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scFv6.C4 DNA vaccine with fragment C of Tetanus toxin increases protective immunity against CEA-expressing tumor

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Abstract

The carcinoembryonic antigen (CEA) is the main tumor-associated antigen of colorectal cancers. Previously, we developed a DNA vaccine using scFv6.C4, a CEA surrogate, against CEA-expressing tumors; 40% of the vaccinated mice were tumor-free after tumor challenge. In order to enhance vaccine efficacy, fragment C of Tetanus Toxin (FrC) was tested as adjuvant. C57BL/6J-CEA2682 mice were electroporated intramuscularly 4 times with uP-PS/scFv6.C4-FrC or uP-PS/scFv6.C4, challenged by *s.c.* injection of 1×10^5 MC38-CEA cells, and tumor growth was monitored over 100 days. The humoral and cellular immune responses were assessed by ELISA, immunocytochemistry, *in-vitro* lymphocyte proliferation, and CTL cytotoxicity assays. Immunization with uP-PS/scFv6.C4-FrC or uP-PS/scFv6.C4-FrC-immunized mice sera. When challenged with MC38-CEA cells, 63% of the FrC-vaccinated mice did not develop tumors, half of the rest had a significant tumor growth delay, and the probability of being free of tumors was on average 40% higher than that of scFv6.C4-immunized mice. Addition of the adjuvant led to higher CD4+ and CD8+ proliferative responses and strong CD8+ CTL response against MC38-CEA cells. DNA immunization with scFv6.C4 and FrC increased antitumor effect via induction of high and specific humoral and cellular immune responses to CEA.

Introduction

Colon and rectum cancers are highly prevalent among men and women, and prevention and treatment are yet major medical and scientific challenges [1, 2]. The carcinoembryonic antigen (CEA) is a 180-KDa membrane-bound highly glycosylated protein, which is the main tumor-

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associated antigen (TAA) of these cancers [3, 4]. The CEA is highly expressed during the fetal development, but its level is reduced to trace level in the normal adult colonic epithelium [3], which is a characteristic of a self-antigen. However, significant levels of autoantibodies against CEA were detected in some patients with CEA-expressing tumors [5–7], evidencing that the CEA self-antigen can activate the immune system.

Previously, our group developed a DNA vaccine against CEA-expressing tumors using scFv6.C4, a CEA surrogate, originated from the anti-idiotypic mAB 6.C4 variable heavy and light chain sequences [8–11]. Similar approaches with anti-idiotypic antibodies have been used in clinical trials with the production of consistent anti-CEA immune responses [12–14].

The scFv6.C4 DNA vaccine was able to both mimic CEA functionally and induce anti-CEA humoral and cellular immune responses [8]. The effectiveness of the preventive immunization with scFv6.C4, as evaluated in transgenic mice for CEA [15], was 40% tumor-free animals after challenge with B16F10-CEA cells. Despite the impressive result, for this vaccine to be

translated into a clinical trial, the vaccine efficacy has to be improved.

Tetanus Toxin Fragment C (FrC) from *Clostridium tetani* has been used as an adjuvant in several DNA vaccine protocols [16–22]. This 50-kDa fragment has a promiscuous universal epitope for MHC class II in its sequence, which can induce a greater presentation and development of humoral and cellular immune responses [23–25]. In preclinical vaccines against lymphomas and melanomas, FrC fused to scFv of idiotypic antibodies increased humoral and cellular responses and caused tumor growth delay [16–18]. Additionally, phase-I and -II clinical trials with FrC fused to specific myeloma and prostatic cancer antigens showed safety and tolerance against the vaccines, inducing antigen specific CD8+T cell responses [26, 27].

In this study, we evaluated the FrC adjuvant effect on DNA vaccination with scFv6.C4 in CEA2682 transgenic mice. Humoral and cellular responses were evaluated in immunized mice before and after challenge with MC38-CEA tumor cells.

Materials and methods

Research Ethics Committee approval

All animal procedures were performed in full compliance with the institutional guidelines, and were approved by the Institutional Research Ethics Committee (http://www. unifesp.br/reitoria/ceua; Approval number: CEUA 703012).

Construction of vectors

To construct the uP/PS-scFv6.C4-FrC plasmid vector, pFrC plasmid (kindly provided by Dr. Natalia Savelyeva from the Cancer Sciences Unit, Faculty of Medicine, University of Southampton, UK) [18] was used as a template for FrC amplification by PCR using the following primers: 5'-AAGCGGCCGCAAAAAACCTTGATTGTT-3' and 5'-AATCTAGAGCGGCCGCTTAGTCGTTG-3' (final concentration: 0.4 mM). The thermocycler was programmed for 95 °C (5 min) and 35 cycles of 95 °C (45 s), 60 °C (45 s), and 72 °C (2 min). After the final cycle, the reaction continued at 72 °C (7 min) and the reaction product was maintained at 4 °C. In the forward and reverse primers, the restriction sites for Not I and Xba I were respectively included, which are underlined. The 1364 bp FrC amplicon was digested with Not I and Xba I, and inserted into the uP-PS/scFv6.C4 plasmid vector [8], which was previously treated with the same enzymes and purified before cloning.

To construct the pT2-scFv6.C4 plasmid vector, uP-PS/ scFv6.C4 was digested with *Pvu II* and *Hind III* to release the 1165-bp fragment with scFv6.C4 and bGH-PolyA. This fragment was treated with Klenow polymerase and inserted into the pT2 vector [28], which was previously digested with Ava I and treated with Klenow polymerase.

Cell culture, transfection and characterization

The human colorectal carcinoma cell line HCT-8 [29], free of mycoplasma, was maintained in RPMI-1640 (Thermo Fisher Scientific; Waltham, MA, USA), supplemented with 10% heat-inactivated fetal bovine serum (Invitrogen; Grand Island, NY, USA), L-glutamine (Gln; 2 mM), penicillin (100 units/ml), and streptomycin (100 μ g/ml). The medium was buffered with sodium bicarbonate (24 mM), plus 2-[4-(2-hydroxyethyl)-1-piperazinyl] ethanesulfonic acid (HEPES) buffer (10 mM) in a humidified atmosphere (5% CO₂; 37 °C). The supplemented medium was named RPMIc.

