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Cloning and expression of recombinant purine nucleoside phosphorylase in the methylotrophic yeast *Pichia pastoris*

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ABSTRACT

Purine nucleoside phosphorylase (PNP) is an enzyme involved in biosynthetic pathway of purine nucleosides. Purine nucleoside phosphorylase catalyzes the cleavage of the glycosidic bond of ribo- or deoxyribonucleosides to form the purine base and deoxyribose- or ribose-1-phosphate. The reversible reaction catalyzed by recombinant PNP of E. coli (EcPNP) has been successfully used for the synthesis of nucleoside analogues. The aim of this study was to clone and expression of recombinant PNP in Pichia pastoris. For expression of recombinant EcPNP in Pichia pastoris, a new recombinant plasmid DNA pPICZ α A-PNP (4256 bp) containing the deoD gene (720 bp) amplified from E. coli strain RKMUz-221 has been cloned. The substrate specificity of the recombinant *EcPNP* expressed in yeast cells was studied by hydrolysis of inosine (9-beta-D-ribofuranosylhypoxanthine) to hypoxanthine and 2-deoxy- β -D-ribofuranosyl. The fraction containing the obtained recombinant EcPNP (≈28 kDa, as determined by SDS-PAGE) demonstrates significant hydrolytic activity, resulting in up to a 51% hydrolysis of inosine within a 5 h timeframe. These findings suggest that the recombinant enzyme holds a promise for applications in enzymatic transglycosylation of purine-type nucleosides.

INTRODUCTION

Nucleoside phosphorylases (NPs) are widely applied for the synthesis of modified nucleosides, which have used as potential anticancer, antiviral, and antibacterial drugs [1-4]. Based on their substrate spectrum, NPs are classified into purine nucleoside phosphorylases (PNP, EC 2.4.2.1) and pyrimidine nucleoside phosphorylases (PyNP, EC 2.4.2.2). Both catalyze the reversible phosphorolysis (transglycosylation) of nucleosides to nucleobases and α -D-pentofuranose-1-phosphates [5-6]. Enzymatic modification of nucleosides promises increased regioselectivity and exquisite control of the transglycosylation and is a better alternative to the commonly used chemical synthesis [6-7].

In recent years, *E. coli* purine nucleoside phosphorylases have attracted increasing interest as a biocatalyst for the synthesis of purine-type nucleosides [8-10]. PNP catalyzes the reversable hydrolysis of the glycosidic bond of pentofuranoses in the presence of inorganic phosphate [10-11].

In transglycosylation reactions, bacterial nucleoside phosphorylases are used either as part of cell lysates (raw) or as recombinant enzymes obtained by genetic engineering. In this regard, obtaining new strains of microorganisms producing recombinant enzymes with a high yield is relevant. *Pichia pastoris* is one of the advanced expression systems

used in biotechnology, characterized by a high yield of recombinant proteins compared to other expression systems and the absence of endotoxins/pyrogens. Therefore, the aim of this study was to clone and express recombinant purine nucleoside phosphorylase in *Pichia pastoris* as a producer on an industrial scale [12-14].

MATERIALS AND METHODS

Chemicals

Restriction enzymes (FastDigest *EcoRI*, FastDigest *XbaI* and FastDigest *SacI*) and T4 DNA ligase used in DNA clonning were purchased from Intivrogen (Thermo Scientific[™], USA). Inosine (Ino), hypoxanthine (6-hydroxypurine), D-ribose, and purine nucleoside phosphorylase (10 U/mg) were purchased from Sigma (Germany). All other chemicals were purchased from Sigma in the highest purity.

