Production of N^{α} **-acetyl T** α **1-HSA through** *in vitro* **acetylation by RimJ**

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ABSTRACT

Thymosin alpha 1 (T α 1) is an important immunomodulating agent with various clinical applications. The natural form of T α 1 is N^{α} -acetylated, which was supposed to be related to *in vivo* stability of the hormone. In this study, fusion protein T α 1-HSA was constructed and expressed in *Pichia pastoris*. RimJ, a N^{α} -acetyltransferase from *E.coli*, was also overexpressed and purified to homogeneity. *In vitro* acetylation of T α 1-HSA in the presence of RimJ and acetyl coenzyme A resulted in N^{α} -acetyl T α 1-HSA. The N^{α} -acetylation was determined by LC-MS/MS. Kinetic assay indicated that RimJ had a higher affinity to desacetyl T α 1 than to T α 1-HSA. Bioactivity assay revealed fully retained activity of T α 1 when the hormone was connected to the N-terminus of the fusion protein, while the activity was compromised in our previously constructed HSA-T α 1. With fully retained activity and N-terminal acetylation, N^{α} -acetyl T α 1-HSA was expected to be a more promising pharmaceutical agent than T α 1.

INTRODUCTION

Thymosin alpha 1 (T α 1), an acidic thymic peptide consisting of 28 amino acids, was first described and characterized by Goldstein et al. [1]. As an endogenous regulator of both innate and adaptive immune systems, T α 1 has been shown to trigger maturational events in lymphocytes, to augment T-cell function, and to promote reconstitution of immune defects [2, 3]. Extensive clinical studies have been conducted to support the role of T α 1 in various indications. The versatility of T α 1 has aroused great interest in pharmaceutical industry. ZADAXIN, developed by SciClone Pharmaceutcials, has been marketed in more than forty countries as the first immuneboosting synthetic peptide for a variety of indications, including Hepatitis B and liver cancer.

One of the biggest challenges for biotechnical production of $T\alpha 1$ by genetic engineering is degradation of the small peptide by proteases in the host cell, leading

to decreased production and interference in isolation from degraded fragments [4]. Most of the strategies aiming at circumventing the above challenge follow the same pattern of production of a larger precursor and subsequent cleavage to release $T\alpha 1$. Esipov et al. reported fused expression of T α 1 and thioredoxin followed by proteolytic cleavage of the precursor [5]. Expression of concatemer T α 1 gene of 6 repeats facilitated purification by increasing molecular size, and Tα1 monomer was released after hydroxylamine incision [6]. Fusion protein of T α 1-Intein was also successfully constructed to release $T\alpha 1$ after intein-mediated N-terminal cleavage [7, 8]. All these approaches of cutting a bigger precursor into $T\alpha 1$ suffer from low cleavage efficiency, imprecise or non-specific incision and expensive cost of the cutting enzymes. In addition, the harsh conditions required for cutting by chemical reagents such as hydroxylamine may structurally modify the target peptides.

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In contrast, fusion of $T\alpha 1$ with a partner that doesn't require subsequent cleavage is a more promising strategy. Human serum albumin (HSA) is the most abundant plasma protein (35-50 g/L human serum). When fused with target protein, HSA usually confers prolonged half-life [9], improved efficacy [10], and reduced toxicity [11]. In our previous work, two fusion proteins, HSA-Ta1 and HSA-linker-Ta1, were constructed and expressed in recombinant Pichia pastoris [12]. Both fusion proteins showed comparable bioactivity with Ta1 and improved pharmacokinetic profiles with prolonged half-life. Since HSA is connected to the N-terminus of $T\alpha 1$, $T\alpha 1$ in the two fusion proteins were desacetylated, while natural T α 1 and the commercialized thymosin α 1 Zadaxin are N^{α} -acetylated. Although desacetyl thymosin α 1 is known to show biological activity equivalent to that of the native hormone, it is less stable *in vivo* [13]. There are several methods, chemical or biochemical, available for the production of N^{α} -acetylated T α 1. Esipov et al. reported in vitro N^a-acetylation of Ta1 by acetic anhydride [5]. Co-expression of the target protein with N^{α} -acetyltransferase from *Escherichia coli* such as RimJ [14] and RimL [15] as well as N^{α} -acetyltransferase from Sulfolobus solfataricus[16] also resulted in partial acetylation of T α 1.