The murine colon adenocarcinoma cell line MC38 [30] was maintained in DMEM (Thermo Fisher Scientific) supplemented with 10% heat-inactivated fetal bovine serum (Invitrogen), Gln (2 mM), penicillin (100 units/ml), and streptomycin (100 µg/ml) in a humidified atmosphere (5% CO_2 ; 37 °C). This medium was buffered with sodium bicarbonate (24 mM) plus HEPES buffer (10 mM). The supplemented medium was named DMEMc.

To promote permanent expression of CEA or scFv6.C4 in MC38 cells, 1×10^5 cells in SMEM (50 µl; Invitrogen) containing pINT (4 µg) [31], and uP-attb-CEA (4 µg) [8], or pSB100x (4 µg) [32] and pT2-scFv6.C4 (4 µg), were transferred into a 4-mm cuvette, and submitted to electroporation (500 V; 150-µs duration; 12 pulses; ECM830, BTX, Harvard Apparatus; Holliston, MA, USA). The transformed cells were named based on the transferred genes (MC38-CEA and MC38-scFv6.C4). The electroporated cells were cloned by limiting dilution, being maintained in DMEMc in a humidified incubator (5% CO₂; 37 °C).

The CEA cDNA integration into the cell genome was assessed by PCR using the following primers: 5'- CTA CCT GTG GTG GGT AAA TGG 3' and 5'- CTT GAC TAT GGA ATT ATT GCG GC -3' (final concentration: 0.4 mM). The thermocycler was programmed for 95 °C (5 min) and 30 cycles of 95 °C (45 s), 51 °C (45 s), and 72 °C (45 s). After the final cycle, the reaction continued (72 °C; 7 min), and the reaction product was then maintained at 4 °C. The expected amplicon was 418 bp. The human colon cell lines HCT8 and CO112 were used as positive controls, which produce an amplicon of 1131 bp.

The scFv6.c4 integration was assessed by PCR, using the primers 5'-TGGGTGAGGCAGACGCCTGAA-3' and 5'-GAGGTCCCAGACCCACTGCCA-3' (final concentration: 0.4 mM). The thermocycler was programmed for 95 °C (5 min) and 30 cycles of 95 °C (45 s), 59 °C (45 s), and 72 °C

(45 s). After the final cycle, the reaction continued at 72 $^{\circ}$ C (7 min) and the reaction product was maintained at 4 $^{\circ}$ C.

As an internal control for PCR, the glyceraldehyde-3-phosphate dehydrogenase housekeeping gene was used with the following primers: 5'-ACCACAGTCCATGCCATC AC-3' and 5'-TCCACCACCCTGTTGCTGTA-3'. The PCR products were analyzed by 1% agarose gel electrophoresis.

Preventive DNA vaccination and tumor cell challenge

The CEA-expressing transgenic mice (CEA2682; kindly donated by Dr Wolfgang Zimmermann; University of Munich, Munich, Germany) [15] were immunized by injection of PBS (70 μ l using insulin syringe) containing the uP-PS/scFv6.C4-FrC (90 μ g) or uP-PS/scFv6.C4 (70 μ g) plasmid (in order to maintain the same molar ratio of scFv6. C4) in each quadriceps muscle. Six electric pulses (100 V; duration: 40 ms per pulse; 1 s interval) were applied through 10-mm tweezer electrodes, which were placed around the DNA injection site (Electroporator ECM830). Three subsequent immunizations were performed at two-week intervals. Blood samples were collected 7 days after each immunization to quantify AB3 antibody production.

A week after the last immunization, mice were challenged by *s.c.* injection of 1×10^5 MC38-CEA cells into the left flank. The tumor size was periodically measured with a caliper for 100 days. Tumor volume (in mm³) was estimated using the following equation:

 $V = 0.52 \times D \times d^2$ (*D*: major diameter; *d*: minor diameter; in mm)

Quantification of CEA-specific antibody response

Sera from vaccinated mice were assessed for anti-CEA antibodies (AB3 = AB1') by ELISA. Initially, CEA (50 μ l) in PBS (1µg/ml; Abcam; Cambridge, UK) was added to each well of 96-well plates and incubated at 37 °C (1 h). Plates were blocked with 1% bovine serum albumin (BSA; Sigma-Aldrich; St. Louis, MO, USA) and 2% non-fat milk in PBS (room temperature, RT; 1 h). The mouse sera diluted in PBS containing 0.1% BSA and 0.2% non-fat milk (1:50) were added and incubated (4 °C; overnight). The wells were washed three times with PBS containing 0.05% Tween-20 (PBS-Tween), and biotinylated rabbit anti-mouse IgG (Dako; Carpinteria, CA, USA) diluted in 0.1% PBS-BSA containing 0.2% non-fat milk (1:1000) was added and incubated (37 °C; 1 h). After washing, horseradish peroxidase-streptavidin (Dako) diluted in 0.1% PBS-BSA containing 0.2% non-fat milk (1:500) was added and incubated (dark chamber; RT; 30 min). The wells were washed before adding ortho-phenylenediamine (OPD; Sigma-Aldrich; 3 mg/ml) in 50 mM citratephosphate buffer (51.4 mM Na₂HPO₄; 24.3 mM acetic acid; pH 5.0) containing 0.03% H₂O₂. The reactions were stopped with H₂SO₄ (2 N; 25 mL). The optical density (I: 492 nm) was read in a microplate (Spectra Max M2^e, Molecular Devices; Sunnyvale, CA, USA) spectrophotometer. Each sample was run in triplicate.

