Membrane-Proximal Epitope Facilitates Efficient T Cell Synapse Formation by Anti-FcRH5/CD3 and Is a Requirement for Myeloma Cell Killing

Highlights

- Prevalence of FcRH5 expression in multiple myeloma is 100%
- Anti-FcRH5/CD3 TDB redirects T cells to kill myeloma cells
- Target clustering and CD45 exclusion activate T cells
- Anti-FcRH5/CD3 TDB is a highly efficacious immunotherapy for myeloma

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In Brief

Li et al. report that the size and epitope location of the target play a key role in the efficiency of T cell activation induced by T cell-dependent bispecific antibodies (TDBs). They develop a TDB targeting FcRH5 expressed in all multiple myeloma tumor cells and show its potential in treating this disease.
Membrane-Proximal Epitope Facilitates Efficient T Cell Synapse Formation by Anti-FcRH5/CD3 and Is a Requirement for Myeloma Cell Killing

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SUMMARY

The anti-FcRH5/CD3 T cell-dependent bispecific antibody (TDB) targets the B cell lineage marker FcRH5 expressed in multiple myeloma (MM) tumor cells. We demonstrate that TDBs trigger T cell receptor activation by inducing target clustering and exclusion of CD45 phosphatase from the synapse. The dimensions of the target molecule play a key role in the efficiency of the synapse formation. The anti-FcRH5/CD3 TDB kills human plasma cells and patient-derived myeloma cells at picomolar concentrations and results in complete depletion of B cells and bone marrow plasma cells in cynomolgus monkeys. These data demonstrate the potential for the anti-FcRH5/CD3 TDB, alone or in combination with inhibition of PD-1/PD-L1 signaling, in the treatment of MM and other B cell malignancies.

INTRODUCTION

Multiple myeloma (MM) is an incurable malignancy of plasma cells characterized by dysregulated growth of abnormal plasma cells in the bone marrow and overproduction of intact monoclonal immunoglobulins that ultimately lead to clinical manifestations including skeletal lesions, renal failure, anemia, and hypercalcemia. Currently the backbone of MM treatment involves combinations of proteasome inhibitors (PIs), immunomodulators, and corticosteroids, with bone marrow transplantation as an additional option for eligible patients. Newer agents are being developed for the treatment of MM, including the monoclonal antibodies targeting CD38 (daratumomab) and SLAMF7 (elotuzumab). Nevertheless, despite progressive improvements in myeloma treatment, the mortality rate remains high and median survival remains less than 5 years (http://seer.cancer.gov/).

Heterogeneous disease biology and genetics, limited availability of predictive preclinical models, and a paucity of known myeloma-specific surface targets remain key challenges in myeloma drug development. FcRH5 (also known as FcRL5, IRTA2, or CD307) has been identified as an attractive B cell lineage-specific surface marker in myeloma (Elkins et al., 2012; Hatzivassiliou et al., 2001; Poislon et al., 2006). High-affinity ligands and biological significance of FcRH5 are largely unknown. FcRH5 is expressed exclusively in the B cell lineage. Expression is detected as early as pre-B cells (Poislon et al., 2006); however, unlike other B cell-specific surface proteins (e.g., CD20, CD19, and CD22), FcRH5 expression is retained in plasma cells. Analogous to its expression in normal plasma cells, FcRH5 is expressed by myeloma tumor cells. Finally, FcRH5 expression has been reported in several B cell malignancies (Ise et al., 2007; Li et al., 2008; Poislon et al., 2006), suggesting broader applicability of this target in hematological malignancies.

Therapies that direct T cells to tumors, including adoptive transfer of genetically engineered T cells and T cell-dependent bispecific antibodies (TDBs) that selectively recruit T cells to tumor cells have been clinically validated in the treatment of B cell leukemias and lymphomas (Bargou et al., 2008; Sadelain, 2015)

Significance

Our study describes how CD3-bispecific antibody “triggers” intracellular T cell signaling and shows that the dimensions of the target molecule and epitope location play a key role in the efficiency of the synapse formation and subsequent T cell activation. These findings are important for future design of T cell-recruiting therapies. Using this information we developed and preclinically validated an anti-FcRH5/CD3 TDB as an immunotherapy for multiple myeloma. The anti-FcRH5/CD3 TDB is highly efficacious in the killing of myeloma cells and depletes bone marrow plasma cells in primates.
and have demonstrated promising activity in myeloma (Garfall et al., 2015; Rapoport et al., 2015). Our previous preclinical studies have validated full-length bispecific antibodies as an optimal TDB format with favorable drug-like properties including long serum half-life and low risk for anti-drug antibodies (Junttila et al., 2014; Sun et al., 2015).

TDBs activate T cells upon ligation with target-expressing cells resulting in potent target cell killing. However, the molecular mechanism that induces T cell activation has not been described in detail. The close proximity of cell membranes forms the basis of the kinetic segregation model for T cell receptor (TCR) triggering (Davis and van der Merwe, 2006). The model proposes that the exclusion of inhibitory molecules, such as CD45 phosphatase, from regions of close cell-cell apposition causes increased kinase activity and leads to phosphorylation of peptide-major histocompatibility complex (pMHC)-bound TCRs within this region. This then initiates receptor triggering and subsequent downstream T cell activation. Exclusion of CD45 from the synapse has been shown to be a passive process driven by the large size of the extracellular domain (James and Vale, 2012). If correct, the model predicts that a tumor target with a large extracellular domain may be suboptimal for synapse formation by CD3-bispecific antibodies. The size of the target protein has previously been linked to the killing activity of bispecific T cell engagers (BiTE) (Bluemel et al., 2010).

Given the potential of FcRH5 as a target for antibody-based therapeutics, the goal of the current study was to develop a TDB targeting FcRH5 (anti-FcRH5/CD3 TDB) for the treatment of MM. Moreover, we characterized the molecular events in the immunological synapse that lead to triggering of the TCR upon stimulation by CD3-bispecific antibodies.

