We have successfully developed a novel protein expression system based on the bacterium Ralstonia eutropha. This system has been developed in our laboratory to overcome some of the shortcomings associated with recombinant protein expression in other bacteria (e.g. poor fermentation performance, inclusion body formation and proteolysis). High level expression of organophosphohydrolase (OPH), an enzyme prone to inclusion body formation in Escherichia coli has been demonstrated. A proteomics approach identified the promoter of the phaP gene as a strong, inducible promoter. By creating a translational fusion between the phaP promoter and oph gene and introducing this fusion into the chromosome, OPH titers of greater than 1 g/L were achieved in high cell density fermentations. Multiple copies of the PphaP-oph translational fusion were introduced into the chromosome to further increase expression. A proportional increase in OPH titer was found with increasing copy number. An OPH titer of approximately 4.3 g/L was measured in high cell density fermentation using a strain containing three copies of PphaP-oph translational fusion. This represents the highest titer reported to date for OPH (approximately 30 times greater than previously reported expression levels). Results have reported in two publications (Srinivasan et al. 2003; Srinivasan et al., 2002).
Scientific progress and accomplishments:

Introduction:

With advances in protein engineering, there has been a surge in the number of newly discovered proteins and protein function as well as the ability to engineer the properties of such proteins. Enhancement of protein production is a primary goal of recombinant microbial process development. This can be achieved by increasing the amount of recombinant protein per cell (specific productivity) and/or increasing the cell concentration per unit time (cell productivity). In order to improve volumetric productivity in a cost effective manner, recombinant proteins are often produced in high cell density fermentations. High cell density fermentation has many advantages over normal fermentations in that they have a higher final product concentration, reduced waste water and higher overall productivity and hence lower setup and operating costs (Chen, Hwang et al. 1992; Andersson, Strandberg et al. 1994).

We proposed the establishment of a novel enzyme expression system designed around a robust and proven fermentation organism. We have developed the molecular biological research tools required to provide a flexible gene transformation and expression system for Ralstonia eutropha (formerly Alcaligenes eutrophus), an organism we have chosen based on its unusually robust fermentation characteristics under industrial fermentation conditions. Moreover, we have successfully developed a high cell density fermentation system, to over express recombinant proteins in R. eutropha. Organophosphohydrolase was chosen as our model enzyme.

The original project objectives are summarized below.

Objectives:

(i) Establish a fermentation system based on R. eutropha to produce maximum protein titers.
(ii) Establish transformation and conjugation protocols for introducing genes into Ralstonia eutropha.
(iii) Identify potent transcriptional control elements.
(iv) Integrate the fermentation and recombinant expression systems.
Results:

1. Fermentation:

We have developed a simple, efficient and reproducible high cell density fermentation protocol based on *R. eutropha* strain NCIMB40124. We have routinely obtained cell densities of over 180g DCW/L in a simple fed batch mode with an industrial medium containing glucose. In order to maximize protein content in the cell, the amount of PHA polymer produced has to be minimized. Previous studies have established that *R. eutropha* produces polymer under phosphate or nitrogen limitations. We performed several experimental fermentations to establish the amount of phosphate that has to be fed for maintaining a high cell density while limiting the polymer content. We were able to demonstrate that feeding the organism with a low carbon: phosphate ratio controlled the PHA concentration. We have established a feeding regime wherein we supply glucose and phosphate during the initial phases in order to increase the cell density to approximately 130 g/L.

Another common problem that occurs in high cell density fermentations is the production of byproducts such as acetate, lactate and ethanol under oxygen limiting conditions. This has been a major drawback in establishing high cell density fermentations in *E. coli* and *Bacillus*. (Dedhia, Hottiger et al. 1994; Gschaedler, Le et al. 1994; Kleman and Strohl 1994). *R. eutropha* produces polymer instead of these compounds to dissipate its reducing equivalents. In our fermentations the dissolved oxygen concentrations dropped to 0% as soon as cell densities of 30 g/L dry cell weight were achieved and remained at 0% throughout the remained of the fermentation. We performed HPLC analysis of the fermentation broths at various times intervals during the fermentation. Concentrations of acetate, lactate or ethanol were below the detection limit of 0.1 g/L.