In this study, a fusion protein T α 1-HSA with a native N-terminus of T α 1 was constructed and expressed in *P.pastoris*. N-terminal acetyl transferase RimJ was overexpressed in *E.coli* and purified to catalyze N-terminal acetylation of T α 1-HSA in the presence of acetyl coenzyme A. With fully retained activity and N-terminal acetylation, N^{α} -acetyl T α 1-HSA was expected to be a more promising pharmaceutical agent than T α 1 and the previously obtained fusion proteins.

RESULTS AND DISCUSSION

Construction of expression vector pPICZaA / Ta1-HSA

In the fusion protein, HSA was connected to the C-terminus of T α 1 such that the N-terminus of T α 1 was available for acetylation. T α 1-HSA gene was introduced downstream of the gene coding for a-factor secretion signal peptide in pPICZ α A. In order to express protein with a native N-terminus, T α 1-HSA gene was cloned flush with a Kex2 cleavage site (Supplementary Figure 1). After double digestion and insertion into pPICZ α A, positive clones of *E.coli* Top 10 were selected by using 100µg/ml Zeocin and confirmed by DNA sequencing. The constructed expression vector pPICZ α A/T α 1-HSA was amplified, extracted and then linearized with *Sac* I. The linear plasmid DNA was transformed into competent *P.pastoris* GS115 prepared by treatment with

lithium chloride. After cultivation on YPD agar plate supplemented with zeocin at 30°C for 48-72 h, positive transformants were selected and confirmed by DNA sequencing.

Production and purification of Tα1-HSA in *P. pastoris* GS115

In order to increase the recombinant expression of T α 1-HSA, induction time (1-7 days) and methanol concentration (0.5-3.0%) were optimized in shakeflask cultures. As shown in Supplementary Figure 2 and Supplementary Figure 3, the optimum induction time was 6 to 7 days, and induction with 1.5% methanol was the most favorable. Because of secretory production led by α -factor, T α 1-HSA could be purified from the supernatant of fermentation broth. Compared with intracellular production, secretory production is more favorable to downstream purification because of less interfering proteins existing in the supernatant. In addition, native N-terminus could be obtained after cleavage of the signal peptide. After a series of purification steps including ultrafiltration, weak cation exchange and affinity chromatography with Blue-Sepharose Fast Flow, the purified protein gave a single band on SDS-PAGE stained with Coomassie brilliant blue R-250 (Figure 1). Its molecular mass was estimated to be around 70 kDa, which was very close to the theoretical molecular weight of the fusion protein.

Construction, production and purification of RimJ

Acetylation of proteins is catalyzed by a variety of acetyltransferases that transfer acetyl groups from acetylcoenzyme A to either the α -amino group of the N-terminal residues ore-amino group of lysine residues at various positions [17]. For the *in vitro* acetylation of T α 1-HSA, expression vector pET-28a(+)/RimJ was constructed and transformed into competent host cell *E.coli* BL21. Positive transformants were screened by 25µg/ml kanamycin and the target gene was confirmed by double digestion and DNA sequencing.

After cultivation at 37°C overnight, cell pellet was obtained after centrifugation and crushed by sonication. A substantial amount of RimJ was overexpressed in *E. coli* BL21 in the soluble form although inclusion body of RimJ was also detected. Since a N-terminal hexahistidine tag was fused with RimJ, a two-step purification containing cation exchange chromatography and Ni²⁺ chelating column was successfully applied to purify RimJ into homogeneity. The single band in column 3 of Figure 2 corresponds to RimJ with a theoretical molecular weight of 22.6kDa.

