

New human single chain anti-idiotypic antibody against benzo[a]pyrene

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Abstract

The naïve library from the lymphocytes of healthy humans was screened by murine single-stranded idiotypic antibodies against benzo[a]pyrene (pSh). The phage clone which contained of anti-idiotypic antibody against benzo[a]pyrene, designated as A4, was chosen for further work because of highly specific to pSh. The available protein databases were searched. The A4 amino acid sequence was unique and 76% identical to a sequence in antibody against interferon γ . The A4 protein was expressed in bacteria and purified by two different methods: His-tagged A4 and CBD-fusion A4. Both the A4 bound to pSh and also to the human single chain idiotypic antibody against the benzo[a]pyrene (T72) by ELISA. The K_d values of A4 for pSh and T72 were very close: 4.44×10^7 M and 5.71×10^7 M, respectively. A4 was a competitor with benzo[a]pyrene for binding sites of both idiotypic pSh and T72 in competitive ELISA. Thus, A4 was a high affinity anti-idiotypic against benzo[a]pyrene which recognised pSh and T72 active sites.

Key words: anti-idiotypic antibody, benzo[a]pyrene, immunology, phage display, polycyclic aromatic hydrocarbons, single-chain antibody.

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Introduction

The anti-idiotypic antibodies (Ab2) contain an internal immunological image of the antigen according to the concept Jerne N.K. [1, 2]. It was suggested that Ab2 be used for immunisation rather than antigen in the case of pathogenic antigen. Eichmann K. and Rajewsky K. 1975 [3] was one of the first works in this field, in which guinea pigs were immunised by Ab2 against *Streptococcus*. The animals acquired of resistance against bacteria after immunisation. Nowadays it has been proposed that Ab2 be used as therapeutic antibodies [4-9]. Ab2 were used against tumour-associated antigens in mice model experiments for protective and therapeutic anti-cancer immunity [10-14]. Ab2 were suggested for the treatment of cancer in humans [15-17], including lung cancer [18-20].

The preliminary immunisation by the murine monoclonal Ab2 against benzo[a]pyrene (BP) slowed tumour growth induced by BP in animals [21]. Ab1 against BP and related Ab2 were found in the blood serums of healthy volunteers and patients with lung cancer [22]. However, the functions of Ab1 and Ab2 against chemical carcinogens in

human cancer pathogenesis still remain poorly understood. It was assumed that Ab1 and Ab2 were able to prevent the emergence of tumours and enhance the carcinogenic effects depending on the concentrations or combination of Ab1 and Ab2 [23]. The recombinant Ab2 against chemical carcinogens should be used to continue the research in this field. Ab2 could be applicable as a source of an antigen in human serum Ab1 detection because Ab2 contains an internal immunological antigen image. Also, purified Ab2 could be used as a standard for the development of quantitative immunoassays for measuring Ab2 in human serum.

Material and methods

Chemicals and reagents

Suppressor *E. coli* strain TG1 (K12, D(lac-pro), supE, thi, hsdD5/F' traD36, proA+B+, lacIq, lacZDM15); non-suppressor *E. coli* strain HB2151 (K12, ara, D(lac-pro), thi/F' proA+B+, lacIq, lacZDM15); *E. coli* strain XL10-Gold (Stratagene, La Jolla, CA, USA) (end, A1, glnV44, recA1, thi-1, gyrA96, relA1, lac, Hte, Δ (m-

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crA)183, Δ (mcrCB-hsdSMR-mrr)173, tetR, F'[proAB, lac-IqZ Δ M15, Tn10, (TetR Amy CmR)]; M13K07 bacteriophage; nad ν e combinatorial library of human scFv genes in M13 bacteriophage [24]; pTT10 [kindly provided to us ICBFM SB RAS Novosibirsk]. The restriction enzymes were obtained from Sibenzymes (Novosibirsk, Russia).

pSh and T72 purification

pSh was mouse idiotype scFvs against BP. T72 was human idiotype scFvs against BP. Both scFvs purifications were processed as indicated in [25] and [26], respectively. pSh and T72 have CBD in each molecule. DNA of pSh and T72 were cloned into plasmid pTT10 [25]. So, amorphous cellulose was used for both protein purifications.

Synthesis of BP-BSA conjugate

BP-BSA was synthesised by covalent coupling of hapten aldehyde group to the BSA amino groups [27].