Escherichia coli genomic DNA extraction

Bacterial genomic DNA was isolated from pure cultures of *Escherichia coli* strain RKMUz – 221 (the strain was obtained from the collection of industrial microorganisms of the Institute of Microbiology of the Academy of Sciences of the Republic of Uzbekistan) by using the previously published protocol [15]. Bacterial cells were grown in liquid nutrient medium (LB Broth Miller, Invitrogen) at 37°C for 12 h. Isolation was carried out in a 1.5 ml tube containing 1 ml of the overnight *E. coli* culture. Centrifuged at max speed for 1min to pellet the cells. Remove as much of the supernatant as we can without disturbing the cell pellet. The cell pellet resuspended in 600 μ l lysis buffer (9.34 ml TE buffer pH 8, 600 μ l of 10% SDS, 60 μ l of proteinase K (20 mg/ml)) and then vortexed. The mixture was incubated 1 h at 37°C. After that, lysate treated an equal volume 2 times using phenol/chloroform without vertex and 1 time chloroform. After centrifuged at max speed for 5 min the upper aqueous phase was carefully transferred to a new tube. For precipitating the DNA, it was added 3 volumes of cold 96% ethanol and mixed gently. Finally, 1 μ l of samples were used directly for PCR in 20 μ l reactions.

Preparation of transfer vector and cDNA (gene) for ligation

1 μg of the transfer vector pPICZαA was sequentially treated using FastDigest *EcoRI* and FastDigest *XbaI* restrictases. Linear DNA 3536 bp was isolated after 0.7% agarose gel electrophoresis using PureLinkTM Quick Gel Extraction Kit [16].

Purine nucleoside phosphorylase cDNA (deoD gene, insert), size of 720 bp was amplified by PCR using as a template genomic DNA isolated from cells of *Escherichia coli* strain RKMUz–221 using the following primers:

Forward – 5'-ccaagaattcatggctaccccacacttaatgc-3',

Reverse-5'-cttgtctagatattactctttatcgcccagcagaac-3'

After electrophoresis in 1% agarose gel the amplificon (insert) was purified using PureLink[™] Quick Gel Extraction Kit [16] and treated with the same enzymes which used for the transfer vector.

Ligation of the vector with cDNA (purine nucleoside phosphorylase gene)

Ligation of the pPICZ α A vector with the purine nucleoside phosphorylase gene (*E. coli* PNP) was carried out in a volume of 10 µl in a molar ratio of 1:3, accordingly, using recombinant the phage T4 DNA ligase (Thermo ScientificTM) [17-18].

Transformation of *E. coli* TOP10 with a ligation mixture

After precipitation with the ligation mixture, the pellet (recombinant DNA) was dissolved in 10 μ l of de-ionized water. Dissolved DNA was transformed into electrocompetent plasmid-free strain *E. coli* TOP10 cells (Invitrogen) according to the method [19].

Identification of recombinant clones containing pPICZ α A- PNP

The molecular weight of plasmid DNA isolated from clones obtained after transformation with a ligation mixture was determined using 0.8% agarose gel electrophoresis. Clones containing DNA with a length of 4256 bp (deoD gene + pPICZ α A transfer vector fragment) were investigated by PCR analysis. PCR amplicons were analyzed by electrophoresis in 1% agarose gel [20].

Sequencing of cloned cDNA

Recombinant cDNAs were sequenced as described [21] in DNA Sequencing with the SeqStudio EDDU protocols using BigDye Terminator v3.1 Cycle Sequencing Kit (Thermo Fisher Scientific, USA). Three identical cycle sequencing reactions (containing 50 ng of the template DNA); 5 pmol of the gene-specific primers; 4 μ L of BigDye Terminator v3.1 Ready reaction Mix; and deionized water to a final vol of 10 μ L were subjected to an initial denaturation step of 96°C for 2 min, followed by 30 cycles of 96°C for 20 s, 60°C for 10 s, 65°C for 4 min in a QuantStudio PCR System (Applied Biosystems, Thermo Fisher Scientific, USA). Sequencing purification was performed using ZR DNA Sequencing Clean-Up Kit as described previously [22]. Automated sequencing traces were obtained in SeqStudio Genetic Analyzer (Applied Biosystems, Thermo Fisher Scientific, USA).

Accession numbers for target gene nucleotide sequences

The nucleotide sequences of the PNP (deoD gene) presented in this study have been entered to the National Centre for Biotechnology Information (NCBI) as GenBank accession number OQ133467.1.