In vitro acetylation and mass spectrometry characterization

 N^{α} -acetyl T α 1-HSA obtained after in vitro acetylation by RimJ was purified with Sephadex G50 and concentrated with centrifuge concentrators (Amicon Ultra-15, 50k MWCO). LC-MS/MS analysis covered 92.17% of the total sequence, including both the N- and C-termini of the fusion protein (Figure 3). The fusion protein had a native N terminus of $T\alpha 1$ and a native C-terminus of HSA. A fragment with m/z of 1466.68767 was captured in the first stage of mass spectrometry and further analyzed as S(acetyl)DAAVDTSSEITTK in the second stage of mass spectrometry (Figure 4) since fragment b2⁺ is 42 larger than its un-acetylated counterpart. Apart from N-terminal acetylation on serine, acetylation on other 13 lysine residues of the fusion protein were also identified, which was speculated to be catalyzed by acetyltransferase in P. pastoris. The molecular mass of N^{α} -acetyl T α 1-HSA was determined to be 69.5kDa.

 N^{α} -Acetylation is one of the most common protein modifications in eukaryotes, but rarely in prokaryotes [18]. However, previous studies have identified three NATs in *E.coli*, namely, RimL, RimJ and RimI, which are responsible for the acetylation of L12, S5 and S16 respectively [19, 20]. Fang *et al.* observed partial acetylation of fusion protein T α 1-L12 when it is recombinantly expressed in *E.coli*. They further disrupted the NATs in *E.coli* one by one and found that when RimJ was disrupted, the fusion protein was completely unacetylated. Based on this finding, we performed *in vitro* acetylation of T α 1-HSA by using purified RimJ. In the presence of AcCoA, a single acetyl group was added to the N-terminal serine residue of T α 1-HSA. Although it is possible to perform *in vivo* acetylation of T α 1-HSA if the fusion protein and RimJ are co-expressed in the host cell, complete N^{α} -acetylation may not be achieved. The final product is very likely to be a mixture of N^{α} -acetyl and N^{α} desacetyl T α 1-HSA, which are extremely difficult to be separated and purified into homogeneity.

Kinetic study of in vitro acetylation

RimJ catalyzes the transfer of acetyl group from AcCoA to the α -NH₂ of serine residue of T α 1-HSA or desacetyl T α 1. The resulting free CoA will react with DTDP to form a product with maximum absorption at 324 nm. The reaction rate was measured by the increase in OD₃₂₄ of the reaction mixture. Theoretically, CoA and N^{α} -acetyl T α 1-HSA or N^{α} -acetyl T α 1 are formed in equal



Figure 1: SDS-PAGE analysis of fractions during T α 1-HSA purification. Lane M, marker; Lane (1) broth supernatant after ultrafiltration with Millipore Cogent M1 Tangential Flow Filtration System (molecular weight cutoff, 30kDa). Lane (2) fractions eluted from CaptoTM MMC column; Lane (3) fractions eluted from Blue-SepharoseTM 6 Fast Flow column.

quantities over the whole time course of acetylation. According to Table 1, a smaller $K_{\rm m}$ value was observed for desacetyl Ta1, showing a higher affinity of RimJ toward Ta1. Higher $V_{\rm max}$ and $K_{\rm cat}$ for desacetyl Ta1 indicated that acetylation of desacetyl Ta1 could be more efficiently catalyzed by RimJ compared with Ta1-HSA. This difference was speculated to be caused by the larger molecular weight and spatial structure of the fusion protein that hindered the collision between enzyme and the substrate.

