The Enhancement of Biodesulfurization Activity in a Novel Indigenous Engineered *Pseudomonas putida*

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ABSTRACT

Background: The combustion of sulfur-rich fossil fuels leads to release of sulfur oxide pollution in the environment. In biodesulfurization process, an organism is able to remove sulfur from fossil fuels without decreasing the caloric value of those substrates. The main aim of this research was to design a recombinant microorganism to remove the highest amount of sulfur compounds in fossil fuels. 

Methods: Three genes (*dszA,B,C*) from *dsz* operon are responsible for the 4S pathway (biodesulfurization pathway) in *Rhodococcus erythropolis* IGTS8 were inserted into the chromosome of a novel indigenous *Pseudomonas putida*. The reaction catalyzed by products of *dszA,B,C* genes require FMNH2 supplied by *dszD* enzyme. Thus, *pVLT31* vector harboring *dszD* gene was transferred into this recombinant strain. 

Results: The results demonstrated a higher biodesulfurization activity when the flavin reductase gene was transferred into recombinant *P. putida* harboring *dszA,B,C*. These results were approved by the Gibbs test and HPLC analysis. 

Conclusion: These analyses showed that this novel indigenous engineered *P. putida* could be a promising candidate for an industrial and environmental application for Biodesulfurization process. 


Keyword: *Pseudomonas aeruginosa*, *Rhodococcus erythropolis* IGTS8, *pVLT31* vector, Biodesulfurization

INTRODUCTION

The combustion of fossil fuels disseminates sulfur oxide compounds. Many researchers have been performed to develop a biocatalyst to remove organic sulfur from coal and petroleum products [1]. The conventional hydro-desulfurization technology is a high pressure and high temperature catalytic process using various transition metal catalysts. However, the biodesulfurization process using microorganisms to remove the organic sulfur from coal and petroleum products could be performed safely under mild condition. Dibenzothiophen (DBT) is generally considered as a model compound for desulfurization in fossil fuels [2].

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subsequently dszA as a second monooxygenase enzyme converting the DBT sulfone to DBT sulfnate.

Finally, the dszB as a desulfinase enzyme catalyzes the rate-limiting step in the pathway to transform DBT sulfone to 2-HBP and sulfite [7, 8]. In this pathway, the monooxygenase C and A require a free FMNH₂ for their activity. Therefore, it is provided as a dszD enzyme in the form of high expression recombinant plasmid in this strain [9, 10]. In this work three genes (dszA,B,C) were inserted stably into the chromosome of newly transformed E. coli expressing recombinant plasmid in this strain [9, 10].

Table 1. Bacterial strains used in this study.

<table>
<thead>
<tr>
<th>Species and Strains</th>
<th>Relevant genotype/phenotype</th>
<th>Reference/origin</th>
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<tbody>
<tr>
<td>E. coli DH5α</td>
<td>[F], endA1, hsdR17(rk·mk'), supE44, thi-1, recA1, gyrA(Nal'), relA1, Δ(lacZYA-argF)U69, (a80lacZΔM15), LacZ recombinant deficient host</td>
<td>[11]</td>
</tr>
<tr>
<td>E. coli HB101</td>
<td>ProA2, leuB6, thi-1, lacY1, hsdS20(rBmB'), recA13, rps120(Stf'), ara-14, galK2, xyl-5, mtl-1, supE44, mcrB, mrr, General recombinant deficient plasmid host</td>
<td>[11]</td>
</tr>
<tr>
<td>Rhodococcus erythropolis IGTS8</td>
<td>Biodesulfurization</td>
<td>NIGEB (National Institute of Genetic Engineering and Biotechnology)</td>
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The sulfur-free medium used in this study was a modification of the standard basal salt medium (BSM) containing (per liter) 2.44 g KH₂PO₄, 5.57 g Na₂HPO₄, 2.0 g NH₄Cl, 0.2 g MgCl₂·6H₂O, 0.001 g CaCl₂·2H₂O, 0.001 g FeCl₃·6H₂O, 0.004 g MnCl₂·4H₂O, DBT as a sulfur source to the final concentration of 60 ppm and glycerol (1.6 ml l⁻¹) as a carbon source to the final concentration of 100 ppm. Occasionally, citrate was added after sterilization of medium. Citrate was used to isolate Pseudomonas strain that are resistant to antibiotic. Indigenous Pseudomonas strains were grown at 40°C. Escherichia coli strains were grown in Luria Bertani (LB) at 37°C. Transformants were selected on 1.5% (w/v) LB agar containing ampicillin or kanamycin (50 µg ml⁻¹ each).

