GMP & T cell therapy, DKFZ) for 3 days at 37 °C, 5% CO₂. For adoptive cell transfer, CD8⁺ T cells were purified by using mouse CD8⁺ T cell isolation MACS Kit (MACS Miltenyi Biotec) according to the manufacturer's instructions.

Generation of bone marrow derived DCs (BMDC)

Bone marrow was isolated from femurs and tibiae of 5–8 weeks old male C57BL/6J mice or Arc/Arg3.1^{-/-} mice. After removal of remaining tissues from the bones, bone marrow was flushed out with PBS and homogenized with a 70 µm cell strainer. Bone marrow, if not otherwise given, was cultured in murine BMDC medium consisting of RPMI-1640 (Sigma-Aldrich) with 10% FBS, 100 U/ml penicillin, 100 µg/ml streptomycin, 25 mM Hepes pH 7.4, 1 mM sodium pyruvate, 5 × 10⁻⁵ M 2-mercaptoethanol (all Sigma-Aldrich) and 2 mM L-glutamine (Thermo-Fisher) in the presence of 20 ng/ml GM-CSF (Peprotech, 315-03) for 6 days at 37 °C, 5% CO₂. We changed medium every other day by carefully replacing the supernatant with a fresh medium containing 20 ng/ml GM-CSF. We harvested non-adherent BMDCs on day six. For vaccination, BMDCs were matured with 100 ng/ml LPS (Sigma-Aldrich) for 24 h and, prior to vaccination, loaded for 4 h with 10 µg/ml hgp100₂₅₋₃₃ or ovalbumin (OVA₂₅₇₋₂₆₄) as control.³⁶

Production of pMXS-Arc/Arg3.1-IRES-GFP DNA construct

The Arc/Arg3.1-gene was cloned into the vector back bone pMXS-IRES-GFP using Gateway clonase enzymes according to manufacturer's manual (Thermo Fischer). pMXS-IRES-GFP vector was a kind gift of Stefan Pusch (CCU Neuropathology, DKFZ Heidelberg).

Firstly, the full-length construct of Arc/Arg3.1 was flanked with attB-sites and cloned via Gateway BP reaction into the backbone of pDONR vector, from which the Arc/Arg3.1-gene was constitutively cloned into pMXS-IRES-GFP backbone vector via Gateway LR reaction.

Transduction of BMDCs

For the package of retrovirus, HEK Phoenix Eco I cells were transfected with the pMXS-Arc/Arg3.1-IRES-GFP construct (pMXS-Arc/Arg3.1) or the control vector pMXS-GFP-IRES-GFP (pMXS-control) using FuGENE® HD transfection reagent

(Promega, E2311). Virus containing cell supernatant was harvested 48 hours after transfection for the subsequent transduction. Before retroviral transduction, freshly isolated bone marrow cells were pretreated with a cytokine cocktail mix consisting of 20 ng/mL IL-3, 50 ng/mL IL-6, 50 ng/mL SCF and 50 ng/mL TPO (all Peprotech) for 4 days.³⁷ 20 ng/mL GM-CSF was added to the cell culture medium starting from day 2 after isolation of BMDCs. BMDCs were subsequently transduced at day 5 in RetroNectin (Takara) pre-coated 6-well plates with Polybrene of 10 µg/ml. Retrovirus containing supernatants were added to the cells, followed by centrifugation of the cell-virus mixtures at 1.200 g for 90 minutes to ensure contact between cells and virus particles. Next day, cells were washed with PBS to remove the remaining virus particles. The transduced BMDCs were maintained in cell culture for additional 4 days and stimulated with 100 ng/ml LPS (Sigma-Aldrich) for 24 h before harvest for vaccination. Transduction efficiency was examined via flow cytometric analysis for GFP⁺ cells.

Tumor challenge and treatment

For tumor inoculation, a cell suspension with 5×10^4 B16 wild type (WT) melanoma cells diluted in 100 µl PBS was mixed with 100 µl Matrigel Matrix (Corning) and injected into the right flank of the mice. To evaluate tumor growth, tumor area (width x length) was measured starting from day 6 after inoculation. For vaccination, 4×10^6 DCs were injected subcutaneously into the right hind leg at day 7 after tumor inoculation, followed by injection of 100.000 IU IL-2 per day (Proleukin, Novartis) for the two following days. A second vaccination with DCs was performed up to 6 days after the first vaccination.¹³ For adoptive T cell transfer, 5×10^6 pmel-1 CD8⁺ T cells were intravenously injected at day 7 after inoculation³⁸ (Fig. 1A).

In vivo bioluminescent imaging

For *in vivo* bioluminescent imaging, we used the IVIS Lumina Series III from Perkin Elmer. Before imaging, mice were shaved at the body regions of interest, injected with 50 mg/kg D-Luciferin i.p. (StayBrite™, BioVision, Mountain View) and anesthesia was induced with isoflurane 3–4%. Bioluminescence images were acquired 10 minutes after D-Luciferin injection with an exposure time of 30, 60 and 90 seconds. During imaging, mice were kept under anesthesia with isoflurane 1,5%.

Quantification of bioluminescence signals was performed by the Living Image 4.3 Software (Perkin Elmer). Therefore, regions of interest were drawn around the regions of the tumor and secondary lymphoid organs (Fig. 3A) and signals were quantified as photons/second.

Isolation of leukocytes from tumor, blood, lymph nodes and spleen

For the isolation of tumor infiltrating lymphocytes, mice were killed by terminal cardiac perfusion with 20 ml PBS nine to eleven days after start of treatment. Whole tumor tissues were excised and digested with HBSS supplemented

with 0,5 mg/ml Collagenase D (Roche) and 20 µg/ml DNase I (Sigma-Aldrich) at 37 °C for 60 minutes. Digested tumors were meshed twice through a 100 µm and a 70 µm cell strainer to obtain single-cell suspension. Erythrocytes were lysed with ACK Lysis Buffer. For the isolation of splenocyte, spleens were excised and meshed twice through a 70 µm cell strainer, followed by lysis of erythrocytes in ACK Lysis Buffer. Tumor draining lymph nodes were excised from the inguinal and axillary region of the tumor bearing side (right side) of the mouse. For further processing, lymph nodes were meshed through a 70 µm cell strainer to obtain a single-cell suspension.

Flow cytometry

Flow cytometry analyses of immune cell subsets *ex vivo* were performed 5 days following the last DC vaccination.

Single-cell suspensions from tumor, spleen and lymph nodes samples were washed thoroughly for cell staining and blocked with anti-CD16/32 (Biolegend) before staining. For extracellular targets, cells were stained for 30 minutes at 4 °C.

For intracellular staining, cells were incubated with 5 µg/mL Brefeldin A (Sigma Aldrich) at 37 °C, 5% CO₂ for 5 h. For IFNγ detection, cells were restimulated with 10 mg/ml hgp100₂₅₋₃₃ at 37 °C, 5% CO₂ for 5 h. Intracellular cell staining was performed for 45 min at 4 °C.