Bioactivity assay of N^α-acetyl Tα1-HSA

Thymosin alpha 1 alone can't directly stimulate the proliferation of lymphocytes, but when used at low concentrations it can increase the proliferative response of lymphocytes to mitogens like phytohaemagglutinin (PHA) and concanavalin A (ConA). MTT proliferation assay was used to determine the growth-promoting effect of N^{α} -acetyl T α 1-HSA, T α 1-HSA and T α 1(ZADAXIN[®]) on lymphocytes. HSA- T α 1 from our previous work was



Figure 2: SDS-PAGE analysis of fractions during Rim J purification. Lane M: marker; lane (1): supernatant after sonication; lane (2): fractions eluted from CaptoTM MMC column; lane (3): fractions eluted from Ni^{2+} chelating column.

		1	11	21	31	41	51	61	71	81	91
Modifications	1	A			A					с с	
5253GP		SDAAVDTSSE	ITTKDLKEKK	EVVEEAENDA	HKSEVAHRFK	DLGEENFKAL	VLIAFAQYLQ	QCPFEDHVKL	VNEVTEFAKT	CVADESAENC	DKSLHTLFGD
Modifications 5253GP	101 1	A C	o cc	С			OC	AA			CC
		KLCTVATLRE	TYGEMADCCA	KOEPERNECF	LOHKDONPNL	PRLVRPEVDV	MCTAFHDNEE	TFLKKYLYEI	ARRHPYFYAP	ELLFFAKRYK	AAFTECCOAA
Modifications 5253GP	201 I	с	A	AC	A				CC	с	С
		DKAACLLPKL	DELRDEGKAS	SAKORLKCAS	LOKFGERAFK	AWAVARLSQR	FPKAEFAEVS	KLVTDLTKVH	TECCHGDLLE	CADDRADLAK	YICENODSIS
Modifications 5253GP	301	cc	С	0		A	0		A	CC	С
		SKLKECCEKP	LLEKSHCIAE	VENDEMPADL	PSLAADFVES	KDVCKNYAEA	KDVFLGMFLY	EYARRHPDYS	VVLLLRLAKT	YETTLEKCCA	AADPHECYAK
Modifications 4 5253GP	401		с			A			AOC	с	A
		VFDEFKPLVE	EPONLIKONC	ELFEQLGEYK	FONALLVRYT	KKVPQVSTPT	LVEVSRNLGK	VGSKCCKHPE	AKRMPCAEDY	LSVVLNQLCV	LHEKTPVSDR
Modifications 5253GP	501	ACC	с			с	A	A A	0		с
		VTKCCTESLV	NRRPCFSALE	VDETYVPKEF	NAETFTFHAD	ICTLSEKERQ	IKKQTALVEL	VKHKPKATKE	QLKAVMDDFA	AFVEKCCKAD	DKETCFAEEG
Modifications	601										
5253GP		KKLVAASOAA	LGL								

Figure 3: Sequence coverage and residue modification of Ta1-HSA detected by LC-MS/MS. A: acetyle; C:carbamidomethyl; O: oxidation.

also assayed in parallel. As shown in Table 2, when used at different concentrations (0.75, 1.5, 3 and 6µM), all forms of Ta1 stimulated the proliferation of murine spleen lymphocytes in a dose dependent manner. In our previous work, we showed that fusion protein HSA-Ta1 and HSAlinker-Ta1, had comparable but slightly decreased growth promoting effect compared with $T\alpha 1(ZADAXIN^{\text{®}})$. The results are reproduced in Table 2, as indicated by the significant difference between the activity of Tα1(ZADAXIN[®]) and HSA-Tα1 at concentrations of 0.75, 3 and 6 μ M. When the position of Ta1 in the fusion protein was changed from C-terminus to N-terminus, Talactivity was fully retained in the fusion protein. In the study by Daniela *et al.*, injection of T α 1 or N₁₄ fragment significantly increased the T cell precursor frequency in old mice, but no effect was induced by injection of the C_{14} fragment of Ta1, indicating that biological activity of the hormone was restricted to the first 14 amino acids [21]. This is one of the possible reasons for the fully retained activity of N^{α} -acetyl T α 1-HSA. A fully exposed N-terminus of Ta1 in N^{α} -acetyl Ta1-HSA is more favorable for the complete biological activity of the hormone.