Transformation of the pPICZαA-PNP vector into *Pichia pastoris* GS115

The recombinant pPICZ α A-PNP vector was linearized with FastDigest *SacI* and the mixture was precipitated with absolute ethanol in the presence of 3M Sodium acetate pH 5.2 to purify and concentrate the DNA. The purified linear DNA vector was transformed into *Pichia pastoris* GS115 yeast using an Electroporator 2510 (Eppendorf, USA). Then, the yeast transformants was grown in YPD selection medium containing the antibiotic ZeocinTM (100 µg/mL).

Expression, purification, and SDS-PAGE identification of recombinant EcPNP

To induce *Ec*PNP expression, *Pichia pastoris* GS115 transformants were inoculated in BMGY medium at 30°C with vigorous shaking (220 rpm), and then transferred to BMMY and incubated at 30°C with vigorous shaking (220 rpm) up to 96 h. Methanol (0.5-1%, v/v) was supplied to the culture medium once a day [23].

Extraction of the enzyme was carried out by destroying the yeast cells using a benchtop two-stage high pressure homogenizer (APV - 2000, SPX Flow, USA). The device can treat liquid samples at pressures up to 2000 bar. The two-stage (two times 1200 bar) was used after spin pellets for 1 min at 14.000 x g at 4°C and resuspend pellets in breaking buffer (Tris-Cl (1 M, pH 8.0) – 10mM, EDTA (0.5 M, pH 8.0) – 1mM, Triton X-100 - 2% (v/v), SDS (10%) - 1% (w/v), NaCl (5 M) - 100 mM, PMSF - 2mM) for the treatment of yeast suspensions. The suspension temperature at the exit of the homogenizer did not exceed 40°C. Treated samples were cooled to 15°C immediately at the outlet of the device using a water-ice bath. After that, the yeast culture liquid medium was added to the homogenate.

Homogenate was precipitated using gradient precipitation with 25%-65% ammonium sulphate to obtain primary purified purine nucleoside phosphorylase. The prepared solution in 65% ammonium sulphate was incubated for 4 h at 40C. The fraction containing the enzyme was separated by centrifugation at 14.000 x g at 4°C for 30 min. The collected pellets (enzyme fraction) were dissolved in BS (150 mM NaCl, 5.2 mM Na₂HPO₄, 1.7mM KH₂PO₄), pH 7.4.

The molecular weight was determined with 10% PAGE electrophoresis in the presence of Na dodecyl sulphate (SDS) according to the Laemmle method [24]. The protein concentration was determined by the Lowry method, using bovine serum albumin (BSA) as the standard [25].

Determination of *Ec*PNP expression

The expression of *EcPNP* in *Pichia pastoris* yeast cells were determined by Purine Nucleoside Phosphorylase Activity Fluorometric Assay Kit (ab204706, Abcam PLC, UK) [26].

Enzymatic hydrolysis of inosine with obtained *EcPNP*

Reaction mixture contained 3.5 mM KH₂PO₄, pH 8.0, 10 mM 9-beta-D-ribofuranosylhypoxanthine (99%, Sigma-Aldrich, Cat. I4125-100G) and 5 μ l *Ec*PNP fraction (total protein cons. 15.8 mg/ml). The reaction mixtures were incubated at 50°C up to 5 h. Substrate and product quantities were determined using HPLC.

HPLC detection

The quantitative determination of the products was performed by HPLC analysis using a Shim-pack GIST C18 5 μ m, 4.6 × 150 mm column (Shimadzu) under the following conditions: flow gradient (100-90% 10 mM KH₂PO₄ in H₂O and 0-10% MeCN) for 30 min, flow rate 0.5 mL/min, detection PDA at 254 nm. The retention times for the substrates and products are: 9-beta-D-ribofuranosylhypoxanthine (Inosine) ~ 20.41 min; 6-hydroxypurine (hypoxanthine) ~ 16.31 min.

RESULTS

Designing, cloning and transformation of the recombinant pPICZ α A-PNP

Plasmid DNA pPICZ α A-PNP (4256 bp) was created on the basis of the transfer vector pPICZ α A (3593 bp), which was designed for intracellular expression of proteins in the yeast *Pichia pastoris*. Figure 1 shows the genetic maps of the cloned plasmid DNA pPICZ α A-PNP.