2. Transformation and Conjugation:

Even though *R. eutropha* grows to very high cell densities, the organism has not been used to produce recombinant proteins. A few genes, most of them involved in PHA production, have been successfully expressed in *R. eutropha* using the pKT230 a broad host range plasmid. (Pries, Steinbuchel et al. 1990). Maintaining the genes in a plasmid offers many advantages such as: (1) manipulation of plasmids is simpler and commonly used in molecular biological applications; (2) plasmids allow us to increase the number of copies (gene dosage) of a given gene thereby increasing expression levels. A major hurdle for establishing transformation procedure in the *R. eutropha* strain is the absence of selectable markers. We found that the strain NCIMB 40124 is resistant to streptomycin and kanamycin, the selectable markers of the plasmid pKT230. We grew the strain on an array of antibiotics and identified that the organism is not resistant to chloramphenicol and tetracycline. We have established the ability to transform recombinant genes into *R. eutropha* by tri-parental mating as described by (Jackson and Srienc 1999) with pKT230, a high copy number plasmid. We have cloned a chloramphenicol acetyltransferse (*cat*) gene into the vector as a selection marker in *R. eutropha*. We have used this technique successfully to transform *R. eutropha* with a plasmid (pKTPPCm) carrying the OPH gene under the control of the *phaP* promoter, chloramphenicol marker and the replication regions of pKT230.
3. Identifying potent transcriptional control elements:

A key element of the project was the search for strong regulatory sequences (promoters) on the chromosome of *R. eutropha*. High expression levels of recombinant proteins can be achieved only if the gene construct for protein expression contains a strong promoter. We were interested in identifying genes that are upregulated during the fermentation process itself or are upregulated in response to the variation of a simple process parameter. Such induction parameters included: (1) a change in temperature; (2) the addition or omission of a specific nutrient e.g., phosphate; (3) microaerobic conditions; (4) change in pH; or (5) change in carbon source e.g., changing glucose to fructose. We performed fermentations where we altered one of the above parameters and collected samples before and after induction. Of these induction conditions, we were able to achieve high densities (greater than 150 g/L dry cell weight) only for two of the conditions: phosphate limitation and changing glucose to fructose. The total protein from these samples was extracted and separated by 2D SDS PAGE. From the 2D SDS PAGE gels we could identify three strongly expressed proteins: a constitutive protein of about 60 kDa (A); an approximately 20 kDa protein (B) induced by fructose and another protein of about 25 kDa; and (C) a 24 kDa protein induced by phosphate limitation.

The gels were subsequently blotted onto a PVDF membrane and the N-terminus of the proteins was sequenced using Edman degradation. We then searched the GENBANK library for identifying the proteins using BLAST. Protein A showed identity to a chaperonin in *B. cepacia*, while Protein B did not show homology to any other protein. Protein C was identical to a 24 kDa protein from *R. eutropha* named GA24. GA24 is the product of *phaP* gene which binds to the surface of the PHA limiting the size of the polymer (Wieczorek, Steinbuchel et al. 1996). This protein has been found to be present to about 5% of the total protein in the cell under phosphate or nitrogen limiting conditions (i.e., under polymer production conditions). Since phosphate limitation is easy to maintain and polymer production has advantages for high cell density fermentations, we decided to use the promoter of this protein for expression of recombinant proteins. From the sequence of *phaP* gene we synthesized primers for the promoter and cloned it from the genomic DNA of *R. eutropha*.
Fig 1. Two-dimensional electrophoresis of whole cell extracts of *R. eutropha* under fermentation conditions: (I) un-induced at $OD_{600}$ 100, (II) un-induced at $OD_{600}$ 300, (III) fructose induction and (IV) phosphate limitation.