Biopanning

The selection was performed by phage display as has been described previously [24]. Three rounds of biopanning were performed using pSh. The microtiter plate was coated with 50 μ l pSh (50 ng/ml) or CBD (50 ng/ml), as negative control, in PBS for one hour at 37°C. The plate was then blocked by adding 100 μ l of blocking solution PBS containing 2% BSA and 0.05% Tween 20 to each well and incubated for one hour at 37°C with shaking. The bacteriophage particles of sampled M13 (containing scFv genes inside and expressing scFvs as part of the surface of the phage protein pIII) were added. The microtiter plate was incubated for one hour at 37°C with shaking. After washing, adsorbed bacteriophage particles were eluted by triethylamine. When individual bacteriophage clones (48 clones) were analysed the bacteriophage particles sorption to CBD as negative control was extrapolated.

DNA sequencing and analysis

scFv DNA from TG1 bacterial clones was isolated by BioSilica columns (Novosibirsk, Russia). The DNA was sequenced using the primers LMB3 and pHEN-SEQ SEQ [28] and a sequencing kit BigDye $\text{\textcircled{R}}$ Terminator v3.1 Cycling Sequencing Kit (Applied Biosystems, Foster City, CA). The sequencing was performed in the inter-institutional centre of DNA analysis of the Siberian Branch of the Russian Academy of Sciences and using equipment of the Core Centre 'Genomic Technologies, Proteomics and Cell Biology' in the All-Russia Research Institute for Agricultural Microbiology.

T4 purification

The purification of His-tagged A4 was performed using Ni $^{2+}$ resin as described in [26]. The resulting DNA

from A4 of M13 phage encoding scFv against pSh was transformed into *E. coli* HB2151 strain for protein expression. Two hundred and fifty μ l of LB containing ampicillin (150 mg/ml) were inoculated with 500 μ l of an overnight culture of transformed *E. coli* and cells were grown at 37°C with vigorous shaking until an absorbance of 0.6–1 OD at 600 nm was attained. The induction of protein synthesis was induced by the addition of 1 mM isopropyl-beta-D-thiogalactopyranoside (Helicon, Novosibirsk, Russia). Overnight after induction, the bacterial cells were harvested by centrifugation and suspended in 6 ml of sonication buffer (PBS containing 100 mM 4-(2-aminoethyl)benzenesulfonyl fluoride (Sigma, St. Louis, MO, USA). The disrupting of the bacterial cells and the chromosomal DNA was with four 30-s cycles at 70 watts in Vibra-cell Sonic power sonicator (Sonics, Newtown, CT, USA). Insoluble cellular membranes were removed by centrifugation at 25,000 \times g for 15 min at 4°C. His-tagged A4 was in the supernatant and was purified by adsorption onto Ni $^{2+}$ resin (Lab Instruments, Moscow, Russia) and elution with elution buffer (250 mM imidazole, pH 6.0), followed by dialysis against a buffer solution (400 mM Tris, pH 8.0, 500 mM NaCl, 1 mM EDTA) for 4 hours at 0°C. The protein refolding occurred during dialysis. Quality control for protein folding was tested by binding of antibodies to antigens. Such preparation of the His-tagged A4 was ~90% pure as assessed by SDS-PAGE. Concentration of purified protein was determined using the BCA Protein Assay (Thermo Fisher Scientific Waltham, Massachusetts, USA) and by spectrophotometry at 280 nm.

The A4 DNA was subcloned into the *Nco*I and *Bam*HI sites of the pTT10 vector. In this case of CBD-fusion A4, the protein was prepared as described in [25].

SDS-PAGE

Gel electrophoresis was performed according to the method of Laemmli in 12.5% acrylamide gels. Proteins were detected in the gels by staining with 0.04% Coomassie G-250 (Bio-Rad Laboratory, Hercules, CA, USA).

Direct ELISA

Noncompetitive direct immunoassay was based on the specific binding of A4 to pSh or T72 [29]. The 96-well microtiter plates were coated with His-tagged A4 at 100 ng/ml at 37°C for one hour. After each step the plates were incubated at 37°C on a shaker for one hour. After each incubation step the plates were washed 3 times with PBS containing 0.05% Tween 20. After His-tagged A4 coating the plates were blocked by adding to each well 250 μ l of blocking solution (PBS containing 0.5% BSA and 0.05% Tween 20). The pSh (from 0.8 ng/ml to 22 ng/ml) or T72 (from 0.2 to 12 ng/ml) were added. The rabbit anti-CBD Ab (1 : 1000) and then horseradish peroxidase-labelled an-

ti-rabbit conjugates of mouse Ab (1 : 5000) were added to the wells successively. The binding was detected by adding of tetramethylbenzidine. The production of coloured reaction was stopped by 2N HCl. The optical density was performed using wavelength of 450 nm on plate reader iMark (Bio-Rad Laboratory, Hercules, CA, USA).