The obtained clones were screened by PCR. Figure 2 shows the result of PCR analysis of recombinant clones. According to the results of PCR, the selected clones contain DNA fragments (gene) with a molecular weight of 720 bp (Figure 2). Thus, PCR indicated the presence of an insert (the PNP-deoD gene) in the recombinant plasmid.

Figure 3 shows a comparative restriction analysis of the recombinant plasmid pPICZ α A-PNP and the original pPICZ α A vector at a single restriction site of FastDigest *SacI*. After electrophoresis in 0.8% agarose gel, linear DNA was detected, the mass of which corresponds to theoretical calculations according to the physical maps of plasmids. At the same time, the difference between the sizes of the two plasmids was evident.

Linearized vector plasmid with FastDigest *SacI* was transformed into *Pichia pastoris* GS115 yeast using a Electroporator 2510 and the yeast transformants was grown in YPD selection medium containing the antibiotic ZeocinTM (100 μ g/mL).



Figure 1. Physical map of the recombinant plasmid pPICZ α A-PNP.



Figure 2. PCR analysis of the recombinant *E. coli* Top10 clones: (A) Clones; (B) K- (pPICZαA); (C) DNA marker.





cDNA (gene) sequencing

Nucleotide sequencing by Sanger was used to verify cloned *E. coli* strain RKMUz - 221 PNPase. The results showed that the purine nucleoside phosphorylase gene has 98.47% sequence similarity with *Escherichia coli* strain BM28 (GenBank accession no. CP10280.1). There were eight different mutations discovered in PNP of *E. coli* strain RKMUz – 221 and all of which were single substitutions (T>G, G>A, G>A, C>T, T>G, T>C, C>A and C>T) (Figure 4).