Immunocytochemistry of HCT-8, MC38, and MC38-CEA cells

The immunocytochemistry was performed as we described previously [8]. Briefly, on day 0, cells were seeded onto 13mm coverslips and incubated in a humidified chamber (5% CO₂; 24 h). On day 1, media were aspirated, and the cells were fixed in 4% paraformaldehyde (1 h), incubated with NH₄Cl (50 mM; 15 min), permeabilized with PBS containing 0.5% Triton X-100 (10 min), blocked with PBS containing 10% BSA (Sigma-Aldrich) and 8% non-fat milk (1 h), and incubated with 1:50 diluted sera from uP-PS/ scFv6.C4-FrC immunized, uP-PS/scFv6.C4-immunized, or non-immunized mice in a humidified chamber (5% CO₂; 4°C; overnight). Monoclonal antibody 1F5H2 [10] (final concentration: 10 µg/ml) was used as a positive control. On day 2, the coverslips were incubated with biotinylated rabbit anti-mouse IgG (Dako; 1:100; 1 h), followed by Alexa 594streptavidin (Invitrogen; 1:1000; 1 h) and 4',6-diamidino-2phenylindole (DAPI) for cell nuclei labeling (Invitrogen; 1:1000; 15 min). At the end, coverslips were rinsed with distilled water and mounted with Fluoromount (Sigma-Aldrich), and images were acquired using a fluorescent microscope (Olympus BX51, Tokyo, Japan).

Immunohistochemistry of MC38-CEA tumor

Subcutaneous tumors formed by injection of MC38-CEA cells were removed from the animals after euthanasia, fixed in formaldehyde (10%; 48 h) and dehydrated by sequential passage in 70% ethanol, 100% ethanol and xylol, and infiltrated with paraffin. Sections (4 µm; Leica RM2255 Microtome; Wetzlar, Germany) were dewaxed and hydrated by sequential passage in xylol, 100% ethanol, 70% ethanol, and distilled water. The sections were incubated with NH₄Cl (50 mM; 15 min) and washed in distilled water (3 times; 5 min per washing). Permeabilization was done with PBS containing 0.5% Triton X-100 (15 min), followed by washing in PBS. Antigen retrieval was performed in citrate buffer (1.8 mM citric acid; 8.2 mM sodium citrate; pH 6.0) in a steamer (15 min), followed by distilled water washes. Endogenous peroxidase was blocked with a solution of methanol with hydrogen peroxide (30%; 15 min in the dark). The sections were washed in distilled water and blocked in PBS containing 10% BSA and 8% non-fat milk (1 h). After PBS washes, avidin and biotin blockage was performed with Avidin/Biotin Blocking Kit (Vector Laboratories; Burlingame, USA). Biotinylated mAB 1F5H2 [10] (final concentration: $50 \mu g/ml$) was incubated in a humidified chamber (5% CO₂; 4 °C; overnight). Next day, the sections were washed with PBS containing 0.25% Tween-20 and incubated with Streptavidin-HRP (Dako; 1:500; 1 h). Peroxidase activity was detected with DAB solution (Dako; Liquid DAB + Substrate Chromogen System) and counterstained with Mayer's Hematoxylin. The slides were dehydrated by sequential passage in ethanol and xylol, and assembled with Entellan (Sigma-Aldrich). Images were acquired using the fluorescent microscope Olympus BX51.

In vitro cellular proliferation assay

After MC38-CEA injection (90-100 days), mice were euthanized, and splenocytes were collected and treated with ammonium chloride potassium buffer (0.15 M NH₄Cl; 10 mM KHCO₃; 0.1 mM Na₂EDTA) to lyse the red blood cells. For the proliferation assay, 2×10^7 splenocytes suspended in PBS were labeled (37 °C; 5 min) with 2.0 µM carboxyfluorescein diacetate succinimidyl ester (CFSE) (Cell-TraceTM; CFSE Cell Proliferation Kit; Invitrogen). Cells were centrifuged $(1500 \times g; 5 \text{ min})$ and washed three times with RPMIc. In a 96-well plate (U-bottom shape), $5 \times$ 10^5 cells per well were plated in RPMIc (200 µl). The cells were stimulated with CEA (2 µg/ml; Abcam), mAB 6.C4 (10 µg/ml) [9], or concanavalin A (2.5 µg/ml; ConA; Sigma-Aldrich). Non-stimulated cells were used as a negative control. All experiments were carried out in triplicate. After incubation in a CO₂ chamber (37 $^{\circ}$ C; 6 days), the cells were washed with MACS buffer (PBS containing 2 mM EDTA and 0.5% BSA; pH 7.2) and labeled in a dark chamber (4 °C; 45 min) with anti-CD4-APC (1:100) or anti-CD8-PE (1:100) antibodies (BD Biosciences; San Jose, CA, USA). The labeled cells were washed (three times) and suspended in MACS buffer (200 µl). The samples were quantified by flow cytometry (FACS Canto II, BD Biosciences), and analyzed by the FlowJo (Three Star; Ashland, OR, USA) software. The gate strategy was used to determine the lymphocyte population based on the SSC-A and FSC-A parameters, followed by determination of the CD8+ (SSC-A, PE) and CD4+(SSC-A, APC) subpopulations. The proliferated cell gate (CFSE low) was established in nonstimulated samples and applied to the stimulated subpopulations. The percentage of CFSE-low cells was normalized by subtracting the percentage observed in nonstimulated samples of the same animal. The samples stimulated with ConA were used as experimental validation (not shown).

Cytotoxicity assay

Splenocytes from mice immunized and challenged with MC38-CEA were prepared as described above. For the cytotoxicity assay, $5-7 \times 10^7$ splenocytes were washed in MACS buffer and labelled with the anti-CD8-PE (BD Biosciences) antibody and sorted by flow cytometry (FACS Aria II, BD Biosciences).