RESULTS

Anti-FcRH5/CD3 TDB Induces Target Clustering and Exclusion of CD45 from the Synapse Resulting in TCR Triggering

We characterized the molecular events in the immunological synapse that lead to triggering of the TCR upon stimulation by CD3-bispecific antibodies. To do this, we utilized a recently described reconstituted system that allows investigation of the initial events that lead to receptor activation in a controlled manner. HEK-T cells are non-immune cells that express the minimal components of the TCR signaling network required to drive receptor activation (James and Vale, 2012). Previous studies using this model have demonstrated that exclusion of CD45 phosphatase from the cell-cell interphase is both necessary and sufficient for TCR-pMHC-driven TCR triggering, supporting the kinetic segregation model (James and Vale, 2012). The HEK-T cells were conjugated with FcRH5-expressing cells in the presence of the CD3 bispecific antibody, and the relative intensities of CD45, FcRH5, and the fluorescently labeled TDB at the conjugate interface were imaged by confocal microscopy. ZAP70 is normally cytosolic but binds to phosphorylated ITAMs on the TCR when the receptor is bound to pMHC. The translocation of ZAP70 provides a convenient microscopy-based assay to evaluate TCR triggering (James and Vale, 2012). TDB binding to the membrane-proximal immunoglobulin (Ig) domain of FcRH5 (1G7; Figure 1A) led to efficient synapse formation, a robust clustering of FcRH5 in the cell-cell interaction site, and exclusion of the CD45 from the synapse (Figure 1B). The combined result of FcRH5 clustering and exclusion of inhibitory molecules was TCR triggering illustrated by ZAP70 translocation to the cell interface (Figure 1B).

We then compared the sequence of events in synapse formation at the cell-cell interface when driven by CD3-bispecific antibody binding (Figures 1A and 1B) with those at the interface caused by the pMHC-TCR interaction itself (Figures 1C and 1D). Overall, the mechanisms leading to TCR triggering, including target clustering, CD45 exclusion, and ZAP70-translocation, showed remarkable similarity between the CD3-bispecific antibody and pMHC-driven ligation (Figures 1B and 1D).

The interface between the two cells can be visualized by taking a three-dimensional volume of the cell-cell conjugate formed by the TDB (Figure 1E). The analysis demonstrated that the segregation of CD45 and the concomitant clustering of FcRH5 caused by TDB binding extended across the entire interface. The analysis also demonstrated a spatial mutual exclusion of the FcRH5 and the CD45 phosphatase. To confirm that this was the case, we analyzed a line profile across an equivalent interface and quantified the relative intensities of CD45, FcRH5, and the TDB (Figure 1F). The quantitation of the fluorescent signal confirmed the strong co-localization between FcRH5 and the TDB, and the complete inverse correlation with CD45 fluorescence intensity. In summary, our results demonstrate that the CD3-bispecific antibody replicates the mechanism of the TCR/pMHC interaction-mediated TCR triggering inducing clustering of the target molecule and exclusion of CD45 from the T cell synapse resulting in activation of TCR signaling. CD45 exclusion has been described in the synapse induced by an Ep-CAM/CD3 BiTE (Offner et al., 2006), demonstrating that the conjugate interface and the molecular mechanism leading to T cell triggering share common features despite distinct structures of these molecules.

A Membrane-Proximal Epitope Is Required for Efficient Synapse Formation and Killing Activity of the Anti-FcRH5/CD3 TDB

Similar to CD45, the extracellular domain of FcRH5 is large (550 and 835 amino acids, respectively) allowing us to test the effect of structural parameters of the tumor target on synapse formation and killing activity. We generated three proof-of-concept TDBs that bind to different regions of FcRH5 (Figure 2A). TDB binding to the membrane-proximal Ig domain of FcRH5 (1G7) led to synapse formation significantly more efficiently compared with TDBs targeting central (10A8) or distal domains (gD) of the target (Figure 2B), driving efficient CD45 exclusion (Figures 2B and 2C) and target clustering (Figures 2B and 2D) at the cell-cell interface. The efficiency of forming a synapse was reflected in the ability of the TDB to induce TCR signaling and mediate killing by human T cells. Using healthy donor CD8+ T cells, 1G7-TDB resulted in very robust SLP76 phosphorylation (Figure 2E), which is indicative of potent TCR signaling, and mediated efficient killing of target cells (Figure 2F; median effective concentration (EC50 = 0.5 nM). In contrast, gD-TDB targeting of a membrane-distal epitope resulted in undetectable TCR signaling and was unable to mediate T cell killing. Monovalent binding affinities of antibodies used (KD = 12 versus 3 nM by...
mediate killing of cells (EC50 = 0.19 nM) when the obstruction activity of each clone was FcRH5 in bispecific format and could demonstrate that the ac-
clones targeting the membrane-proximal domain for the specific TDB clones, we tested a total of five unique antibody are related to the epitope rather than being properties of theure S1A). To confirm that the differences in the killing activity
target expression level being the cause for the activity differ-
were retargeted to kill MOLP-2 cells, only membrane-proximal
target cells and the potency correlated with FcRH5 expression
The cytotoxic activity of TDB required FcRH5 expression on
and killing of MOLP-2 cells (Figures 3A and 3B). Anti-FcRH5/
healthy donors resulted in dose-dependent T cell activation
CD3 TDB also had an effect on Treg cell activation (Figure S2D).
The anti-FcRH5 clone 1G7 was humanized and paired with a hu-
manized anti-CD3 arm that is cross-reactive to the cynomolgus
monkey to generate an anti-FcRH5/CD3 TDB. Anti-FcRH5/CD3
TDB is specific to FcRH5 and binds to the membrane-proximal
domain of the target (Figures S2A–S2B). Anti-FcRH5/CD3 TDB
binds to FcRH5-expressing myeloma cell lines (MOLP-2),
healthy donor B cells, bone marrow plasma cells, and primary
myeloma tumor cells (Figure S2C). Preclinical characterization of anti-FcRH5/CD3 TDB activity to confirm its mechanism of ac-
tion was performed. Treatment of FcRH5-positive MOLP-2 cells
with the anti-FcRH5/CD3 TDB and CD8+ or CD4+ T cells from healthy donors resulted in dose-dependent T cell activation
and killing of MOLP-2 cells (Figures 3A and 3B). Anti-FcRH5/
CD3 TDB also had an effect on Treg cell activation (Figure S2D).
The cytotoxic activity of TDB required FcRH5 expression on target cells and the potency correlated with FcRH5 expression level (Figure 3C). Stimulation of effector T cells with the anti-FcRH5/CD3 TDB in the presence of target cells led to a robust proliferation of T cells, with 95% of the CD8+ cells undergoing as many as six cell divisions in 5 days (Figure 3D).