E.Coli strain	BM28	1	A <mark>T</mark> GGC <mark>TACCC</mark>	CACACATTAA	TG <mark>C</mark> AGAAA <mark>T</mark> G	GG <mark>C</mark> G <mark>ATTTC</mark> G	CTGACGTAGT	50
RKMUz-221		1	atggctaccc	cacacattaa	tgcagaaatg	gg <mark>cgatttc</mark> g	ctgacgtagt	50
E.Coli strain	BM28	51	TTTGATG <mark>CC</mark> A	GG <mark>C</mark> GACCCGC	TG <mark>C</mark> GTGCGAA	G <mark>TATATTGC</mark> T	GAAAC <mark>TTTCC</mark>	100
RKMUz-221		51	tttgatg <mark>cc</mark> a	gg <mark>c</mark> gacccgc	tgcgtgcgaa	gtatattgct	gaaac <mark>tttcc</mark>	100
E.Coli strain	BM28	101	TTGAAGA <mark>TGC</mark>	CCG <mark>T</mark> GAAGTG	AACAACG <mark>TTC</mark>	GCGGTATGCT	GGG <mark>CTTCACC</mark>	150
RKMUz-221		101	ttgaaga <mark>tgc</mark>	CCg <mark>t</mark> gaag <mark>t</mark> g	aacaacg <mark>tt</mark> c	gcgg <mark>tatgct</mark>	ggg <mark>cttcacc</mark>	150
E.Coli strain	BM28	151	GG <mark>TACTTACA</mark>	AAGG <mark>CCGC</mark> AA	AA <mark>TTTCC</mark> GTA	A <mark>T</mark> GGG <mark>TCAC</mark> G	G <mark>TAT</mark> GGG <mark>TAT</mark>	200
RKMUz-221		151	gg <mark>tactt</mark> aca	aagg <mark>cc</mark> gcaa	aa <mark>ttt<mark>cc</mark>gt</mark> a	a <mark>t</mark> ggg <mark>tcac</mark> g	g <mark>tat</mark> ggg <mark>tat</mark>	200
E.Coli strain	BM28	201	CCCGTCCTGC	TCCATCTACA	CCAAAGAACT	GA <mark>TCACC</mark> GAT	TTCGGCGTGA	250
RKMUz-221		201	CCCg <mark>t</mark> CC <mark>t</mark> gc	t <mark>ccatc</mark> taca	ccaaagaact	ga <mark>tcacc</mark> ga <mark>t</mark>	ttcggcgtga	250
E.Coli strain	BM28	251	AGAAAA <mark>TT</mark> AT	<mark>CC</mark> G <mark>C</mark> G <mark>T</mark> GGGT	TCCTGTGGCG	CAGTTCTGCC	G <mark>CACGT</mark> AAAA	300
RKMUz-221		251	agaaaa <mark>tt</mark> at	<mark>CC</mark> g <mark>C</mark> g <mark>t</mark> ggg <mark>t</mark>	t <mark>cc</mark> tgtggcg	cag <mark>ttctgcc</mark>	g <mark>cac</mark> g <mark>t</mark> aaaa	300
E.Coli strain	BM28	301	CTGCGCGACG	TCGTTATCGG	TATGGGTG <mark>CC</mark>	TG <mark>CACC</mark> GATT	<mark>CC</mark> AAAG <mark>TT</mark> AA	350
RKMUz-221		301	ctgcgcgacg	tcgttatcgg	t <mark>at</mark> gggtg <mark>cc</mark>	tg <mark>cacc</mark> gatt	<mark>CC</mark> aaag <mark>tt</mark> aa	350
E.Coli strain	BM28	351	CCGCATCCGT	TTTAAAGA <mark>CC</mark>	A <mark>TGACTTTGC</mark>	CGCTATCGCT	GACTTCGACA	400
RKMUz-221		351	ccgcatccgt	ttt <mark>aaaga<mark>tc</mark></mark>	a <mark>tgactttgc</mark>	cgctatcgct	gacttcgaca	400
E.Coli strain	BM28	401	TGG <mark>T</mark> G <mark>C</mark> GTAA	CGCAGTAGA <mark>T</mark>	G <mark>CAGCT</mark> AAAG	CACTGGGTAT	TGATGCTCGC	450
RKMUz-221		401	tggtgcgtaa	cgcggtagac	g <mark>c</mark> gg <mark>ct</mark> aaag	cactgggcat	tgatgctcgc	450
E.Coli strain	BM28	451	G <mark>T</mark> GGG <mark>TAACC</mark>	TGTT <mark>CTCC</mark> GC	TG <mark>ACC</mark> TGTTC	TACTCTCCGG	A <mark>C</mark> GG <mark>C</mark> GAAA <mark>T</mark>	500
RKMUz-221		451	g <mark>tt</mark> gg <mark>t</mark> aacc	tgtt <mark>ctcc</mark> gc	tgacctgttc	tactctccgg	acggcgaaat	500
E.Coli strain	BM28	501	G <mark>TTC</mark> GACG <mark>T</mark> G	A <mark>T</mark> GGAAAAAT	ACGGCA <mark>TTC</mark> T	CGGCG <mark>T</mark> GGAA	A <mark>T</mark> GGAAG <mark>C</mark> GG	550
RKMUz-221		501	g <mark>ttcgac</mark> g <mark>t</mark> g	a <mark>t</mark> ggaaaaa <mark>t</mark>	acgg <mark>catcc</mark> t	CggCg <mark>C</mark> ggaa	a <mark>t</mark> ggaagcgg	550
E.Coli strain	BM28	551	CTGGTATCTA	CGGCGTCGCT	G <mark>CA</mark> GAA <mark>TTT</mark> G	G <mark>CGC</mark> GAAAG <mark>C</mark>	CC <mark>T</mark> GACCATC	600
RKMUz-221		551	ctggtatcta	cggcgtcgct	g <mark>ca</mark> gaatttg	g <mark>cgc</mark> gaaagc	cctgaccatc	600
E.Coli strain	BM28	601	TG <mark>CACC</mark> G <mark>TA</mark> T	C <mark>T</mark> GACCACAT	CC <mark>GCACT</mark> CAC	GAG <mark>C</mark> AGACCA	C <mark>TGCCGC</mark> TGA	650
RKMUz-221		601	tgt <mark>acc</mark> gtgt	ccgaccacat	ccgcactcac	gag <mark>c</mark> aga <mark>cc</mark> a	c <mark>tgccgct</mark> ga	650
E.Coli strain	BM28	651	G <mark>CGTCAGACT</mark>	ACC <mark>TT</mark> CAAC <mark>G</mark>	ACA <mark>T</mark> GA <mark>TC</mark> AA	AA <mark>TC</mark> GCACTG	GAA <mark>TCC</mark> G <mark>TTC</mark>	700
RKMUz-221		651	gcgtcagacc	acc <mark>tt</mark> caacg	aca <mark>tgat</mark> caa	aa <mark>tcgcact</mark> g	gaa <mark>tcc</mark> gtt <mark>c</mark>	700
E.Coli strain RKMUz-221	BM28	701 701	TGCTGGGCGA tgctgggcga	TAAAGAG <mark>T</mark> AA taaagagtaa	720 720			