T α 1 is a N^{α} -acetylated peptide that is mainly used as an immune-modulating agent to enhance the Th1 immune response. Chemically synthesized T α 1 is used worldwide for the treatment of some immunodeficiencies, malignancies, and infections. A biotechnological approach using the recombinant gene expression will be much more promising. In this study, we constructed fusion protein T α 1-HSA and N^{α} -acetyltransferase RimJ, and purified them into homogeneity. *In vitro* acetylation of T α 1-HSA by RimJ was performed in the presence of AcCoA. LC-MS/MS identified the N^{α} -acetylation on the N-terminus of T α 1, which is the natural form of the hormone and supposed to be involved in its *in vivo* stability. MTT proliferation assay indicated that the *in vitro* activity of T α 1 was fully retained in the fusion protein. N^{α} -acetylation may further confer therapeutic advantages to N^{α} -acetyl T α 1-HSA.

In eukaryotes, N-terminal acetylation of proteins is involved in the biological functions, stability and interactions with other proteins and/or peptide receptors. In the case of rat glycine N-methyltransferase, its N-terminal deacetylated form recombinantly produced in *E.coli* lacks the co-operative behavior of the native enzyme [22]. Similarly, the melanotropic action of α -melanocyte stimulating hormone (α -MSH) is increased by N-terminal acetylation [23]. However, early studies already showed that N^{α} -acetylation did not affect the *in* vitro biological activities of Ta1 [13]. This was confirmed in our comparative study on the in vitro activity of Ta1-HSA and N^{α} -acetyl T α 1-HSA. The N-terminal acetylation during or after the biosynthesis of eukaryotic proteins also serves to protect intracellular proteins from proteolysis. For example, enzymatic acetylation of the N-terminus of cytoplasmic actin converts the protein into a more stable form with insensitivity to aminopeptidase digestion [24]. Many researchers have proposed that N^{α} -acetylation will affect the *in vivo* stability of Ta1. We also suspected that N^{α} -acetylation will influence the *in vivo* stability even the in vivo activity of the newly obtained fusion protein Ta1-HSA, although the in vitro activity was not affected. In our previous work, fusion of partner HSA to Tal successfully increased the in vivo half-life of Ta1, which was advantageous for reducing dosing frequency and cost of treatment. Taking into consideration of the fully retained activity of $T\alpha 1$ and potential stability benefits brought by N^{α} -acetylation, N^{α} -acetyl T α 1-HSA is likely to be a more promising therapeutic agent than Tα1(ZADAXIN[®])



Figure 4: MS/MS spectrum of MH⁺1466.68767.

Table 1: Kinetic parameters of *in-vitro* acetylation of Ta1 and Ta1-HSA by RimJ

Substrate	$K_{\rm m}(\mu{ m M})$	V _{max} (M min ⁻¹)	K_{cat} (min ⁻¹)	$K_{\text{cat}}/K_{\text{m}}(\min^{-1} \mu \mathbf{M}^{-1})$
Τα1-HSA	0.58	10-7	0.13	0.22
desacetyl Ta1	0.26	1.49×10 ⁻⁶	0.22	0.85

Table 2: Growth-promoting effect of different forms of Te	α1 on murine immunocyte (n=5)
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	Concentration (µM)	Proliferation rate±SD (100%)
N ^α -acetyl Tα1-HSA	6.00	130.2±7.3
	3.00	80.1±4.2
	1.5	77.4±3.7
	0.75	51.9±1.9
Τα1-ΗSΑ	6.00	123.8±4.6
	3.00	87.0±3.7
	1.5	74.2±4.4
	0.75	50.3±2.8
HSA-Ta1	6.00	110.2±6.7*
	3.00	72.1±2.6*TM
	1.5	65.4±3.4
	0.75	$47.9 \pm 2.5^*$
Tα1(ZADAXIN®)	6.00	127.5±6.2
	3.00	84.6±4.7
	1.50	72.0±4.1
	0.75	54.6±2.3