**MATERIALS AND METHODS**

Restriction endonucleases were purchased from Fermentas (Germany). All enzymes were used in accordance with manufacturers recommendation. DBT and 2-HBP were purchased from Fisher (Germany) and Gibbs reagent, 2, 6-dichloroquinone-4-chloromide from Sigma (USA). Ethyl acetate, acetonitril and all other chemicals were purchased from Merck (Germany).

**Bacterial strain and plasmids.** The bacterial strains and plasmids used in this study are listed in Tables 1 and 2, respectively.

**Media and growth conditions.** Deionized water was used to prepare all media and stock solutions. The genomic DNA of R. erythropolis IGTS8 was extracted by phenol/chloroform extraction method [11]. PCR was carried out for the identification and amplification of dszA,B,C genes of R. erythropolis IGTS8. The sequence of forward and reverse primers were 5’GAATTCGCGATGACTCAAC AACGAC 3’ and 5’ AAGCTTCCAGGAGGTGAA GCCGGGAA 3’, respectively. Restriction sites for EcoRI and HindIII introduced at the 5’ ends of forward and reverse primers. Fast start taq DNA polymerase and a high fidelity kit (Roche, Germany) were used for PCR. The annealing temperature was 65°C. The PCR product with 3.8 kb length was purified and concentrated by using a high pure PCR product purification kit (Roche, Germany). The PCR product containing dszA,B,C genes was digested by EcoRI and HindIII and cloned into the pVLT31 containing tac promoter. Ptac dsz fusion together. pVLT31 plasmid was transformed into competent E. coli DH5. The bacteria were harvested and
Table 2. Plasmids used in this study that is previously been described by Gallardo et al. [12].

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Genotype/phenotype</th>
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<tbody>
<tr>
<td>pRK600</td>
<td>Km&lt;sup&gt;r&lt;/sup&gt;, oriColE1/PK 2-Mob&lt;sup&gt;+&lt;/sup&gt;, PK2-Tra&lt;sup&gt;+&lt;/sup&gt;, pESOX1 into pVLT31</td>
</tr>
<tr>
<td>pESOX3</td>
<td>TC&lt;sup&gt;r&lt;/sup&gt;, 3.8 kb, dsz operon subclone of pESOX1 into pVLT31</td>
</tr>
<tr>
<td>pESOX4</td>
<td>Km&lt;sup&gt;r&lt;/sup&gt;, Ap&lt;sup&gt;r&lt;/sup&gt;, 5.8 kb fragment subclone of pESOX3 into pBSL118</td>
</tr>
<tr>
<td>pVLT31</td>
<td>TC&lt;sup&gt;r&lt;/sup&gt;, Broad-host-range plasmid</td>
</tr>
<tr>
<td>pBSL118</td>
<td>Km&lt;sup&gt;r&lt;/sup&gt;, Ap&lt;sup&gt;r&lt;/sup&gt;, Mini-Tn&lt;sup&gt;5&lt;/sup&gt; transposon carrier</td>
</tr>
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</table>

pVLT31 plasmid was extracted and digested by EcoRV restriction enzyme. DszA,B,C genes and tac promoter in a fragment were the result of EcoRV restriction enzyme. Then, Ptac::dsz fragment was ligated in pBSL118 plasmid (pBSL118 harboring Ptac::dsz is named pESOX4). The pESOX4 Plasmid contains the RP4-mediated mobilization function and carries a mini-Tn<sup>5</sup> transposon that causes the stable migration of the heterologous DNA fragment from plasmid into the chromosome of P. putida. The pESOX4 transformed into the competent E. coli CC118pir bacterium. The tri-parental filter-mating method was applied by using E. coli CC118pir as the donor and E. coli HB101 as the helper to transfer genetic information to P. putida as a recipient cell. Bacteria were cultivated in a M9 medium containing kanamycin antibiotic and citrate as only carbon source [12].