Figure 4. The alignment of the cloned *EcPNP* sequence with the sequences of representative *E. coli* (BM28) from GenBank.

Expression and purification of *EcPNP*

Fluorometric assay (ab204706, Abcam PLC, UK) was performed to study the expression level of the recombinant enzyme. The highest level of PNP expression (activity) was enriched at the 72 h of cultivation when adding 0.5% - 1.0% methanol to the medium every 24 h. The yeasts were homogenized as described in material and methods. Then homogenate was separated by centrifuging at 14.000 g for 30 min after gradient precipitation with 25%-65% ammonium sulphate. The fraction contains 15.8 mg/ml total proteins. The fraction containing PNP was analyzed with 10% SDS-PAGE electrophoresis by staining with Coomassie G-250 (Figure 5). Figure 5 shows the \approx 28 kDa band which corresponds to the recombinant enzyme based on its nucleotide sequence.



Figure 5. SDS-PAGE of fraction containing *rEc*PNP: (A) Tri-color restrained protein marker I (10-180kD), Bioland Scientific; (B) fraction after gradient precipitation with 25%-65% ammonium sulphate (3 and 5 μ g protein per well).

Enzymatic hydrolysis of purine nucleosides by EcPNP expressed in Pichia pastoris

The catalytic activity of the fractions contained *Ec*PNP was determined by hydrolysis of inosine (Figure 6). The level of hydrolysis and the identification of the formed hypoxanthine after hydrolysis were carried out by HPLC for 0-5 h.

As can be seen from the graph (Figure 7), the fraction containing recombinant *Ec*PNP leads to the hydrolysis of inosine within 5 h by more than 50% under our experimental conditions (Figure 8), which confirms its high hydrolytic activity.



Figure 6. Enzymatic hydrolysis of Inosine (9-beta-D-ribofuranosylhypoxanthine) by purine nucleoside phosphorylase (PNP).



Figure 7. Time-course of enzymatic hydrolysis of Inosine catalyzed by recombinant *Ec*PNP expressed in *P. pastoris.* The graph shows the percentage of inosine hydrolyzed over a time period of 0 to 5 h.



Figure 8. HPLC analysis of enzymatic hydrolysis of Inosine catalyzed by recombinant PNP. i-ii) The quantity of hydrolyzed Inosine in reaction mixture over time from 0 min to 5h.

DISCUSSION

The current study described the designing and cloning of the recombinant plasmid pPICZ α A-PNP for the expression of the *Ec*PNP of conditionally pathogenic *E. coli* strain RKMUz-221 in *Pichia pastoris* yeast and enzymatic activity of recombinant *Ec*PNP. Besides, the study showed the *EcPNP* in the yeast for the first time.

