SUPPLEMENTAL MATERIAL

Imiquimod clears tumors in mice independent of adaptive immunity by converting pDCs into tumor-killing effector cells

Barbara Drobits, Martin Holcmann, Nicole Amberg, Melissa Swiecki, Roland Grundtner, Martina Hammer, Marco Colonna, Maria Sibilia

Supplemental Figure 1 shows TLR expression and cytokine induction of Imiquimod treated skin as well as gating strategies to identify pDCs in the skin.

Supplemental Figure 2 demonstrates the bone marrow chimerism by molecular analysis (PCR) and shows tumor growth in $Myd88^{-1/2}$ chimeric mice

Supplemental Figure 3 confirms the efficient and specific depletion of the respective immune cell population in tumor-bearing mice. It also shows that pDCs upregulate CD8α after Imiquimod treatment.

Supplemental Figure 4 shows that pDC were specifically depleted in tumor-bearing *Bdca2*-DTR mice after DT treatment. Moreover, it shows the apoptosis observed in Imiquimod treated tumor tissue.

Supplemental Figure 5 confirms cell purity after FACS sorting and shows that Imiquimodactivated pDCs upregulate cytotoxic molecules in a TLR7- and IFNAR1-dependent manner.

Supplemental Table 1 shows primer sequences for RT- and qRT-PCRs.

1



Supplemental Figure 1 Effects of Imiquimod in the skin

(A) RT-PCR analysis showing TLR1-9, 11 expression in the indicated cells and tissues of mice treated for 7 days with Imiquimod (Imi) or left untreated. Results are representative of at least three independent experiments. (B) Primary keratinocyte cultures isolated from C57BL/6 (WT) mice were stimulated with Imi (12 μ g/ml) or LAL reagent water (control) for 24 hours and cytokines such as IL-6, TNF- α , IL-1 β or CCL2 were measured in the supernatants. (C) FACS analysis showing representative dot plots of pDCs infiltrating the dermis of WT mice 3 days after Imi treatment. CD45⁺ cells within the dermal cell suspension were further gated for mPDCA1⁺B220⁺ and CD11c⁺MHCII⁺. Data are representative for at least 2 independent samples. (D) H&E staining of skin sections from mice of the indicated genotype. Skin was treated with Imi for 7 days or left untreated (Co). Magnification x400. The dotted lines delineate the dermal-epidermal junction. Data are representative for at least 3 independent samples.



Supplemental Figure 2 Tumor induction and generation of bone marrow chimeras

(A) Mice were injected intradermally with B16-F10 melanoma cells. Mice developed tumors after 9 days which were treated topically with Imi every other day. (B) Experimental scheme for tumor induction in bone marrow (BM) chimeras: 8-9 weeks old mice were lethally irradiated and reconstituted intravenously with BM cells. Tumor cells were intradermally injected 12 weeks later and the same experimental protocol as depicted in A was followed. (C and D) BM chimerism was verified by PCR with primers detecting the respective wild-type (WT) and knock out alleles in BM cells isolated from mice reconstituted with either WT, $Tlr7^{-/.}$ or $Myd88^{-/.}$ BM. Results are representative for at least 2 independent batches. (E and F) Relative tumor volume in BM chimeras of the indicated genotypes following Imi treatment. WT and $Myd88^{-/.}$ mice were lethally irradiated and reconstituted intravenously with BM cells of the indicated genotypes. After 12 weeks reconstituted mice were injected intradermally with B16-F10 melanoma cells and tumors treated with Imi or left untreated (n = 7-11 per group). Data represent mean \pm SEM of at least 2 independent experiments. * P < 0.05, ** P < 0.005



Supplemental Figure 3 Analysis of immune cells in mice depleted of specific immune cell populations

(A) Increased activation of tumor infiltrating T cells (CD3) and NK cells (CD49b) shown by upregulation of CD69 on the respective cells in Imi treated tumors (B) Experimental protocol for cell depletion experiments. Tumor bearing mice were injected with antibodies depleting the indicated cell population before starting the topical treatment with Imi. (C and D) FACS analysis showing depletion efficacy in tumor draining lymph nodes (tdLN) of mice treated with specific anti-NK cell antibodies (C), anti-CD4 antibodies or anti-CD8 α antibodies (D). (E and F) FACS analysis for CD8 α expression on pDCs (SiglecH⁺B220⁺) in cultured splenocytes (E) and BM-derived pDCs (CD11b⁻B220⁺) of WT, *Tlr7^{/-}* or *Ifnar1^{-/-}* mice (F) stimulated with Imi (2.5 µg/ml) for 24 hours. Results are representative for at least 2 independent batches. * *P* < 0.05