Results are expressed as mean±SD (n=5), *indicate statistically significant difference (P 0.05) as compared with activity of T α 1(ZADAXIN[®]) at the same concentration.

and HSA-T α 1 or HSA-linker- T α 1. Comparative investigations on the *in vivo* stability and activity of N^{α} -acetyl T α 1-HSA, T α 1-HSA and T α 1(ZADAXIN[®]) are underway to further explore the therapeutic potential of N^{α} -acetyl T α 1-HSA and its advantages over T α 1-HSA and T α 1(ZADAXIN[®]).

MATERIALS AND METHODS

Microorganisms, vectors and materials

P. pastoris host strain GS115 and plasmid pPICZ α A used for expression of T α 1-HSA were purchased from Invitrogen Co. (Shanghai, China). *E.coli* host strain BL21 and plasmid pET-28a(+) for expression of RimJ were purchased from EMD Biosciences (Novagen). *E. coli* DH5 α and *E.coli* Top10

used for plasmid amplification were from TianGentech Co.(Beijing, China). Restriction endonucleases *Xho* I, *Not* I, *Nde* I, *Bam* HI and *Sac* I, DNA polymerases pfu, dNTP, and T4 DNA ligase were purchased from TaKaRa (TaKaRa Ltd., Dalian, China).

Medium composition and culture conditions

Inocula of *E. coli* strains were cultured at 37°C and 200rpm in Luria-Bertani (LB) medium containing 0.5% (w/v) yeast extract, 1% (w/v) Tryptone and 1% (w/v) NaCl. To prepare the solid medium, 2% agar was added. When appropriate, zeocin (100 mg/ml) or kanamycin (25 μ g/ml) was added to the LB medium. For expression of the fusion protein by engineered strain GS115, BMGY medium was used to prepare seed culture and BMMY medium was used for flask fermentation.

Construction of expression vector pPICZaA / Ta1-HSA

A codon-optimized full length T α 1-HSA gene was synthesized based on the protein sequence of T α 1 and HSA by GenScript Co.,Ltd (Nanjing, China). Restriction sites *Xho* I and *Not* I were introduced at the 5'-and 3'-terminus respectively. In order to obtain a fusion protein with a native N-terminus, a Kex2 cleavage site was cloned directly downstream of the *Xho* I site to achieve precise incision of the signal peptide. After transformation into *E. coli* TOP10, positive clones were screened out by using 100µg/ml Zeocin. The target sequence was confirmed by double digestion and DNA sequencing.

Transformation and screening of *P. pastoris* GS115 with high expression capacity of Tα1-HSA

Recombinant plasmid pPICZ α A/T α 1-HSA amplified in *E. coli* TOP10 was linearized by *Sac* I, followed by transformation into competent *P.pastoris* GS115 prepared by treatment with lithium chloride. After plating onto YPD agar plate with 100 mg/ml zeocin and cultivation at 30°C for 48-72 h, positive clones were picked out and stocked in slant culture. The selected clones were first inoculated into 25 ml BMGY seed culture and incubated at 30°C until OD₆₀₀ reached 10-15. The cell pellets were collected by centrifugation at 1500 rpm for 10 min and re-suspended in 50 ml BMMY medium. The fermentation was performed at 30°C in 500ml shaking flasks. The culture conditions were optimized by single factor experiments on days of induced expression (1-7 days) and methanol concentration (0.5-3.0%).