Flow cytometry was measured by using BD FACS Canto II or Attune NxT analyzers.

Data were analyzed with FlowJo V10.

For the characterization of *in vitro* generated murine BMDCs, a single-cell suspension of $1-3 \times 10^6$ cells were stained with following extracellular antibodies: fixable viability dye – eFluor 780 (Thermo Fischer, 65086514); anti-CD11c-APC (Biolegend, clone N418, 117310); anti-I-A/I-E-BV711 (Biolegend, clone M5/114.15.2, 107643).

For *ex vivo* identification of cytotoxic T cells from the tumor and secondary lymphoid organs, we used following antibodies: fixable viability dye – APC-Cy7/eFluor 780 (Thermo Fischer, 65086514); anti-CD45-BV510 (Biolegend, clone 30-F11, 103138); anti-CD3-BV711 (Biolegend, clone 17A2, 100241); anti-CD8-AF700 (Biolegend, clone 53-6.7, 100730); anti-CD4-PE-Texas Red (Thermo Fischer, clone RM4-5, MCD0417); anti-CD90.1-PE (Biolegend, clone OX-7, 202524). T-cells were identified by gating for CD45⁺CD3⁺ population on CD45⁺ live cells. From there, further gating was performed on CD8⁺ for cytotoxic T-cells and CD90.1⁺ for pmel-1 gp100 specific T-cells.

For *ex vivo* identification of DCs from the tumor and secondary lymphoid organs, the single-cell suspension was stained using following extracellular antibodies: fixable viability dye – eFluor 780 (Thermo Fischer, 65086514); anti-CD45-BV510 (Biolegend, clone 30-F11, 103137); anti-CD45.2-eFluor 450 (Thermo-Fischer, clone 104, 48045482); anti-CD11c-APC (Biolegend, clone N418, 117310); anti-I-A/I-E-BV711 (Biolegend, clone M5/114.15.2, 107643); anti-CD8a-PerCP-Cy5.5 (Thermo Fischer, clone 53-6.7, 45008182) and anti-CD103-PE (Biolegend, clone 2E7, 121406). Dendritic cells were identified as CD11c⁺ from CD45⁺ live cells. Injected DCs were gated as CD45.2⁺CD11c⁺ cells (Fig. S1A) and so

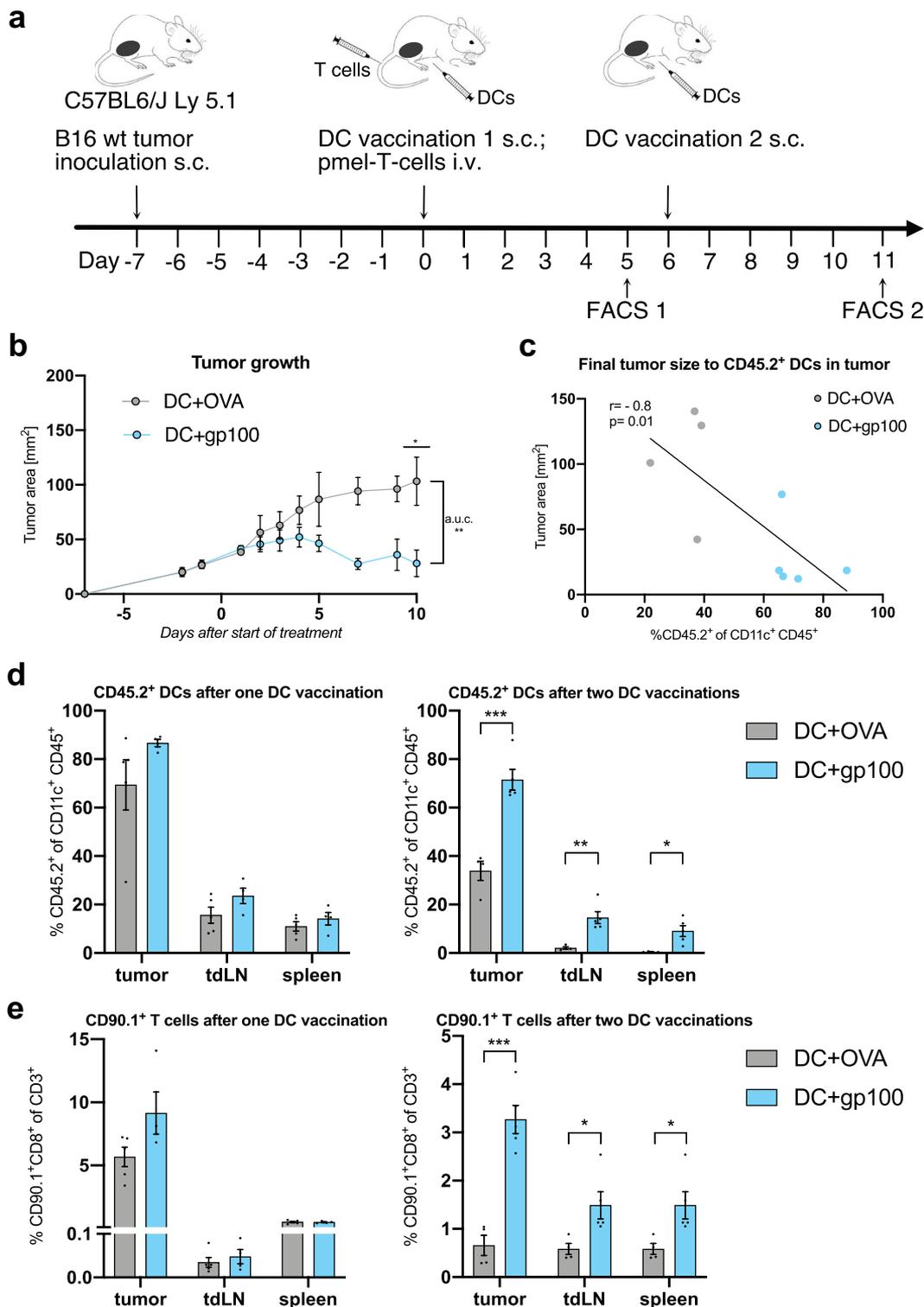


Figure 1. Vaccination with TAA-loaded BMDCs induces T cell mediated antitumor immune response (n=4-5 per group). (A) Scheme of B16 melanoma inoculation followed by combination treatment with DC vaccination and adoptive T cell transfer starting on day seven after tumor inoculation. Flow cytometry analysis was performed five days after first or second DC vaccination respectively. (B) Tumor growth curves of treated mice measured from two days before until ten days after start of treatment. (C) Correlation of final tumor sizes to tumor infiltrating CD45.2+CD11c+ DCs. (D-E) Flow cytometry analysis of frequencies of injected CD45.2+ DCs among all CD11c+ DCs (D) and CD90.1+CD8+ pmel1 T cells among all CD3+ T cells (E) in the tumor, tdLN and the spleen as measured five days after first or second vaccination. All data are presented as mean SEM. For (B), (D) and (E) we performed a two-tailed student's t test to determine statistical significance (* p<0.05; ** p<0.01, *** p<0.001, **** p<0.0001). For (C) we calculated Pearson's correlation coefficient to determine correlation.

distinguished from recipient mice intrinsic dendritic cells. For further phenotypic characterization, identified dendritic cells were gated for CD8a⁺, CD103⁺ and MHCII⁺ cell population.