The MC38, MC38-CEA, and MC38-scFv6.C4 cells were used as targets. Concomitantly, 2×10^4 tumor cells were plated in duplicates in 96-U-well plates with sorted T CD8 + cells in three different target: effect ratios: 1:5 $(10 \times 10^4 \text{ T})$ CD8+), 1:2 (4×10^4 T CD8+), and 1:1 (2×10^4 T CD8+). The final volume was completed to 200 µl with RPMIc. The cells were incubated in a humidified chamber (5% CO₂; 16 h). Wells containing only tumor cells were used as controls. The LDH activity assay (In Vitro Toxicology Assay Kit, Lactic Dehydrogenase based; Sigma-Aldrich) was performed in 50 µl medium following the manufacturer's instructions. The lysis percentage was calculated using the following formula: % cell lysis = $100 \times [(A - B)/(C - B)]$, where A: OD_{690nm} tumor plus target, B: OD_{690nm} target spontaneous release (background), and C: OD_{690nm} target maximus lysis.

scFv6.C4 in silico analysis

The complementarity determining regions (CDRs) and structural regions (FR) of scFv6.C4 light and heavy chains were identified through the contact definition and with the IgBLAST algorithm [33, 34]. The forward and reverse sequences of these regions were individually aligned with the amino acid sequence of CEA (NP_004354.3) using the BLASTp and EMBOSS Needle algorithms [35, 36].

Prediction of CD8+ T-cell epitopes was performed in IEDB Analysis Resource (v2.19) using artificial neural network (ANN) method [37], considering the C57BL/6 MHC I alleles H-2-Db and H-2-Kb. Selection of predicted binders was based on the percentile rank of MHC binding affinity $\leq 1\%$ for each combination (MHC allele, length) to cover most of the immune responses [38, 39]. Prediction of linear B-cell epitopes was performed in IEDB Analysis Resource (v2.19) using Bepipred Linear Epitope Prediction [40]. The predicted residues with scores above the threshold were considered as an epitope. The predicted T and B cells' epitopes with scores above the threshold were individually aligned with the CEA amino acid sequence (NP_004354.3) using the BLASTp and EMBOSS Needle algorithms [35, 36] to assess similarities.

The results were presented as percentage of similarity between sequences, which represents the sum of the percentages of identical and chemically similar amino acids.

Statistical analysis

Statistical analyses were performed using the IBM SPSS Statistics (v. 21; New York, NY, USA) software, and graphs were plotted using the GraphPad Prism (v. 5.0; La Jolla, CA, USA) software. The anti-CEA antibody titers were analyzed by GEE (General Estimating Equations) using linear distribution, defined according to the QIC parameter, followed by Bonferroni. The significance level was set at 5%. The data are presented as mean and standard deviation. Survival analysis was performed by Cox Regression, in which the observed outcome was the time necessary to reach 0.5 cm^3 tumor volume. The reported Hazard Ratio (HR) corresponds to the mean of all observed time. The effect of the different groups of animals on the proliferation and cytotoxicity assays were assessed by GLzM using linear distribution, defined according to the AIC parameter, followed by Bonferroni. Sample size was chosen based upon experiences from previous experiments and the numbers of samples per group were indicated in the legends. The significance was 5%. Data are presented as mean and standard deviation.

Results

In vivo tumor model with MC38 cells expressing CEA

To establish a murine colon adenocarcinoma cell line that permanently expresses human CEA, the murine colon adenocarcinoma cell line MC38 was electroporated with the integrative vector system composed of pINT(\u03c6C31) and uPattb-CEA; the CEA-expressing cells were isolated by the limiting dilution technique. The CEA expression on transfected cells were detectable by immunocytochemistry with mAB 1F5H2 [10], even a year after clonal selection (Fig. 1a). Integration of the CEA gene was confirmed by PCR (Fig. 1b). Tumorigenesis of the selected MC38-CEA cells was validated after subcutaneous injection in CEA2682 mice. Visible tumors appeared about 20 days later and reached 1 cm³ 40 days after injection, as shown by the standard tumor growth curve with a 95% prediction band (Fig. 1c). Tumors collected after 100 days maintained high CEA expression in most tumor cells (Fig. 1d).

Humoral responses and protection against tumor challenge induced by uP-PS/scFv6.C4-FrC DNA vaccination

To evaluate the immune response after vaccination with the uP/PS-scFv6.C4-FrC vector, CEA2682 mice were immunized four times with 2-week intervals. The DNA vaccination with plasmid solution was performed by *i.m.* injection followed by electroporation based on our previous experience [8, 41]. Blood samples were collected 1 week after each immunization to determine the AB3 antibody titers (Fig. 2a). Mice immunized with the uP/PS-scFv6.C4 vector, which was used in a previous study [8], were used for comparison. Although animals immunized with uP/PS-scFv6.C4-FrC had a significant increase in AB3 antibody titer after the first (0.185 ± 0.025 vs 0.132 ± 0.010; P = 0.042), third (0.266 ± 0.028 vs0.205 ± 0.025; P = 0.002), and fourth (0.322 ± 0.019 vs0.266 ± 0.028; P = 0.003) immunizations in comparison with the immediately previous measure, no difference was observed in the AB3 titer between animals immunized with uP/PS-scFv6.C4-FrC and uP/PS-scFv6.C4 vectors (Fig. 2b).

To evaluate the effectiveness of the preventive DNA uP-PS/scFv6.C4-FrC vaccine, 1×10^5 MC38-CEA cells were injected subcutaneously into the left flank of mice one week after the last immunization, and tumor growth was measured periodically. In the uP-PS/scFv6.C4-FrC-immunized mice, 63% remained free of tumor over 100 days of observation, and in the uP-PS/scFv6.C4-immunized mice only 47%. All mice without immunization developed tumor within 40 days after tumor injection. Survival analysis by Cox regression shows that the probability of uP-PS/scFv6. C4-FrC immunized mice to be free of tumor is 15.2 times higher than non-immunized mice (CI 95% HR 3.36-68.19; P < 0.001) and 1.4 times higher than the group immunized with uP-PS/scFv6.C4 (CI 95% HR: 0.434–4.58; P = 0.568) (Fig. 2c). These results show that the vaccine regimen can delay tumor growth and increase animal survival, or even can completely inhibit tumor growth. The summary of tumor cell challenge experiments is shown in the Table 1 to facilitate visualization of these results.