In the case of CBD-fusion A4 the direct ELISA was the same except for the details. The 96-well microtiter plates were coated with CBD-fusion A4. Then after blocking pSh or T72 were added. Mouse anti-cMyc Ab (1 : 1000), which

bound pSh or T72 and horseradish peroxidase-labelled anti-mouse conjugates of rabbit Ab (1 : 5000) were used.

Competitive ELISA

The competitive ELISA was evaluated as non-competitive ELISA (described above), except of the 96-well microtiter plates were coated with 100 ml of conjugate BP-BSA at 2 ng/ml for overnight at 6°C. The pSh or T72 (4 and 15 ng/ml, respectively, corresponding to half of the maximum saturation concentration – IC₅₀) were added in

Table 1. Analysis of the nucleotide sequences encoding V-, D-, and J-segments of heavy (A) and light (B) chains of A4. The comparison of the DNA sequences of A4 to germline segments

#	Germline segments	% identity	FR/CDR	Mutations		Amino acid residues replacements		
				R	S	1	2	3
A4	IGHV1-69*13	93.75%	FR	10	0	a2>g, Q1>R (+ - -) g3>a, Q1>R (+ - -) t5>g, V2>G (- - -) g6>t, V2>G (- - -) c7>g, Q3>E (+ + -) c16>g, Q6>E (+ + -) t49>g, S17>A (- + -) g54>a	c117>g, I39>M (+ + -) a118>c, S40>H (+ - -) g119>a, S40>H (+ - -)	-
			CDR	6	1	g82>t, G28>Y (+ - -) g83>a, G28>Y (+ - -) g104>c, S35>T (+ - +) a106>g, S36>G (+ + -) t111>c g112>t, A38>Y (- - -) c113>a, A38>Y (- - -)	-	-
	IGHJ6*02	93.10%					-	
	IGHD2-15						-	
B								
#	Germline segments	% identity	FR/CDR	Mutations		Amino acid residues replacements		
				R	S	1	2	3
A4	IGKV3-20*01	95.04%	FR	3	1		g153>t, R51>S (- - -) t158>c, L53>P (- - -) a164>t, Y55>F (- + -)	t312>c
			CDR	13	2	a80>g, Q27>R (+ - -) g85>a, V29>I (+ - +) g110>c, S37>T (+ - +)	g167>c, G56>A (- + -) g169>a, A57>T (- - -)	g315>a a320>t, Y107>F (- + -) g322>a, G108>N (- - -) g323>a, G108>N (- - -) c327>t c329>a, S110>Y (+ - -) a330>t, S110>Y (+ - -) c331>t, P111>Y (+ - -) c332>a, P111>Y (+ - -) t333>c, P111>Y (+ - -) c334>a
	IGKJ2*01	89.74%					-	

R and S were significant and insignificant nucleotide substitutions, respectively. The (+ + -) indicated of comparison of two amino acid residues (before and after replacement): hydrophobicity, size and physic-chemical characteristics. Percent of homology with embryonic segments was given only for V and J segments of the scFvs

the presence of competitor (A4) at a concentration between 0.0016 to 0.1 mg/ml. Both His-tagged A4 and CBD-fusion A4 were used. For the rabbit anti-CBD Ab (10.8 ng/ml), which bound pSh or T72 and horseradish peroxidase-labelled anti-rabbit conjugates of mouse Ab (1 ng/ml) were

used. In case of CBD-fusion A4 the mouse anti-cMyc Ab (1 : 1000), which also bound pSh or T72 and horseradish peroxidase-labelled anti-mouse conjugates of rabbit Ab (1 : 5000) were used.

Surface plasmon resonance

The kinetics of interaction between A4 and pSh/T72 was performed by the surface plasmon resonance instrument ProteOn XPR36 (BioRad Laboratory, Hercules, CA, USA) using purified proteins. A4 was immobilised using the amino groups on the surface of the biochip. pSh or T72 were in flow through the chip surface as analytes at concentrations of 0.266 mM, 0.532 mM, 1.06 mM, 2.13 mM and 0.199 mM, 0.399 mM, 0.798 mM, 9.97 mM, respectively. BSA was immobilised on the biochip as a negative control. The binding of pSh (T72) to BSA was taken into account at final constant calculations. Both His-tagged A4 and CBD-fusion A4 were used in surface plasmon resonance experiments and gave us the same results.