Southern-blot hybridization analysis. To confirm the cloning of dszA,B,C genes, DNA hybridization experiment was performed by Southern-blot method as described by Maniatis et al. [11]. DNA was labeled non-radioactively by using the random primer method with a Dig label and detection kit (Bohering Mannheim, Germany). Genomic DNA was electrophoresed on a 0.7% agarose gel then incubated in 0.25 M HCl at 20°C for 10 min, in the denaturation solution for 45 min and in the neutralization solution for 30 min. The denaturation solution contained NaOH (50 ml of 10 M solution) and NaCl (87.66 g) made up to 1 L with distilled water. The neutralization solution contained Tris (121.14 g), NaCl (87.66 g) and Tri-sodium citrate (88.2 g) in distilled water (L). Separated DNA transferred from gel to nitrocellulose membrane. The hybridization between the Dig-labeled probe and immobilized DNA on the membrane was carried out by using the procedure as described by Maniatis et al. [11].

Cloning of dszD gene into recombinant P. putida. Plasmid pTZ57RT containing dszD gene of R. erythropolis IGTS8 was digested by EcoRI and HindIII restriction enzymes. dszD gene was purified and ligated in plasmid pVLT31 comprising tetracycline resistance site and tac promoter. Then, it was cloned into the recombinant P. putida containing dszA,B,C in its chromosome by electroporation method [11]. After cloning, the bacteria were cultivated in M9 medium containing tetracycline antibiotic and citrate as a carbon source. In order to identify bacteria containing dszD gene, PCR technique was employed. The nucleic acid sequences of the PCR primer were designed using conserved nucleic acid sequence of the flavin reductase enzyme of R. erythropolis IGTS8. The primers were as follow: 5'-GAA TTC ATG TCT GAC AAG CCG AAT GCC-3' (forward) and 5'-TCT AGA CTA TTG ACC TAA CGG AGT CGG-3' (reverse). Annealing temperature was 55°C for 1 min (30 cycles).

Quantitative Gibbs assay. Recombinant P. putida containing dszA,B,C in the chromosome and dszD on pVLT31 vector and R. erythropolis IGTS8 were grown in LB medium at 30°C. Bacteria were cultured to reached to an optical density of 2.0 at 600 nm, harvested by centrifugation and resuspended in BSM medium(400 ml) to reach to an optical density of 0.05 at 600 nm.. Then supplemented by DBT in acetone (250 µl of 40 mM solution) as a sulfur source until the final concentration of DBT reached 60 ppm and glycerol (200 µl) as a carbon source until the final concentration of glycerol reached 100 ppm and shacked 200 rpm at 30°C. A volume of 40 ml of this solution was removed every 4 h and its pH was adjusted to 2 by using concentrate HCl. For Gibbs assay, the pH of solution was adjusted to 8 with 10% (w/v) sodium carbonate. Gibbs reagent (2, 6 dichloroquinon -4-chloroamide, 10 µl of a10-mM solution in acetone) was then added to the solution and kept at 30°C for 30 minute. The solution was then centrifuged (8000 ×g) for 5 minute to remove cells. Absorbance of the supernatant was determined at 610 nm [11]. Biodesulfurization activity of recombinant P. putida and R. erythropolis IGTS8 was compared in 6, 12, 18, 24, 30 and 36 h. Standard Gibbs curve [8] was designed and 2-HBP production of other samples was measured based on comparing with 2-HBP concentration and OD of standard peak.