Scatchard analysis for 1G7 and 10A8, respectively) do not explain the differences in the synapse formation or signaling.
We next confirmed that the TDB activity is driven primarily by
the location of the epitope and the size of the extracellular domain (ECD) by targeting cells that express a heavily truncated FcRH5 that retains the 1G7 and gD epitopes (Figure 2G). The activity of the proximal 1G7-TDB increased by 25-fold (Figure 2H; EC50 = 20 pM) and the gD-TDB was able to effectively mediate killing of cells (EC50 = 0.19 nM) when the obstruction caused by the ECD was removed. The possibility of differential target expression level being the cause for the activity difference between cell lines was ruled out by flow cytometry (Figure S1A). To confirm that the differences in the killing activity are related to the epitope rather than being properties of the specific TDB clones, we tested a total of five unique antibody clones targeting the membrane-proximal domain for the FcRH5 in bispecific format and could demonstrate that the activity of each clone was ~20-fold higher compared with 10A8 (Figure 2I). These findings were confirmed using the MOLP-2 myeloma cell line, which endogenously expresses FcRH5 at a low level comparable with that of MM patients. When T cells were retargeted to kill MOLP-2 cells, only membrane-proximal TDBs induced killing of the MOLP-2 cells. Targeting the mid region of FcRH5 would not lead to sufficiently potent TCR triggering to kill MOLP-2 cells (Figure S1B). Together these data demonstrate that formation of the immunologic synapse by a CD3-bispecific antibody is dependent on the dimensions of the target molecule, and that rational epitope selection based on membrane proximity can overcome the hindrance caused by a large target protein that would otherwise lead to suboptimal synapse formation.

The Anti-FcRH5/CD3 TDB Induces Target-Dependent Cell Killing and T Cell Proliferation
The anti-FcRH5 clone 1G7 was humanized and paired with a hum-
manized anti-CD3 arm that is cross-reactive to the cynomolgus
monkey to generate an anti-FcRH5/CD3 TDB. Anti-FcRH5/CD3 TDB is specific to FcRH5 and binds to the membrane-proximal domain of the target (Figures S2A–S2B). Anti-FcRH5/CD3 TDB binds to FcRH5-expressing myeloma cell lines (MOLP-2), healthy donor B cells, bone marrow plasma cells, and primary myeloma tumor cells (Figure S2C). Preclinical characterization of anti-FcRH5/CD3 TDB activity to confirm its mechanism of action was performed. Treatment of FcRH5-positive MOLP-2 cells with the anti-FcRH5/CD3 TDB and CD8+ or CD4+ T cells from healthy donors resulted in dose-dependent T cell activation and killing of MOLP-2 cells (Figures 3A and 3B). Anti-FcRH5/CD3 TDB also had an effect on Treg cell activation (Figure S2D). The cytotoxic activity of TDB required FcRH5 expression on target cells and the potency correlated with FcRH5 expression level (Figure 3C). Stimulation of effector T cells with the anti-FcRH5/CD3 TDB in the presence of target cells led to a robust proliferation of T cells, with 95% of the CD8+ cells undergoing as many as six cell divisions in 5 days (Figure 3D).

Figure 1. Anti-FcRH5/CD3 TDB Induces Target Clustering and Exclusion of CD45 from the Synapse Resulting in TCR Trig-
erg
(A) Schematic of the interface between the FcRh5-expressing target cell and the reconstituted HEK-T cell, with protein dimensions shown approximately to scale. The remaining components of the HEK-T cells, including the normally cytoplasmic kinase, ZAP70, have been omitted for clarity.
(B) Representative images of TDB-mediated conjugates (1G7-TDB) between an FcRH5-expressing HEK cell and a reconstituted HEK-T cell, showing CD45 segregation, FcRH5 clustering, and ZAP70 recruitment at the cell interface.
(C) Schematic of the interface between the pMHC-expressing target cell and the reconstituted HEK-T cell, with protein dimensions shown approximately to scale. The remaining components of the cells, including the normally cytoplasmic kinase, ZAP70, have been omitted for clarity.
(D) Representative images of conjugates between a pMHC-expressing Raji B cell and a reconstituted HEK-T cell, showing CD45 segregation, pMHC clustering, and ZAP70 recruitment at the cell interface.
(E) A reconstructed en face view of a conjugate interface equivalent to that shown in (B). (F) Line profiles of CD45 (green), FcRH5 (blue), and TDB (red) intensities across a conjugate interface equivalent to that shown in (B). In all images, box color denotes that used in the overlay image. Scale bars, 5 μm (B) and (D) or 2 μm (E) in length.
Expression of FcRH5 in Normal Tissues and MM

FcRH5 is expressed in the B cell lineage starting from pre-B cells, but unlike most B cell markers, its expression is retained in plasma cells (Polson et al., 2006). Analysis of FcRH5 RNA expression in the Genotype-Tissue Expression (GTeX) sample set (Ardlie et al., 2015), consisting of 8,555 samples from 544 donors over 53 tissues, demonstrated expression in Epstein-Barr virus-transformed lymphocytes, spleen, and the terminal ileum of the small intestine (Figure 4A). The RNA signal detected in spleen and intestine is likely derived from infiltrating B cells. Further analysis demonstrated a strong correlation with the expression profile of known B cell and plasma cell markers (CD19, CD20, and BCMA; Figure 4B). Overall the selective expression in B lineage cells and tissues predicts a favorable safety profile for this target.

