

Construction, Expression and Purification of DNA Pol I ITB₁ and its Deletion Mutants

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(Received: 18 June 2009; accepted: 27 July 2009)

A gene encoding DNA polymerase I, namely DNA Pol I ITB₁, was cloned from *Geobacillus thermoleovorans*. Heterologous expression of DNA Pol I ITB₁ in *Escherichia coli* was carried out under expression vector pET30a(+). The vector contains his-tagged in the upstream of the gene, thus the expressed protein carried poly his on the N-terminal. Recombinant plasmid containing DNA Pol I ITB₁ gene was constructed by inserting *NcoI* – *BamHI* gene fragment of pITB₈ containing the whole coding region of DNA Pol I ITB₁ into pET30a(+) resulting pITB₂₀ plasmid. The deletion mutants of the genes were constructed through *in frame* deletion of the gene by using *EcoRI*, and *XhoI* restriction enzymes resulting pITB₂₁, and pITB₂₂ plasmids respectively. The expression of the wild type and the deletion mutants were carried out in *Escherichia coli* BL21-DE3. High expression levels of the genes were shown on SDS-PAGE. The proteins were purified by immobilized metal-ion affinity chromatography (IMAC) using Ni-NTA resin and single band protein products were shown on the gel following SDS PAGE analysis.

Key words: DNA Polymerase I, Deletion mutant, Heterologous expression, His-tag.

DNA polymerases are present in all organisms and involve in genomic replication and repair. DNA Pol I is the most abundant DNA polymerase found in *E. coli* and also the first polymerase characterized¹. DNA Pol I consists three discrete structural domains, namely 5'→3' exonuclease, 3'→5' exonuclease and 5'→3'

polimerized domains. The 5'→, 3' exonuclease degrades duplex DNA from its 5' end. It enables DNA polymerase I to remove RNA primers of Okazaki fragment and fill with DNA sequences. The 5'→3' exonuclease is also capable of excising DNA lesion, such as thimin dimers, during DNA repair. The 3'→5 exonuclease degrades single or double stranded DNA from their 3'end. The ability to remove mismatched nucleotides provides proofreading activity of DNA replication¹.

More than 100 DNA polymerase genes have been cloned and studied from various organisms, including thermophiles and archaea². As expected, these enzymes have been shown an elevation temperature activity and poses thermal stability compared to the mesophilic enzymes. Thermostable DNA Pol I isolated from

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thermophilic microorganisms play an important role in molecular biology through their used in Polymerase Chain Reaction (PCR), particularly. PCR has become powerful method for the identification and amplification of genes, direct sequencing and clinical diagnosis. At the early development of PCR, the experiment used thermolabile Klenow Fragment, which required addition of the enzyme for every cycle. The introduction of a thermostable DNA polymerase allowed the automation of the process^{3,4}.

Thermostable DNA Pol has been studied from a wide range of bacteria. DNA polymerase from *T. aquaticus* (Taq polymerase) was the first cloned and expressed in *E. coli*⁵. A number of archaeobacterial DNA polymerases have also been isolated and purified³. Thereafter, many of DNA Pol I from *Thermus* strains have been studied. *Tfl*, *Tth*, *Tfi* and *Top* Polymerase have been applied to PCR^{3,6,7,8}. However, their base-insertion fidelity is low since some DNA Pols have no 3'→5' exonuclease activity. The high fidelity of DNA Pol, which has 3'→5' exonuclease activity dependent proofreading activity, should be required for error correction during the polymerization. Several thermostable DNA polymerases with proofreading activity (*Pfu*, *Vent*, *Deep Vent*, and *Pwo*) have also been studied and introduced from high-fidelity PCR amplification³. A few moderately thermostable DNA polymerases have been isolated and purified from thermophilic *Bacillus* species^{9,10}. Bst DNA polymerase was isolated from *B. stearothermophilus*^{11,12,13}. Bca DNA polymerase was isolated and cloned from *B. caldotenax*^{13,14}. Bst DNA polymerase has been used for DNA sequencing.

Most of the native thermostable enzymes are synthesized at very low levels by the thermophilic bacteria and therefore cumbersome to purify¹⁵. All of thermostable DNA Polymerases were produced in a biologically active form in *E. coli* expression vector^{16,17}, however the commercial available DNA Pols have some advantages and disadvantages properties, therefore a new and improved thermostable DNA Pol are still needed.

