

Engineering adoptive T cell therapy to co-opt Fas ligand-mediated death signaling in ovarian cancer enhances therapeutic efficacy

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ABSTRACT

Background In the USA, more than 50% of patients with ovarian cancer die within 5 years of diagnosis, highlighting the need for therapeutic innovations. Mesothelin (MSLN) is a candidate immunotherapy target; it is overexpressed by ovarian tumors and contributes to malignant/invasive phenotypes, making tumor antigen loss disadvantageous. We previously showed that MSLN-specific T cell receptor (TCR)-engineered T cells preferentially accumulate within established tumors, delay tumor growth, and significantly prolong survival in the ID8_{VEGF} mouse model that replicates many aspects of human disease. However, T cell persistence and antitumor activity were not sustained. We therefore focused on Fas/FasL signaling that can induce activation-induced cell death, an apoptotic mechanism that regulates T cell expansion. Upregulation of FasL by tumor cells and tumor vasculature has been detected in the tumor microenvironment (TME) of human and murine ovarian cancers, can induce apoptosis in infiltrating, Fas (CD95) receptor-expressing lymphocytes, and can protect ovarian cancers from tumor-infiltrating lymphocytes.

Methods To overcome potential FasL-mediated immune evasion and enhance T cell responses, we generated an immunomodulatory fusion protein (IFP) containing the Fas extracellular binding domain fused to a 4-1BB co-stimulatory domain, rather than the natural death domain. Murine T cells were engineered to express an MSLN-specific TCR (TCR₁₀₄₅), alone or with the IFP, transferred into ID8_{VEGF} tumor-bearing mice and evaluated for persistence, proliferation, cytokine production and efficacy. Human T cells were similarly engineered to express an MSLN-specific TCR (TCR₅₃₀) alone or with a truncated Fas receptor or a Fas-4-1BB IFP and evaluated for cytokine production and tumor lysis.

Results Relative to murine T cells expressing only TCR₁₀₄₅, T cells expressing both TCR₁₀₄₅ and a Fas-4-1BB IFP preferentially persisted in the TME of tumor-bearing mice, with improved T cell proliferation and survival. Moreover, TCR₁₀₄₅/IFP⁺ T cells significantly prolonged survival in tumor-bearing mice, compared with TCR₁₀₄₅-only T cells. Human T cells expressing TCR₅₃₀ and a Fas-4-1BB IFP exhibit enhanced functional activity and viability compared with cells with only TCR₅₃₀.

Conclusions As many ovarian tumors overexpress FasL, an IFP that converts the Fas-mediated death signal into

pro-survival and proliferative signals may be used to enhance engineered adoptive T cell therapy for patients.

INTRODUCTION

More than 20,000 women are diagnosed with ovarian cancer annually, and >50% will die within 5 years.¹ This mortality rate has changed little in the last 20 years, highlighting the need for therapy innovation.² T cells engineered to selectively target proteins uniquely overexpressed in tumors represents a rapidly evolving strategy to control tumor growth without toxicity to healthy tissues. Mesothelin (MSLN) contributes to the malignant and invasive phenotype in ovarian cancer,^{3,4} and has limited expression in healthy cells,⁵ making it a candidate target.⁶ Studies targeting MSLN with monoclonal antibodies,⁷ vaccination⁸ and chimeric antigen receptor (CAR)-expressing T cells⁹ have shown modest anti-tumor activity, validating MSLN as a viable target antigen.

T cells engineered to target MSLN (TCR₁₀₄₅) can preferentially accumulate within established tumors on adoptive transfer, delay tumor growth, and significantly prolong survival in the ID8_{VEGF} murine ovarian cancer model of established, disseminated disease.¹⁰ However, the previous study also revealed that elements in the tumor microenvironment (TME) limit engineered T cell persistence and the ability to eradicate cancer cells. The Fas death receptor is expressed on antigen-experienced T cells, and FasL expression in the tumor vasculature of human and murine ovarian cancers can induce apoptosis of Fas-expressing T cells,^{11,12} representing an obstacle to T cell accumulation in ovarian cancer.¹² To overcome this T cell-evasion mechanism, we generated a panel of immunomodulatory fusion proteins

(IFPs) containing the Fas extracellular binding domain fused to a 4-1BB co-stimulatory domain rather than the natural death domain.¹³ We previously demonstrated that this IFP can improve therapeutic efficacy of engineered T cells in mouse models of pancreatic cancer and acute myeloid leukemia,¹³ but the mechanism of in vivo action and the potential broader utility of this strategy remain undefined.

We have now confirmed our hypothesis that T cells expressing TCR₁₀₄₅ and a Fas-4-1BB IFP would persist better within ID8_{VEGF} ovarian tumors, with less apoptosis and potentially enhanced T cell proliferation in situ. IFP⁺ T cells persisted longer than cells only expressing TCR₁₀₄₅ when FasL was present on tumor cells. T cells engineered with TCR₁₀₄₅ and the Fas-4-1BB IFP were more therapeutically effective, improving survival of tumor-bearing mice without on-target, off-tumor toxicity. We have also validated that human CD8 T cells expressing a MSLN-specific TCR and a Fas-4-1BB IFP exhibit enhanced functional activity compared with T cells expressing only the TCR or the TCR and a truncated Fas receptor. These studies validate that a rationally designed fusion protein can address Fas-mediated apoptotic T cell death, otherwise an obstacle to the efficacy of engineered T cell therapy.

METHODS

Cell lines

ID8_{VEGF} cells, which were transduced to overexpress vascular endothelial growth factor (VEGF) to recapitulate the elevated levels observed in human disease,¹⁴ were a gift from Dr Matthias Stephan in 2014. ID8 cells were cultured in DMEM (Gibco) containing 10% Fetal Bovine Serum (FBS, Hyclone), 1% Penn/Strep (Gibco), and 0.1% Insulin-Transferrin-Selenium (Sigma). ID8_{VEGF} cell lines were passaged fewer than 10 times before use in experiments. PLAT-E cells (ATCC) passaged fewer than 35 times were used for retrovirus production for all T cell transductions. All cell lines were confirmed negative for mycoplasma prior to use. Cell lines were not authenticated in the past year.

Mouse strains

All mice were co-housed and provided with nesting material for enrichment. Cages were maintained on the same row of the multi-tier caging system. 5×10^6 ID8_{VEGF15} cells were injected i.p. into >8-week-old female C57BL/6J mice (Jackson Laboratories).

ID8_{VEGF} FasL CRISPR KO

ID8_{VEGF} cells were edited using CRISPR knockout technology by Synthego. Briefly, founder ID8_{VEGF} cells (mycoplasma-free) were sequenced and synthetic single guide RNA (sgRNA) was designed to target FasL (guide target sequence: CTCCTTTGGTCCGGCCCTCT). Specific guide RNA was complexed with *Streptococcus pyogenes* Cas9 (PAM motif: AGG) into a ribonucleoprotein and delivered into ID8_{VEGF} cells by electroporation.

PCR-amplification and Sanger sequencing was used to sequence the transfected cells to verify knockout efficiency. Cells from the edited pool were seeded using single cell dilution and expanded to establish clonal lines. Clones were sequenced to verify the clone contained a homozygous edit and that the progeny were derived from a single cell, and a single clone (E9) was selected for experiments.

Cytotoxicity assays

Naïve P14 T cells were activated for 72 hours with anti-CD3 and CD28 antibodies, then cultured alone or co-cultured with tumor cells for 18–24 hours in 24-well tissue culture plates. T cells were then gently removed and transferred to FACS tubes for intracellular cleaved-caspase 3 (CC3) staining. The BD Fix/Perm kit (cat: 554714) was used for staining with anti-CC3.

Retroviral constructs

The codon-optimized murine Vβ9 and Vα4 TCR chains, connected by a porcine teschovirus-1 2A element (“P2A”; Life technologies), recognize the Msln₄₀₆₋₄₁₄ epitope presented in H2-D^b, and were cloned from the Mig-R1 retroviral vector¹⁶ into the pENTR vector and subsequently Gateway cloned into the pMP71 retroviral vector for all TCR₁₀₄₅ studies. A construct encoding Fas-4-1BB_{tm} and TCR₁₀₄₅ was ordered from GeneArt (ThermoFisher) in the pDONR221 vector and gateway cloned into the pMP71 retroviral vector for all TCR₁₀₄₅ studies.

TCR transduction of T cells

Murine T cell transduction has been described previously¹⁰ and can be accessed at DOI: dx.doi.org/10.17504/protocols.io.smrec56. Briefly, PLAT-E cells were transfected with DNA encoding TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm}, the media was replaced at 24 hours, and the viral supernatant used for T cell transduction 48 and 72 hours. Splenic T cells isolated from P14 Thy1.1⁺ mice were stimulated with anti-CD3 and anti-CD28 antibodies in the presence of IL-2 and transduced with retroviral supernatant by spinfection in polybrene at 24 and 48 hours after activation. T cell restimulation has been described previously¹⁰ and can be access at DOI: dx.doi.org/10.17504/protocols.io.spqedmw. Briefly, Thy1.2⁺ splenocytes were irradiated and pulsed with Msln₄₀₆₋₄₁₄ peptide for >90 min to prepare APCs. Transduced T cells were co-cultured with peptide-pulsed APCs for 5–7 days in the presence of IL-2. T cells were screened by flow cytometry for transduction efficiency 5 days after activation or restimulation.

Human T cell transduction and rapid expansion protocol have been described previously and can be accessed at DOI: dx.doi.org/10.17504/protocols.io.sxvefn6. Briefly, 293T cells were transfected with DNA encoding TCR_{HIVgag}, TCR₅₃₀, TCR₅₃₀/FasTr, TCR₅₃₀/Fas_{tm}-4-1BB, or TCR₅₃₀/Fas-4-1BB_{tm}, the media was replaced at 24 hours, and the viral supernatant used for T cell transduction at 48 hours. CD8⁺ T cells were thawed and activated with anti-CD3 and -CD28 beads in the presence of

IL-2 and transduced by lentiviral supernatant by spinfection in polybrene between 8 and 24 hours after activation. Cells were expanded by culturing with irradiated PBMC and LCL cells in the presence of anti-CD3 antibody (OKT3) and IL-2. T cells were screened by flow cytometry for transduction efficiency and used for experiments 7 days after activation or restimulation.