Results

Selection and DNA sequence analysis of specific phages

The selection of scFvs against pSh (mouse idotype against BP) was carried out by phage display. The naive combinatorial library of human scFvs was used [24], the size of which was 1.9×10^{10} cfu/ml, indicating that the library satisfied with high sequence diversity. The library was panned three times against immobilised pSh to microtiter plate. As a result of analysis of 48 individual bacterial clones, the 14 positive clones with the strongest response to the pSh were selected. The phagemid DNA from the 12 bacterial clones were isolated and sequenced. DNA sequencing of 12 clones showed that all contained inserts phagemid DNA encoding scFvs. Only 7 sequenced DNA samples were unique and the rest of them contained repetitions. Only one clone A4 was chosen for further analysis and work because of the preliminary experiments showed that A4 bound to pSh with high affinity (data not shown).

Analysis of the amino acid and DNA sequences of A4

The analysis of the nucleotide sequences encoding V-, D-, and J-segments of heavy and light chains of A4 was done by the IMGT V-QUEST (Table 1). V-, J-, and D-segments of A4 heavy chain belonged to IGHV1-69*13, IGHJ6*02, and IGHD2-15 family segments, respectively. Light chain of A4 applied to the family of κ -chains. V- and J-segments of A4 light chain belonged to IGKV3-20*01 and IGKJ2*01 family segments, respectively. By comparing the A4 nucleotide sequence with germline segments, it could be assumed that V-segments of the A4 were low

Heavy chain			
FR1	CDR1	FR2	CDR2
RGELVESGAEVKKPGASVKVSCAS	GYTFTGYY	MHWVVRQAPGQGLEWMGG	IIPFGTA
FR3	CDR3	FR4	
NYAQKFRVITADKSTSTAYMELSSLRSEDVAVYYC	ARDRVPAAMGVSIDYYYYGMDV	WGQGTLLTVSS	
Light chain			
FR1	CDR1	FR2	
EIVLTQSPGTLSLSPGERATLSCRAS	RSISSTY	LAWYQQKPGQAPSLPIF	
CDR2	FR3	CDR3	FR4
ATS	SRATGIPDRFSGSGGTDFLTISRLEPEDEFAVYYC	QQFNYYT	FGQGTKVEIK

Fig. 1. Amino acids sequence of A4 CDR and FR delimitations were from the IMGT V domain directory

Table 2. The A4 CDR3 formation by gene V-, D-, and J-segments

V-segment			J-segment
A4 HC	~MELSSLRSED TAVYYCAR	–	DRVPAAMGVSID YYYYYGM DV~
A4 LC	~LTISRLEPEDFAVYYC QQFNS	Y	YTFGGG TKLEIK~

The CDR3 is in bold. Amino acid chains start with a conservative amino acid residue – LM89 [30]. HC – heavy chain, LC – light chain

conservative to V germline segments. The percentage identity ranged was 93.75% for the heavy chain and 95.04% for the light chain.

Searching the National Centre for Biotechnology Information database (NCBI, USA) using the BLAST algorithm revealed that A4 was unique and did not have any homology among published antibodies. The amino acid sequence was nearly identical to a sequence in antibody against INF- γ (AHM25306.1) – Max score 360, Query cover 100%, Ident 76% (data not shown).

Figure 1 shows the A4 amino acid sequence consisting of 236 amino acids excluding the 18 amino acid residues linker connecting the heavy and light chains. A4 is composed of 129 amino acid residues of the heavy chain and 107 amino acid residues of the light chain. The Figure 1 shows the analysis of the constant and variable amino acid sequences regions of the heavy and light chains. Interestingly, the shortest of the LCDR2 was only three amino acid residues. The HCDR3 was the longest and consisted of 23 amino acid residues.

The CDR3 region is the most variable part of the scFv, in the formation of which Variable-, Diversity-, and Joining-segments attended. To understand and clarify the recognition of the A4 properties, the maturation mechanisms comprising V/D/J recombination and variability at junctional site of those A4 was studied and compared with their predecessor germline sequences. Table 2 presents an analysis of segment boundaries in the formation of A4. Interestingly, the HCDR3 contained no D-segment. The main part of the HCDR3 was encoded by J-segment and only two amino acids by V-segment. In the case of A4 light chain there was one triplet for Y insertion between V- and J-segments.