A number of thermophilic microorganisms have been isolated from few hot spring around Indonesia^{18,19,20}. DNA pol I gene from one of the isolated has been cloned and

sequenced², namely DNA Pol I ITB₁. Thermal stability of the protein have been studied through Molecular Dynamic Simulation^{21,22}. However, structure function of the protein need to be elucidated. In order to further probe to structure function of the protein, in this report we would like to present over-expression and purification of DNA Pol I ITB₁ and its deletion mutants in *E. coli*.

MATERIAL AND METHODS

Bacterial Strains and Plasmids

The strains used for cloning was *E. coli* DH5a (supE44 lacU169 (Q90 LacZM1) hsdR17 recA1 endA1 gyrA96 thi-1 reiA1). *E. coli* BL21(DE3)(F⁻ ompT hsdSb (rB⁻mB⁻) gal dem(DE3) was used for heterologous expression of the gene. The pITB₈ that contains DNA Pol I ITB₁ gene was used for construction of DNA Pol I ITB₁ deletion mutants, while pET30a(+) (Novagen,UK) was used as expression system.

Growth Condition and DNA Manipulation

E. coli strains were grown aerobically at 37°C in Luria Bertani (LB) broth or plated on LB containing appropriate antibiotics when required. *E. coli* BL21 (DE3) was grown at 37°C on LB medium supplemented with 34 µg/ml kanamycin. All routine DNA isolation and manipulation were performed as described by Sambrook *et al*²³. Restriction enzymes and other modifying enzymes were purchased from Promega (Madison, USA). Small-scale preparation of plasmid DNA from *E. coli* cells was performed using plasmid miniprep kit (Qiagen, Hilden, Germany).

Construction of Recombinant Vector

Recombinant vector (pITB₂₀), carrying DNA PolI wild type gene was constructed by inserting *NcoI*-*Bam*HI fragment of DNA PolI gene fragment from pITB₈ plasmid into pET30a(+) (Fig. 1A). The ligation process was carried out by standard method²³. Meanwhile recombinant vectors (pITB₂₁ and pITB₂₂), carrying *Eco*RI and *Xho*I deletion fragments respectively, were constructed from pITB₈ plasmid. *Eco*RI or *Xho*I fragment of pITB₈ was removed by restriction of *Eco*RI or *Xho*I restriction enzyme. The rest of the vectors were religated resulting pITB₈-A and pITB₈-B plasmids respectively (Fig 1B, C). Furthermore, DNA PolI gene fragment from

pITB₈-A and pITB₈-B were removed by *Nco*I and *Bam*HI restriction digest. The fragments were inserted into linearized pET30a(+) vector with the same (*Nco*I and *Bam*HI) enzymes (Fig. 1B,C).

Expression and Purification of Recombinant Proteins

E. coli strain BL21(DE3) transformed by pITB₂₀, pITB₂₁ and pITB₂₂ were grown at 37°C in 1000 ml LB containing 34 mg/ml kanamycin to an optical density (OD_{660}) = 0.5 reached. IPTG was then added to the final concentration of 1 mM. The cells were harvested after 4 h by centrifugation (9 g of cell mass) and the pellet was resuspended in 20 ml of B buffer (50 mM phosphate, pH 7.9, 500 mM NaCl, 1 mM PMSF and 1 mg/ml lysozyme). The cells were disrupted by sonication, and the insoluble debris was removed by centrifugation. The cleared lysate was heated at 70°C in water bath for 10 minute, cooled on ice for 20 min, and then centrifuged at 16,000g, 4°C for 20 min. The supernatant was then applied directly onto Ni²⁺-NTA agarose column pre-equilibrated with 4 vol of B buffer. After loading, the column was washed several times with 10 ml of the same buffer until the UV absorption returned to the baseline. His6-tagged DNA Pol I ITB-1 was eluted by B buffer containing 200 mM imidazole. Protein fractions resulting from Ni-NTA chromatography were analyzed following SDS-PAGE and comassie brilliant blue staining. The eluted fractions were pooled and dialyzed against a buffer containing 50 mM phosphate, pH 7.9 and 50 mM NaCl²³.