T cell isolation

Tumors were dissociated in 3 mL of RPMI with 10% FBS using the *m_imptumor_01* setting on a gentleMACS dissociator (Miltenyi Biotec). Samples were transferred to a conical tube with 35 mL of Collagenase (RPMI containing 1% HG solution, 0.1% MgCl₂, 0.1% CaCl₂, 5% FBS, and 20,000U of Collagenase Type IV) and mixed on a MACSmix rotator at 37°C for 10 min. Samples were filtered through cell strainers (70 μm Falcon) and lymphocytes were purified on a 44/67% percoll gradient (800×g at 20°C for 20 min). Spleens were dissociated by mechanical separation through a cell strainer and ACK lysis (Gibco, cat: A10492-01) was performed to remove red blood cells.

Flow cytometry

MSLN₄₀₆₋₄₁₄/H2-D^b and MSLN₅₃₀₋₅₃₈/HLA-A*02.01 tetramers conjugated to APC were prepared by the Fred Hutch Immune Monitoring Core. All cells were stained with LIVE/DEAD fixable Aqua (405 nm, cat: L34966) or fixable Blue (350 nm, cat: L23105) in 1× DPBS prior to surface or intracellular staining. UltraComp eBeads (eBioscience, cat: 01-2222) were used for all compensation. For *ex vivo* experiments, cells from either untreated mice or endogenous CD44⁺ CD62L⁺ CD8⁺ T cells from the spleen of treated mice were used for negative controls and gating. For *in vitro* experiments, fluorescence minus one or irrelevant engineered T cells were used for negative controls and gating. For murine FasL staining, cells were blocked with human and mouse serum and then stained with purified Armenian hamster anti-mouse CD178 (clone: MFL3) followed by secondary staining with polyclonal goat anti-Armenian hamster IgG PE (Invitrogen). The eBioscience Fix/Perm kit (cat: 00-5523-00) was used for staining with anti-Ki67 (cat: 51-36524X) with a mouse IgG₁ isotype as a control (cat: 51-35404X). Cells were resuspended in FACS buffer (1× DPBS containing 2% FBS Hyclone and 0.72% 0.5M EDTA) or 0.5% Paraformaldehyde and acquired with an LSR2-2, Fortessa or Symphony Instrument (BD).

Intracellular cytokine stimulation

The stimulation protocol for intracellular cytokine staining has been described previously¹⁰ and can be found at DOI: [dx.doi.org/10.17504/protocols.io.sqded6](https://doi.org/10.17504/protocols.io.sqded6). Briefly, cells were treated with protein transport inhibitor containing Brefeldin A (GolgiPlug) and plated at 1×10⁶ cells per well in a flat-bottom 96-well plate. Cells were stimulated for 5 hours at 37°C with T cell media or 1 mg/mL of Msln₄₀₆₋₄₁₄ peptide (GQKMNAQAI; murine T cells)

or Msln₅₃₀₋₅₃₈ (VLPLTVAEV; human T cells). Peptides were ordered from ELIM peptide (>80% purity). The BD Fix/Perm kit was used for intracellular staining. In some experiments, cells were fixed in 0.5% paraformaldehyde until data acquisition.

Cell proliferation

The Click-iT Plus EdU imaging kit (cat: C10640) was reconstituted at 10 mM in DMSO and used to analyze *in situ* cell proliferation. For *in vitro* experiments, 3×10⁶ cells were plated with 5 μL of the 10 mM EdU solution and incubated for 24 hours. Cells were treated with the eBioscience Fix/Perm kit and subsequently stained using Click-iT Plus EdU imaging kit reagents: Click-iT reaction buffer, copper protectant, Alexa Fluor picolyl azide (AF647 fluorescent), and Click-iT reaction buffer additive. Samples were analyzed by flow cytometry within 4 hours. For *in vivo* EdU experiments, EdU was diluted to 5 mg/mL of saline. Mice were injected *i.p.* with 50 mg EdU/kg and cells were isolated 24 hours later by enzymatic digestion. Cells were stained using the Click-iT Plus EdU imaging kit and analyzed by flow cytometry within 4 hours.

Quantitative PCR

3×10⁶ transduced T cells were resuspended in RLT lysis buffer (supplemented with β-ME) and RNA extracted with the Qiagen RNeasy Plus RNA isolation kit. RNA integrity was analyzed on Tape Station analyzer and cDNA was generated using iScript Reverse Transcription Supermix for RT-qPCR (Biorad). qPCR was run using qPCR SYBR Green Assay with mouse BCL2 PrimePCR assay (Biorad) and with RPL13a reference gene (Primers: Fwd.: TTCTCCTCCAGAGTGGCTGT, Rev.: GGCTGAAG-CCTACCAGAAAG) on the 384 well ABI QuantStudio5 instrument. The delta delta CT method was used for analysis.

Adoptive immunotherapy

ID8_{VEGF}-tumor-bearing mice received either engineered T cells (1×10⁷, transduced and re-stimulated *in vitro*) or engineered T cells (1×10⁷) transduced without restimulation *in vitro* but then stimulated *in vivo* with 5×10⁷ peptide-pulsed irradiated splenocytes as a vaccine. Cell infusions were followed by IL-2 (2×10⁴ IU, *s.c.*) daily for 10 days to promote T-cell expansion and survival. For therapy with serial T-cell infusions, mice received this same treatment protocol every 2 weeks. In indicated experiments, treated mice received one dose of Cyclophosphamide (180 mg/kg) *i.p.* to lymphodeplete hosts approximately 6–8 hours prior to only the first T-cell transfer. Mice were randomized by one investigator and treated by a second. Power analysis guided enrolment numbers to power the study for a large effect (>50% increase in median overall survival).

Impedance cytotoxicity assay

1×10⁴ OVCAR3 tumor cells were plated on gold-electrode E-plates (xCELLigence, Agilent), plates were connected to the xCELLigence RTCA MP instrument and allowed

to adhere for 24 hours. When cells reached logarithmic growth, T cells were added at varying E:T ratios (5:1 to 0.625:1) in triplicate. Irrelevant T cells (TCR_{HIVgag}) were used to calculate tumor-specific killing above background.

Immunohistochemistry

Histology preparation has been described previously¹⁰ and can be found at DOI: dx.doi.org/10.17504/protocols.io.sppedmn. Briefly, harvested tissues were fixed in 10% neutral buffered formalin for at least 72 hours, embedded in paraffin, sectioned (4 μm) and stained with hematoxylin and eosin or primary antibodies for markers of interest using a Leica Bond Instrument. Following antigen retrieval, slides were blocked with Leica Bond Peroxide Block and then 10% normal goat serum, stained with primary antibodies for 30 or 60 min, and Leica Bond polymer was applied. Leica Bond Mixed Refine (DAB) detection was performed and a Leica hematoxylin counterstain was added. Slides were cleared with xylene, mounted, and scanned in brightfield (20x) using the Aperio ScanScope AT slide scanner. Digital images were imported into Aperio eSlide manager.

Halo analysis

Images were analyzed using HALO (Indica Labs). Cells were determined based on thresholds set for nuclear size, segmentation, contrast threshold, and maximum cytoplasm radius. FasL and CD31 expression was analyzed using positive staining set by the minimum optical density (OD) above the background (set on regions of non-specific staining). Co-localization was analyzed by using image registration to align both FasL and CD31 stains and then using nearest neighbor analysis. Cell location within tumors was evaluated by concentric partitioning analysis with Cytonuclear v2.0.9 per partition. Lung tissue was annotated, and the total number of cells was identified using cell by cell analysis. CD8⁺ or CD3⁺ cells were identified by positive staining set by the minimum optical density (OD) above the background. MSLN expression analysis was performed by annotating the tumor region and using the Area Quant analysis to determine the percentage of area with positive MSLN staining set by the minimum OD above the background.

Statistics

The Student's t-test was used to compare normally distributed two-group data. A one-way Anova with post hoc analysis pairwise for multiple comparisons was used to compare data from experiments with more than two groups. Survival curve analysis was performed using the Log-rank (Mantel-Cox) and Gehan-Breslow-Wilcoxon tests. All error bars represent SD.

RESULTS

FasL expression on ovarian tumor cells and effector T cells induces CD8 T cell death

FasL expression by solid tumors promotes tumor metastasis¹⁷ and immune evasion.¹⁸ FasL is overexpressed in ovarian tumor vasculature¹² and has higher expression in the ovarian TME than in normal ovarian tissue.¹⁹ We evaluated the distribution of FasL expression in high-grade serous ovarian cancer. Serial sections from matched primary and metastatic high-grade serous tumor samples were stained for the vascular marker CD31 and FasL (figure 1A–B); merged images were analyzed by nearest-neighbor Halo infiltration analysis. Above-background FasL expression was detected in the vasculature of 12/17 primary and 14/17 metastatic tumors, consistent with previous reports,^{12,19} but was also detected in the epithelial tumor regions of 11/17 primary and 13/17 metastatic tumors. Imaging revealed heterogeneous FasL expression in patient samples (figure 1C), and we used concentric partitioning with cytonuclear Halo image analysis (figure 1D) to further evaluate the location of FasL⁺ cells and the intensity of FasL expression in tumors. Analysis of 100 μm concentric regions (denoted in figure 1D–F as numbered 'rings') revealed similar numbers of FasL⁺ cells in epithelial regions of primary (figure 1E) and metastatic tumors (figure 1F). While we observed a trend toward fewer FasL⁺ cells in the more central regions of metastatic tumors, this did not reach statistical significance. Analysis of FasL expression in 200 μm concentric regions (denoted in figure 1D and G–H as 'rings a–e') revealed the highest levels often found near the tumor edge (figure 1G–H). Thus, T cells infiltrating ovarian tumors can encounter FasL death signals not only while exiting the vasculature but also on encountering and then infiltrating epithelial tumors.