To assess the affinity of AB3 antibody on CEA, sera obtained after the last immunization and after tumor challenge were tested by immunocytochemistry on the CEAexpressing human colorectal cell line HCT-8 and murine cell line MC38-CEA. The MC38 cell line was used as a negative control. Pre-immune sera and sera from nonimmunized mice were used as negative controls, while sera from the uP-scFv6.C4-immunized mice were used for comparison (Fig. 3). All the CEA-expressing cell lines were strongly marked with sera from uP/PS-scFv6.C4-FrC immunized and tumor-challenged mice, whereas the preimmune sera or sera from non-immunized mice showed no reaction. Although fluorescent images are difficult to quantify, the staining of uP-scFv6.C4-FrC sera can be clearly observed, mainly in MC38-CEA cells. These results confirm the effectiveness of the scFv6.C4-FrC recombinant protein in mimicking CEA and inducing AB3 specific antibody.



Fig. 1 Establishment of the MC38-CEA tumor cell lineage. The MC38 cells were electroporated with uP-attB-CEA and uP-INT (φ C31) and cloned by the limiting dilution method. **a** CEA expression was detected by immunocytochemistry in three time periods: before, right after, and twelve months after clonal selection. CEA staining is shown in red, and nuclei staining in blue (DAPI). Bar = 50 µm. **b** CEA integration into the genome was analyzed by PCR. 1: 100 bp ladder plus, 2: MC38 (negative control), 3: MC38-CEA, 4: HCT-8 (positive control), 5: CO112 (positive control), 6: reaction without template.

The expected amplicon size is 418 pb. **c** Tumor growth rate was determined after *s.c.* injection of 1×10^5 MC38-CEA cells into the left flank of C57bl/6-CEA2682 mice. Each point represents the temporal measure of one animal (n = 8 animals). The continuous red line represents the standard tumor growth curve and the dotted lines represent the 95% prediction band d) CEA expression detected by immunohistochemistry in MC38-CEA tumor. Cell nuclei were stained with hematoxylin. Bar = 100 µm

Cellular responses induced by uP-PS/scFv6.C4-FrC DNA vaccination

To assess the specific T-cell proliferative activities, splenocytes from vaccinated and MC38-CEA-challenged mice were harvested and stimulated with CEA or mAB 6.C4 (Fig. 4). ConA ($2.5 \mu g/ml$) and no stimulation were used as positive and negative controls, respectively. As there were mice with and without tumor after vaccination and tumor-challenge, splenocytes from these mice were analyzed separately.

Under CEA stimulation, a significantly higher proliferation of CD4+ T-cells was observed in scFv6.C4-FrC immunized animals that did not develop any tumors (4.59% \pm 0.28%) as compared to animals immunized with scFv6.C4 only (2.06% \pm 0.56%; P = 0.003) and non-immunized animals with tumor (1.93% \pm 0.35%; P < 0.001). In the animals with tumor, no difference in CD4+ proliferation was observed. On the other hand, CD8+ proliferation was higher in the scFv6.C4-FrC immunized animals that were with tumor (12.50% \pm 0.60%), as compared to animals immunized with scFv6.C4 only (1.29% \pm 0.46%; *P* < 0.001) and non-immunized (8.59% \pm 0.46%; *P* < 0.001). Considering the tumor-free animals, CD8+ proliferation in the scFv6.C4 group was higher than in the scFv6.C4-FrC group (8.52% \pm 0.74% vs. scFv6.C4-FrC 3.42% \pm 0.42%; *P* < 0.001).

When cells were stimulated with mAB 6.C4, a higher CD4+ proliferation was observed in both scFv6.C4-FrC animals that developed or did not develop tumors as compared to other groups. The main difference (almost 10-fold) was observed in the scFv6.C4-FrC animals that were with tumor (4.36% ± 0.46%) as compared to scFv6. C4 ($0.49 \pm 0.35\%$; P < 0.001) and non-immunized animals ($0.59 \pm 0.30\%$; P < 0.001). The CD8+ proliferation under mAB 6.C4 stimulus was also significantly higher in scFv6.C4-FrC animals with tumor ($10.26 \pm 0.60\%$) as compared to scFv6.C4 ($5.65 \pm 0.46\%$; P < 0.001) and non-immunized animals ($1.02\% \pm 0.43\%$; P < 0.001).



Fig. 2 Humoral response and protection against MC38CEA tumor challenge after uP-PS/scFv 6.C4-FrC DNA vaccination. **a** Immunization scheme. The arrows indicate electroporations performed with the uP-PS/scFv 6.C4-FrC vector every 14 days. Blood samples were collected 7 days after each immunization, as indicated by drops. The tumor challenge was performed 7 days after the last immunization, as indicated by cell drawings. The animals were euthanized between days 90 and 130 for cellular and humoral response evaluation. **b** CEA-specific AB3 antibodies in mice immunized with uP-PS/scFv6.C4 -FrC were detected by ELISA. Blood samples were diluted (1:50) for the assays. Sera from mice immunized with the uP-PS/scFv6.C4 vector

To evaluate the CTL immune response, two target cells (MC38-CEA or MC38-scFv6.C4) were initially constructed to express CEA and scFv6.C4, respectively. Individually sorted CD8+ cells from tumor-challenged animals (which developed or not tumors) were used for cytotoxic assay in different targets: effector ratios, using MC38 cells as a negative control (Fig. 5).

Analyzing 1:5 ratio, about 4% of MC38 cells were lysed by CD8+ from non-immunized mice, and this was considered as non-specific basal activity.