Immunoblot

We performed immunoblotting on whole-cell lysates. 40 µg of protein were subjected to SDS-polyacrylamide gel

electrophoresis and transferred to nitrocellulose. After blocking, we incubated the membranes with antibodies directed to Arc/Arg3.1 (mouse, 1:4000; Worley Lab) as previously described³⁹ or H3 (rabbit, 1:1000; Cell Signaling, cat. 9715) overnight at 4 °C and washed and incubated them with a species-specific secondary antibody (1:20000; LI-COR Biosciences) for 1 hour at room temperature. Labeling was visualized using enhanced chemiluminescence (LI-COR Biosciences). Quantification was carried out by densitometry using ImageJ software. For uncropped immunoblots, see Fig. S2B.

mRNA sequencing

Purification of RNA from FACS sorted migratory DCs from sdLN of C57BL/6 J mice was done with the RNeasy Mini (Qiagen) according to the manufacturer's protocol. RNA-seq libraries were prepared using the NEBNext Ultra RNA Library Prep Kit for Illumina (New England Biolabs) and sequenced on an HiSeq 2000 sequencer (Illumina) generating 50 base pair single-end reads. The reads were aligned to the Ensembl mouse reference genome (mm10) using STAR v.2.4. The overlap with annotated gene loci was counted with featureCounts v.1.5.1.

All analyses were performed in the R environment (v.4.0.4) using publicly available packages.

Statistical analysis

Data analyses were performed with GraphPad Prism 8, if not stated otherwise. All data are presented as means \pm SEM as indicated in figure legends. Data were analyzed by two-tailed Student's t-test for comparison of two groups and one-way ANOVA combined with correction for multiple testing for comparison of three groups. Correlation was determined by calculation of Pearson's correlation coefficient. $p < .05$ was considered statistically significant (* $p < .05$; ** $p < .01$, *** $p < .001$, **** $p < .0001$).

Data availability

Data generated for this study are available from the correspondent author upon reasonable request.

Results

TAA-loaded BMDCs in the tumor microenvironment induce T cell mediated antitumor immune response

Therapeutic efficacy of a tumor antigen-specific DC vaccine was assessed by application of BMDCs loaded with the tumor-associated antigen hgp100₂₅₋₃₃ in combination with gp100-specific pmel-1 T cells to B16 melanoma bearing mice. For comparison, BMDCs loaded with OVA₂₅₇₋₂₆₄ were injected as an unspecific control vaccination (Fig. 1A). According to clinical application in melanoma patients, DC vaccine was applied subcutaneously.⁴⁰

TAA-loading of DCs determined response to adoptive T cell therapy, since tumor growth control was only achieved following tumor-antigen specific DC vaccination (Fig. 1B). Of note,

higher frequencies of tumor infiltrating CD45.2⁺ donor DCs were associated with smaller tumor sizes (Fig. 1C, Fig. S1A). A boost vaccination with TAA-loaded BMDCs significantly increased the frequencies of CD45.2⁺ DCs within the tumor tissue and the secondary lymphoid organs in comparison to the control boost vaccination with OVA-loaded BMDCs (Fig. 1D). In line, a second vaccination with TAA-loaded BMDCs was associated with an increased recruitment of tumor-specific CD90.1⁺ T cells toward the tumor tissue and secondary lymphoid organs at day 18 after tumor injection (Fig. 1E).

Arc/Arg3.1 expression is crucial for migration of donor BMDCs following DC vaccination

Our previous findings suggest a crucial role of DC migration toward tumors and secondary lymphoid organs for mounting an effective T cell mediated antitumor immune response. To determine the relevance of Arc/Arg3.1 expression in DCs for an antitumor immune response, therapeutic efficacy of DC vaccination using BMDCs isolated from Arc/Arg3.1-deficient (Arc/Arg3.1^{-/-}) mice³⁴ and Arc/Arg3.1-expressing wild-type mice (WT, Arc/Arg3.1^{+/+}) was explored.

Migration of CD45.2⁺ donor DCs to the tumor (Fig. 2A) and to the secondary lymphoid organs (Fig. 2B, C) was reduced after vaccination with TAA-loaded Arc/Arg3.1^{-/-}-BMDCs in comparison to Arc/Arg3.1^{+/+}-BMDCs.

In line with previous findings,³² Arc/Arg3.1 deficiency did not impair *in vitro* BMDC maturation and activation, respectively (Fig. S1B). *In vivo*, Arc/Arg3.1 deficiency was associated with an increased MHC class II expression on donor-derived TAA-loaded DCs in the tumor (Fig. 2D). cDC subtypes including CD8a⁺ and CD103⁺ cDC1 and CD11b⁺ cDC2 were represented among tumor infiltrating CD45.2⁺ DCs (Fig. S1C). Notably, the frequency of CD8a⁺ DCs among all CD11c⁺ donor DCs in the TME depended on both TAA-loading and Arc/Arg3.1 expression on injected BMDCs (Fig. 2E).

Collectively, our findings imply that Arc/Arg3.1 is critical for migration of subcutaneously injected TAA-loaded DCs to the tumor and secondary lymphoid organs.

Vaccination with Arc/Arg3.1-expressing BMDCs promotes recruitment of activated TAA-specific T cells to the tumor microenvironment

We next investigated the role of Arc/Arg3.1 expression in DC vaccines for the recruitment of tumor-specific T cells. Luminescence signals from adoptively transferred luciferase-expressing CD8⁺ effector T cells (pmel luc mcherry)⁴¹ at the tumor site as well as at the DC vaccine injection site were monitored (Fig. 3A). While TAA-loading of donor DCs was critical for T cell recruitment to the vaccine injection site, tumor trafficking of antigen-specific T cells was dependent on Arc/Arg3.1 expression of DCs: Four days after adoptive transfer, tumor infiltration of gp100-specific CD8⁺ T cells was significantly enhanced after vaccination with gp100-loaded WT-BMDCs as compared to gp100-loaded Arc/Arg3.1^{-/-}-BMDCs or OVA-loaded WT-BMDCs (Fig. 3B). Luminescence signal at the tumor site increased starting from day two until day four after adoptive transfer and decreased at the DC vaccine injection site starting on day three after