FasL is also expressed on activated T cells (figure 1I).^{20,21} To evaluate if FasL signaling from fellow T cells can induce fratricide, we activated wild-type P14 CD8 T cells, expressing a TCR (TCR_{gp33}) specific for the gp33-41 epitope of lymphocytic choriomeningitis virus (LCMV), with anti-CD3 and CD28 antibodies in vitro for 8 hours. We then treated the T cells with media or a FasL blocking antibody (Kay-10 clone) and stained for cleaved caspase 3 (CC3) 3 days later. FasL blockade significantly reduced CC3 expression (figure 1J), suggesting that activated T cells engage in Fas/FasL apoptosis-inducing signaling. To determine if FasL expression on ID8_{VEGF} tumor cells also induces CD8 T cell death, we co-cultured wild type ID8_{VEGF} cells with P14 CD8 T cells previously activated in vitro with anti-CD3 and CD28 antibodies (±pretreatment with FasL-blocking antibody), and stained for CC3 in T cells 3 days later. Significantly decreased CC3 staining was observed when tumor-cell FasL signaling was inhibited by the antibody (figure 1K); concurrent T cell FasL blockade further decreased CC3 levels. To verify these results suggesting tumor cell-induced apoptosis of T cells, we used CRISPR/Cas9 targeting to generate a FasL knockout ID8_{VEGF} cell line (ID8_{VEGF}^{FasL^{-/-}}; denoted E9;

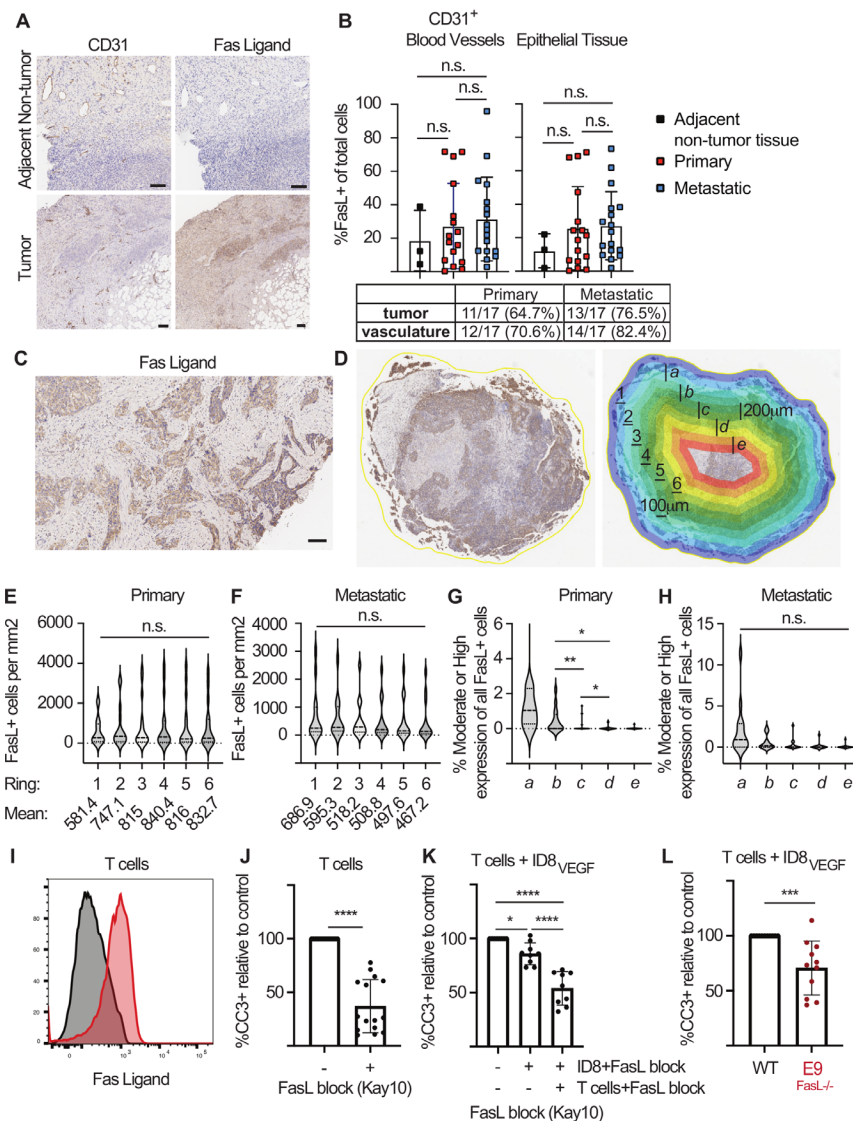


Figure 1 Fas ligand signaling from T cells and ID8_{VEGF} tumor cells induce death in effector CD8 T cells. (A) Immunohistochemistry (IHC) staining for CD31 and Fas Ligand in human high-grade serous ovarian cancer. Images are representative of 17 primary and 17 metastatic patient samples. Scale bar=500 μ m. (B) Halo quantification of FasL⁺ cells in CD31⁺ vasculature or tumor epithelium. Samples were considered positive if >10% of cells were FasL⁺. Two-way ANOVA for multiple comparisons. n.s.=not significant. (C) Representative IHC staining for FasL, with higher intensity staining near the tumor edge. Scale bar=100 μ m. (D) Example of concentric partitioning analysis in Halo. Consecutive 100 (denoted '1-6') or 200 μ m (denoted 'a-e') rings are annotated on each sample and are referred to in (E-H). (E, F) Quantification of FasL⁺ cells in 100 μ m concentric rings from the outer edge of the sample to the center. Concentric rings, as in (D), were annotated as Ring 1 (0-100 μ m), ring 2 (100-200 μ m), ring 3 (200-300 μ m), ring 4 (300-400 μ m), ring 5 (400-500 μ m), ring 6 (500-600 μ m) on primary (E, F) metastatic tumor samples. Mixed-effects analysis for multiple comparisons. (G, H) Percent of FasL⁺ cells with moderate or high staining intensity in 200 μ m concentric rings from the outer edge of the sample to the center. Concentric rings, as in (D), were annotated as Ring 1 (0-200 μ m), ring 2 (200-400 μ m), ring 3 (400-600 μ m), ring 4 (600-800 μ m), ring 5 (800-1000 μ m) on of G) primary and (H) metastatic tumor samples. Mixed-effects analysis for multiple comparisons. *P<0.5, **p<0.01. (I) FasL flow cytometry staining on activated CD8 T cells 7 days after activation with peptide-pulsed irradiated splenocytes. Results are representative of 4 independent experiments. (J) Cleaved Caspase 3 (CC3) flow cytometry staining in activated CD8 T cells 3 days after culture with or without pre-treatment with anti-FasL blocking antibody (clone: Kay10). Data are displayed as a percentage of CC3⁺ staining relative to untreated T cells. Cumulative data from five independent experiments. Student's unpaired t-test. ****P<0.0001. (K) CC3 flow cytometry staining in activated CD8 T cells 3 days after culture alone or coculture with ID8_{VEGF} tumor cells. T cells or tumor cells were pre-treated with FasL (Kay10) blocking antibody as indicated. Data displayed as a percentage relative to T cells cocultured with ID8_{VEGF} tumor cells without FasL blockade. Cumulative data from three independent experiments. One-way ANOVA for multiple comparisons. *P=0.0353; ****p<0.0001 (L) CC3 flow cytometry staining in activated CD8 T cells 3 days after co-culture with wild type ID8_{VEGF} or CRISPR edited ID8_{VEGF}^{FasL^{-/-}} tumor cells (E9 clone). Data displayed as a percentage relative to T cells co-cultured with wild type ID8_{VEGF} tumor cells. Cumulative data from four independent experiments. Student's unpaired t-test. ***p=0.0008. All error bars indicate SD. ANOVA, analysis of variance; ns, not significant.

online supplemental figure 1). CC3 staining was reduced in activated T cells co-cultured with E9 ID8_{VEGF}^{FasL^{-/-}} cells, but not in activated wild-type ID8_{VEGF} cells (figure 1L). Thus, effector CD8 T cells are susceptible to FasL signals from both ID8_{VEGF} tumor cells and fellow CD8 T cells.

TCR₁₀₄₅/Fas-4-1BB IFP⁺ T cells exhibit enhanced survival *in vivo*

We previously isolated the high-affinity murine TCR₁₀₄₅ specific for the MSLN₄₀₆₋₄₁₄ epitope and demonstrated that CD8 T cells transduced with TCR₁₀₄₅ mediate anti-tumor activity against ovarian and pancreatic cancers without toxicity to normal tissues.^{10,16} We also previously developed an IFP containing the Fas extracellular binding domain and a 4-1BB co-stimulatory domain; expression of this fusion protein improved the efficacy of T cell therapy in mouse models of acute myeloid leukemia and pancreatic cancer.¹³ We now tested whether the Fas-4-1BB_{tm} IFP could improve therapeutic activity in a mouse model of ovarian cancer in which FasL/Fas signaling is known to reduce T-cell efficacy.¹² Naive transgenic P14 CD8 T cells were activated with anti-CD3 and CD28 antibodies and transduced with either a bi-cistronic vector encoding the alpha and beta chains of TCR₁₀₄₅, or a tri-cistronic vector encoding both TCR₁₀₄₅ chains and a Fas-4-1BB_{tm} IFP (TCR₁₀₄₅/Fas-4-1BB_{tm}, figure 2A), linked by P2A elements to ensure equimolar expression. P14 T cells engineered with either TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm} expressed similar levels of the Vβ9 component of TCR₁₀₄₅, but only TCR₁₀₄₅/Fas-4-1BB_{tm} T cells expressed high levels of Fas, reflecting high levels of transduced IFP (figure 2B). We previously reported that Fas-4-1BB_{tm}-expressing T cells produce increased levels of IL-2,¹³ and we validated that the TCR₁₀₄₅/Fas-4-1BB_{tm} fusion protein also increased IL-2 production by transduced T cells (figure 2C). Blocking FasL during *in vitro* stimulation reduced IL-2 production by TCR₁₀₄₅/Fas-4-1BB_{tm} T cells, but not TCR₁₀₄₅ cells, suggesting FasL signals promote IL-2 production by IFP⁺ T cells (figure 2D–E).