A strong CTL activity was observed in CD8+ cells derived from scFv6.C4-FrC-immunized animals that did not develop tumors, with specific lysis of MC38-CEA (77.83 \pm 2.24%), which was 15-fold higher than that of scFv6.C4 (5.12 \pm 2.24%; *P* < 0.001), and almost 7-fold higher than in non-immunized and non-challenged animals (naïve group) (12.39 \pm 2.59; *P* < 0.001).

were used as controls. Data are expressed as mean \pm SD of OD_{490nm} of each group (uP-PS/scFv6.C4-FrC (n = 14) and uP-PS/scFv6.C4 (n = 39)). Number 1: P = 0.042 compared to pre-immune sera; Number 2: P = 0.002 compared to the second immunization; Number 3: P = 0.003 compared to the third immunization. **c** Tumor-free animals estimated by Cox regression. Mice with tumors smaller than 500 mm³ were considered as survivors. Non-immunized and uP-PS/scFv6. C4-FrC (n = 11) and uP-PS/scFv6.C4 (n = 17)). The animals were observed for 100 days; however, no change was observed on the survival rate since day 65

In the group of animals that developed tumors, specific lysis of MC38-CEA cells by CTL from scFv6.C4-FrC immunized animals $(31.27 \pm 0.91\%)$ was almost 4-fold higher than that from uP/PS-scFv6.C4-immunized animals $(8.11 \pm 0.91; P < 0.001)$ and 2.5-fold higher than that from non-immunized animals $(12.80 \pm 0.65; P < 0.001)$.

The MC38-scFv6.C4 lysis (1:5 ratio) by cells of tumorfree scFv6.C4-FrC animals ($52.45\% \pm 2.70\%$) was 5-fold higher than that of uP/PS-scFv6.C4 ($10.03 \pm 2.70\%$; P < 0.001). Regarding animals that developed tumors, MC38scFv6.C4 lysis by CD8+ cells from uP/PS-scFv6.C4-FrC immunized animals ($22.76 \pm 0.47\%$) was about 3.6-fold higher than that of uP/PS-scFv6.C4 ($6.23 \pm 0.47\%$; P < 0.001) and 2-fold higher than that in non-immunized animals ($12.26 \pm 0.38\%$; P < 0.001).

A non-specific lysis of MC38 cells was observed in scFv6.C4-FrC animals that developed $(19.06 \pm 1.78\%)$ or

Table 1 Summary of tumor cell challenge experiments

	Mice without tumor	Mice with delayed tumor growth	^a Mice with normal tumor growth	Hazard ratio	Hazard ratio
Non- immunized	—	_	100%	1.0	—
scFv6.4	47%	35%	18%	_	1.0
scFv6.4-FrC	63%	18.5%	18.5%	^b 15.2 (CI 95% 3.36–68.19)	^c 1.4 (CI 95% 0.43–4.58)

CI confidence interval

^aNormal tumor growth refers to the speed of tumor growth of the non-vaccinated mice

^b15.2 times the chance of being tumor free in relation to the non-immunized group after challenge

^c1.4 times the chance of being free of tumor in relation to the scFv6.4 group after challenge



Fig. 3 Evaluation of humoral response by immunocytochemistry using sera from uP-PS/scFv6.C4-FrC immunized mice. Blood samples (diluted to 1:50) were collected before immunization, after immunization, and after tumor challenge. The MC38 and HCT-8 human colorectal cells were used as negative and positive controls, respectively.

Samples obtained from non-immunized and uP-PS/scFv6.C4-immunized animals were used for comparison. CEA staining is shown in red, and nuclei staining in blue (DAPI). Images are representative of 10 animals per group. Bar = $100 \,\mu m$

did not develop $(15.82 \pm 1.34\%)$ tumors, but both were lower than the lysis observed in MC38-CEA and MC38scFv6.C4 target cells. An overview of all outcomes after vaccination is schematized in the Fig. 6.

In silico analysis of scFv6.C4

Initially, the amino acid sequences of the complementarity determining regions (CDRs) and framework regions (FRs) of the light and heavy variable chains of scFv6.C4 were deduced based on the IgBLAST algorithm by contact definition (Fig. 7a). Using the BLASTp and EMBOSS Needle algorithms, scFv6.C4 and CEA sequences were aligned and the most significant alignment results are shown in Fig. 7b. Eight scFv6.C4 regions have more than 50% similarities to the CEA sequence; most of them are localized in the light chain. Only two heavy-chain regions show 50% similarity, and 6 light chain regions show similarities varying between 50.0–85.7%. Curiously, the reverse sequences.

Comparing the CEA antigenic epitopes [42–44], three scFv6.C4 regions (CDR-H1, CDR-L2-R, and CDR-L3-R) are similar to the CEA A1B1 sequence. Therefore, these regions can be similar to the GOLD IV antigenic region. The CDR-L2, CDR-L1-R, and FR-L1-R sequences have similarity to the CEA A3B3 region, where the GOLD I and III epitopes are present. In addition, scFv6.C4 CDR-H3 and FR-L1 sequences are similar to the CEA A2B2 sequence, which correspond to the GOLD II antigenic region. These results indicate a high collective similarity between the CEA and scFv6.C4 sequences.

The predicted epitopes for T and B cells were inferred from the scFv6.C4 amino acid sequence in IEBD Analysis Resource. Seven MHC-I and eleven B-cell predicted epitopes were selected based on the previously defined parameters. Four MHC-I and three B-cell predicted epitopes aligned with CEA showed similarities higher than 50%. The MHC-I-H2-Kb epitopes 1, 2 and 3 showed similarity to GOLD II antigenic region whereas the epitope 4 to GOLD V. B-cell epitopes 1 was similar to



Fig. 4 Cellular response of uP/PS-scFv6.C4-FrC immunized animals by proliferation assay. Splenocytes of mice challenged with MC38-CEA were harvested and labeled with 2.0 μ M CSFE and stimulated with CEA or mAB 6.C4 for 6 days. CD4 +, and CD8 + CFSE-low cells were

counted by flow cytometry. Non-immunized and uP/PS-scFv6.C4-immunized animals were used for comparison. Data are expressed as mean \pm SD ((uP-PS/scFv6.C4-FrC (n = 4), uP-PS/scFv6.C4 (n = 8) and non-immunized (n = 5)). ** $P \le 0.01$, *** $P \le 0.001$

GOLD V, the epitope 2 to GOLD II, and the epitope 3 to GOLD I/III (Fig. 7c).