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HPLC analysis. To recognize standard peak, a certain value (0.1 mM) of pure 2-HBP was inserted in BSM medium and injected (standard peak). After sample preparation according to the Maniatis et al. [11], each sample was injected and the production of 2-HBP was monitored and the peak area on HPLC was compared with standard 2-HBP peak. The time course for DBT desulfurization for all the strains were carried out by evaluation of the producing of 2-HBP. The 2-HBP production of recombinant P. putida and R. erythropolis IGTS8 was measured after 12, 24 and 36 h. The properties of HPLC analysis were model 1100 Cecil (England), C18 column, elution phase performed with 50:50 (v/v) acetonitrile/water mobile phase at 1 ml min⁻¹. Detection was realized with an UV detector at 280 nm, flow rate 0.9 ml/min [11, 13].

RESULTS

Cloning of dszA, B, C genes into the chromosome of P. putida. dszA,B,C genes (3.8 kb) of R. erythropolis IGTS8 was amplified using PCR method (Fig. 1) and ligated into the plasmid pVLT31 under control of tac promoter to make the construct pTSOX3. Then, a 5.8-kb fragment containing dsz operon and tac promoter of pTSOX3 plasmid was digested with EcoRV restriction enzyme and ligated into EcoRV site of a suicide vector (pBSL118) which carries the mini-Tn5 transposon genes to make the construct pTSOX4. Afterwards, the construct, pTSOX4 was transferred into the E. coli CC118λpir cells. To confirm the accuracy of cloning, the pESOX4 plasmid was digested by EcoRV restriction enzyme and ligated into EcoRV site of a suicide vector (pBSL118) which carries the mini-Tn5 transposon genes to make the construct pTSOX4. Afterwards, the construct, pTSOX4 was transferred into the E. coli CC118λpir cells. To confirm the accuracy of cloning, the pESOX4 plasmid was digested by EcoRV restriction enzyme. According to Figure 2, two bands of dszA,B,C gene under heterologous tac promoter (5.8 kb) and plasmid (4.7 kb) reveal; Lane 5 and 6, plasmid without insert.

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Southern-blot. To confirm the presence of \( dszA,B,C \) gene into the chromosome of recombinant \( P. \) \textit{putida} (\( pTSOX4 \)), Southern-blot was performed. Southern-blot of chromosomal DNA demonstrated the accuracy of insertion of \( dszA,B,C \) gene into chromosome of \( P. \) \textit{putida}. According to Figure 3, Lane 2 is blot of chromosomal DNA of SOX4 which demonstrated the accuracy of insertion of \( dszA,B,C \) gene into chromosome of \( P. \) \textit{putida}. The data confirmed that the \( dsz \) cluster was functional when stably inserted in a single-copy into the chromosome of \( P. \) \textit{putida}.

Cloning of \( dszD \) gene into recombinant \( P. \) \textit{putida}. Plasmid \( pTZ57RT \) containing \( dszD \) gene was digested by \( EcoRI \) and \( HindIII \) (Fig. 4). In Figure 4, lanes 2 and 3 reveal bands of \( dszD \) gene (586 bp) and \( pTZ57RT \) plasmid. The \( dszD \) gene was ligated in \( pVLT31 \) plasmid and transferred into recombinant \( P. \) \textit{putida}. Oxidoreductase gene is necessary for enhancing DBT desulfurization activity. To screen \( P. \) \textit{putida} containing \( dszD \) gene, PCR technique was employed. In Figure 5, lanes 5-7 reveal PCR band of oxidoreductase gene (586 bp).