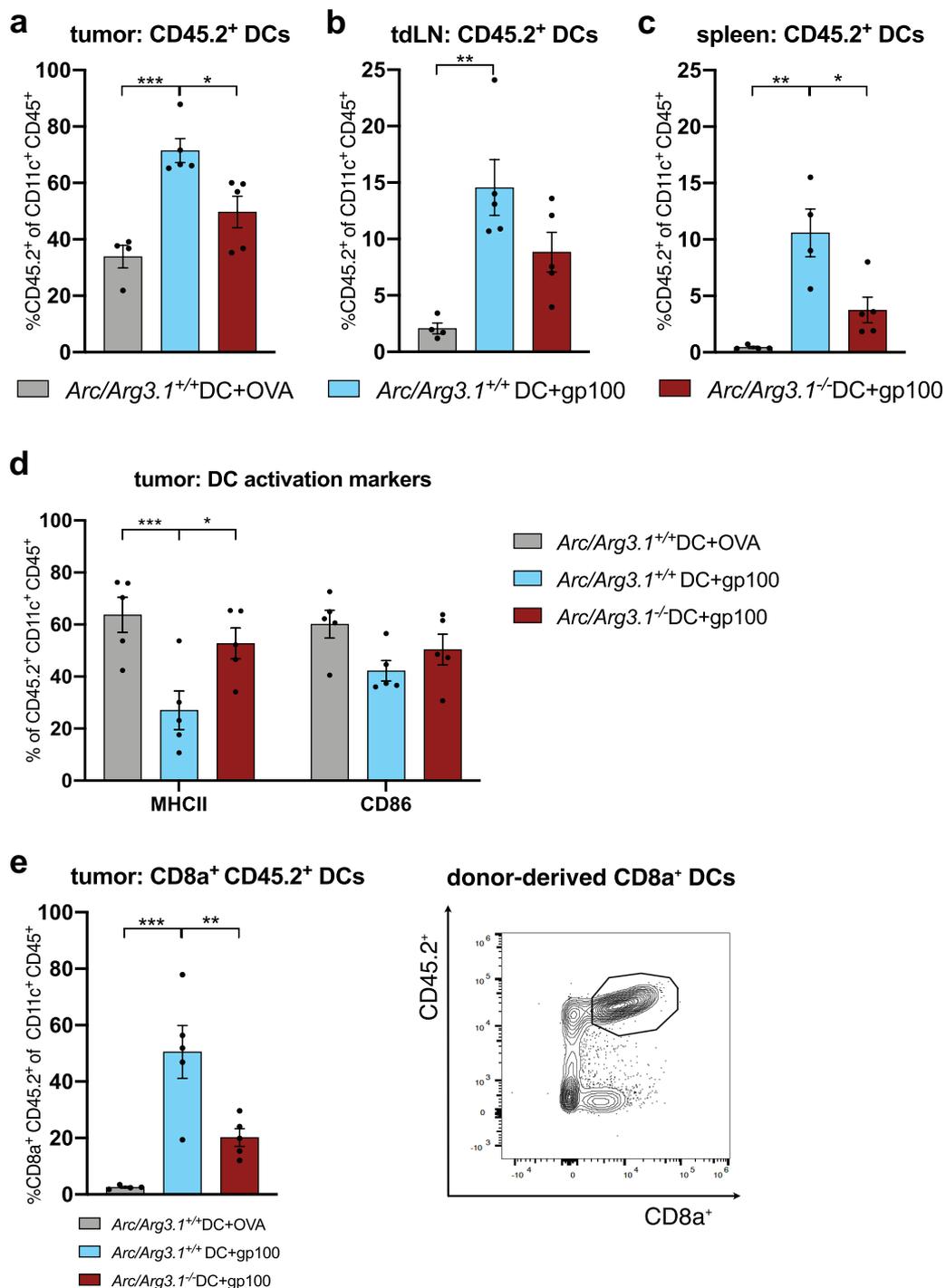


Figure 2. Arc/Arg3.1-dependent migration of injected TAA-loaded BMDCs to the tumor and secondary lymphoid organs following DC vaccination (n=4-5 per group). Flow cytometry analysis of injected CD45.2⁺ DCs eleven days after start of treatment. (A-C) Frequency of injected CD45.2⁺ DCs among all CD11c⁺ DCs in the tumor (A), tdLN (B) and the spleen (C). (D) Expression of DC activation markers MHCII and CD86 on tumor infiltrating CD45.2⁺ DCs among all CD11c⁺ DCs in the tumor and respective gating strategy for CD45.2⁺ CD8a⁺ DCs. (E) Frequency of donor-derived CD45.2⁺ CD8a⁺ DCs among all CD11c⁺ DCs in the tumor and respective gating strategy for CD45.2⁺ CD8a⁺ DCs. All data are presented as mean \pm SEM. We performed a one-way ANOVA in combination with Tukey's test to determine statistical significance (* p<0.05; ** p<0.01, *** p<0.001).

treatment indicating a migration of tumor-specific CD8⁺ effector T cells from the site of DC vaccination to the tumor site (Fig. 3B). In line, flow cytometry analyses revealed an increased infiltration of CD90.1⁺ T cells to the tumor and secondary lymphoid organs following vaccination with Arc/Arg3.1-expressing BMDCs in comparison to the controls (Fig. 3C) and expression profiling of Arc/Arg3.1-expressing migratory DCs revealed expression of T cell recruiting chemokines (Fig. S1D).

Arc/Arg3.1-overexpressing BMDCs in the tumor and secondary lymphoid organs following DC vaccination

To further investigate the effect of Arc/Arg3.1 expression for DC vaccination, Arc/Arg3.1-overexpressing BMDCs were generated.⁴² Following transduction of WT BMDCs with the retroviral construct pMXS-Arc/Arg3.1-IRES-GFP (pMXS-Arc/Arg3.1), transduction efficiency with 30% GFP⁺ cells was