RESULTS

Construction of the Recombinant Vectors

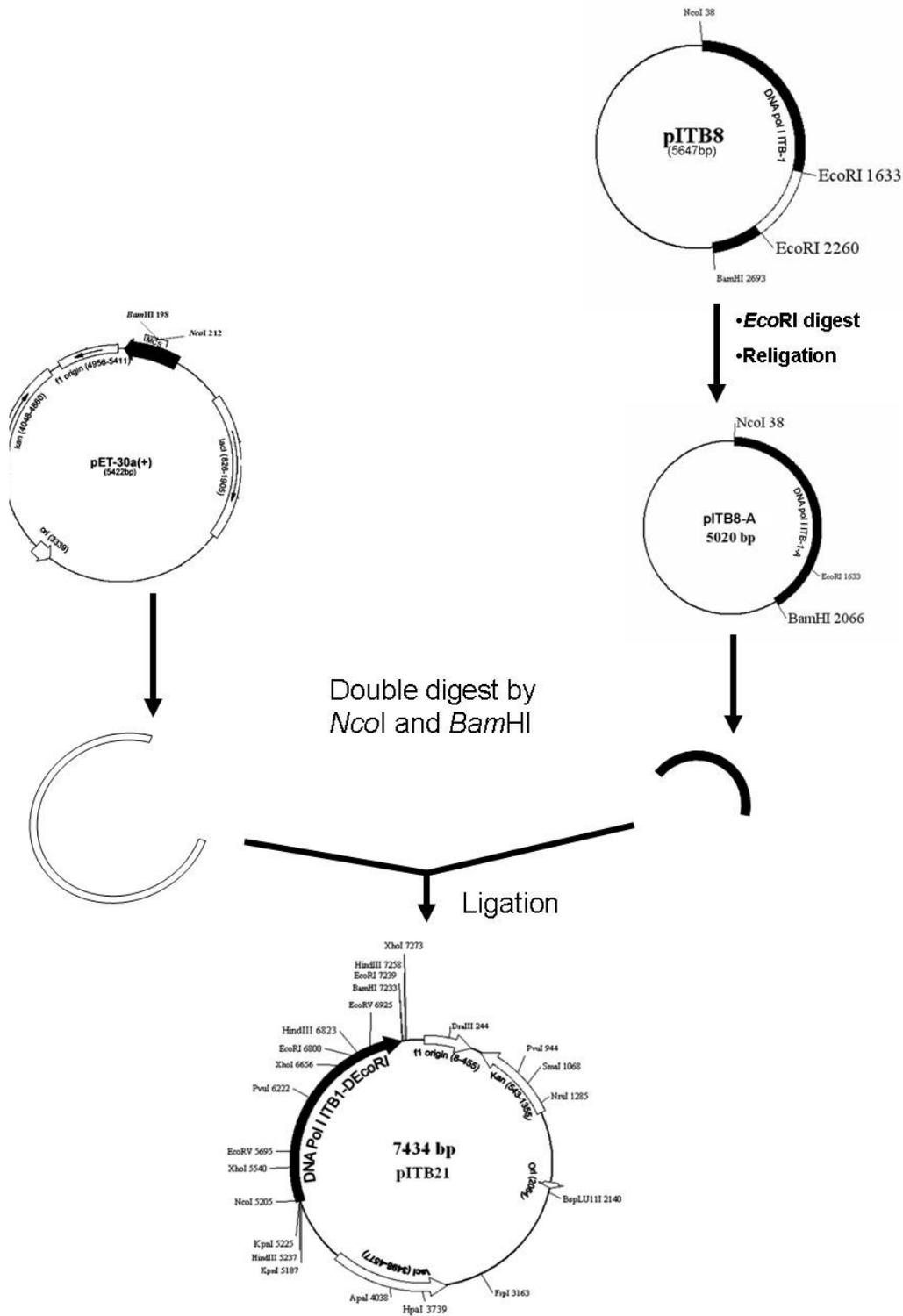
pET system (Novagen, Madison, USA) is one of the useful and powerful recombinant protein expression systems in *E. coli*. The pET vector has a strong T7 promoter and could be harbored in combination with pLysS to provide additional stringency^{15,24,25}. The pITB₂₀, pITB₂₁ and pITB₂₂ have been successfully constructed by ligation of the *Nco*I-*Bam*HI fragments of the genes as illustrated in Fig.1A, B, and C. The parent plasmid, pITB₈ is a recombinant pGEMT plasmid carrying *Kpn*I-*Bam*HI PCR fragment of DNA polymerase I ITB₁²⁶.