Expression of FcRH5 in CD138+CD38+ MM cells and normal bone marrow plasma cells was evaluated by flow cytometry using bivalent 1G7 antibody. In all samples tested, all patient-derived tumor cells, and all normal plasma cells expressed FcRH5, suggesting 100% prevalence in myeloma (Figure 4C). Considerable inter-patient variability in expression level was detected in MM samples. Generally, FcRH5 expression levels in tumor cells was not significantly elevated compared with normal plasma cells, suggesting that developing a tumor cell-selective, normal plasma cell-sparing anti-FcRH5/CD3 TDB may not be feasible. FcRH5 expression level in normal B cells was observed to be lower compared with normal plasma cells and MM tumor cells (Figures 4C and S2C), a similar finding as a previous report (Elkins et al., 2012). To understand the prevalence of expression in a broader patient population we performed a bioinformatic analysis of FcRH5 mRNA expression in CD138-purified plasma cells from 170 non-treated newly diagnosed MM patients and 6 healthy donors (microarray dataset GSE39754 from the NCBI Gene Expression Omnibus). All myeloma samples were positive for FcRH5 RNA (Figure 4D). At the mRNA level, FcRH5 expression was significantly higher in myeloma samples compared with healthy donor samples. Expression of FcRH5 was higher in 155 out of 170 (91%) malignant samples compared with the highest expression level detected in the normal samples. Only one clinical value of interest, response to the USP7 inhibitor P5091, is available for the samples, and there was no significant correlation between this treatment response and FcRH5 expression (p = 0.62; ANOVA). The FcRH5 gene is located in the chromosomal breakpoint in 1q21 (Hatzivassiliou et al., 2001).
Analysis of ~20 primary MM biopsies demonstrated a significant association between FcRH5 RNA expression and 1q21 gain (Figures 4E–4F), demonstrating that the 1q21 gain can lead to FcRH5 overexpression in high-risk myeloma patients. The selective expression for B lineage cells and tissues predicts a favorable safety profile for this target. Overall, 100% prevalence in myeloma, the predicted favorable safety profile and overexpression in high-risk patients indicate FcRH5 as a promising target for MM.

The Anti-FcRH5/CD3 TDB Mediates Potent Killing of Normal Plasma Cells and Patient-Derived Primary Myeloma Cells

The ability of the anti-FcRH5/CD3 TDB to kill plasma cells was analyzed by targeting bone marrow mononuclear cells (BMMCs) isolated from bone marrow aspirates of healthy donors (Figure 5A). Anti-FcRH5/CD3 TDB treatment induced potent dose-dependent killing of normal plasma cells (EC50 = 85–180 pM). Similarly robust cytotoxic activity was detected when BMMCs from MM patients were exposed to the anti-FcRH5/CD3 TDB (Figure 5B). The anti-FcRH5/CD3 TDB demonstrated near-complete and highly potent killing of primary myeloma tumor cells (EC50 = 60–1,200 pM).

As FcRH5 expression is variable in myeloma (Figures 4C–4D) and anti-FcRH5/CD3 activity correlated with expression level (Figure 3C), we investigated whether patients whose tumor cells expressed low levels of FcRH5 would be predicted to respond to the anti-FcRH5/CD3 TDB. The MOLP-2 myeloma cell line was identified as a benchmark cell line that has similar expression levels of FcRH5 as plasma cells and primary MM cells (Figure 4C). We also identified additional cell lines that express extremely low levels of FcRH5 and determined the number of FcRH5 molecules per cell using Scatchard analysis. The 1G7 binding sites in these cell lines ranged from 160 to 2,200 FcRH5 molecules per cell. Even with very low target copy number, anti-FcRH5/CD3 induced killing of all tested cell lines. Despite the limited maximal killing seen in the case of one cell line, EC50 values for all cells were in the pM range (EC50 = 2–230 pM, Figure 5C). Occupancy calculations indicate that as few as ~50 TDB molecules (2% occupancy at MOLP-2; EC50 = 58 pM) are sufficient to induce T cell activation and target cell apoptosis.
Figure 4. Expression of FcRH5 in Normal Tissues and Multiple Myeloma

(A) FcRH5 RNA-seq analysis of the Genotype-Tissue Expression (GTEx) sample set. Boxes represent the interquartile range (IQR, 25th to 75th percentile), the horizontal line is the median. Whiskers extend to the most extreme data point that is within 1.5*IQR of the 25th and 75th percentiles. Data points beyond the whiskers represent outliers.

(B) Correlation of FcRH5 expression with CD19, CD20, and BCMA expression in the GTEx samples.

(C) FcRH5 protein expression in primary multiple myeloma tumor cells and healthy donor peripheral B cells and bone marrow plasma cells. FcRH5 expression was analyzed by flow cytometry normalized to expression in MOLP-2 internal and assay control. Data are represented as the mean ± SEM.

(D) FcRH5 mRNA expression in anti-CD138 purified plasma cells from newly diagnosed non-treated multiple myeloma patients measured using Affymetrix GeneChip Human Exon 1.0 ST.

(legend continued on next page)
Anti-FcRH5/CD3 TDB Suppresses Growth of Established MOLP-2 Tumors in Mice Reconstituted with Human Immune Cells

Modeling anti-myeloma activity of the anti-FcRH5/CD3 TDB in mice is challenging since anti-CD3 antibodies do not cross-react with mouse CD3 and there is no mouse FcRH5 ortholog. Therefore we established a mouse model with a reconstituted human immune system by transplanting CD34+-selected human hematopoietic stem cells into irradiated mice (humanized NOD/SCID gamma [huNSG] mice). Human CD8+ cells harvested from spleens of huNSG mice were shown to be able to kill MOLP-2 cells in vitro with comparable efficiency as human peripheral CD8+ T cells from healthy donors (Figure 6A). Twenty weeks post transplantation, huNSG mice were inoculated with 20 million MOLP-2 cells subcutaneously. Mice with established tumors (100–200 mm3) were treated with a weekly intravenous dose of vehicle or 0.5 mg/kg of anti-FcRH5/CD3 TDB. Anti-FcRH5/CD3 TDB treatment resulted in tumor regression in all animals (Figure 6B), indicating that anti-FcRH5/CD3 suppresses tumor growth in vivo.