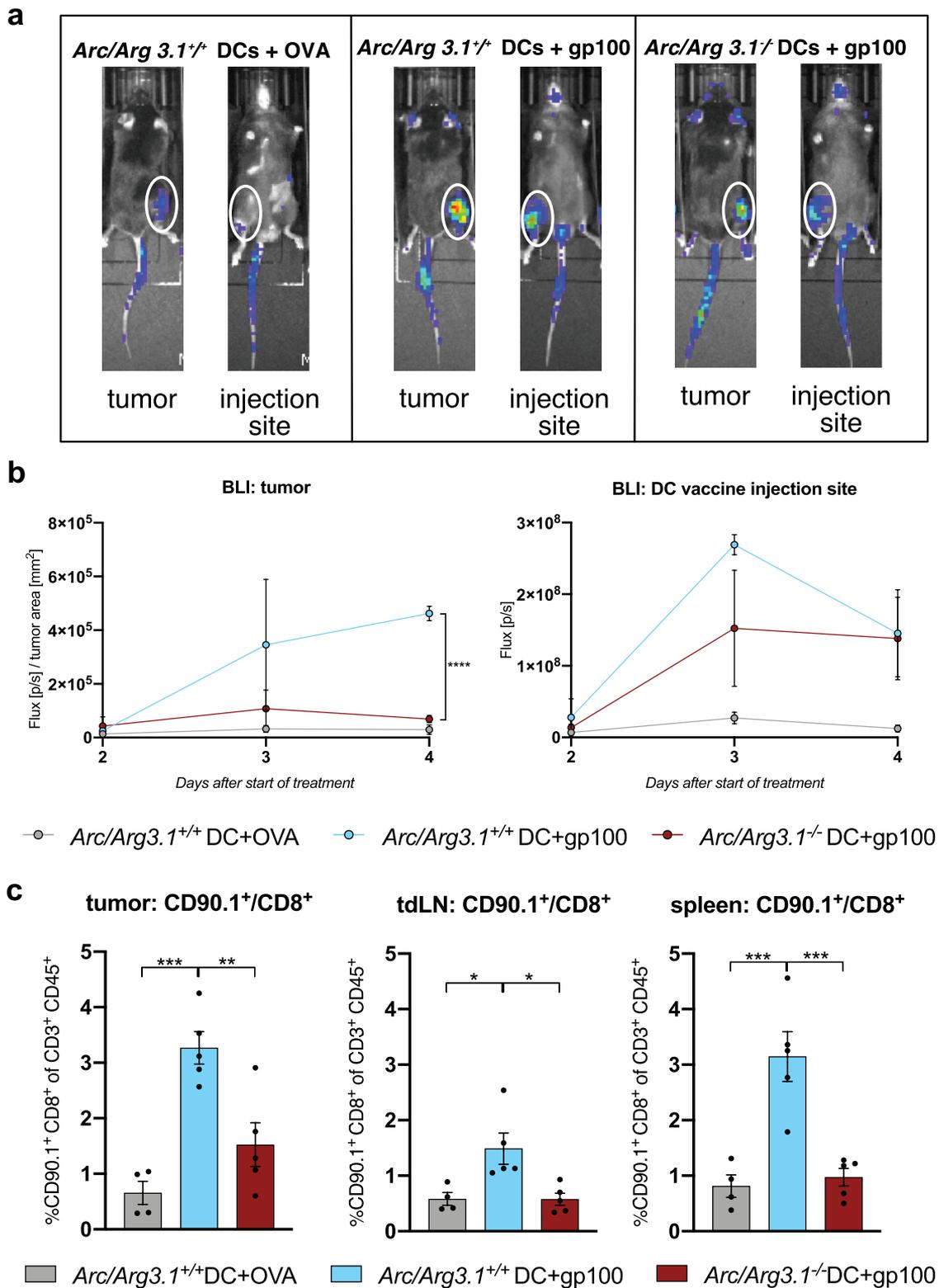


Figure 3. Recruitment of antigen-specific T cells to the tumor microenvironment depends on *Arc/Arg3.1* expression in injected BMDCs. (A-B) In vivo bioluminescence imaging (IVIS) of adoptively transferred pmel luc mcherry T cells two to four days after start of treatment. (A) Photographic images of bioluminescence signals from luciferase expressing T cells in vivo in the tumor and at the DC vaccine injection site four days after start of treatment. (B) Quantification of bioluminescence signals from luciferase expressing T cells in the tumor and at the DC vaccine injection site measured from two days until four days after start of treatment. Signal is measured in photon/s and normalized to tumor size at respective days of measurements ($n=3$). (C) Flow cytometry analysis of frequency of CD90.1+CD8+ pmel T cells among all CD3+ T cells in the tumor, tdLN and the spleen eleven days after start of treatment ($n=4-5$ per group). All data are presented as mean \pm SEM. For (B)-(C) we performed a one-way ANOVA in combination with Tukey's test to determine statistical significance (* $p<0.05$; ** $p<0.01$, *** $p<0.001$).

quantified by flow cytometry (Fig. 4A, S2A) and DC phenotype was confirmed by CD11c and MHCII expression (Fig. 4B, S2A).⁴³ Immunoblot verified *Arc/Arg3.1* overexpression in *pMXS-Arc/Arg3.1*-transduced DCs (Fig. 4C, S2B).