We also previously showed that TCR₁₀₄₅-T cells infiltrate ID8_{VEGF} tumors, but that antitumor activity is limited by low persistence.¹⁰ To evaluate if TCR₁₀₄₅/Fas-4-1BB_{tm} T cells persist better in mouse ovarian tumors than control TCR₁₀₄₅ cells, T cells were transferred into ID8_{VEGF} tumor-bearing mice, following an established protocol.¹⁰ Briefly, 5×10⁶ ID8_{VEGF} cells were injected intraperitoneally (i.p.) into 8 week-old female C57Bl/6 mice. After tumor nodules were readily detectable by high resolution ultrasound (>6 weeks after tumor injection), mice were treated with cyclophosphamide ≥6 hours to render the host lymphopenic, and then received 1×10⁷ engineered T cells and a vaccine of 5×10⁷ irradiated splenocytes pulsed with MSLN₄₀₄₋₄₁₆ peptide to enhance engraftment.¹⁰ Prior to transfer, >93% of the transduced T cells expressed TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm}, as indicated by staining for the Vβ9 chain of TCR₁₀₄₅ (figure 2B). By twenty-one days after T cell transfer, the number of T cells in TCR₁₀₄₅ T cell-engrafted tumors was not significantly greater than the number of

endogenous T cells in tumors from untreated mice, but 3-fold more T cells persisted in TCR₁₀₄₅/Fas-4-1BB_{tm} T cell-treated vs untreated tumors (figure 2F). As co-stimulation through 4-1BB promotes T cell proliferation and survival,^{22,23} enhanced persistence of intratumoral TCR₁₀₄₅/Fas-4-1BB_{tm} T cells could be due to increased T cell proliferation, reduced T cell death or both. To evaluate T cell proliferation, we assessed Ki67 expression and EdU incorporation by tumor-infiltrating engineered T cells. Congenically distinct (Thy1.1⁺ or Thy1.1⁺Thy1.2⁺) P14 T cells were transduced with TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm} and equal numbers were co-transferred into tumor-bearing mice. Prior to T cell transfer, a similar proportion of TCR₁₀₄₅ and TCR₁₀₄₅/Fas-4-1BB_{tm} T cells expressed Ki67 (figure 2G), suggesting expressing Fas-4-1BB_{tm} does not change the proportion of cycling, activated cells *in vitro*. At 3 or 7 days post-transfer, TCR₁₀₄₅/Fas-4-1BB_{tm} T cells preferentially accumulated within tumors (figure 2H–I). Although there was no difference in the proportion of Ki67⁺Edu⁺ cells at either time point (figure 2J), 1.7-fold more Ki67⁺Edu⁺ TCR₁₀₄₅/Fas-4-1BB_{tm} T cells were present 7 days post-transfer (figure 2K). To address enhanced proliferation *in situ* and/or reduced cell death in the TCR₁₀₄₅/Fas-4-1BB_{tm} T cell population, we stained intratumoral T cells with Annexin V and Propidium Iodide (PI). Three- and 7 days post-transfer, 1.2-fold and 1.5-fold fewer TCR₁₀₄₅/Fas-4-1BB_{tm} T cells were Annexin V⁺/PI⁺ than TCR₁₀₄₅ T cells, respectively (figure 2L), suggesting both enhanced proliferation and survival of TCR₁₀₄₅/Fas-4-1BB_{tm} T cells within ID8_{VEGF} tumors.

To further interrogate the mechanism of TCR₁₀₄₅/Fas-4-1BB_{tm} T cell persistence, transcripts for the prosurvival Bcl2 protein were quantified by qPCR 8 days postactivation *in vitro* (figure 2M) and detected at higher levels in TCR₁₀₄₅/Fas-4-1BB_{tm} T cells relative to TCR₁₀₄₅ T cells. Intracellular staining of T cells isolated from tumors 3 days post-transfer also revealed higher Bcl2 protein expression in TCR₁₀₄₅/Fas-4-1BB_{tm} T cells (figure 2N). Together, these data suggest TCR₁₀₄₅/Fas-4-1BB_{tm} T cells achieve enhanced persistence in ID8_{VEGF} tumors by improved T cell survival and proliferation within the TME.

TCR₁₀₄₅/Fas-4-1BB IFP⁺ T cells sustain enhanced IL2 production in solid tumors

We previously reported Fas-4-1BB_{tm} IFP-enhanced cytokine production *in vitro*.¹³ To evaluate if this advantage was maintained *in vivo*, we co-transferred P14 T cells expressing TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm} into tumor-bearing mice. Twenty-one days after cell transfer, both tumor-infiltrating T cell populations expressed PD-1, Lag-3, Tim-3 and TIGIT (figure 3A, relative to naïve T cells in the spleen). Fas-4-1BB_{tm} IFP⁺ T cells expressed reduced PD-1 and elevated Tim-3 and Lag-3 inhibitory receptor proteins, relative to their TCR₁₀₄₅ counterparts. A higher proportion of intratumoral Fas-4-1BB_{tm} IFP⁺ T cells retained CD62L expression, a protein associated with a central memory phenotype, compared with TCR₁₀₄₅ T cells in the same mouse (figure 3B,C). After

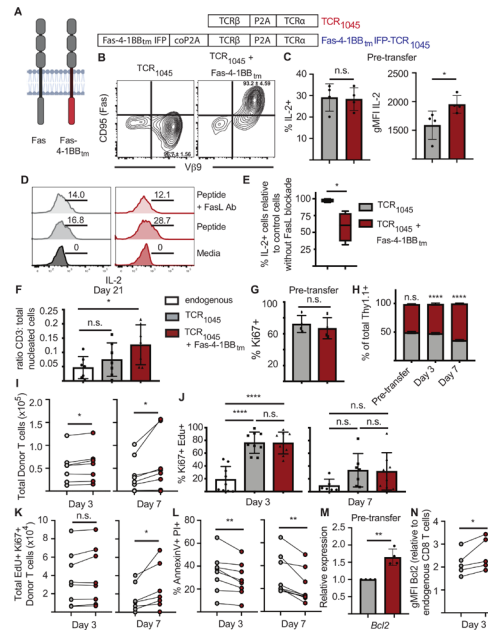


Figure 2 Expression of a Fas-IFP enhances accumulation of CD8 T cells in vivo (A) Schematic of monomeric endogenous Fas receptor, a Fas-4-1BB_{tm} immunomodulatory fusion protein, and vectors encoding TCR₁₀₄₅ or TCR₁₀₄₅ and a Fas-4-1BB_{tm} immunomodulatory fusion protein (IFP). Genes are separated by P2A or codon-optimized (co) P2A elements to ensure equimolar expression. (B) CD95 (Fas) and Vβ9 expression on transduced P14 Thy1.1⁺ CD8 T cells. T cells were transduced with retroviral vectors containing TCR₁₀₄₅ or TCR₁₀₄₅ and Fas-4-1BB_{tm} IFP and re-stimulated with irradiated splenocytes pulsed with Msln₄₀₆₋₄₁₄ in the presence of IL-2. Cells were screened by flow cytometry 7 days after restimulation. Data representative of >5 independent experiments. Quadrant values indicate mean and SD from five independent experiments. (C) Intracellular cytokine staining for IL-2 production by P14 Thy1.1⁺ CD8 T cells expressing either TCR₁₀₄₅ (gray) or TCR₁₀₄₅ and Fas-4-1BB_{tm} IFP (red) after 5-hour stimulation with Msln₄₀₆₋₄₁₄ peptide presented as a percent of engineered T cells (left panel) and as geometric mean fluorescence intensity (gMFI, right panel). Cumulative data from three independent experiments (1–3 technical replicates per experiment). Unpaired t-test, **p=0.0040. n.s.=not significant. (D, E) In vitro intracellular cytokine staining for IL-2 production by P14 Thy1.1⁺ TCR₁₀₄₅ (gray) or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP (red) CD8 T cells, with or without FasL blockade (clone: Kay10), after 5 hour stimulation with Msln₄₀₆₋₄₁₄ peptide. (D) Representative flow cytometry plots from one experiment. The average percentage of IL-2⁺ cells is displayed for each condition (samples run in triplicate). (E) Data are displayed as a percent difference between cells treated with FasL blocking Ab (clone: Kay10) compared with cells treated with isotype control Ab. Cumulative data from four independent experiments. Paired t-test. *P<0.05. (F) Immunohistochemistry (IHC) staining for CD3⁺ T cells in ID8_{VEGF} tumors 21 days after T cell transfer. P14 Thy1.1⁺ CD8 T cells expressing TCR₁₀₄₅ or TCR₁₀₄₅ and Fas-4-1BB_{tm} IFP were injected i.p. into ID8_{VEGF} tumor-bearing mice. Mice were pre-treated with 180 mg/kg cyclophosphamide >6 hours prior to cell transfer. All mice received 1 × 10⁷ engineered T cells, 5 × 10⁷ irradiated splenocytes pulsed with Msln₄₀₆₋₄₁₄ peptide, and daily IL-2 s.c. for 10 days (1 × 10⁴ IU). CD3 staining in untreated mice (white bar) included as a reference for endogenous T cell infiltration. Cumulative data from three independent experiments, n=7 per group. One-way ANOVA Tukey's multiple comparisons test, *p=0.0442. n.s.=not significant (G) Intracellular flow cytometry staining for Ki67 expression in Thy1.1⁺ CD8⁺ Vβ9⁺ T cells 7 days after in vitro restimulation of engineered T cells. Data from four independent experiments. Unpaired t-test. (H–N) Thy1.1⁺ or Thy1.1/1.2⁺ P14 T cells expressing TCR₁₀₄₅ (gray) or TCR₁₀₄₅ and Fas-4-1BB_{tm} IFP (red) were co-transferred at a 1:1 ratio into ID8_{VEGF} tumor-bearing mice with 5 × 10⁷ irradiated splenocytes pulsed with Msln₄₀₆₋₄₁₄ peptide, and daily s.c. IL-2 (1 × 10⁴ IU), at 3 or 7 days after co-transfer, T cells were isolated from tumors, enumerated and evaluated by flow cytometry for indicated markers. (H) Proportion of donor T cells within ID8_{VEGF} tumors after co-transfer. Data pooled from three independent experiments, n=8 (day 3) or n=7 (day 7) mice per group. Two-way ANOVA for multiple comparisons. n.s. (TCR₁₀₄₅ from pre-transfer to D3 and TCR₁₀₄₅/Fas-4-1BB_{tm} IFP pre-transfer to D3). ****p<0.0001 (TCR₁₀₄₅ from D3 to D7 and TCR₁₀₄₅/Fas-4-1BB_{tm} IFP from D3 to D7). (I) Quantification of intratumoral donor T cells. Counts of the cotransferred T cell populations from each individual mouse are connected with a line. Paired t-test. *P<0.05. (J) Flow cytometry staining of intratumoral endogenous and donor T cells three or seven days after transfer for Ki67 expression and EdU incorporation. EdU was injected i.p. into mice 24 hours prior to T cell isolation. 1-way ANOVA for multiple comparisons. ****p<0.0001. n.s.=not significant. (K) Quantification of EdU⁺ Ki67⁺ intratumoral donor T cells. Counts of the cotransferred cell populations from each individual mouse are connected with a line. Paired t-test. *P<0.05. (L) Flow cytometry staining of intratumoral donor T cells three or seven days after transfer for Annexin V and Propidium Iodide (PI). Cell populations from the same mouse are connected with a line. Data from three independent experiments, n=8 (day 3) or n=9 (day 7). Paired t-test. **P<0.01. (M) qPCR for *Bcl2* expression in TCR₁₀₄₅ (gray) or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP (red) T cells 8 days after restimulation in vitro. Data pooled from four independent experiments. Unpaired t-test **p=0.0016. (N) Flow cytometry staining of intratumoral engineered T cells 3 days after transfer for intracellular Bcl2. Data are displayed relative to expression in endogenous CD8 T cells from the spleen of the same mouse. Cell populations from the same mouse are connected with a line. Data from three independent experiments, n=5. Paired t-test. *P=0.0376. All error bars represent SD. ANOVA, analysis of variance.