Nowadays, *Pichia pastoris* is most effectively used in the large-scale production of heterologous recombinant proteins [12]. The successful creation of the recombinant pPICZ α A-PNP plasmid is an important stage in the expression of the target protein in *Pichia pastoris* yeast. The obtained clones of pPICZ α A-PNP after transformation into *E. coli* TOP10 were screened by PCR and restriction analysis, which confirmed the presence of the insert (the PNP-deoD gene) in the recombinant plasmid. The recombinant plasmid pPICZ α A-PNP isolated from selected clones was then transformed into *Pichia pastoris* GS115 yeast for intracellular expression of protein. The selection of recombinant *Pichia clones* is carried out on a medium containing the antibiotic ZeocinTM, which ensures the survival of only transformed yeasts [23]. The nucleotide sequencing of the *Ec*PNP gene of *E. coli* strain RKMUz – 221 showed 98.47% sequence similarity with *E. coli* strain BM28 [27] and eight different mutations in the PNP, represented as single nucleotide substitutions. It was interesting to see if these mutations would affect the structure and, most importantly, the functional activity of

the PNP enzyme, since some mutations may have no effect, while others may alter the enzymatic activity or stability of proteins. The identification of these mutations can provide important information for understanding the genetic diversity of PNP enzymes and their potential applications in biotechnology.

For the determination of influence of mutations in cDNA and enzymatic activity of the recombinant *EcPNP* in the stage of expression in *Pichia pastoris* cells used a fluorometric assay [26]. Fluorometric assay showed that the highest activity of expressed *EcPNP* was enriched at 72 h of cultivation after induction with methanol (0.5% - 1.0%). The specific activity of recombinant *EcPNP* was studied by hydrolysis of inosine to hypoxanthine and D-ribose because inosine as a purine type nucleoside is main substrate for purine nucleoside phosphorylase [28]. For this purpose, the recombinant EcPNP containing fraction was separated from the yeast homogenate by gradient precipitation with 25%-65% ammonium sulphate. Because by using gradual changes in ammonium sulfate concentration, different proteins in a mixture can be precipitated sequentially based on their solubility properties [29-30]. In this protein purification stage using gradient ammonium sulfate precipitation, the optimal ammonium sulfate concentration needed for protein precipitation was determined based on the molecular weight of the recombinant protein. The salt concentration was titrated to find the value that resulted in maximum protein recovery while minimizing contamination from other protein impurities. The course of enzymatic hydrolysis of inosine by recombinant EcPNP was analyzed using HPLC. The degree of hydrolysis of the inosine in reaction mixture was quantified by HPLC for 1-5 h. More than 50% of the inosine was hydrolyzed within 5 h under our experimental conditions, which indicates the high hydrolytic activity of the recombinant EcPNP expressed in Pichia. It should be noted that the cell lysate of normal Pichia pastoris GS115 does not exhibit hydrolytic activity (HPLC chromatogram isn't provided). Thus, the revealed hydrolytic activity of recombinant *EcPNP* indicates the ability to efficiently catalyze purine nucleosides, such as inosine, and can be used in the development of new antiviral or cytotoxic prodrugs based on modified nucleosides.

CONCLUSIONS

A new recombinant pPICZ α A-PNP plasmid, consisting of 4256 base pairs, was successfully cloned to express the recombinant PNP of *E. coli* strain RKMUz-221 in the yeast *Pichia pastoris*. The molecular weight of the obtained recombinant *Ec*PNP, determined by electrophoresis was approximately 28 kDa. The enzymatic hydrolysis results revealed that the recombinant *Ec*PNP exhibited significant activity by hydrolyzing over 50% of inosine (9-beta-D-ribofuranosylhypoxanthine) within 5 hours. These findings demonstrate the potential of the obtained recombinant *Ec*PNP for generating modified nucleosides. Moreover, the expression of the recombinant enzyme in *Pichia pastoris* yeast provides a cost-effective and scalable approach for large-scale production.

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AUTHOR CONTRIBUTIONS

ShA and SS provided direction for this research idea; JA and SS: writing – review the manuscript, JA, ShKh, SG and SS: cloning, HPLC, data analysis; AM, AB: synthesis and purification of oligonucleotides (primers); KhN: DNA sequencing; OA, TS, and OY: cultivation of *Pichia pastoris* strains; FE and KhD: isolation of DNA, protein fractionation, SDS-PAGE. All authors have read and agreed to the published version of the manuscript.

CONFLICTS OF INTEREST

There is no conflict of interest among the authors.

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