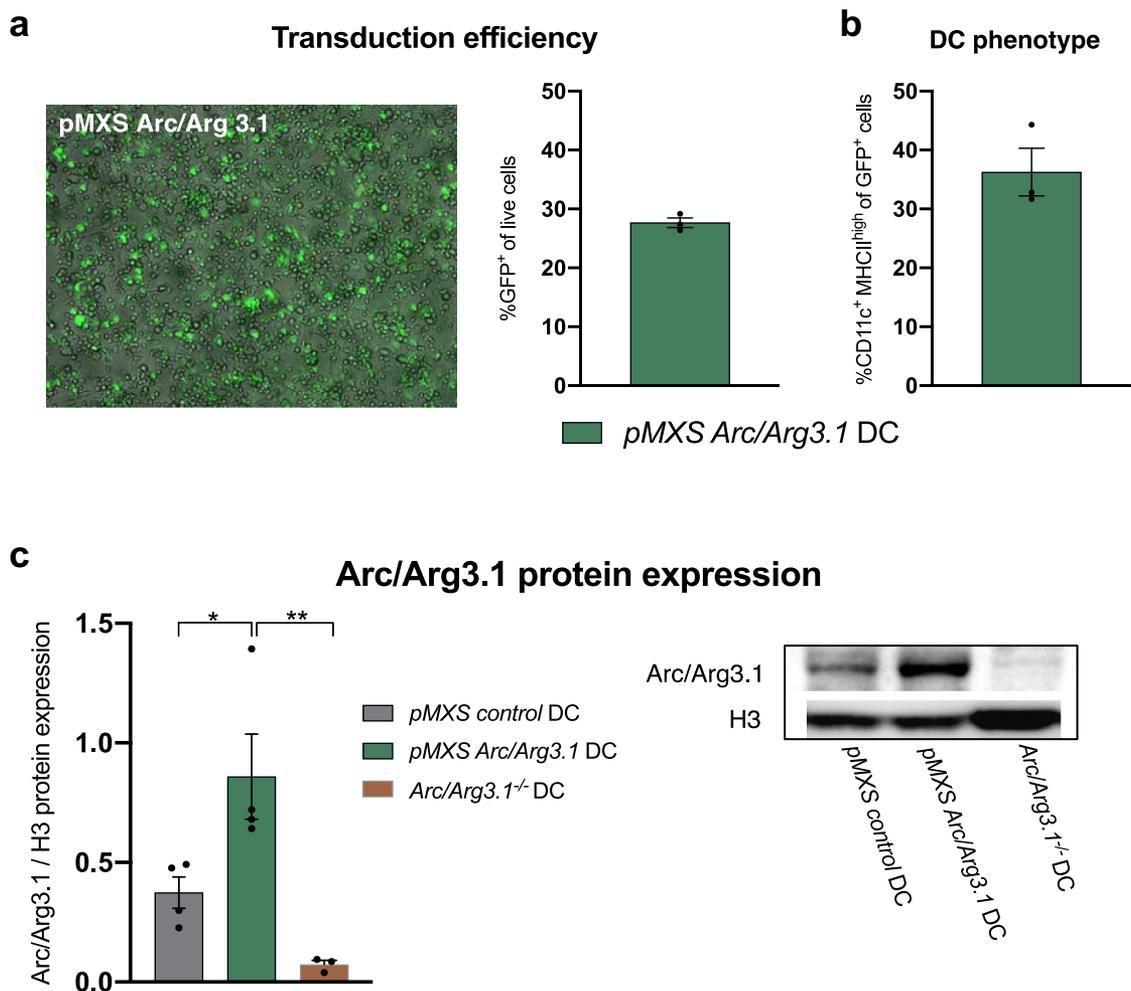


Figure 4. Retroviral transduction of BMDCs for the overexpression of Arc/Arg3.1. (A) Fluorescence microscopy of GFP and flow cytometry analysis of GFP⁺ cells after retroviral transduction with pMXS-Arc/Arg3.1-IRES-GFP (n=3). (B) Flow cytometry analysis of CD11c⁺ MHCII⁺ BMDCs among GFP⁺ cells after retroviral transduction with pMXS-Arc/Arg3.1-IRES-GFP (n=3). (C) Immunoblot of Arc/Arg3.1 from pMXS-control transduced, pMXS-Arc/Arg3.1 transduced and Arc/Arg3.1^{-/-} BMDCs (n=3-4 per group). All data are presented as mean SEM. For (C) we performed a one-way ANOVA in combination with Tukey's test to determine statistical significance (* p<0.05; ** p<0.01).

Following vaccination of B16 melanoma bearing mice with TAA-loaded Arc/Arg3.1-overexpressing DCs, donor DCs could be detected in the tumor and secondary lymphoid organs based on their GFP expression (Fig. 5A). Hereby, increased Arc/Arg3.1 expression enhanced DC migration to the tdLN as demonstrated by a positive correlation between MFI GFP representing pMXS-Arc/Arg3.1 expression and the frequency of CD45.2⁺ donor DCs in the tdLN (Fig. 5B). This positive correlation could not be detected when applying pMXS-control transduced BMDCs (Fig. 5B). Arc/Arg3.1 overexpression of BMDCs did not impair DC activation as assessed by MHC II expression (Fig. S3A) nor influence cDC subpopulation frequencies within the tumor (Fig. S3B). Even so, an increase in Arc/Arg3.1 expression did not provide a therapeutic benefit on tumor growth following DC vaccination (Fig. S3C, D).

Arc/Arg3.1-overexpressing BMDCs shape the tumor immune microenvironment

Correlation analyses of CD45.2⁺ donor DCs to the presence of CD90.1⁺ T cells within the TME revealed a significant positive

correlation between antigen-specific T cell infiltration and the infiltration of injected BMDCs in the tumor (Fig. 6A) and tdLN (Fig. 6B) exclusively after vaccination with Arc/Arg3.1-overexpressing DCs. However, Arc/Arg3.1 overexpression was not sufficient to increase activation and proliferation of prior *in vitro* stimulated antigen-specific T cells in the tumor compared to control gp100-loaded DCs (Fig. 6C).

In summary, our results demonstrate that Arc/Arg3.1-expressing DCs in the TME are crucial for intratumoral accumulation of antigen-specific T cells.

Discussion

Clinical implications suggest the usage of DC vaccination in combination with an adoptive transfer of cytotoxic T cells as immunotherapy against cancer.¹⁴ However, durable anti-tumor immune responses and therapeutic tumor control following DC vaccination are still limited and need to be further improved.⁶

DC vaccination with BMDCs loaded with the TAA gp100 was therapeutically effective against gp100-expressing B16