Expression and purification of A4

The preliminary experiments showed that the anti-idiotypic A4 bound to mouse idiotype antibody pSh with high affinity (data not shown), which is why DNA of A4 was expressed in *E. coli* and proteins purified in preparative amounts by affinity chromatography on a nickel resin as mentioned in the 'Materials and methods' section. Also A4 DNA was subcloned into pTT10 vector for A4 expression as a CBD-fusion. In the last case cellulose was used for A4 purification as indicated in [25]. Figure 2 shows an electrophoretogram of CBD-fusion A4 after SDS-PAGE electrophoresis. The purified A4 migrated as major bands of ~51 kDa consistent with its predicted molecular weights

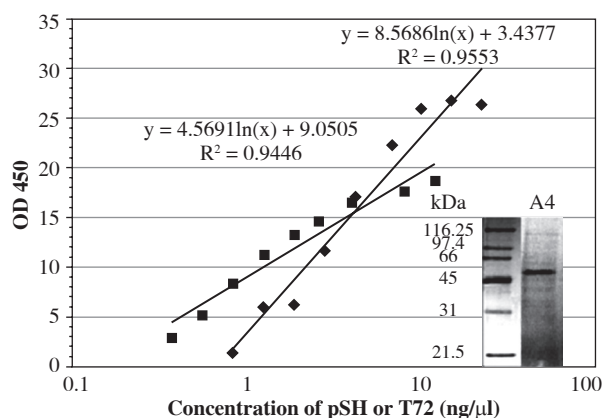


Fig. 2. The result of ELISA binding of pSh (rhombus) and T72 (foursquare) to microtiter plates immobilized A4. The electrophoreses was on 12.5% acrylamide gels under reducing conditions and stained with Coomassie R-250. A4 was expressed as CBD-fusion and purified on cellulose. A4 migrated as ~51 kDa protein corresponding to protein ladder

of the processed form of CBD-fusion scFv, i.e. without a leader peptide.

The Affinity of A4

Direct ELISA was used for A4 binding estimation to murine idiotype pSh and human idiotype T72 (Fig. 2). Both His-tagged A4 and CBD-fusion A4 were used in ELISA experiments and gave us the same results (data not shown). pSh was used for phage library screening. However also A4 showed a positive reaction with the T72 in the assay used, despite the fact that the active sites of pSh and T72 were different [25, 26]. A4 binding had a dose-dependent manner in both cases and was very similar.

The optical biosensor ProteOn (Bio-Rad, Hercules, California, USA) was used to determine the dissociation constants for purified A4 and pSh (T72) by surface plasmon resonance. A4 was immobilised onto chip GLM using amino groups. Increasing concentrations of pSh or T72 were in the solution: 0.266 mM, 0.532 mM, 1.06 mM, 2.13 mM and 0.199 mM, 0.399 mM, 0.798 mM, 9.97 mM, respectively. BSA was immobilised on the chip as

Table 3. Equilibrium constants for binding of surface-immobilized A4 to pSh and T72

	ka (M ⁻¹ s ⁻¹)	kd (s ⁻¹)	Kd (M)	Ka (M ⁻¹)	χ ² (RU)	Residuals
pSh	9.97 × 10 ⁺²	4.43 × 10 ⁻⁴	4.44 × 10 ⁻⁷	2.2 × 10 ⁺⁶	23.23	from -20 till 20
T72	4.42 × 10 ⁺³	2.52 × 10 ⁻³	5.71 × 10 ⁻⁷	1.7 × 10 ⁺⁶	34.89	from -20 till 40

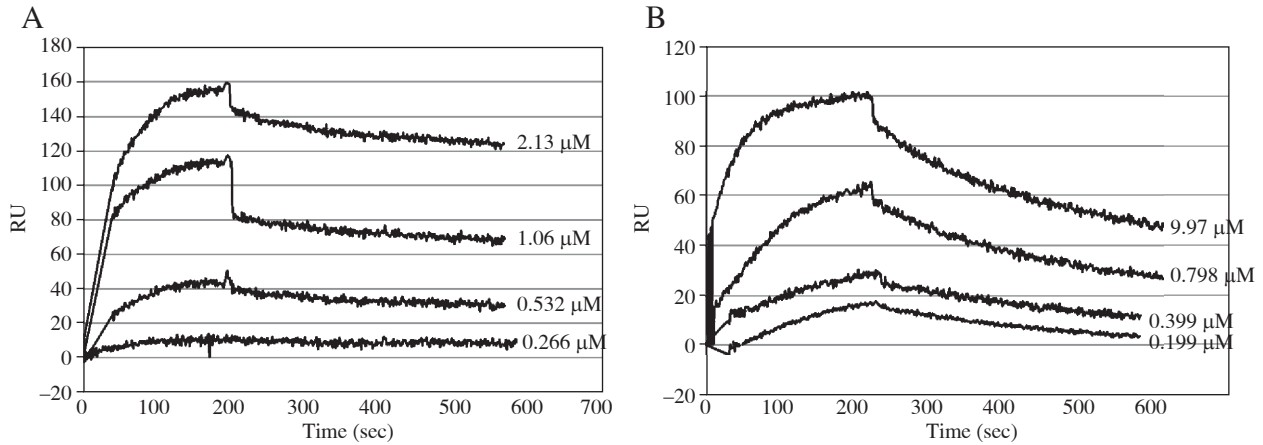


Fig. 3. Association-dissociation curves of (A) pSh and (B) T72 with chip GLM immobilized A4