Cynomolgus Monkey Is an Appropriate Preclinical Model for the Anti-FcRH5/CD3 TDB

Flow cytometry analysis was used to confirm both the reactivity of anti-FcRH5 1G7 to FcRH5 and expression of the target in B cells and plasma cells in cynomolgus monkey (Figures S3A–S3C). FcRH5 expression was detected throughout the B cell line-age in a similar manner to human (Polson et al., 2006), and the anti-FcRH5/CD3 TDB binds to FcRH5 and CD3 with comparable affinity. Treatment with anti-FcRH5/CD3 TDB of target cells expressing primate FcRH5 or MOLP-2 cells expressing human FcRH5 resulted in robust killing using peripheral T cells from either human or cynomolgus monkey with comparable efficiency (Figures S3D and S3E). Adding anti-FcRH5/CD3 TDB to peripheral blood mononuclear cell (PBMC)/BMMC samples from cynomolgus monkey also resulted in a dose-dependent and robust killing of B cells (Figure S3F) and bone marrow plasma cells (Figure S3G). These results validate the cynomolgus monkey as an appropriate safety and efficacy model for the anti-FcRH5/CD3 TDB.

Anti-FcRH5/CD3 TDB Has a Long Serum Half-Life in Cynomolgus Monkeys

A single-dose study was conducted to evaluate efficacy, pharmacokinetic (PK) and pharmacodynamic (PD) properties of the anti-FcRH5/CD3 TDB in cynomolgus monkeys. Monkeys were treated with a single intravenous dose with slow infusion of vehicle or 1, 2, or 4 mg/kg of anti-FcRH5/CD3 TDB. Blood samples were collected for analysis of PK/PD response and cytokines for 7 days after the anti-FcRH5/CD3 TDB was administered. The study was terminated at day 8. The anti-FcRH5/CD3 TDB demonstrated dose-proportional exposure (Cmax and area under the curve) between 1 and 4 mg/kg and with clearance ranging from 29 to 33 mL/day/kg in all cohorts (Figure 7A). The Cmax at the 4 mg/kg dose level was 129 µg/mL, ~2,000-fold higher than that required to reach
the in vitro killing EC50 for human plasma cells and MOLP-2. Receptor occupancy calculations suggested near-total saturation of FcRH5 engagement on peripheral blood B cells at Cmax at all dose levels (Figure S4A). In summary, these results demonstrate that the anti-FcRH5/CD3 TDB has PK characteristics that support an intermittent weekly or less frequent dosing schedule.

**Anti-FcRH5/CD3 TDB Depletes B Cells and Bone Marrow Plasma Cells in Cynomolgus Monkeys**

Flow cytometry of peripheral blood demonstrated a robust pharmacologic effect at all dose levels. Anti-FcRH5/CD3 treatment resulted in T cell activation and a transient decrease in T cells likely reflecting a margination response within 24 hr (Figures 7B, 7C, S4B, and S4C). CD4+ and CD8+ T cells recovered to baseline levels by the end of the study. In contrast, B cells remained to be undetectable in blood 7 days after anti-FcRH5/CD3 TDB administration indicating that they were depleted by exposure to the molecule (Figure 7D). All dose levels resulted in complete depletion of B cells in spleen and bone marrow (Figures 7E and 7F). Anti-FcRH5/CD3 TDB treatment also induced a robust, dose-dependent depletion of B cells from the lymph nodes (Figures 7G and S4D).

Depletion of primate bone marrow plasma cells is a key efficacy endpoint in the preclinical development of the anti-FcRH5/CD3 TDB. Complete depletion of plasma cells following anti-FcRH5/CD3 TDB treatment was observed in the animals treated at 2 and 4 mg/kg (Figure 7H). Anti-FcRH5/CD3 treatment also resulted in a dose-dependent reduction of IgG of 37% and 44% in the 2 and 4 mg/kg groups, respectively (Figure 7I), an expected secondary outcome resulting from plasma cell depletion. These figures compare favorably with calculations based on the half-life of IgG suggesting that complete depletion of plasma cells would decrease IgG level ~30%–40% by day 7. In summary, anti-FcRH5/CD3 TDB induced a robust PD response in cynomolgus monkeys consistent with its mechanism of action. Complete plasma cell depletion with subsequent decrease in serum IgG levels provides compelling evidence of TDB activity in the bone marrow microenvironment.

**Anti-FcRH5/CD3 TDB Induces Transient Cytokine Release in Cynomolgus Monkey**

Consistent with the mechanism of action, treatment with the anti-FcRH5/CD3 TDB at all dose levels tested induced a rapid, generally mild/moderate cytokine release (Figure S5), including elevations in IL-6, IL-5, IFN-γ, IL-2, IL-13, and MCP-1 as well as the anti-inflammatory response peaking at 2–6 hr. All cytokines returned to normal baseline levels within 24 hr. In summary, no signs of severe or prolonged cytokine release were observed at dose levels that are expected to saturate target and sufficient for complete depletion of B cells and plasma cells. A single dose at the ≤4 mg/kg dose level did not result in detectable neurotoxicity.

**PD-L1 Blockade Enhances the Activity of Anti-FcRH5/CD3 TDB**

A strong TCR stimulation signal normally leads to immunosuppressive feedback that limits T cell activity. Signaling through the PD-1/PD-L1 axis is a critical component of this feedback and a therapeutically validated immune escape mechanism in several tumor indications. PD-L1 is frequently expressed by myeloma cells (Gorgun et al., 2015), and the signaling axis may limit T cell activity in myeloma patients.

In vitro stimulation (48 hr) of human healthy donor CD8+ cells with anti-FcRH5/CD3 TDB in the presence of target-expressing cells resulted in significant PD-1 induction in T cells (Figure 8A). This feedback signal was also observed in vivo. A significant increase in the number of PD-1-positive T cells was observed when cynomolgus monkeys were treated with anti-FcRH5/CD3 TDB at all tested dose levels. PD-1 induction was detected in both CD8+ and CD4+ T cells in blood, spleen, lymph nodes, and bone marrow (Figures 8B and S6). The ability of anti-FcRH5/CD3 TDB-primed CD8+ T cells to kill PD-L1-expressing target cells was modest (Figure 8C); however, blocking PD-1/PD-L1 signaling using an anti-PD-L1 antibody in combination with anti-FcRH5/CD3 significantly increased the efficiency of killing (Figure 8C). Together, these results show that anti-FcRH5/CD3 TDB-mediated activation of T cells leads to induction of PD-1 in T cells in vitro and in vivo. Although PD-1/PD-L1 signaling can limit anti-FcRH5/CD3 TDB-mediated killing, PD-L1 blockade can overcome this inhibition and lead to enhanced activity of the anti-FcRH5/CD3 TDB. Our data provide strong scientific rationale for the clinical assessment of anti-FcRH5/CD3 TDB combined with anti-PD-L1 blockade in MM patients.