All of the recombinant plasmids have

been confirmed by restriction digest analysis using appropriate restriction enzymes. The size of pITB₂₀ is around 8 kb, meanwhile pITB₂₁ and pITB₂₂ are 7.5 and 7.0 kb respectively. The size of pITB₂₀ was confirmed by double digest of the plasmid using *Bam*HI and *Nco*I. Following agarose gel electrophoresis, the result showed that two bands represents fragment DNA with the sizes of 5.4 kb from pET30a(+) vector and 2.6 kb from DNA PolI insert respectively (Fig 2A). pITB₂₁ and pITB₂₂ carries deletion fragment of *Eco*RI with the size of 0.6 kb and *Xho*I with the size of 1.1 kb respectively. Agarose gel electrophoresis following double digest by *Bam*HI and *Nco*I showed that two fragments were appeared from both plasmids with the respected sizes (Fig. 2 B, and C). Further analysis to confirm the constructed plasmid was carried out by sequencing of the fragments. Sequence analysis showed that all recombinant plasmids carried ATG start codon originally from pET30a(+) vector, six histidine codons and in-frame junction on *Nco*I and *Bam*HI sites (data not shown). No other mutations were found within the coding sequence of the genes.

Expression and purification of DNA Pol I and Its Mutant Proteins

The whole coding region of DNA Pol I ITB and its deletion mutant genes were successfully cloned into plasmid pET30a(+) through *Nco*I and *Bam*HI restriction sites resulting on pITB₂₀, pITB₂₁, and pITB₂₂ respectively. In these plasmids the gene are controlled under promoter of bacteriophage T7. The plasmids were used to transform *E. coli* BL21(DE3) which is suitable for the expression of plasmid since this strain carrying T7 RNA polymerase from bacteriophage DE3. The gene under T7 promoter remaining transcriptionally silent until the expression a chromosomal copy of T7 RNA Polymerase was induced. The expression of DNA Pol I ITB1 and its deletion mutant proteins were carried out under the induction of IPTG when the culture cells reached on the logarithmic phase. The results showed that the proteins were over-expressed up to 15% of the total protein following densitometric measurement on the gel (data not shown). The size of the over-expressed proteins were expected, 100 kDa for the wild type, 75 kDa for the *Eco*RI