Supplemental Figure 4 pDCs are the effector cells in mediating the tumoricidal effect of Imiquimod

(A) Experimental protocol for pDC depletion: Diphteria Doxin (DT) (4.5 ng per g body weight) or PBS (control) was administered intraperitoneally (i.p) in tumor bearing *Bdca2*-DTR⁺ mice every other day. First Imi treatment was performed one day after depletion start. (B) FACS analysis showing pDC (CD11c⁺B220⁺SiglecH⁺) depletion efficacy in tumor-bearing *Bdca2*-DTR mice treated with DT. (C) Representative immune-fluorescence staining of active caspase-3 in tumor tissue of WT (n = 7-8 per group), *Bdca2*-DTR + DT (pDCs depl.) (n = 8-9 per group) and *Tlr7^{-/-}* mice (n = 3 per group) treated with Imi or left untreated. Magnification x200



Supplemental Figure 5 Imiquimod stimulated pDCs kill tumor cells

(A) FACS sorted B220⁺CD11b⁻ cells of in vitro generated BM-derived pDCs. (B) Representative dot plots of TRAIL expression on WT pDCs (CD11b⁻B200⁺) after 6 hours of Imi (2.5 µg/ml) stimulation. (C) Quantification of TRAIL expression by FACS on WT, *Ifnar1^{-/-}* and *TIr7^{-/-}* pDCs after 6 hours of Imi stimulation. (D) Flow cytometric analysis showing intracellular granzyme B (GzmB) staining of pDCs after stimulation with Imi for 4 hours. (E) Quantification of FasL expression on WT, *Ifnar1^{-/-}* and *TIr7^{-/-}* pDCs after Imi stimulation for 6 hours analyzed by FACS. (F) Representative staining of Isotype (IgG) or Fas antibodies on B16-F10 melanoma cells. (G) Killing assay performed with B16-F10 melanoma treated with Imi, recombinant TRAIL (10, 20, 50 ng/ml) or supernatants of Imi stimulated or unstimulated WT pDCs. Graphs are representative for one experiment of at least 2 independent batches.* *P* < 0.05

Supplemental Table 1

Primer Sequences for RT-PCR

Tlr1: 5'-CAATGTGGAAACAACGTGGA-3'; 5'-TGTAACTTTGGGGGAAGCTG-3';

Tlr2: 5'-AAGAGGAAGCCCAAGAAAGC-3'; 5'-CGATGGAATCGATGATGTTG -3';

Tlr3: 5'-CACAGGCTGAGCAGTTTGAA-3'; 5'-TTTCGGCTTCTTTTGATGCT-3';

Tlr4: 5'-ACCTGGCTGGTTTACACGTC- 3'; 5'-CTGCCAGAGACATTGCAGAA- 3';

Tlr5: 5'-AAGTTCCGGGGAATCTGTTT-3'; 5'-GCATAGCCTGAGCCTGTTTC-3';

TIr6: 5'-TTCCCAATACCACCGTTCTC- 3'; 5'-CTATGTGCTGGAGGGTCACA-3';

TIr7: 5'-AATCCACAGGCTCACCCATA-3'; 5'-CAGGTACCAAGGGATGTCCT-3';

TIr8: 5'-GTTATGTTGGCTGCTCTGGTTCAC-3'; 5'- TCACTCTCTTCAAGGTGGTAGC-3';

TIr9: 5'-ACTGAGCACCCCTGCTTCTA-3'; 5'-AGATTAGTCAGCGGCAGGAA-3';

Tlr11: 5'-TTGATGTATTCGTGTCCCACTGC-3'; 5'-CCACTCTTTCTCTCCTCGTG';

Gapdh: 5'-CTCATGACCACAGTCCATCG-3'; 5'-CACATTGGGGGTAGGAACAC-3'

Primer Sequences for qRT-PCR

Trail: 5'-GTGTCTGTGGCTGTGACTTACA-3'; 5'-AATGCCCTTTCCGAGAGGA-3',

Gzmb: 5'-ATTCCCCACCCAGACTATAATCC-3'; 5'-TTACTCTTCAGCTTTAGCAGCATGA-3';

Actin: 5'-ACCAACTGGGACGATATGGAGAAGA-3'; 5'TACGACCAGAGGCATACAGGGACAA-3';