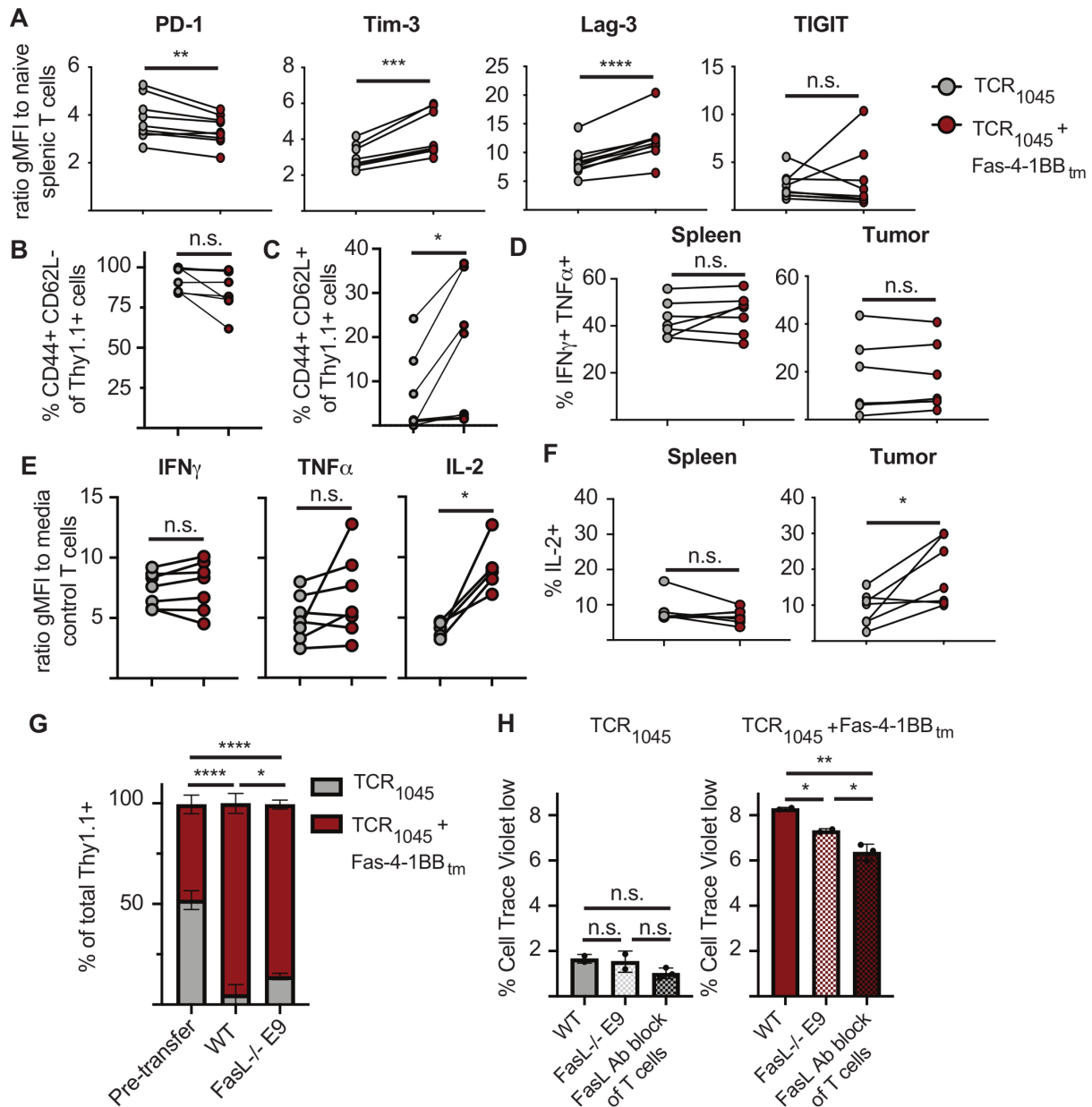


Figure 3 Fas-IFP-expressing T cells remain susceptible to T cell dysfunction in vivo Thy1.1⁺ or Thy1.1/1.2⁺ P14 T cells expressing TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP were co-transferred at a 1:1 ratio i.p. into ID8_{VEGF} tumor-bearing mice with 5 × 10⁷ irradiated splenocytes pulsed with Msln₄₀₆₋₄₁₄ peptide, and daily s.c. IL-2. In (E) cells were co-transferred into ID8_{VEGF} wild type or FasL^{-/-} E9 tumors. (A) at 21 days after co-transfer, T cells were isolated from tumors and evaluated by flow cytometry for expression of PD-1, Tim-3, Lag-3, and TIGIT. TCR₁₀₄₅ T cells (gray) and TCR₁₀₄₅/Fas-4-1BB_{tm} IFP⁺ T cells (red) from the same mouse are connected with a line. Data are displayed as a ratio of the geometric mean fluorescence intensity (gMFI) of Thy1.1⁺ T cells compared with endogenous CD44⁻ CD62L⁺ naïve CD8 T cells from the spleen of the same mouse. Cumulative data from two independent experiments (n=7 mice). Paired t-test. **P=0.0064; ***p=0.0005; ****p<0.0001; n.s.=not significant. (B, C) Flow cytometry staining of Thy1.1⁺ or Thy1.1/1.2⁺ donor P14 T cells for CD44 and CD62L. Data from experiments in A). Paired t-test. *P<0.05. (D, F) Ex vivo intracellular cytokine staining for IFN- γ and TNF- α or IL-2 production by P14 Thy1.1⁺ TCR₁₀₄₅ (gray) or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP (red) CD8 T cells isolated from spleen or tumor, after 5 hour stimulation with Msln₄₀₆₋₄₁₄ peptide. Cumulative data from two independent experiments (n=7 mice). Paired t-test. *P<0.05 (G) Proportion of donor T cells within ID8_{VEGF} wild type or FasL^{-/-} E9 tumors 7 days after co-transfer. Data pooled from three independent experiments, n=3 (WT) or n=3 (E9) mice per group. Two-way ANOVA for multiple comparisons. ****p<0.0001 (TCR₁₀₄₅ T cells pre-transfer vs WT and TCR₁₀₄₅/Fas-4-1BB_{tm} IFP T cells pre-transfer vs WT). *P<0.0474 (TCR₁₀₄₅ T cells, WT vs E9), *p<0.0345 (TCR₁₀₄₅/Fas-4-1BB_{tm} IFP T cells, WT vs E9). (H) In vitro Cell Trace Violet (CTV) proliferation assay of T cells after co-culture with wild type or FasL^{-/-} E9 ID8_{VEGF} tumor cells. Tumor cells were irradiated, pulsed with Msln₄₀₆₋₄₁₄ peptide, and plated for >4 hours before adding T cells. In some conditions, T cells were pre-treated with anti-FasL blocking antibody (clone: Kay10). T cells were added at a 5:1 T cell to tumor cell ratio. Cells were co-cultured for 7 days, then stained for flow cytometry. The percent of live Thy1.1⁺ V β 9⁺ T cells with reduced CTV staining compared with control CTV⁺ T cells cultured without tumor cells is shown. Cumulative data from two independent experiments. 1-way ANOVA for multiple comparisons. *P<0.04, **p=0.0035. ANOVA, analysis of variance.

isolation from tumor vs spleen, a lower fraction of engineered T cells from the tumor produced the effector cytokines interferon- γ (IFN γ) and tumor necrosis factor- α (TNF α) when stimulated with MSLN₄₀₆₋₄₁₄ peptide ex vivo (figure 3D), consistent with previously reported declining function in the TME.¹⁰ The IFP apparently does not sustain effector function in the TME as no differences were detected between TCR₁₀₄₅ and TCR₁₀₄₅/Fas-4-1BB_{tm} T cells in the fraction of cells producing these effector cytokines (figure 3D) or on a per-cell basis (figure 3E). However, the larger number of cytokine-producing IFP⁺ cells in the TME does suggest overall enhanced effector activity in IFP⁺ T cell-treated tumors. Similar to in vitro (figure 2C), a higher percentage and total number of TCR₁₀₄₅/Fas-4-1BB_{tm} vs TCR₁₀₄₅ intratumoral T cells produced IL-2 (figure 3E,F). As 4-1BB signaling induces IL-2 production by T cells,^{24 25} these data are consistent with TME-delivered FasL signals promoting sustained 4-1BB co-stimulation, thereby supporting T cell survival and proliferation. However, the data also suggest that IFP⁺ T cells are not rendered resistant to TME-mediated inhibitory signals.