Discussion

In our previous studies, we described the construction of scFv6.C4, a CEA epitope surrogate isolated from antiidiotypic mAB 6.C4, and showed its capacity to raise specific humoral and cellular immune responses to CEA [8, 9, 11]. To evaluate the vaccine efficacy of scFv6.C4, CEA2682 transgenic mice were preventively immunized with uP-PS/scFv6.C4 and challenged with B16F10-CEA, a murine melanoma cell line expressing CEA (Denapoli et al., 2016). This vaccination induced sufficient antitumor responses to retard tumor growth and a population of immunized mice remained free of tumor. However, about 60% of them did not survive (Denapoli et al., 2016). The B16F10 tumor cell line is known to be a very aggressive and highly proliferative [45]. In mice, 5×10^5 B16F10-CEA cells injected subcutaneously reaches 200 mm³ in 12 days and 8×10^3 cells reaches the same size in 22 days (Denapoli et al., 2016). After reaching 200 mm³, cell growth rate changes to even faster and becomes very difficult to halt. So, we speculate that the window time for the immune system to fight against the tumor could be very narrow. To evaluate this speculation, here we used a murine colon adenocarcinoma cell lineage expressing CEA (MC38-CEA), which took about 40 days to reach 1 cm^3 after injection of $1 \times 10^5 \text{ MC38-}$ CEA cells (Fig. 1c), whereas the same number of B16F10-CEA cells reached the same size in less than 15 days [8]. To generate MC38-CEA cell lineage, we used the phiC31 recombinase system because it allows CEA integration into the genome of MC38 cells (Fig. 1b) and promotes a long-term gene expression both in vitro and in vivo (Fig. 1a, d). The slower growth rate of MC38-CEA cells and their proximity to human colorectal tumor have



Fig. 5 CTL activity in CD8+ cells from uP/PS-scFv6.C4-FrC immunized animals by LDH activity assay. CEA and scFv6.C4-specific CTL lysis was carried out using CD8 + cells sorted by FACS from tumor-challenged animals that developed tumors or the animals that did not develop tumors. The cells were incubated for 16 h together with tumor target cells (target tumor: CD8+) in the ratios 1:5, 1:2, and



Fig. 6 Schematic representation of all outcomes after vaccination. Intensities of responses were shown in number of "+" signs, and "-" sign indicates no response

made them the model of choice in many other studies [21, 46–49, 50–56].

However, the challenge of uP/PS-scFv6.C4-immunized mice with MC38-CEA increased the survival rate from 40% (with B16F10-CEA cells) to 50%. In other words, only 10% increase was obtained compared to the challenge with B16F10 cells (Fig. 2c). This result showed the necessity to increase the immune response to CEA-expressing tumors irrespective of the tumor cell line for challenge because the extension of the window of time for the immune response to

act on tumor growth affected the survival rate well less than expected.

scFv6.C4-immunized animals were used for comparison. Naive group

represents non-immunized and non-challenged animals. MC38 cells

were used as a negative control. Data are expressed as mean ± standard

deviation, SD (uP-PS/scFv6.C4-FrC (n = 4), uP-PS/scFv6.C4 (n = 4),

non-immunized (n = 6) and naïve (n = 4)). *** $P \le 0.001$

The uP/PS-scFv6.C4-FrC-immunized mice raised an anti-CEA antibody response in CEA transgenic mice, but the antibody titer was not higher than that of the antibody response induced by scFv6.C4 alone (Fig. 2b). Nevertheless, the staining observed in CEA-expressing tumor cells with sera from the scFv6.C4-FrC-immunized mice was stronger than with sera from scFv6.C4-immunized mice (Fig. 3). The fluorescence intensity after immunocytochemistry staining is the sum of all individual antibodyantigen recognition. As the antibody titer of mice immunized with uP/PS-scFv6.C4-FrC or uP/PS-scFv6.C4 was similar, the stronger immunocytochemistry staining with the serum from uP/PS-scFv6.C4-FrC mice may indicate the presence of more antibodies that recognize other epitopes that can synergize in halting of tumor growth. Several of our results support this hypothesis: 63% of the vaccinated mice did not develop tumors and half of the rest had a significant delay in tumor growth. In addition, the probability of being free of tumors was on average 40% higher than that of mice immunized with scFv6.C4 alone (Fig. 2c).

The cellular immunity of uP/PS-scFv6.C4-FrC-immunized mice was assessed by the proliferation rate and CTLspecific tumor cell lysis assays. The proliferative activity of CD4+ and CD8+ cells in mice immunized with the FrC adjuvant showed to be higher than those immunized with scFv6.C4 alone (Fig. 4). Comparison between scFv6.C4-FrC-immunized mice with and without tumor after tumor challenge showed that there is an apparent increase in CD8