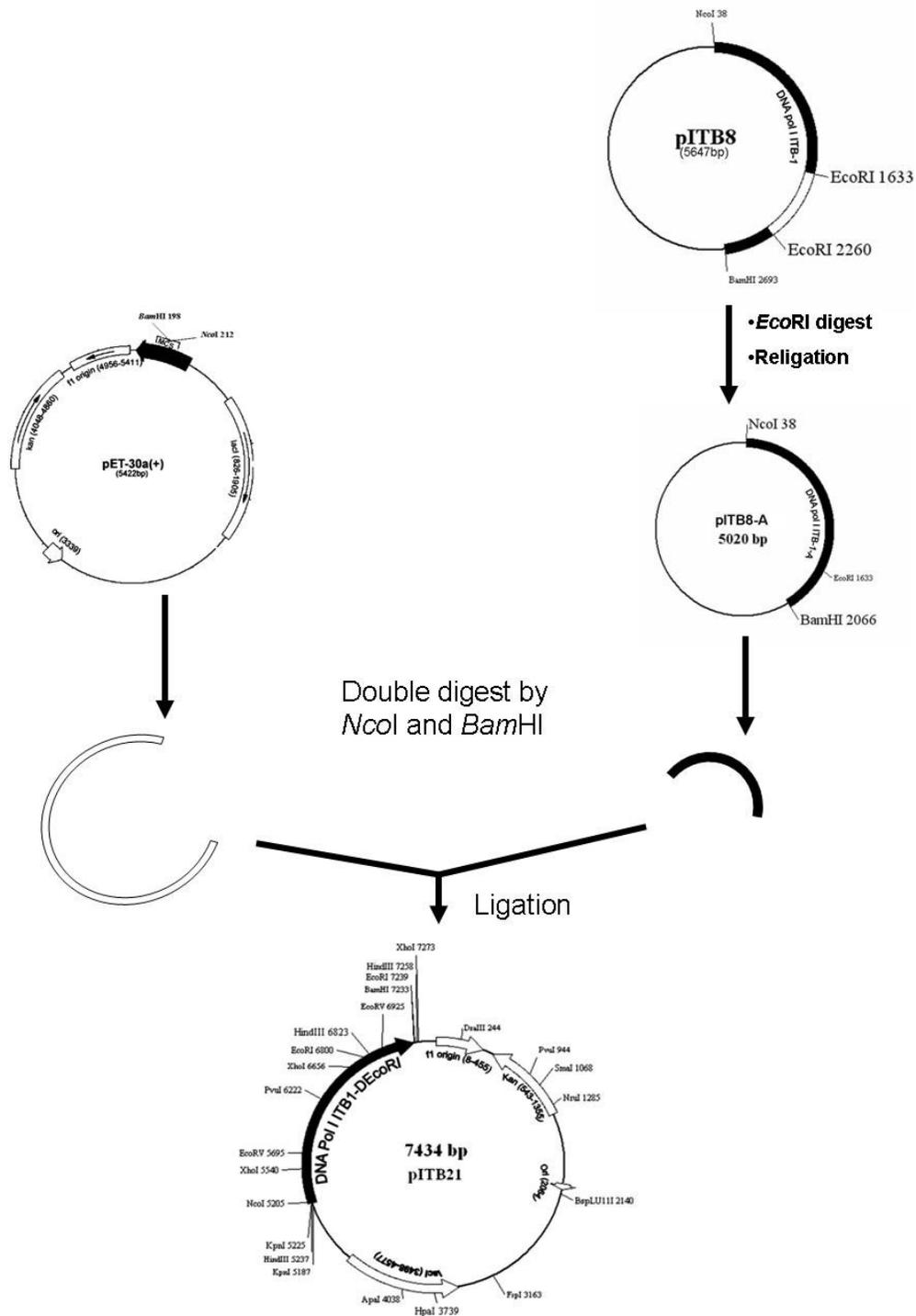


Fig. 1B. Construction Strategy of pITB₂₁. *EcoRI* fragment of DNA PolI gene was removed from pITB₈, then the vector was religated resulting pITB₈-A. *NcoI* and *BamHI* fragment of DNA PolI gene from pITB₈-A was inserted into linearized pET30a(+) digested by *NcoI* and *BamHI* restriction enzymes