FasL signal from tumor epithelium contributes to, but is not required for, preferential accumulation of TCR₁₀₄₅/Fas-4-1BB_{tm} T cells in the TME

To determine if tumorous FasL expression is required for preferential accumulation of TCR₁₀₄₅/Fas-4-1BB_{tm} T cells, we generated tumor-bearing mice with wild type ID8_{VEGF} or E9 ID8_{VEGF}^{FasL^{-/-}} cells and co-transferred P14 T cells expressing TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm}. Seven days later, TCR₁₀₄₅/Fas-4-1BB_{tm} T cells preferentially accumulated in both tumors, but the enrichment of TCR₁₀₄₅/Fas-4-1BB_{tm} T cells was lower in ID8_{VEGF}^{FasL^{-/-}} tumors (figure 3G). These data suggest that FasL signaling from the tumor epithelium promotes, but is not essential for, IFP⁺ T cell persistence. To evaluate if the enhanced proliferation of TCR₁₀₄₅/Fas-4-1BB_{tm} T cells is due to FasL signaling from tumor cells and/or T cells, T cells were treated with Cell Trace Violet and co-cultured with wild type or E9 ID8_{VEGF}^{FasL^{-/-}} tumor cells for 7 days. In some conditions, T cells were pre-treated with FasL blocking Ab. ID8_{VEGF} tumor cells as stimulators induce only modest T cell proliferation. Blocking FasL from tumor cells by genetic knockout (ID8_{VEGF}^{FasL^{-/-}}) or from fellow T cells by antibody blockade did not significantly impact proliferation of TCR₁₀₄₅ T cells. However, knockout of FasL from the tumor cells reduced proliferation by IFP⁺ T cells and this was further reduced when FasL was also blocked on T cells (figure 3H). Together, this data suggests that the tumor epithelium and neighboring T cells both provide FasL signals that support IFP⁺ T cell proliferation, persistence and cytokine production.

Adoptive immunotherapy with TCR₁₀₄₅/Fas-4-1BB_{tm} T cells significantly prolongs survival of ovarian tumor-bearing mice

Evaluating whether TCR₁₀₄₅/Fas-4-1BB_{tm} T cells control progressive ovarian cancer more effectively than TCR₁₀₄₅

T cells, we used an established treatment protocol that previously revealed TCR₁₀₄₅ T cells prolong survival of ID8_{VEGF} tumor-bearing mice.¹⁰ Briefly, ID8_{VEGF} tumor-bearing mice were treated with a single dose of cyclophosphamide ≥ 6 hours prior to T cell transfer, and then received 1×10^7 engineered T cells and 5×10^7 irradiated splenocytes pulsed with MSLN₄₀₄₋₄₁₆ peptide every 14 days (lymphodepletion occurred only before the first T cell transfer). Mice received 10^4 U IL-2 daily for 10 days after each T cell transfer to promote T cell expansion and persistence. Mice treated with TCR₁₀₄₅/Fas-4-1BB_{tm} T cells had a significantly longer median survival (123 days) relative to control mice (77 days) or mice treated with TCR₁₀₄₅ T cells (102 days) (figure 4A).

Since MSLN is expressed on the lining of the pleural and pericardial cavities, we evaluated if IFP expression enhanced T cell accumulation/activity in the lungs. At euthanasia we evaluated CD8 T cell infiltration by IHC staining, and the proportions of intralung CD8 T cells were not statistically different between treatment groups (figure 4B), suggesting no selective accumulation of engineered T cells in lung tissues.

To assess inflammation, a pathologist evaluated H&E-stained lung and heart sections from treated and untreated mice for metastatic tumor growth and neutrophil infiltration. No treatment-related myocarditis or cardiac lesions were observed. We detected metastatic tumor growth in lungs from 2/7 untreated mice, 9/9 TCR₁₀₄₅ T cell-treated mice, and 7/12 TCR₁₀₄₅/Fas-4-1BB_{tm} T cell-treated mice, with longest surviving mice harboring the greatest number of metastatic lung nodules (excluding samples with poor fixation or staining from the analysis). The increased metastasis in treated mice may reflect the prolonged survival, with longer time for metastatic lesion development. No inflammation was observed in lungs of mice without metastatic lesions, suggesting the absence of T cell activation by normal tissues. Mice with metastatic intra-lung tumor growth were scored to determine if the presence of lung metastases increased inflammation after T cell treatment. Mild to moderate inflammation, defined as lymphoplasmacytic and neutrophilic perivascularitis, was observed in the lungs of some treated mice (figure 4C) and was scored slightly higher in treated compared with untreated mice, but this did not reach statistical significance. No mice showed signs of respiratory distress during the experimental course.

Moreover, antigen-loss immune escape was not clearly driven by TCR₁₀₄₅/Fas-4-1BB_{tm} T cells. IHC showed that MSLN expression was still present in the tumors of treated as well as untreated mice (figure 4D), consistent with the sustained upregulation of exhaustion markers we observed on tumor-infiltrating T cells (figure 3A).

A human Fas-4-1BB IFP improves primary T cell killing of ovarian cancer

To evaluate if a Fas-4-1BB IFP might improve activity against human ovarian cancer, three unique donors were transduced to express a human TCR specific for MSLN

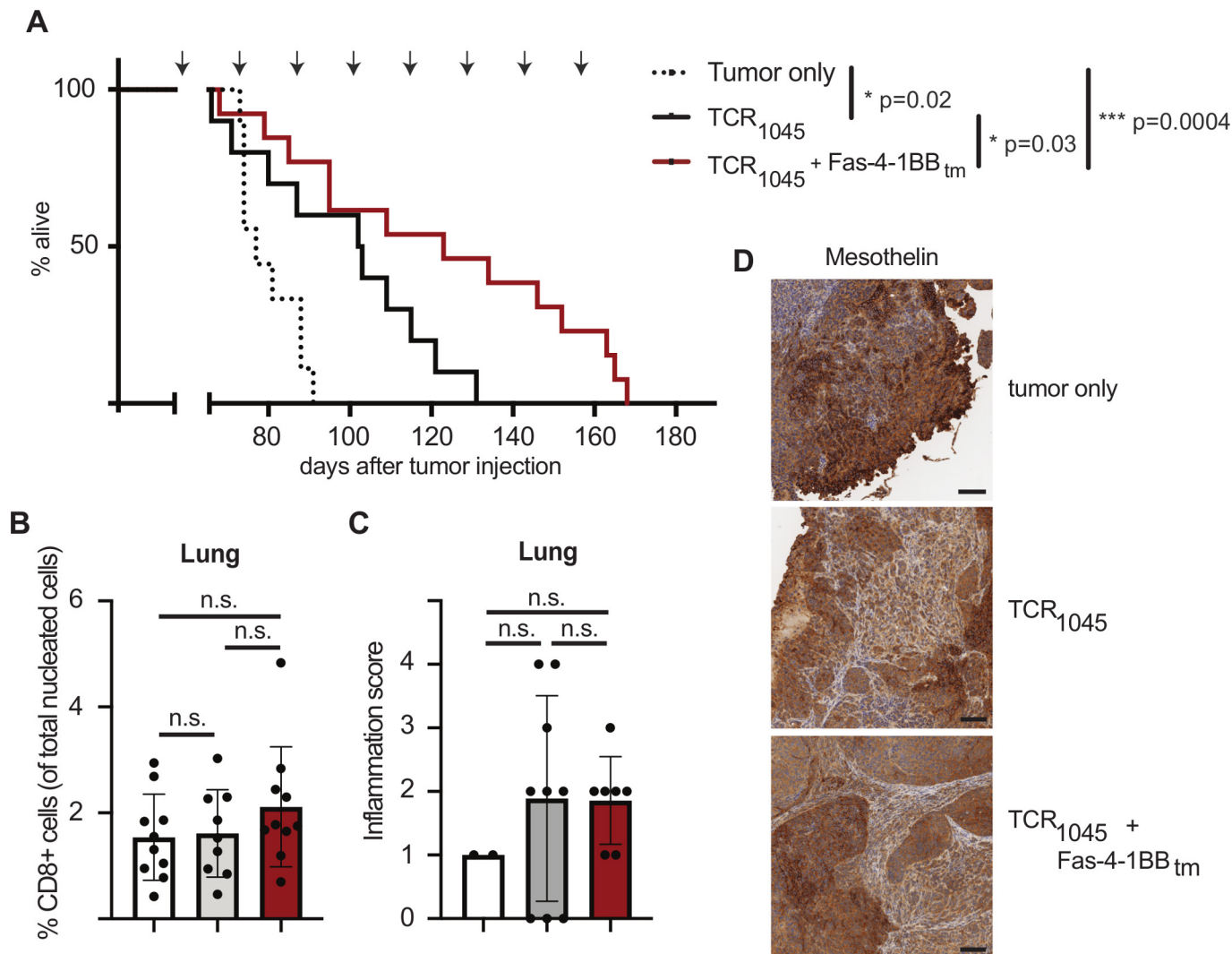


Figure 4 A Fas-IFP enhances antitumor efficacy in vivo (A) Overall survival of ID8_{VEGF} tumor-bearing mice treated with repeated doses of P14 Thy1.1⁺ CD8 T cells transduced with TCR₁₀₄₅ or TCR₁₀₄₅ and Fas-4-1BB_{tm} IFP. Tumor-bearing mice received a single dose of cyclophosphamide (180 mg/kg) before the first T cell infusion followed by injections of 1×10^7 TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm} T cells and peptide-pulsed irradiated splenocytes (5:1 APC:T cell ratio) i.p. every 14 days with 1×10^4 U IL-2 s.c. for 10 days after each infusion. Treatment was initiated 45–52 days after tumor injection, when tumors were detectable by US. Arrows above survival curve indicate the timing of T cell infusions. Survival data are aggregated from three independent experiments, n=9–13 total per group. Log-rank (Mantel-Cox) test. (B) IHC quantification of CD8 + T cells in lungs of untreated (white), TCR₁₀₄₅ (gray) or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP (red) treated mice at necropsy. (C) Histology scoring of hematoxylin and eosin IHC stained lungs from untreated (white), TCR₁₀₄₅ (gray) or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP (red) treated mice at necropsy. All lungs contained metastatic tumor. Scoring ranged from 0 (tissue within normal limits), to 4 (neutrophilic interstitial pneumonia with or without lymphoplasmacytic and neutrophilic perivascularitis) and was performed by a trained pathologist. (B, C) Cumulative data from three independent experiments, n=9–10 per group, except the untreated mice in (C), for which only 2 mice had metastatic tumors in the lungs. One-way ANOVA with multiple comparisons. All error bars represent SD (D) Immunohistochemistry (IHC) staining for MSLN in tumors of untreated, TCR₁₀₄₅ or TCR₁₀₄₅/Fas-4-1BB_{tm} IFP treated mice at necropsy. Scale bar=100 μm. Images are representative of 9–10 mice per group from three independent experiments. ANOVA, analysis of variance; IFP, immunomodulatory fusion protein; MSLN, Mesothelin; n.s., not significant.

peptide 530–538 (TCR₅₃₀) with or without a truncated Fas or a Fas-4-1BB IFP. Primary human T cells were transduced with either a bi-cistronic vector containing the alpha and beta chains of TCR₅₃₀, a tri-cistronic vector containing TCR₅₃₀ and a truncated Fas (FasTr), or a tri-cistronic vector containing TCR₅₃₀ and a Fas-4-1BB fusion protein with the transmembrane domain from Fas (Fas_{tm}-4-1BB). T cells were transduced and restimulated twice with irradiated feeder cells and anti-CD3 antibody and

then evaluated for tetramer binding and expression of Fas (figure 5A). TCR₅₃₀ expression varied between donors but was similar between all constructs within each donor (figure 5B). Fas expression was not statistically different between the TCR₅₃₀/FasTr and TCR₅₃₀/Fas_{tm}-4-1BB constructs, but the truncated Fas trended toward the highest expression (figure 5C).