Purification of Tα1-HSA

When the fermentation process was completed, the culture medium was harvested and centrifuged at 4°C and 8000 rpm for 20 min. The supernatant was concentrated by ultrafiltration using Millipore Cogent M1 Tangential Flow Filtration System (molecular weight cutoff, 30kDa) and then loaded onto a SephadeG-25 column(2.6cm×60cm) to remove pigment. A weak cation exchanger (CaptoTM MMC, GE Health, 2cm×25cm) pre-equilibrated with sodium acetate -acetic acid buffer (25mM, pH 4.6) was then applied. The bound protein fractions were eluted using Na₂HPO₄-NaH₂PO₄ buffer (50mM, pH7.2) containing 1.0 M NH₄Cl. Fractions containing the target protein were pooled and further loaded on a Blue-Sepharose[™] 6 Fast Flow (GE Health, 2cm×25cm) column pre-equilibrated with 0.05M citric acid-0.1M Na₂HPO₄ (pH 7.0). The column was washed with the same buffer to baseline and the bound protein was eluted with 0.05M KH₂PO₄ containing 1.5M KCl (pH 7.0). The collection of target protein was stored at 4°C for further analysis. SDS-PAGE was carried out to determine the homogeneity of purification and the molecular mass of the recombinant fusion protein as previously described [25]. Coomassie brilliant blue R-250 was used for staining.

Construction of expression vector pET-28a(+)/ RimJ

The genomic DNA of *E.coli* DH5 α was isolated. The complete open reading frame of RimJ gene was amplified using forward primer 5'-GGAATTC<u>CATATG</u>TTTGG CTATCGCAG-3' and reverse primer 5'-CGC<u>GGATCC</u> TTAGCGGCCGGGCGTCCAGTC-3' containing restriction sites *Nde* I and *Bam* HI, respectively. The PCR products were separated on 1% agarose gel electrophoresis and the resulting fragments were digested and inserted into pET-28a(+) vector, which produced RimJ fused to an N-terminal hexahistidine tag. After amplification in *E. coli* BL21, the target gene was confirmed by DNA sequencing.

Expression and purification of RimJ

Transformed E. coli BL21 was allowed to grow in liquid LB medium overnight at 37°C and 200 rpm and then transferred into 50ml AIM medium in 500 ml shake flask. 12h after cultivation at 37°C and 200 rpm, cell pellet was obtained after centrifugation at 4000rpm for 20 min at 4°C and re-suspended in phosphate buffer (pH7.0). After washing for three times, the wet cell mass was sonicated for 20 min at 10°C. Supernatant was harvested by centrifugation at 12,000×g for 20 min at 4°C, and loaded onto a weak cation exchanger (CaptoTM MMC, GE Health, 2cm×25cm) pre-equilibrated with PBS buffer (50 mM, pH 8.0). After elution with Na₂CO₂- NaHCO₂ buffer (pH 10.0) containing 1.0M NH₂Cl, fractions containing RimJ were collected and loaded onto a 10ml Ni²⁺ chelating Sephrose Fast Flow column. After washing with the binding buffer (50 mM sodium phosphate buffer, 500 mM NaCl, 50 mM imidazole, pH 7.5) to baseline, the bound protein was eluted by a washing buffer (50 mM sodium phosphate buffer, 500 mM NaCl, 500 mM imidazole, pH 7.5). Imidazole was then removed through dialysis against 50mM PBS (pH7.0).

In vitro acetylation of Ta1-HSA by RimJ and mass spectrometry characterization

In vitro acetylation was carried out according to the previously reported method [15]. Reaction mixture contained 300 μ M 4,4'-DTDP(dithiodipyridine, AldrithioITM-4), 50 μ M AcCoA (acetyl coenzyme A), 0.8 μ M RimJ and 50 μ M T α 1-HSA. Addition of 50mM PBS buffer (pH7.0) resulted in a final volume of 1 ml. Reaction mixtures were incubated for 12h at 25°C, followed by purification with Sephadex G50 (2.6cm×60cm) and concentration with centrifuge concentrators (Amicon Ultra-15, 50k MWCO). The resulting solution was loaded on a 12% gel. Protein band of expected molecular mass was incised, destained and subjected to in-gel tryptic digestion at 37°C overnight. The resulting peptides were extracted with 50% ACN/5% FA and then with 100% ACN. Peptides were dried and re-suspended in 2%ACN/0.1% FA. The peptides were separated by a reversed-phase analytical column (Acclaim PepMap RSLC, Thermo Scientific) and analyzed by Q ExactiveTM Hybrid Quadrupole-OrbitraTM Plus Mass Spectrometer (ThermoFisher Scientific).