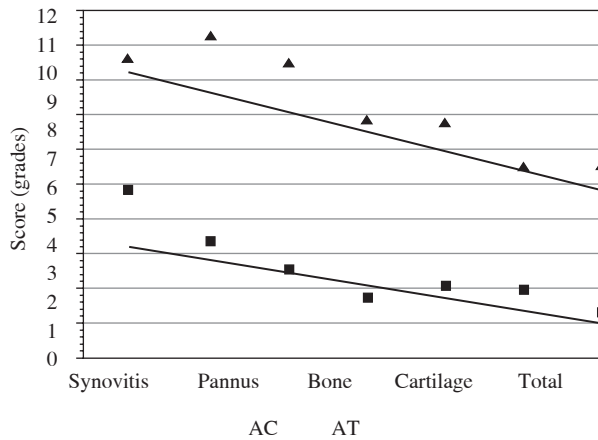


Fig. 4. The result of competitive ELISA binding of pSh (triangle) and T72 (square) to immobilized BP in the presence of increasing concentration of A4

a control. Figure 3 shows the sensorgram curves A4 to pSh (A) and T72 (B). The K_d values for His-tagged A4 and CBD-fusion A4 were the same.

The simple 1 : 1 interaction model ($A + B = AB$) was used for the calculation of values of constants. Table 3 shows the final calculated results for the association rate constants – ka, dissociation rate constants – kd, dissociation

constants – K_d and association constants – K_a for A4 binding to pSh and T72. K_d values for A4 to pSh and T72 were very close 4.44×10^{-7} M and 5.71×10^{-7} M, respectively. It was correlated with ELISA result (Fig. 2) where pSh and T72 binding to A4 curves were almost coincided.

The competitive ELISA was assessed to define anti-idiotypic A4 mimicked BP epitope and interacted with active centers of idiotype antibodies against BP (pSh and T72) (Fig. 4). An immunological plate was coated with BP-BSA. The T72 and pSh (concentration at half saturation of the maximum BP binding – IC_{50}) were in solution in the presence of increasing competitor concentrations of A4. A4 inhibited the binding of BP-BSA with both T72 and pSh in a dose dependent manner. Moreover, A4 inhibition of T72 binding to BP-BSA was stronger than in the case of pSh to BP-BSA.

Discussion

Earlier, high affinity murine scFv Ab1 against BP with $K_d = 0.7 \times 10^{-8}$ M [25, 31] was obtained and monoclonal antibodies with $K_d = 0.68 \times 10^{-10}$ M [32], as well as human scFv against BP with $K_d = 2.93 \times 10^{-7}$ M [26]. The high affinity of human anti-idiotypic scFv against BP was described for the first time in the current article.

The A4 against pSh (murine idiotype against BP) was found after screening of the naive combinatorial library of scFv genes from human leukocyte, which has been de-

scribed in [25]. Nucleotide sequence analysis A4 DNA was distributed on gene families and subfamilies based on the analysis of heavy and light chains of scFv (Table 1). Interestingly, IGHV 1-69*13, which encoded the V-domain of A4 heavy chain, was found mainly in immunoglobulins expressed in B cells in chronic lymphocytic leukaemia [33]. IGHJ6*02, which encoded the J-domain of the A4 heavy chain, was heavily mutated in leukaemia [34]. IGKV3-20*01, V-domain coding A4 light chain, played an important role in the pathogenesis of eye lymphoma [35]. The percentage of homology analysed A4 V-segments with segment germ lines was very low: 93.75% and 95.04% for the heavy and light chains, respectively. The A4 light chain belonged to κ chains (70% of the total light chains of Ab). Also, Table 2 shows CDR3L and CDR3H formation from V-, D-, and J-segments of DNA.