We previously reported that T cells expressing both TCR₅₃₀ and a Fas-4-1BB IFP produce more IFN γ than

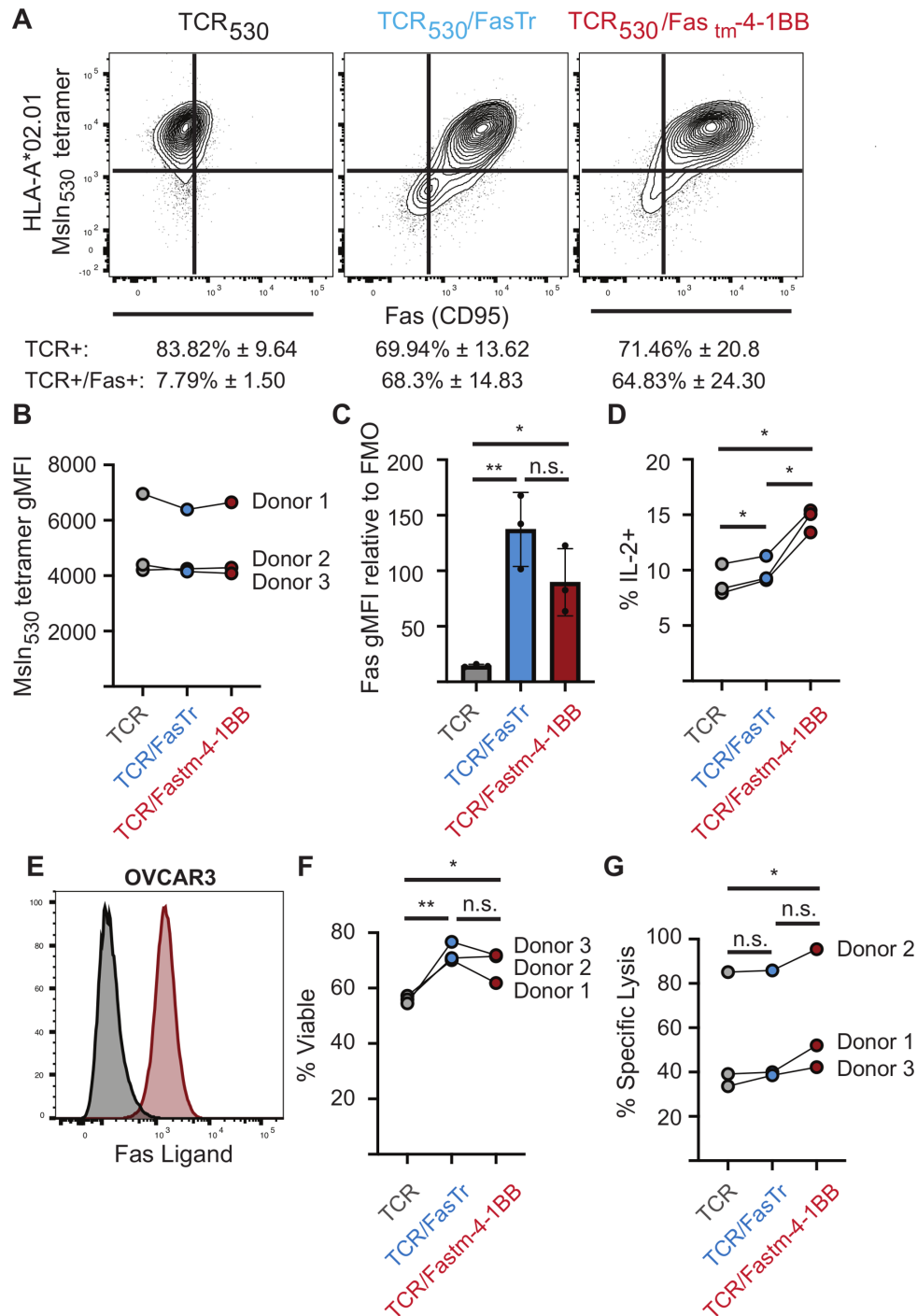


Figure 5 A human Fas-IFP enhances ovarian tumor cell killing Three unique donors were transduced to express an MSLN-specific TCR (TCR₅₃₀, gray), TCR₅₃₀ and a truncated Fas (TCR₅₃₀/FasTr, blue) and TCR₅₃₀ and a Fas_{tm}-4-1BB IFP (TCR₅₃₀/Fas_{tm}-4-1BB, red). (A) Flow cytometry staining for HLA-A*02.01 Msln₅₃₀₋₅₃₈ tetramer binding and Fas expression. Representative flow plots from one donor after two restimulations are shown. The average transduction efficiency and SD of each construct for three unique donors are listed below. (B) Geometric MFI of HLA-A*02.01 Msln₅₃₀₋₅₃₈ tetramer staining for all donors. Results from each unique donor are connected with a line. (C) Geometric MFI of Fas expression relative to the fluorescence minus one (FMO) control for all donors. Analyzed with one-way ANOVA with multiple comparisons. *P=0.0283, **p=0.0028. (D) In vitro intracellular cytokine staining for IL-2 production after 5-hour stimulation with Msln₅₃₀₋₅₃₈ peptide. Results from each unique donor are connected with a line. Analyzed with repeated measures one-way ANOVA for multiple comparisons. *P<0.04. (E) Flow cytometry staining for FasL on OVCAR3 tumor cells. The gray histogram represents unstained tumor cells. Representative histogram from three independent experiments. (F) Viability staining of T cells after 3 days of coculture with OVCAR3 tumor cells. Results from each unique donor are connected with a line. Analyzed with repeated measures one-way ANOVA for multiple comparisons. *p=0.0198, **p=0.0052 (G) Specific lysis of OVCAR3 cells after 155 hours of coculture with transduced T cells. Results from each unique donor are connected with a line. Analyzed with repeated measures one-way ANOVA for multiple comparisons. *P=0.025. ANOVA, analysis of variance; IFP, immunomodulatory fusion protein; ns, not significant.

their TCR₅₃₀ and TCR₅₃₀/FasTr counterparts.¹³ To determine if the 4-1BB co-stimulatory domain could promote increased IL-2 production, as observed in murine T cells (figure 2C), T cells were stimulated for 5 hours with Msln₅₃₀ peptide. Significantly more TCR₅₃₀/Fas_{tm}-4-1BB T cells produced IL-2 than TCR₅₃₀ and TCR₅₃₀/FasTr T cells (figure 5D), despite slightly lower expression of the fusion protein (figure 5A,C), suggesting co-stimulatory signaling from the 4-1BB component of the IFP supports enhanced cytokine production.

To determine if the FasTr and Fas-IFP constructs reduce FasL-induced T cell death, T cells were co-cultured for 3 days with human ovarian cancer cells (OVCAR3) which express FasL (figure 5E). The co-culture period was limited to 72 hours to allow for analysis of the disruption of the death signal through dominant negative mechanisms by truncated Fas or the IFP while limiting the contribution to survival from the co-stimulatory/survival signals from the 4-1BB domain. T cells expressing FasTr or a Fas-4-1BB IFP exhibited greater viability than their TCR₅₃₀ counterparts (figure 5F), suggesting that during this brief 3-day period of co-culture both the FasTr and IFP can similarly interfere with death from endogenous Fas signaling.

To determine if FasTr or Fas-IFP T cells can lyse human ovarian cancer cells better than TCR₅₃₀ T cells, T cells expressing an irrelevant TCR or T cells expressing TCR₅₃₀ with or without FasTr or a Fas-4-1BB IFP were co-cultured with OVCAR3 tumor cells 155 hours. OVCAR3 cells were allowed to adhere to E-plates overnight, T cells added, and tumor cell lysis was quantified by cellular impedance (xCELLigence, Agilent). T cells expressing TCR₅₃₀ and the Fas_{tm}-4-1BB IFP resulted in greater OVCAR3 lysis than TCR₅₃₀ or TCR₅₃₀/FasTr T cells (figure 5G). TCR₅₃₀/FasTr T cells did not kill OVCAR3 tumor cells more than control TCR₅₃₀ T cells, suggesting co-stimulation from the IFP is necessary for the improved cytolytic capability of TCR₅₃₀/Fas-4-1BB_{tm} T cells. These results are consistent with our previous finding that the Fas-4-1BB IFP, but not the decoy Fas receptor, enhances T cell lytic ability.¹³

DISCUSSION

FasL/Fas signaling can mediate T cell death, including activation-induced cell death, an apoptotic mechanism that regulates T cell expansion during repeated stimulation. Tumor cells often upregulate FasL, which may protect from tumor-infiltrating lymphocytes and other inflammatory cell types. The immune-competent ID8_{VEGF} model of ovarian cancer naturally expresses FasL,² providing an opportunity to interrogate strategies for overcoming this immune-evasion mechanism. We previously demonstrated that TCR₁₀₄₅ T cells could prolong survival of ID8_{VEGF} tumor-bearing mice harboring late-stage disease,¹⁰ but that all mice eventually succumb to disease, due at least

in part to immune-suppressive mechanisms operative in the TME. CRISPR/Cas9 knock-in genetic modification of T cells with a pooled library demonstrated that a synthetic Fas-4-1BB fusion protein improved T cell fitness during in vitro expansion,²⁶ and we previously demonstrated that T cells expressing a Fas-4-1BB fusion protein improved tumor cell killing in vitro and in vivo.¹³ Following transfer into ID8_{VEGF} tumor-bearing mice, we have now shown that T cells engineered to express both TCR₁₀₄₅ and a Fas-4-1BB IFP persist better in the ovarian TME than T cells modified with only TCR₁₀₄₅, and significantly further prolong host survival. We have also demonstrated that human T cells expressing a Fas-4-1BB fusion protein exhibit enhanced proliferation,¹³ cytokine production, and specific lysis of ovarian tumor cells in vitro. Thus, engineering strategies that address immune-suppressive features of solid tumors have the potential to significantly improve therapeutic benefit for patients.