Kinetic assays

Kinetic studies were conducted at 25°C in a total volume of 1ml. The reaction mixture contained 300 μ M 4,4'-DTDP, 50 μ M AcCoA, 0.8 μ M RimJ and different concentrations of T α 1-HSA (5-100 μ M). Reactions were started by adding RimJ into the reaction mixture. When the N-terminus of T α 1-HSA was acetylated, the acetyl-depleted form of AcCoA, CoA, began to react with DTDP and resulted in the reaction product with maximum absorption at 324 nm (ϵ_{324} =19800 M⁻¹cm⁻¹). OD₃₂₄ was measured every 3 minutes. Kinetic parameters K_m , V_{max} and K_{cat} were calculated by the double reciprocal plot method. *In vitro* acetylation of desacetyl T α 1 was also investigated in parallel for comparison.

Bioactivity assay of N^{α} -acetyl T α 1-HSA *in vitro*

The growth-promoting effect of N^{α} -acetyl T α 1-HSA on lymphocytes was determined by standard MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) proliferation assay [26]. Spleen lymphocytes were prepared from 5 to 8 weeks old female BALB/c mice by pressing the animal spleen through a fine stainless mesh as previously described [27]. The cells were separated and suspended in RPMI 1640 medium containing 10% fetal bovine serum, 100 Uml-1 of penicillin and 100µg ml-1 of streptomycin and kept in an incubator with 5% CO₂ at 37°C. Cells were seeded in a 96-well plates (4.0×10^{5}) well) in the presence of 5µg/ml concanavalin A (ConA) for six hours. Then a serial dilutions of N^{α} -acetyl T α 1-HSA were added to the wells. Cells stimulated with 5µg/ml concanavalin A alone was used as control. The activity of ZADAXIN, HSA-T α 1 and N^{α}-desacetyl T α 1-HSA were also determined for comparison. After a total incubation of 72h, MTT solution was added to each well to a final concentration of 0.5 mg/ml and incubated for 4 hours. Supernatants in each well was discarded and 100 µL of DMSO was added to dissolve the formed crystal of formazan for about 10 min. Optical density of each well was measured at 570 nm using a Bio-Rad plate reader. Proliferation rate was calculated according to the following formula: proliferation rate = $(OD_{570 \text{ sample}})$ OD_{570 control}) /OD_{570 control}. T-test was performed to evaluate statistical significance. All procedures involving animals have been approved by the Animal Ethics Committee in China pharmaceutical university.

Abbreviations

AcCoA= acetyl coenzyme A: AIM=auto induction medium; BMGY=buffered glycerol-BMMY=buffered complex medium; methanolcomplex medium; 4,4'-DTDP= dithiodipyridine, AldrithiolTM-4; HAS= human serum albumin; LB= Luria-Bertani; phytohaemagglutinin=PHA; MTT=3-(4,5dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; $T\alpha 1$ = thymosin alpha 1; YPD=yeast extract-peptonedextrose.

Author contributions

Jing Chen constructed the plasmids for expression of HSA-T α 1 and Rim J. Haibin Li purified both proteins and conducted acetylation reaction and bioactivity assay. Tao Wang did all the data analysis. Jianhua Chen designed all the experiments and wrote the manuscript. Shuyang Sun and Jia Liu helped with cloning and protein purification. All authors read through and approved the final manuscript.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

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