A4 was purified in two different ways: using cellulose (Fig. 2, insert) and Ni²⁺-resin (data not shown). Both ways gave us the same major bands on SDS-PAGE. However, the molecular weights of the two A4 were different, because of A4 different fusions. CBD-fusion A4 migrated as band of ~51 kDa and His-tagged A4 of ~31 kDa, when analysed by SDS-PAGE. CBD-fusion A4 and His-tagged A4 gave us the same results in ELISA and ProteOn experiments. Both purified A4 bound both pSh and T72 in ELISA (Fig. 2), despite the fact that pSh and T72 had different binding sites for A4. Measured K_d values for binding A4 (His-tagged A4 and CBD-fusion A4) to pSh and T72 by surface plasmon resonance were very close 4.44×10^{-7} M and 5.71×10^{-7} M, respectively (Table 3). The competitive ELISA was held in order to prove that A4 recognised the active centers of pSh and T72. The result is shown in Fig. 4. A4 competed with BP-BSA in binding to both pSh and T72. Thus, the A4 was an anti-idiotypic antibody and bound the active centers of pSh and T72. The amino acid sequences of pSh and T72 were presented by Ustinov *et al.* [25, 26], respectively. The identity between pSh and T72 was low, because of different amino acid sequences: Max score 185, Query cover 92%, Ident 47% (data not shown). However A4 carried an internal immunological image of BP, so it could recognise of completely different idiotypic antibodies.

A4 was purified and analysed for further use in the development of cancer immunodiagnostic techniques [36]. A4 could be used as an antigen to replace hazardous BP-BSA in immunoassay measure the Ab1 detection in human blood serum and also as a standard for the quantitative analysis of Ab2 against BP in human blood serum. Also, A4 could be used in creating new approaches in human cancer immunoprophylaxis. However, firstly we need to figure out immune response and inhibition pathogenic effects induced by A4 compared with those induced by BP in mouse.

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The authors declare no conflict of interest.

References

1. Jerne NK (1974): Towards a network theory of the immune system. *Ann Immunol (Paris)* 125C: 373-389.
2. Jerne NK (1984): Idiotypic networks and other preconceived ideas. *Immunol Rev* 79: 5-24.
3. Eichmann K, Rajewsky K (1975): Induction of T and B cell immunity by anti-idiotypic antibody. *Eur J Immunol* 5: 661-666.
4. Tornetta M, Fisher D, O'Neil K, et al. (2007): Isolation of human anti-idiotypic antibodies by phage display for clinical immune response assays. *J Immunol Methods* 328: 34-44.
5. Tzioufas AG, Routsias JG (2010): Idiotype, anti-idiotypic network of autoantibodies: pathogenetic considerations and clinical application. *Autoimmun Rev* 9: 631-633.
6. van Schie KA, Wolbink GJ, Rispen T (2015): Cross-reactive and pre-existing antibodies to therapeutic antibodies – Effects on treatment and immunogenicity. *MAbs* 7: 662-671.
7. Tohidkia MR, Barar J, Asadi F, et al. (2012): Molecular considerations for development of phage antibody libraries. *Drug J Target* 20: 195-208.
8. Chin SE, Ferraro F, Groves M, et al. (2015): Isolation of high-affinity, neutralizing anti-idiotypic antibodies by phage and ribosome display for application in immunogenicity and pharmacokinetic analyses. *J Immunol Methods* 416: 49-58.
9. Lim SY, Chan CEZ, Lisowska MM, et al. (2015): The molecular engineering of an anti-idiotypic antibody for pharmacokinetic analysis of a fully human anti-infective. *PLoS One* 10: e0145381.
10. Yuan W, Xia G, Zhao C, et al. (2012): Anti-idiotypic single chain mimicking CA125 linked with tuftsin provides protective immunity against ovarian cancer in mice. *Mol Med Rep* 5: 388-394.
11. Wang JJ, Li YH, Liu YH, et al. (2010): The ability of human bispecific anti-idiotypic antibody to elicit humoral and cellular immune responses in mice. *Int Immunopharmacol* 10: 707-712.
12. Wang JJ, Liu YH, Li GC (2015): Induction of protective and therapeutic anti-cancer immunity by using bispecific anti-idiotypic antibody G22-I50 for nasopharyngeal carcinoma. *Int Immunopharmacol* 28: 1026-1033.
13. Luo C, Wang JJ, Li YH, et al. (2010): Immunogenicity and efficacy of a DNA vaccine encoding a human anti-idiotypic single chain antibody against nasopharyngeal carcinoma. *Vaccine* 28: 2769-2774.
14. Chang DK, Kurella VB, Biswas S, et al. (2016): Humanized mouse G6 anti-idiotypic monoclonal antibody has therapeutic