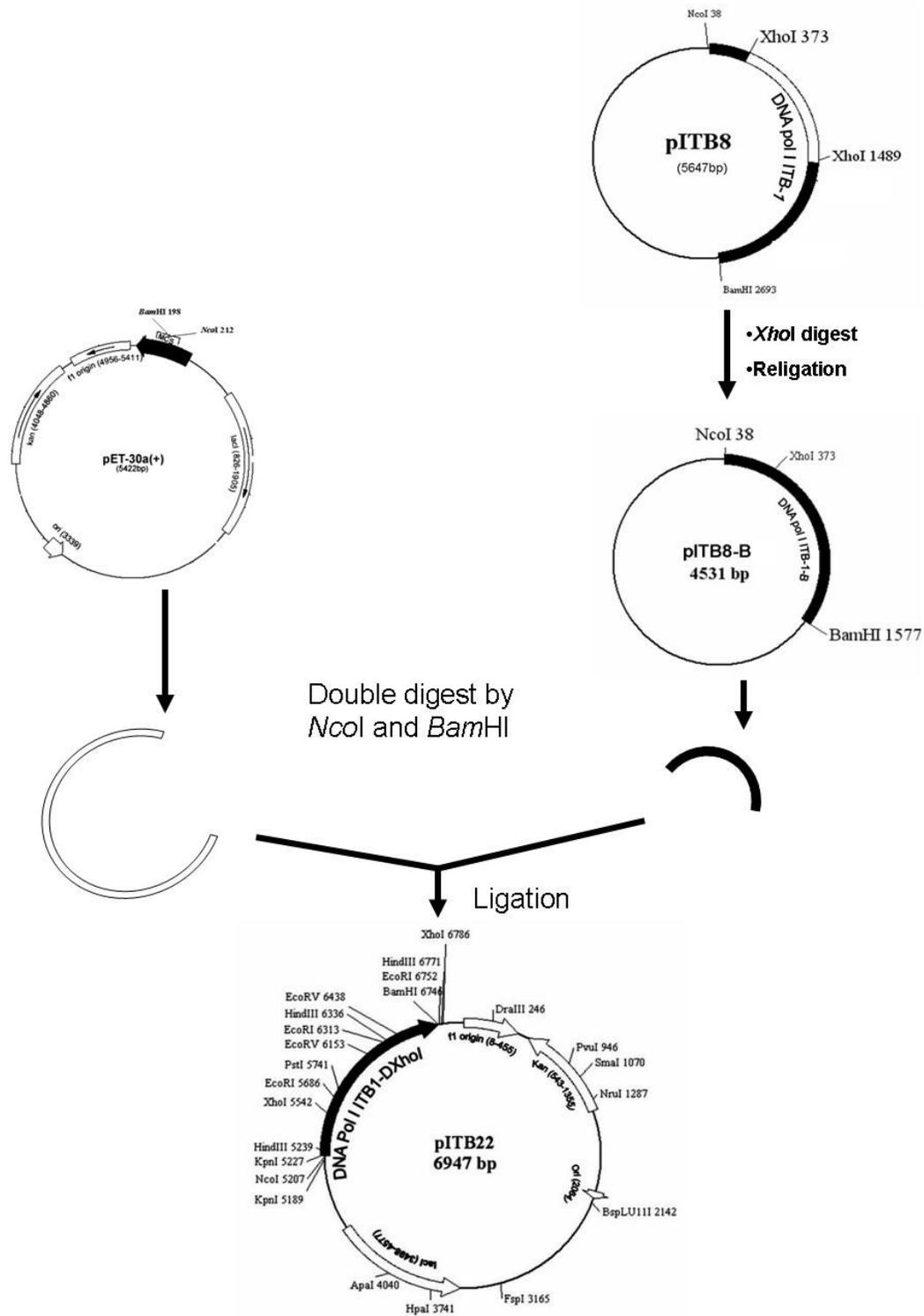


Fig. 1C. Construction Strategy of pITB₂₁. *XhoI* fragment of DNA PolI gene was removed from pITB₈, then the vector was religated resulting pITB₈-B. *NcoI* and *BamHI* fragment of DNA PolI gene from pITB₈-B was inserted into linearized pET30a(+) digested by *NcoI* and *BamHI* restriction enzymes

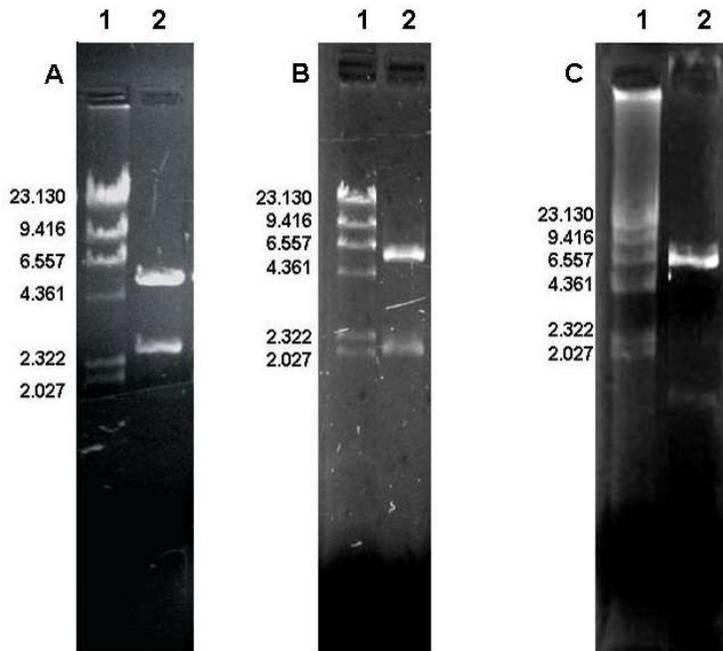


Fig. 2. Electrophoregram of Agarose Gel Electrophoresis. (A) pITB₂₀, (B) pITB₂₁, (C) pITB₂₂ digested with *NcoI* and *BamHI*. Lane 1 (A,B,C) Lambda DNA digested by *HindIII*. Lane 2 (A, B, C) Double digest fragment with *NcoI* and *BamHI*