a	b CDR-H1	GYIFTSYD	(50%)	с		
> scFv 6.C4 heavy chain	CEA (GOLD V)	::. GYVIGTQQ	()	CEA (GOLD II) MHCI-H2-Kb-1	TITVYAEP :. . . .	(50%)
MDLMA (leader) FR-H1-QVKLQQSGTEVVKPGASVKLSCKAS CDR-H1-GYIFTSYD	CDR-H3 CEA (GOLD II)	GDYYRRYFDL : YTYYRPGVNL	(50%)	CEA (GOLD II)	NTTYLWW : ::	(71.4%)
FR-H2-IDWVRQTPEQGLEWIG CDR-H2-WIFPGEGSTEYNEKFKG FR-H3-RATLSVDKSSSTAYMELTRLTSEDSAVYFCAR	FR-L1-R CEA (GOLD I/III)	CTMTVREGPSASMIAPSQTLEI	(50%)	CEA (GOLD II) MHCI-I-H2-Kb-3	SIRYIYW TYYRPGVNL . : DYYRRYFDL	(55.5%)
CDR-H3-GDYYRRYFDL WGQGTTVTVSSSAVYFCAR (constant/FR4)	FR-L1 CEA (GOLD II)	IELTQSPAIMSASPGERVTMTC .:. . : ::: DDPTISPSYTYYRPGVNLSLSC	(54,5%)	CEA (GOLD V) MHCI-I-H2-Kb-4	IGYVIGTQ . ::. SGYIFTSY	(50%)
 scFv 6.C4 light chain D (leader) FR-L1-IELTQSPAIMSASPGERVTMTC 	CDR-L1-R CEA (GOLD I/III)	YIYRISSSAS : .: . YVCGIQNSVS	(60%)			
CDR-L1- SASSSIRYIY FR-L2- WYQQKPGSSPRLLIY CDR-L2- DTSNVAP	CDR-L3-R CEA (GOLD IV)	TYPYGSWEQ .: ::: WFVNGTFQQ	(66,7%)	CEA (GOLD V) B cell-1	AYSGREIIYPN . ::. . QQSGTEVVKPG	(60%)
FR-L3- GVPFRFSGSGSGTSYSLTINRMEAEDAATYYC CDR-L3- QEWSGYPYT FGGGTKLELKRAAA (constant/FR4)	CDR-L2 CEA (GOLD I/III)	DTSNVAP :: DTPIISP	(71,4%)	CEA (GOLD II) B cell-2	SVDHSDPV . SVDKSSST	(50%)
	CDR-L2-R CEA (GOLD IV)	PAVNSTD ::: .: PSISSNN	(85,7%)	CEA (GOLD I/III) B cell-3	KSITVSASGTS :. . FRFSGSGSGTS	(54.5%)

Fig. 7 In silico analysis of scFv6.C4 regions. **a** Amino acid sequences of the complementarity determining (CDRs) and framework regions (FRs) of the light and heavy variable chains of scFv6.C4. **b** scFv6.

C4 sequences with more than 50% similarity to CEA. c) scFv6.C4 B-cell predicted binders. Similarity was defined as the sum of the percentages of identical (|) and chemically similar amino acids (:)

+ cell proliferation in the group of mice with tumor. However, sorted CD8+ cells from mice without tumor showed higher CTL activity against the MC38-CEA (77.8%) and MC38-scFv6.C4 (52.5%) cells using the target:effector ratio 1:5 (Fig. 5), which could be achieved with the total splenocytes extract from scFv6.C4-immunized mice only at the 1:50 ratio [8], and this CTL activities were about 10 times higher than other studies using anti-idiotypic CEA vaccines and MC38-CEA tumor model [48]. Therefore, this high and specific CTL activities should be responsible for tumor elimination. The high lymphocyte proliferative activity seen in mice with tumor seems to occur to compensate the low specific lytic activity that was not able to halt tumor progression. Increased protective immunity was seen in the treatment of lymphomas and melanomas after the use of FrC as an adjuvant [17, 18], and cytotoxic response by another group using a plasmid vector carrying FrC fused with CEA for vaccination in wild-type animals [20], but it has never been reported in CEAexpressing transgenic mice yet.

Another important difference between mice with and without tumor after tumor challenge is that the group without tumor showed strong CD4+ and CD8+ proliferative responses with CEA, whereas the mice with tumor showed similar proliferative responses with CEA or mAB 6. C4. The immunization with scFv6.C4 should elicit immune responses against the sequences specific to scFv6.C4 and against the sequences common to both CEA and scFv6.C4 because of their similarities (Fig. 7), however, as the CEA2682 transgenic mice express CEA constitutively, we hypothesized that the endogenous CEA may have favored the selection of clones that are more reactive to CEA than scFv6.C4.

Generation of antibodies and lymphocytes able to recognize CEA after immunization with scFv6.C4 depends on amino acid sequence similarities between CEA and scFv6.C4 regions and epitopes (Fig. 7). In fact, we found eight scFv6.C4 regions, four MHC-I and three B-cell predicted epitopes with high (above 50%) similarities to the CEA epitopes (GOLD I to GOLD V). The mAB 3H1 epitope (surrogate of CEA) is a similar anti-idiotypic epitope that has already been tested clinically. It has only three regions whose similarities are higher than 50% to CEA [55], which is much lower than that found in scFv6.C4. More regions with high similarities between epitope surrogates and CEA should be advantageous in vaccination because it can broaden immune responses and, consequently, more CEA epitopes can be targeted later.

It is important to remind that although vaccination with scFv6.C4 induces the breakdown of tolerance to CEA, which can both cause autoimmune disease and attack their own cells and tissues. However, in our experimental conditions, the immunized mice apparently remained healthy during more than 100 days of follow up. Similar observations were made by others in such vaccine studies [8, 57–59].

In conclusion, preventive DNA vaccination of CEAexpressing transgenic mice with the uP-PS/scFv6.C4-FrC vector raised humoral and cellular responses, which were sufficient to maintain 63% of mice free of tumor over 100 days after challenge with MC38-CEA cells against 47% of mice vaccinated with uP-PS/scFv6.C4. The FrC adjuvant activity in delaying and preventing tumor growth is likely to be associated with the induction of high and specific humoral and cellular immune responses to CEA. FrC has proven to be safe and tolerable as a cancer vaccine adjuvant in phase I/II clinical trials [26, 27], as well as in clinical trials for neurological diseases [60]. Therefore, its use as adjuvant with scFv.6C4 for vaccination of patients with CEA-expressing cancer is promising.

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Authors' contributions BFZ: conception and design of the study, acquisition of data, analysis and interpretation of the data, drafting of the manuscript; CPF: acquisition of data, analysis and interpretation of data; JRCV: analysis and interpretation of the data; SWH: conception and design of the study, drafting of the manuscript, critical review of the manuscript for important intellectual content, and final approval of the version to be submitted.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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