- tic potential against IGHV1-69 germline gene-based B-CLL. *MAbs* 10: [Epub ahead of print].
15. Koprowski H, Herlyn D, Lubeck M, et al. (1984): Human anti-idiotypic antibodies in cancer patients: Is the modulation of the immune response beneficial for the patient? *Proc Natl Acad Sci U S A* 81: 216-219.
 16. Herlyn D, Ross AH, Koprowski H (1986): Anti-idiotypic antibodies bear the internal image of a human tumor antigen. *Science* 232: 100-102.
 17. Reinsberg J (2007): Detection of human antibodies generated against therapeutic antibodies used in tumor therapy. *Methods Mol Biol* 378: 195-204.
 18. Grant SC, Kris MG, Houghton AN, et al. (1999): Long survival of patients with small cell lung cancer after adjuvant treatment with the anti-idiotypic antibody BEC2 plus Bacillus Calmette-Guérin. *Clin Cancer Res* 5: 1319-1323.
 19. Neningen E, Díaz RM, de la Torre A, et al. (2007): Active immunotherapy with 1E10 anti-idiotypic vaccine in patients with small cell lung cancer: report of a phase I trial. *Cancer Biol Ther* 6: 145-150.
 20. Hernández AM, Vázquez AM (2015): Racotumomab-alum vaccine for the treatment of non-small-cell lung cancer. *Expert Rev Vaccines* 14: 9-20.
 21. Chagnaud JL, Faibre S, Geffard M (1994): Curative effects on rat sarcomas obtained after a treatment combining two monoclonal antibodies. *Anti-Cancer Drugs* 5: 361-366.
 22. Ustinov VA, Matveeva VA, Kostyanko MA, et al. (2013): Antibodies against benzo[a]pyrene in immunized mouse and in lung cancer patients. *Exp Oncol* 35: 207-210.
 23. Glushkov AN (2014): Immunological disbalance in carcinogenesis. *Medical Hypotheses* 83: 166-171.
 24. Batanova TA, Ulitin AB, Zhirakovskaya EV, et al. (2006): Construction and characterization of combinatorial naive phage library of human scFvs. *Mol Genetics Microbiol Virol* 3: 35-41.
 25. Ustinov VA, Averjanov AV, Glushkov AN (2014): Purification and characterization of mouse single-chain antibody against polycyclic aromatic hydrocarbons. *Journal of Immunoassay and Immunochemistry* 35: 428-441.
 26. Ustinov VA, Studennikov AE, Vavilov VA, et al. (2015): Generation and Characterization of Human Single-Chain Antibodies Against Polycyclic Aromatic Hydrocarbons. *Immunological Investigations* 44: 536-552.
 27. Kostyanko MV, Glushkov AN (1998): Synthesis of hapten-protein conjugate. Patent RF 2141114.
 28. Vikhrova MA, Shveygert MV, Khrapov EA, et al. (2010): Selection of naturally occurring autoantibodies to interleukin-18 from phage display library. *Hum Antibodies* 19: 71-78.
 29. Glushkov AN, Kostyanko MV, Chernov SV, et al. (1998): Immunoassay of antibodies to benz[a]pyren. *Experim Oncol* 20: 74-76.
 30. Lefranc MP, Pommie C, Ruiz M, et al. (2003): IMGT unique numbering for immunoglobulin and T cell receptor variable domains and Ig superfamily V-like domains. *Dev Comparative Immunol* 27: 55-77.
 31. Karsunke XYZ, Wang H, Weber E, et al. (2012): Development of single-chain variable fragment (scFv) antibodies against hapten benzo[a]pyrene: a binding study. *Anal Bioanal Chem* 402: 499-507.
 32. Karsunke XYZ, Pschenitzka M, Rieger M, et al. (2011): Screening and characterization of new monoclonal anti-benzo[a]pyrene antibodies using automated flow-through microarray technology. *Journal of Immunological Methods* 371: 81-90.
 33. Que X, Widhopf GF, Amir S, et al. (2013): IGHV1-69-encoded antibodies expressed in chronic lymphocytic leukemia react with malondialdehyde-acetaldehyde adduct, an immunodominant oxidation-specific epitope. *PLoS One* 8: e65203.
 34. Muggen AF, Pillai SY, Kil LP, et al. (2015): Basal Ca(2+) signaling is particularly increased in mutated chronic lymphocytic leukemia. *Leukemia* 29: 321-328.
 35. Zhu D, Lossos C, Chapman-Fredricks JR, et al. (2013): Biased immunoglobulin light chain use in the *Chlamydomonas psittaci* negative ocular adnexal marginal zone lymphomas. *Am J Hematol* 88: 379-384.
 36. Glushkov A (2013): Clinical immunology carcinogenesis: new challenges and prospects. *Rus J Immunology* 7: 27-34.