**DISCUSSION**

Several CD3-bispecific antibodies or antibody fragment-based molecules are in clinical development and clinical
Figure 7. Anti-FcRH5/CD3 TDB Depletes B Cells and Bone Marrow Plasma Cells in Cynomolgus Monkey

A single intravenous dose of vehicle (blue) or anti-FcRH5/CD3 TDB (red, 1 mg/kg; brown, 2 mg/kg; green, 4 mg/kg) was administered to three cynomolgus monkeys/group.

(A) Blood samples were collected at indicated time points and human IgG was detected by ELISA.

(B and C) The effect of anti-FcRH5/CD3 TDB on CD4+ (B) and CD8+ (C) T cell activation in peripheral blood.

(D–G) The absolute count of CD20+ B cells in peripheral blood (D), spleen (E), bone marrow (F), and mandibular lymph node (G).

(H and I) The effect of anti-FcRH5/CD3 TDB on bone marrow plasma cells (H) and serum IgG (I) levels. The difference between before and after treatment was analyzed by unpaired t test. Data in E–I are represented as the mean ± SEM. See also Figures S3–S5.
proof-of-concept has been established by blinatumomab in hematological malignancies (Bargou et al., 2008). Optimally, the CD3-bispecific molecules show extremely potent preclinical activity regardless of the target molecule or the molecule format. In our studies, using a plethora of tumor targets and antibody clones, we have detected extreme variability in the activity of the molecules that could not be explained by the affinities of the molecules. In this study we describe the molecular events in the synapse induced by a CD3-bispecific full-length antibody and show that the events closely follow the principles of kinetic segregation, and are not significantly different compared with TCR activation by pMHC ligation. Our studies confirm that FcRH5 is suboptimal for bispecific antibody-mediated T cell triggering due to its large ECD that interferes with efficient synapse formation. By using antibodies that bind to various different epitopes we show that the efficiency of synapse formation correlates with the proximity of binding epitope to cell membrane. The difference between the epitopes in the end result (killing of myeloma cells) is dramatic: membrane-proximal antibodies kill with picomolar concentrations, whereas more distal antibodies are essentially inert. Potency in the context of BiTE-mediated killing has been correlated with similar structural features of the target molecule (Bluemel et al., 2010) complementing our molecular studies of synapse and mechanism of T cell triggering.

Anti-FcRH5/CD3 TDB killed patient-derived myeloma cells and healthy donor-derived plasma cells at picomolar concentrations. Non-clinical pharmacology studies with anti-FcRH5/CD3 TDB in mice are challenging. First, anti-FcRH5/CD3 TDB is not reactive to mouse CD3. Second, an FcRH5 ortholog does not exist in the mouse; thus genetically engineered mouse models are not suitable for testing the molecule. The only available mouse tumor model that can be used is human myeloma cell line (MOLP-2) xenografted to immune-compromised mice supplemented with human T cells. As these tumors are grafted subcutaneously, the MOLP-2 xenografts do not model activity in the bone marrow environment. A further clear limitation of this type of xenograft model is that the immune system engrafted in the mice likely does not exactly recapitulate the adult human immune system, potentially not accounting for the contribution of other cell types, such as Treg cells, to TDB treatment. In contrast, cynomolgus monkeys can be used as a compelling efficacy model to demonstrate in vivo activity in the bone marrow compartment. A single dose of the anti-FcRH5/CD3 TDB depleted plasma cells and B cells from tissues and led to expected reduction of serum IgG levels.

Cytokine release has been reported consistently across CD3-targeting bispecific molecule platforms with variable frequency and severity. Clinical cytokine release syndrome (CRS) has been reported in CD19-targeting agents, e.g., blinatumomab and CD19 CAR-T cells. As expected, the anti-FcRH5/CD3 TDB induced mild/moderate cytokine release immediately after dose administration, but no extensive or prolonged cytokine release was observed in cynomolgus monkeys. The predictive value of the detected cytokine levels in primates to CRS in myeloma patients is unclear. However, several potential mitigation strategies are available for cytokine-related adverse effects (dose fractionation, corticosteroids, or IL-6 signaling blockers).

The anti-FcRH5/CD3 TDB is predicted to be broadly active in myeloma as the prevalence of the target expression is 100%, and as few as ~200 copies of FcRH5 on a MM cell are sufficient to induce tumor cell killing. In addition to myeloma, evidence of frequent FcRH5 expression has been reported in multiple B cell malignancies such as chronic lymphocytic leukemia, mantle cell lymphoma, diffuse large B cell lymphoma, and follicular lymphoma (Ise et al., 2007; Li et al., 2008; Polson et al., 2006). This suggests a more general applicability for anti-FcRH5/CD3 in B cell-mediated malignancies in addition to MM.

Gain or amplification of chromosome 1q21 is one of the most commonly detected genetic abnormalities in MM and is considered a predictive marker of aggressive disease (Boyd et al., 2012). FcRH5 was originally identified in cloning of this chromosomal region and has been shown to be deregulated in cell lines with 1q21 abnormalities (Hatzivassiliou et al., 2001). Our analysis of primary myeloma samples demonstrates that FcRH5 mRNA is elevated in myeloma patients with 1q21 gain. Although it is unlikely that FcRH5 plays a functional role in the myeloma...
progression, its overexpression provides an intriguing diagnostic hypothesis for the anti-FcRH5/CD3 TDB. Our in vitro assays demonstrate a correlation between target expression level and activity of the molecule, suggesting that MM with gain of 1q21 may be exquisitely sensitive to the anti-FcRH5/CD3 TDB, thus providing clinical benefit to a patient population that otherwise has very limited treatment options.