FasL expression in solid tumors is heterogenous, and high expression may simultaneously support metastatic spread¹⁷ and immune evasion.¹⁸ Fas-4-1BB IFP⁺ T cells preferentially accumulated relative to IFP⁻ T cells even in E9 ID8_{VEGF}^{FasL^{-/-}} tumors, indicating that FasL expression by tumor epithelium is not required for the improved persistence of IFP⁺ T cells in situ. Since effector T cells also express FasL, the addition of a Fas-4-1BB IFP may improve therapeutic efficacy even in patients with tumors expressing low FasL levels. However, therapeutic efficacy may be greatest in tumors with high FasL expression as tumor-cell FasL expression enhanced T cell proliferation in vitro and accumulation of IFP⁺ T cells in vivo.

We previously demonstrated that IFP⁺ T cells produced more IFN γ , TNF α and IL-2 than control T cells in vitro.¹³ However, cells isolated from tumor-bearing mice and stimulated ex vivo produced similar levels of IFN γ and TNF α when isolated from tumor. Since the IFP⁺ T cells do produce more IL-2 ex vivo, have an increased frequency of cells with central memory characteristics (CD62L expression, low PD-1) and preferentially persist in tumors, these results suggest the improved tumor control observed in tumor-bearing mice may be largely due to increased persistence of tumor-specific T cells with enhanced proliferative capacity rather than enhanced cytolytic function of individual cells. These results are consistent with findings in mouse models and patients, in which T cells with a progenitor exhausted phenotype have improved persistence, proliferation and response to checkpoint blockade and correlate with improved tumor control.^{14 27-29} Thus, engineering approaches such as introducing IFPs that promote increased persistence and differentiation potential of adoptively transferred tumor-specific T cells should offer an opportunity to improve the therapeutic efficacy of cellular therapies.

Our co-transfer studies revealed that TCR₁₀₄₅/IFP⁺ T cells expressed lower levels of PD-1 but higher levels of Tim-3 and Lag-3 compared with TCR₁₀₄₅ T cells within the same TME, an unexpected finding given that inhibitory receptors are expressed in response to TCR signaling. Since expression of these molecules is regulated by distinct transcription factors, and we previously demonstrated that signaling through the IFP modulates transcription factor expression,¹³ IFP signaling may establish distinct transcription factor profiles in the two T cell populations, accounting for these differences. Ongoing single cell transcriptomic and epigenetic studies comparing TCR₁₀₄₅ and TCR₁₀₄₅/IFP⁺ T cells may reveal further insights into the regulation of these receptors.

The Fas-4-1BB IFP utilizes a decoy Fas receptor to provide co-stimulatory signals, which are often limited in solid tumors. Cell-intrinsic engineering strategies using a truncated Fas receptor can successfully disrupt death-receptor signaling and improve the efficacy of T cell therapy in a mouse melanoma model,¹⁹ but such dominant-negative Fas molecules still lack co-stimulatory signals that may be critical for T cell persistence in some TMEs. 4-1BB agonists, soluble 4-1BB ligand and other agents that provide systemic co-stimulation can promote anti-tumor immunity but are not cell intrinsic and can also trigger inflammation.³⁰ The Fas-4-1BB IFP selectively targets co-stimulation to tumor-specific T cells, resulting in intratumoral T cells expressing more anti-apoptotic molecules and IL-2, together promoting T cell survival/proliferation and antitumor efficacy. As FasL is highly expressed in many solid tumors,¹⁹ and associated with poor prognosis,¹¹ Fas-4-1BB IFPs may provide an opportunity to enhance engineered adoptive T cell therapy against many malignancies.

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REFERENCES

- Lheureux S, Karakasis K, Kohn EC, *et al*. Ovarian cancer treatment: the end of empiricism? *Cancer* 2015;121:3203–11.
- Vaughan S, Coward JI, Bast RC, *et al*. Rethinking ovarian cancer: recommendations for improving outcomes. *Nat Rev Cancer* 2011;11:719–25.
- Gubbels JAA, Belisle J, Onda M, *et al*. Mesothelin-MUC16 binding is a high affinity, N-glycan dependent interaction that facilitates peritoneal metastasis of ovarian tumors. *Mol Cancer* 2006;5:50.
- Chang K, Pastan I. Molecular cloning of mesothelin, a differentiation antigen present on mesothelium, mesotheliomas, and ovarian cancers. *Proc Natl Acad Sci U S A* 1996;93:136–40.
- Chang K, Pastan I, Willingham MC. Isolation and characterization of a monoclonal antibody, K1, reactive with ovarian cancers and normal mesothelium. *Int J Cancer* 1992;50:373–81.
- Cheever MA, Allison JP, Ferris AS, *et al*. The prioritization of cancer antigens: a national cancer Institute pilot project for the acceleration of translational research. *Clin Cancer Res* 2009;15:5323–37.
- Hassan R, Thomas A, Alewine C, *et al*. Mesothelin immunotherapy for cancer: ready for prime time? *J Clin Oncol* 2016;34:4171–9.
- Le DT, Wang-Gillam A, Picozzi V, *et al*. Safety and survival with GVAX pancreas prime and Listeria Monocytogenes-expressing mesothelin (CRS-207) boost vaccines for metastatic pancreatic cancer. *J Clin Oncol* 2015;33:1325–33.
- Beatty GL, Haas AR, Maus MV, *et al*. Mesothelin-specific chimeric antigen receptor mRNA-engineered T cells induce anti-tumor activity in solid malignancies. *Cancer Immunol Res* 2014;2:112–20.
- Anderson KG, Voillet V, Bates BM, *et al*. Engineered adoptive T-cell therapy prolongs survival in a preclinical model of advanced-stage ovarian cancer. *Cancer Immunol Res* 2019;7:1412–25.
- Peter ME, Hadji A, Murmann AE, *et al*. The role of CD95 and CD95 ligand in cancer. *Cell Death Differ* 2015;22:549–59.
- Motz GT, Santoro SP, Wang L-P, *et al*. Tumor endothelium FasL establishes a selective immune barrier promoting tolerance in tumors. *Nat Med* 2014;20:607–15.
- Oda SK, Anderson KG, Ravikummar P, *et al*. A Fas-4-1BB fusion protein converts a death to a pro-survival signal and enhances T cell therapy. *J Exp Med* 2020;217. doi:10.1084/jem.20191166. [Epub ahead of print: 07 12 2020].
- Miller BC, Sen DR, Al Abozy R, *et al*. Subsets of exhausted CD8⁺ T cells differentially mediate tumor control and respond to checkpoint blockade. *Nat Immunol* 2019;20:326–36.
- Janát-Amsbury MM, Yockman JW, Anderson ML, *et al*. Comparison of ID8 MOSE and VEGF-modified ID8 cell lines in an immunocompetent animal model for human ovarian cancer. *Anticancer Res* 2006;26:2785–9.



- 16 Stromnes IM, Schmitt TM, Hulbert A, *et al.* T cells engineered against a native antigen can Surmount immunologic and physical barriers to treat pancreatic ductal adenocarcinoma. *Cancer Cell* 2015;28:638–52.
- 17 Heath RM, Jayne DG, O'Leary R, *et al.* Tumour-Induced apoptosis in human mesothelial cells: a mechanism of peritoneal invasion by Fas Ligand/Fas interaction. *Br J Cancer* 2004;90:1437–42.
- 18 Chen L, Park S-M, Tumanov AV, *et al.* CD95 promotes tumour growth. *Nature* 2010;465:492–6.
- 19 Yamamoto TN, Lee P-H, Vodnala SK, *et al.* T cells genetically engineered to overcome death signaling enhance adoptive cancer immunotherapy. *J Clin Invest* 2019;129:1551–65.
- 20 Strasser A, Jost PJ, Nagata S. The many roles of Fas receptor signaling in the immune system. *Immunity* 2009;30:180–92.
- 21 Kági D, Vignaux F, Ledermann B, *et al.* Fas and perforin pathways as major mechanisms of T cell-mediated cytotoxicity. *Science* 1994;265:528–30.
- 22 Snell LM, Lin GHY, McPherson AJ, *et al.* T-cell intrinsic effects of GITR and 4-1BB during viral infection and cancer immunotherapy. *Immunol Rev* 2011;244:197–217.
- 23 Lee H-W, Park S-J, Choi BK, *et al.* 4-1BB promotes the survival of CD8+ T lymphocytes by increasing expression of Bcl-xL and Bfl-1. *J Immunol* 2002;169:4882–8.
- 24 Saoulli K, Lee SY, Cannons JL, *et al.* CD28-independent, TRAF2-dependent costimulation of resting T cells by 4-1BB ligand. *J Exp Med* 1998;187:1849–62.
- 25 Oh HS, Choi BK, Kim YH, *et al.* 4-1BB signaling enhances primary and secondary population expansion of CD8+ T cells by maximizing autocrine IL-2/IL-2 receptor signaling. *PLoS One* 2015;10:e0126765.
- 26 Roth TL, Li PJ, Blaeschke F, *et al.* Pooled knockin targeting for genome engineering of cellular immunotherapies. *Cell* 2020;181:728–44. e21.
- 27 Chan JD, Lai J, Slaney CY, *et al.* Cellular networks controlling T cell persistence in adoptive cell therapy. *Nat Rev Immunol* 2021;21:769–84.
- 28 Siddiqui I, Schaeuble K, Chennupati V, *et al.* Intratumoral Tcf1⁺PD-1⁺CD8⁺ T Cells with Stem-like Properties Promote Tumor Control in Response to Vaccination and Checkpoint Blockade Immunotherapy. *Immunity* 2019;50:195–211. e10.
- 29 Sade-Feldman M, Yizhak K, Bjorgaard SL, *et al.* Defining T cell states associated with response to checkpoint immunotherapy in melanoma. *Cell* 2018;175:998–1013. e20.
- 30 Bartkowiak T, Curran MA. 4-1BB agonists: multi-potent potentiators of tumor immunity. *Front Oncol* 2015;5:117.