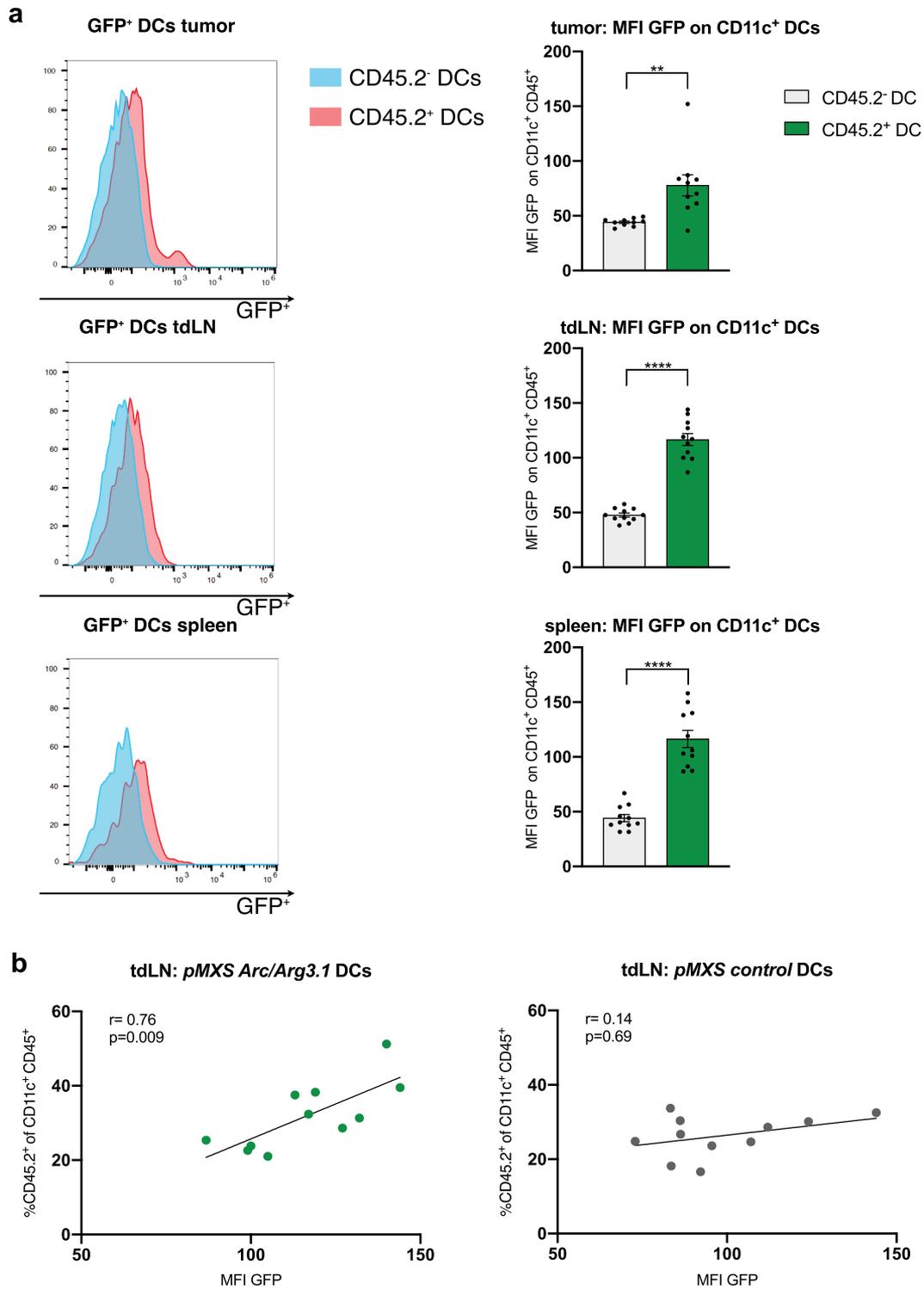


Figure 5. Arc/Arg3.1-overexpressing BMDCs in the tumor and secondary lymphoid organs following DC vaccination. Flow cytometry analysis of CD11c⁺ DCs in the tumor nine days after start of treatment. (A) Quantification of GFP signal (MFI) in flow cytometry on injected CD45.2⁺CD11c⁺ BMDCs and endogenous CD45.2⁻CD11c⁺ BMDCs in the tumor, tdLN and the spleen (n=11). (B) Correlation of donor derived CD45.2⁺CD11c⁺ DCs to MFI of GFP on CD45.2⁺ CD11c⁺ DCs in tdLN (n=11). All data are presented as mean \pm SEM. For (A) we used a two-tailed student's t test to determine statistical significance (* $p<0.05$; ** $p<0.01$, *** $p<0.001$, **** $p<0.0001$). For (B), Pearson's correlation coefficient was calculated to determine correlation.

melanoma (Fig. 1B). Activation of gp100-specific pmel-1 T cells by gp100-loaded DCs in the TME enabled further recruitment of injected DCs, as observed by a higher frequency of donor-derived BMDCs in the tumor and secondary lymphoid organs following two sequential vaccinations with gp100-loaded BMDCs as compared to the control (Fig.

1D).^{13,44} Since an increased tumor infiltration of injected DCs was associated with therapeutic response (Fig. 1C), we developed the rationale to improve DC migration to the TME to enhance the therapeutic efficacy of DC vaccination.^{29,45} Of note, gp100 is also expressed in healthy skin; thus, autoimmune destruction of melanocytes resulting

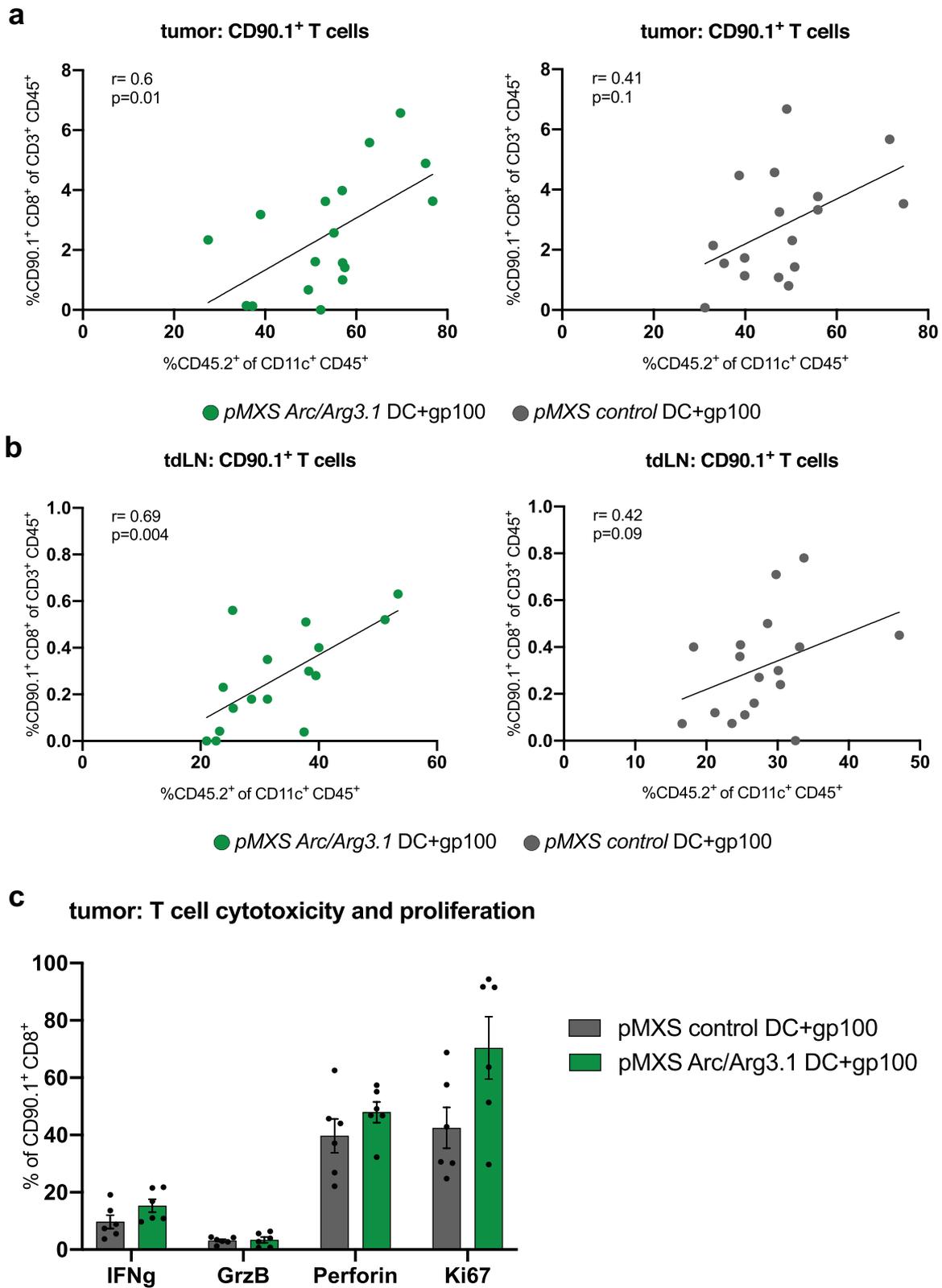


Figure 6. Antigen-specific T cells in the tumor microenvironment following vaccination with Arc/Arg3.1-overexpressing BMDCs. Flow cytometry analysis of CD45.2⁺CD11c⁺ DCs and CD90.1⁺CD8⁺ T cells in the tumor and tumor draining lymph nodes. (A)–(B) Correlation of CD90.1⁺CD8⁺ T cells to donor-derived CD45.2⁺CD11c⁺ DCs in the tumor (A) and tdLN (B) (n=17). (C) Expression of T cell activation and proliferation markers on tumor infiltrating CD90.1⁺CD8⁺ T cells. All data are presented as mean \pm SEM. For (A) and (B) Pearson’s correlation coefficient was calculated to determine correlation.

in vitiligo should be considered for clinical application.^{35,46} Yet, such side effects were not observed within this study.