Quantitative Gibbs assay. Quantitative Gibbs assay was carried out based on the color change of the solution. The time course for DBT desulfurization of Recombinant \( P. \) \textit{putida} (containing \( dszA,B,C \) in its chromosome and \( dszD \) on \( pVLT31 \) plasmid) and \( R. \) \textit{erythropolis} IGTS8 was carried out by measuring the release of 2-HBP using quantitative Gibbs assay. 2-HBP production by recombinant \( P. \) \textit{putida} was compared with \( R. \) \textit{erythropolis} IGTS8 (Fig. 6A). Biodesulfurization activity of these samples was compared in 6, 12, 18, 24, 30 and 36 h. According to Gibbs assay, 2-HBP production of \( P. \) \textit{putida} was 0.166 mM and 0.228 mM after 18 and 36 h, respectively. The lag phase of \( P. \) \textit{aeruginosa} was low (3-4 h) and the highest value of 2-HBP production (0.229 mM) by recombinant \( P. \) \textit{putida} was achieved between 16-20 h. The 2-HBP production of \( R. \) \textit{erythropolis} IGTS8 were 0.039 mM and 0.239 mM after 18 and 36 h, respectively and the highest value of 2-HBP production (0.239 mM) by \( R. \) \textit{erythropolis} IGTS8 was achieved after 36 h and this increasing was continued (Fig. 6A).

HPLC assay. HPLC analysis was carried out by evaluating the production of 2-HBP. The 2-HBP production of recombinant \( P. \) \textit{putida} and \( R. \) \textit{erythropolis} IGTS8 was measured after 12, 24 and 36 h using the high-performance liquid chromatography method. The 2-HBP production in this comparison was monitored by comparing the peak area of each sample on HPLC. The data obtained from HPLC analysis showed that 2-HBP production of recombinant \( P. \) \textit{putida} (0.192 mM) was higher than that of \( Rhodococcus \) \textit{erythropolis} IGTS8 (0.047 mM) in 21 h. Biodesulfurization activity of \( R. \) \textit{erythropolis} IGTS8 was low in primary 21 h, and increased after 22 h and 2-HBP production of recombinant \( P. \) \textit{putida} and \( R. \) \textit{erythropolis} IGTS8 was 0.229 mM and 0.196 mM, respectively after 36 h (Fig. 6B).
DISCUSSION

Economical analysis indicate that designing a recombinant industrial strain depends on the enhancing of desulfurization rate and significant improvements in the stable biocatalysts adapted to the extreme conditions encountered in petroleum refining [14]. *R. erythropolis* IGTS8 is the most studied bacterium having the genes and enzymes responsible for DBT degradation. The rate of biosulfurization activity and the stability of this bacterium in oil and petroleum are low.

In addition, sulfur compounds inhibit desulfurizing promoter in this organism [3, 15]. The strategy in the metabolic engineering is to change the host strain for the *dsz* genes entirely and promoter replacement for the expression of the *dsz* genes in a heterologous host [16, 17]. Gallardo *et al.* [12] previously reported that the *dsz*A,B,C gene from *R. erythropolis* IGTS8 could be engineered as a DNA cassette under the control of heterologous regulatory signals to increase the ability of *P. putida* K2442 and *Pseudomonas aeruginosa* PG201 to efficiently desulfurize DBT.

Moreover, Matsubara *et al.* [3] cloned *dsz* genes of *R. erythropolis* IGTS8 into *E. coli* and showed that biodesulfurization activity of recombinant *E. coli* increased in an acceptable level.

In this study, *dsz*A,B,C genes were inserted stably into the chromosomes of newly indigenous engineered *P. putida* isolated from Iranian soil. The *flavin reductase* gene also transferred into recombinant *P. putida* by pVLT31 vector. This new indigenous bacterium is an ideal biocatalyst for desulfurizing enzyme system due to the solvent-tolerant characteristic and optimum growth temperature at 40°C which is suitable for industrial biodesulfurization process. In addition, this strain produces *Rhamonolipid biosurfactant* which accelerates two-phase separation step in the biodesulfurization process through increasing emulsification. Moreover, it has a high growth rate which cause to remove sulfur compounds faster than *R. erythropolis* IGTS8 and has the highest biodesulfurization activity in shortest time. In addition to a higher optimal growth temperature, ability in production of *rhamnolipid biosurfactant* and solvent toleration was the other privileges of this recombinant strain which is applicable in biodesulfurization processes.
ACKNOWLEDGMENTS

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REFERENCES


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