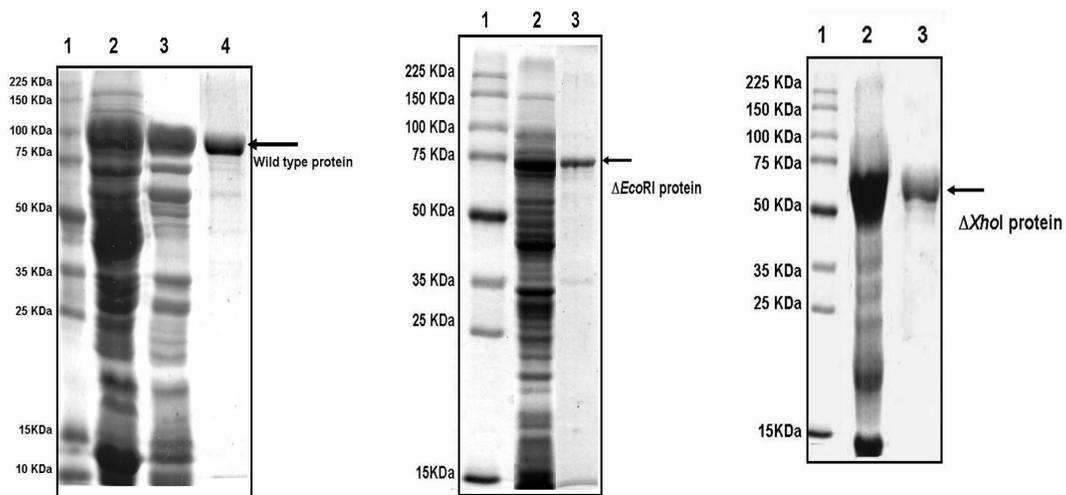


Fig. 3A. Electrophoregram of SDS-PAGE from DNA Pol I ITB₁ Wild Type. (1) marker protein, (2) crude extract, (3) crude extract after heated at 60°C for 10 min, (4) purified protein following IMAC purification

Fig. 3B. Electrophoregram of SDS-PAGE from DNA Pol I ITB₁ *EcoRI* Deletion Mutant. (1) marker protein, (2) crude extract, (3) purified protein following IMAC purification

Fig. 3C. Electrophoregram of SDS-PAGE from DNA Pol I ITB₁ *XhoI* Deletion Mutant. (1) marker protein, (2) crude extract, (3) purified protein following IMAC purification

deletion, and 60 kDa for *XhoI* deletion respectively (Fig 3A, B, and C).

Purification of recombinant proteins were performed by Ion Metal Affinity Chromatography (IMAC) system since the genes under pET30a(+) containing His-tag (6 histidine residues) in the N-terminal of the proteins. The purification using IMAC system was based on the specific interaction between transitional metal ion (Co²⁺ or Ni²⁺) with a donor electron from amino acid residues^{27,28}. In the case of DNA Pol I ITB₁, the histidine was used as a donor electron meanwhile Ni²⁺ was the acceptor. The soluble crude extracts of the proteins were directly subject to Ni-NTA affinity chromatography. The proteins were eluted by addition of imidazoles. Fig 3A, B, and C (lane 3) showed the electrophoregram of purified proteins for the wild type, *EcoRI* and *XhoI* deletion mutants respectively. It showed that DNA Pol I ITB₁ wild type and its deletion mutants have been well purified and ready for further used.

CONCLUSIONS

DNA Pol I ITB₁, *DEcoRI* and *DXhoI* genes were successfully cloned into pET30a(+) expressions vector resulting pITB₂₀, pITB₂₁ and pITB₂₂ recombinant plasmids. Restriction and sequence analysis of all of recombinant plasmids confirmed that the DNA Pol I ITB-1 genes were clone in right and correct positions. The genes from pITB₂₀, pITB₂₁, and pITB₂₂ have been successfully expressed in *E. coli* BL21 (DE3) and purified using Ni-NTA resin.

ACKNOWLEDGMENTS

This research was support by Competitive Grant (Hibah Bersaing, Dikti) from Ministry of National Education, Republic of Indonesia to Fida Madayanti, and BPPS scholarship program to Hira Helwati.

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