T cell activation by anti-FcRH5/CD3 TDB induced upregulation of PD-1 in T cells. This negative feedback signaling has been detected with other CD3 targeting bispecific molecules regardless of the format of the molecule (Bacac et al., 2016; Junttila et al., 2014; Osada et al., 2015), and is likely a class effect for molecules with this mechanism of action. As PD-1/PD-L1 signaling can inhibit the killing activity of T cells, optimal clinical use of T cell-recruiting bispecific antibodies may include combination with inhibitors for this pathway.

**EXPERIMENTAL PROCEDURES**

**Antibodies**
Antibodies were from BD Biosciences unless otherwise mentioned. Anti-human PD-1 was from Abcam. Goat anti-human IgG and goat anti-mouse IgG were from Jackson ImmunoResearch. Anti-PC-FTC (clone Vs38c) was from Dako, SLP-76 from Cell Signaling Technology, p-SLP76 (Ser376) and anti-PD-L1 antibodies were generated at Genentech.

**Fluorescent Labeling of Antibodies**
For detection of FcRH5 from MM samples and healthy donor plasma and B cells by flow cytometry, anti-FcRH5 antibody 1G7 was labeled with phycoerythrin by SouthernBiotech. For microscopy, the TDBs were labeled with Alexa Fluor 647 using the appropriate protein labeling kit (Thermo Fisher Scientific) according to the manufacturer’s instructions. TDBs were diazylated into PBS, pH 7.2, prior to labeling and a dye/protein ratio of ~4 was routinely achieved.

**Stable Cell Lines**
To evaluate the immunological synapse formation, SVT2 cells were infected with retrovirus encoding full-length FcRHS with N-terminal gd expression tag or truncated FcRHS (deletion of AA1-744) with N-terminal gd tag. To evaluate the target dependency of TDB killing, FOX-NY cells were infected with lentivirus encoding full-length FcRHS and single-cell-derived clones with differential expression level of FcRHS were selected. To evaluate the effect of PD-1/PD-L1 signaling to TDB activity, 293 cells were infected with lentivirus encoding FcRHS followed by transfection of human PD-L1 encoding plasmid using Lipofectamine (Invitrogen).

**Vectors and Transient Transfection for Microscopy**
FcRHS with N-terminal gd expression tag was fused to the fluorescent protein mRuby2 by first inserting FcRHS into the pHIR-SIN lentiviral vector before cotransfection with HEK293-FcRH5 cells (2:1) and 1 μg/mL of TDBs. Western blot analysis of CD8+ T cells were labeled with carboxyfluorescein succinimidyl ester and co-cultured with MOLP-2 cells in a 3:1 ratio and co-cultured with Anti-FcRH5/CD3 TDB for 24 hr. The T cell activation assay has been described previously (Junttila et al., 2014).

**Microscopy Imaging and Analysis**
To image cell conjugates, 3 × 10⁶ cells were harvested from culture and resuspended in 100 μL of 20 nM TDB in RPMI-1640 (without phenol red). After 20–30 min incubation to allow cell conjugation, cells were washed with PBS, resuspended in DMEM/F12 imaging medium (Evrogen) and added to 35 mm imaging dishes (Mattek). An Andor spinning disc confocal microscope system was used to image the cells at 37°C. All images were analyzed and all presented images were manipulated in an equivalent manner using ImageJ. The presented images were background subtracted and then cropped to focus on the pair of cells and the contrast was optimized. The degree of protein clustering and segregation was determined by using the intensity of fluorescently labeled proteins in the plasma membrane. The plasma membrane was selected by manually drawing a line and the average fluorescence intensity of the plasma membrane within the cell-cell interface was divided by the average fluorescence intensity of the plasma membrane outside the cell-cell interface to calculate the degree of clustering or segregation. To generate an image of the interface of a pair of cells conjugated by TDBs from a z stack, the image stack was first deconvolved and then cropped to highlight the interface region using Huygens software.

**Production of TDBs**
Full-length bispecific antibodies were produced as described elsewhere (Junttila et al., 2014; Sun et al., 2015). In brief, the two half antibodies containing the “knob” or the “hole” mutations in the CH3 domains were expressed by transient transfection of CHO cells and then affinity purified with Protein A. Equal amounts of the two half antibodies were incubated with a 200 molar excess of reduced glutathione at pH 8.5 overnight at 32°C to drive the formation of the knob-hole disulfide bonds. The assembled bispecific antibody was purified from contaminants through hydrophobic interaction chromatography.

**In Vitro Cytotoxicity Assays: Cell Lines**
PBMCS and CD8+ separation, CellTiter-Glo (Promega) and flow cytometry-based viability assays (48 hr) were described previously (Junttila et al., 2014). CD4+ T cells were isolated from PBMCS by the Human CD4+ T cell Isolation Kit (Miltenyi Biotec). CD4+ or CD8+ cells were used as effectors in a 3:1 effectortarget ratio.

**In Vitro Cytotoxicity Assay: Human Plasma Cells and Primary MM Samples**
Human BMMCs from MM patients were procured from Conversant Bio. Human bone marrow aspirates of healthy donors were procured from AlCells. All human biospecimens were collected, processed, and distributed in full ethical and regulatory compliance with the sites from which human biospecimens were collected. This includes independent ethical review, institutional review board approval (where appropriate), independent regulatory review, and ethical review for collection sites. All sites were located in the US and the EU. In vitro experiments using human healthy donor blood, bone marrow, or vendor-procured live tumor material are routinely performed at Genentech and do not require approval by an internal ethical review committee.

Human bone marrow aspirates of healthy donors were diluted in PBS and BMMCs were isolated by conventional gradient separation (Lymphoprep, STEMCELL). Flow cytometry viability assay was used to test the effect of 72 hr anti-FcRHS/CD3 TDB treatment on BMMC plasma cells. Myeloma BMMCs were mixed with freshly isolated healthy donor CD8+ T cells and co-culture treated with anti-FcRHS/CD3 TDB for 72 hr. PI-negative CD38+CD138+ cells were counted by flow cytometry. The killing activity was calculated as: {number of live target cells without TDB – number of live target cells with TDB}/(number of live target cells without TDB) x 100%.