Arc/Arg3.1 expression in DCs was critical for the migration of subcutaneously injected peptide-loaded BMDCs (Fig. 2A) and led to an increase of CD45.2⁺ CD8a⁺ DCs in the TME (Fig. 2E). Previous observations demonstrated that Arc/Arg3.1 expression is not stimulated by DC migration promoting chemokines CCL19/CCL21 and that CCR7 expression on DCs was not impaired by Arc/Arg3.1-deficiency.³² The reduced migration of Arc/Arg3.1^{-/-}DCs to the tumor as well as to the secondary lymphoid organs (Fig. 2A-C) further indicates a chemokine-independent migration of LPS-activated Arc/Arg3.1-expressing DCs.

In the tumor microenvironment, resident *Batf3*-dependent cDC1s initiate effective T cell recruitment by secretion of T cell recruiting chemokines CXCL9/CXCL10,⁴⁷ which directed us to further investigate the antigen-specific T cell response following DC vaccination with Arc/Arg3.1-expressing BMDCs. Indeed, T cell trafficking to the TME was dependent on Arc/Arg3.1 expression in injected DCs (Fig. 3B, C). Moreover, an increased frequency of adoptively transferred gp100-specific T cells was associated with an increase in donor derived gp100-loaded DCs in the tumor and tdLN exclusively after injecting Arc/Arg3.1-overexpressing DCs (Fig. 6A, B). The expression of T cell recruiting chemokines by Arc/Arg3.1-expressing migratory DCs (Fig. S1D) supports the hypothesis that Arc/Arg3.1-expressing DCs in the TME are involved in the recruitment of antigen-specific T cells. In the lymphoid organs, resident CD8a⁺ cDC1s are essential for cross-presentation of tumor-derived antigens to T cells leading to T cell proliferation and activation.^{48,49} Also, cross presentation by a distinct *Batf3*-dependent DC subpopulation within the tumor microenvironment itself mediated T cell activation and determined tumor rejection.²⁵ It remains to be elucidated, whether processing of tumor antigens by injected donor-derived DCs for cross presentation to CD8⁺ cytotoxic T cells might be a reason for the observed decrease of MHC class II expression on donor-derived gp100-loaded DCs in the tumor (Fig. 2D).⁵⁰

The migratory capacity of Arc/Arg3.1-expressing DCs serves as a potential target to enhance the therapeutic efficacy of DC vaccination by increasing the amount of Arc/Arg3.1-expressing DCs among *in vitro* generated BMDCs.

However, Arc/Arg3.1 overexpression in genetic-modified BMDCs was not sufficient to further enhance the therapeutic effect of DC vaccination on tumor growth as compared to vaccination with control-vector transduced BMDCs (Fig. S3C, D). The increase in Arc/Arg3.1-expressing DCs to 30% pMXS-Arc/Arg3.1⁺ DCs among all generated BMDCs following genetic modification (Fig. 4A) might be scarce to engender a therapeutic benefit for DC vaccination and thus limits its clinical application as antitumor therapy. Therapeutic efficacy might be augmented by an increase in transduction efficiency or the injection of purified Arc/Arg3.1-expressing DCs for vaccination. Although vaccination with Arc/Arg3.1-expressing BMDCs was associated with increased T cell infiltration to the tumor, the T cell mediated antitumor response might be limited by T cell exhaustion in the tumor microenvironment. Since the presence of Arc/Arg3.1-overexpressing DCs in the TME does not alter the cytotoxic potential of

activated tumor-specific T cells, the vaccination with Arc/Arg3.1-expressing DCs might not be sufficient to unleash an effective T cell response in the tumor. A combination with immune checkpoint blocking antibodies could be evaluated to increase the therapeutic effect of Arc/Arg3.1-expressing DCs as antitumor therapy.

Our study depicts the role of Arc/Arg3.1-dependent DC migration to the tumor and lymphoid organs for the trafficking of antigen-specific T cells as essential part of an effective antitumor immune response after DC vaccination. T cell infiltration to the tumor was significantly reduced following DC vaccination when DC migration was impaired by deficient Arc/Arg3.1 expression in injected BMDCs (Fig. 3B, C) and an enhancement of Arc/Arg3.1 expression in injected BMDCs also significantly increased T cell infiltration to the tumor (Fig. 6A). The usage of DCs with superior migratory capability for DC vaccination might serve as a potential therapeutic approach to enhance T cell mediated immune response against the tumor.

List of Abbreviations

ACT	adoptive T cell transfer
Arc/Arg3.1	activity-regulated cytoskeleton-associated protein/activity-regulated gene 3.1
BMC	bone marrow cell
BMDC	bone marrow derived dendritic cell
CTL	cytotoxic T cell
DC	dendritic cell
cDC	classical DC
MHC	major histocompatibility complex
TAA	tumor-associated antigen
tdLN	tumor draining lymph nodes
TME	tumor microenvironment
WT	wildtype.

Acknowledgements

We acknowledge the support by the Center for Preclinical Research, the Core Facility for Flow Cytometry and for Light Microscopy at the German Cancer Research Center and the Flow Cytometry Core Facility at the Medical Faculty Mannheim of the Heidelberg University. We thank Paul Worley, Baltimore, USA, for providing anti-Arc/Arg3.1 antibody and Dietmar Kuhl, Hamburg, Germany for providing Arc/Arg3.1^{-/-} mice.

Authors contributions

X.W.Z., K.S. and M.P. conceptualized the studies and designed the experiments. X.W.Z., K.H. and F.C. developed methodologies and performed research and experiments. K.J., J.K.S., S.B., M.S.W., K.L. and M. K. performed *in vitro*, *in vivo* and *ex vivo* experiments. E.G., F.U. and M.A.F. provided expertise and helped developing methodologies. X.W.Z., K.H., J.K.S., F.U., M.A.F., M.P. and K.S. wrote the manuscript with input from all co-authors.

Disclosure of potential conflicts of interest

The authors declare no competing interests.

Funding

This work was supported by grants from the Deutsche Forschungsgemeinschaft (SFB1366-TPC01, Project number: 394046768, to K.S. and M.P., PL-315/8-1 to M.P.), the Helmholtz Association (ZT00-27 to M.P.), the DKFZ-MOST Program (Ca-188 to M.P.), the German Cancer Aid (70113515 to M.P., 70113115 to X.W.Z.), the Hertie Foundation (P1200013 to K.S.), the Helmholtz International Graduate School for Cancer Research and the Graduate Academy Baden-Württemberg to M.K. and F.C.

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