**T Cell Activation**
Human CD4+ T cells, CD8+ T cells, or Treg cells (CD4+CD25+CD127low) were mixed with MOLP-2 cells in a 3:1 ratio and co-cultured with Anti-FcRH5/CD3 TDB for 24 hr. The T cell activation assay has been described previously (Junttila et al., 2014).

**T Cell Proliferation**
CD8+ T cells were labeled with carboxyfluorescein succinimidyl ester and co-cultured with MOLP-2 cells (1:1) and 1 μg/mL TDB for 5 days.

**Western Blot Analysis**
pSLP76 (Ser376) and SLP76 were analyzed in human CD8+ T cells co-cultured with HEK293-FcRH5 cells (2:1) and 1 μg/mL of TDBs.
RNA Expression in Normal Tissues and Myeloma Samples
mRNA expression was analyzed in the GTEx RNA sequencing sample set (Ar-dille et al., 2015) consisting of 8,555 samples from 544 donors over 53 tissues and in the NCBI GEO: GSE389754 dataset (Affymetrix GeneChip Human Exon 1.0 ST Array) from the NCBI GEO repository (Chauhan et al., 2012). CD138 purified plasma cell samples in the NCBI GEO: GSE389754 dataset represent newly diagnosed patients with MM before initiation of primary treatment.

RNA Isolation, cDNA Synthesis, and Gene Expression Analysis Total RNA was extracted from decalcified formalin-fixed paraffin-embedded (FFPE) bone marrow biopsy tissues collected from MM patients. Two reference genes, SDHA and VPS33B, were evaluated for each sample and used to calculate expression of FcRH5. Gene expression of FcRH5 was determined by using the delta Ct (dCt) method (Ct gene of interest –Ct geometric mean of reference genes). Detailed description of method in the supplement.

Cytogenetic Fluorescent In Situ Hybridization 1q21 + copy control 1 fluorescent in situ hybridization (FISH) probe (Biocare Medical; previously CymoGen Dx) was used to analyze the 1q21 region. The 1q21 probe covers the chromosomal band 1q21.3 while the control probe is located in the peri-centricromeric 1p12 region of chromosome 1. FISH analysis on FFPE tissue was performed as described previously (Koeppen et al., 2014; O’Brien et al., 2008). A minimum of 100 non-overlapping tumor cells from each sample was enumerated. Cutoff of gain was 3 or more copies in >20% of the tumor cells. Detailed description of method in the supplement.

huNSG/MOLP-2 Mouse Xenograft Model All mouse experimental procedures conformed to the guiding principles of the American Physiology Society and were approved by Genentech’s Institutional Animal Care and Use Committee (IACUC). Female huNSG mice were obtained from The Jackson Laboratory. Animals were inoculated with 20 million MOLP-2 tumor cells in Hank’s balanced salt solution/Matrigel, subcutaneousy. Treatments were administered intravenously once a week from each sample was enumerated. Cutoff of gain was 3 or more copies in >20% of the tumor cells. Detailed description of method in the supplement.

Cynomolgus Monkey Study The PK and PD properties of anti-FcRHiS/CD3 TDB were evaluated in naive, male cynomolgus monkeys (cynos) at Charles River Laboratories (CRL). Cynos were treated with a single-dose, intravenous infusion (1 hr) of vehicle, 1, 2, or 4 mg/kg anti-FcRHiS/anti-CD3 TDB blood samples were collected by venipuncture via the femoral vein pre-study and at selected time points for 7 days after dosing for analyses of hematology, serum chemistry, coagulation, and PK and PD endpoints (cytokines, flow cytometry of T lymphocytes, B lymphocytes, activated T lymphocytes, and PD-1 and circulating cyno IgG). Bone marrow was collected in anesthetized animals by aspiration from the humerus pre-study and on day 8 for evaluation of B lymphocytes and plasma cells by flow cytometry. The study was terminated at day 8. All procedures were approved by the CRL IACUC and were performed in compliance with the Animal Welfare Act, the Guide for the Care and Use of Laboratory Animals, and the Office of Laboratory Animal welfare.

Anti-FcRHiS/CD3 Pharmacokinetics in Cyno Anti-FcRHiS/CD3 TDB in serum were determined by generic ELISA. Sheep anti-human IgG antibody was used as the capturing reagent and sheep anti-human IgG conjugated to horseradish peroxidase (HRP) was used as the detection reagent. Serum concentration-time data from available samples were analyzed by a non-compartmental with IV bolus input model (Phoenix WinNonlin, Version 6.3; Pharsight Corporation). Nominal sample collection time and nominal dose concentrations were used in the data analysis. All TK analyses were based on individual animal data.

Flow Cytometry Analysis for Cyno Plasma Cells Cyno bone marrow aspirate were diluted (1:10) into ammonium-chloride-potassium lysis buffer twice. Cyno bone marrow cells were stained with anti-CD45, anti-CD20, and anti-CD38. After wash, cells were fixed and permeabilized with IntraStain Kit (Dako). Cells then were stained with anti-PC (clone Vs38c). The cyno plasma cells were classified by flow cytometry as CD45-CD20-CD38-PC+.

ELISA Analysis for Cyno IgG Level Total cyno serum IgG was quantified using standard colorimetric-based sandwich ELISA. A goat anti-monkey IgG (Bethyl Laboratories, A140-202A) and a HRP conjugated goat anti-monkey IgG (Bethyl Laboratories, A140-202P) were used as the capture and detection antibody, respectively. Cyno IgG (Cell Sciences CS120163A) was used as the protein quantification standard.

PD-1 Induction and Cytotoxicity Assay with anti-PD-L1 Total CD8+ T cells and MOLP-2 cells were co-cultured (1:1) with 1,000 ng/mL of TDB for 48 hr and stained with anti-PD-1-APC. Cytotoxicity assay is described above.

SUPPLEMENTAL INFORMATION Supplemental Information includes Supplemental Experimental Procedures and six figures and can be found with this article online at http://dx.doi.org/10.1016/j.ccell.2017.02.001.

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