4. Development of the OPH expression system in *R. eutropha*

Our initial strategy to produce OPH was to construct a $P_{phAP}::oph$ translational fusion and introduce this fusion into the cell on a plasmid (pKT230). Good OPH expression results were obtained from shake flasks experiments. However scale-up to high cell density fermentation resulted in very low specific enzyme activities (<1 U/mg protein). Plasmid stability was measured at numerous time points during several fermentation experiments. It was found that only 30% of the cells retain the plasmid, after 20 hours after inoculation and that less than 10% of the cells retained the plasmid after 50 hours.
In order to express OPH in high cell density fermentations of *R. eutropha*, a translational fusion between the *phaP* promoter and the *oph* gene was created and introduced into the suicide plasmid pJQPPCm. This suicide plasmid was used to integrate the recombinant gene into the *phaP* locus of *R. eutropha* using bi-parental mating techniques. Integration into the chromosome overcomes the problems of maintaining plasmid stability over multiple generations during the course of a fermentation experiment.

A Southern blot was performed to confirm that single copies of the $P_{phaP}::oph$ translational fusion had been integrated in the *phaP* locus.

*Fig 2: Southern blot analysis of the OPH integrant strain to confirm single copy integration.*
Fig 3: Western blot of fermentation samples from a high cell density fermentation of *R. eutropha* expressing OPH from a single chromosomal copy.

Fig 4: Growth and OPH activity from a high cell density fermentation of *R. eutropha* expressing OPH from a Single Chromosomal Copy.

Feed 1: 600 g/L Glucose; 220 mM H3PO4; 2.2 g/L MgSO4.7H2O; 0.15 mM CoCl2

Feed 2: 600 g/L Glucose; 15 mM CoCl2
Figure 6 shows high levels of expression (circa. 121 U/mg using the paraoxon assay). This enzyme concentration represents approximately 1.5% of the total protein and thus in this fermentation about 1 g/L of soluble, active OPH was produced. Moreover the Western blot shows that the basal level expression of the protein is low prior to induction with phosphate limitation.

Results from sections 1, 2, 3 and 4 culminated in an Applied and Environmental Microbiology publication (Srinivasan et al., 2002).

5. Increasing oph gene dosage

In prokaryotes, gene dosage has typically been increased by the used of medium and high copy number plasmids. In lower order eukaryotes, gene expression has been achieved random, multiple integration of a gene of interest into the host chromosome (Werten et al., 1999). Multiple copies of the P\textsubscript{phaP}::oph translational fusion were therefore introduced into the R. eutropha chromosome in an attempt to increase gene dosage. Single, double and triple copies of the P\textsubscript{phaP}::oph translational fusion were introduced into the R. eutropha chromosome.

Southern blot analysis showed not only that the multiple copies had been integrated into the chromosome, but also that the integration is stable throughout the time course of the fermentation.
Fig 5: (A) Southern blot analysis of *R. eutropha* strains SS17, SS18 and SS19. Genomic DNA of single copy (SS17; lanes 1 and 2), double copy (SS18; lanes 3 and 4) and triple copy (SS19; lanes 5 and 6) was digested with HindIII. Lanes 1, 3, and 5 correspond to samples collected during fermentation before induction. Lanes 2, 4, and 6 correspond to samples collected after induction. (B) Map of the genomic DNA region analyzed. The open reading frame of the *oph* gene is indicated in the figure while *H* refers to the HindIII restriction sites.

Introducing multiple copies of the $P_{phaP}::oph$ translational fusion increased the OPH expression levels in high cell density fermentations. Moreover, a proportional increase in OPH expression level was observed with increasing copy number.

Results from the fermentation are summarized in Fig 6. By integrating three copies of the $P_{phaP}::oph$ translational fusion into the chromosome, a titer of approximately 4.3 g/L was measured in high cell density fermentation. This represents the highest titer reported to date for this enzyme and is approximately 30 times greater than previously reported expression level in *E. coli* fermentations.
Fig 6: Summary of post-induction profiles for OPH expression in fermentations conducted with strain containing single, double and triple copies of the $P_{phaP}::oph$ translational fusion.

The results summarized in Section 5 culminated in a recent Biotechnology and Bioengineering publication (Srinivasan et al., 2003).

Scientific personnel:

A full time graduate student (Sriram Srinivasan) was supported by the grant.
References:


A Novel High-Cell-Density Protein Expression System Based on *Ralstonia eutropha*

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We describe the development of a novel protein expression system based on the industrial fermentation organism *Ralstonia eutropha* (formerly known as *Alcaligenes eutrophus*) NCIMB 40124. This new system overcomes some of the shortcomings of traditional *Escherichia coli*-based protein expression systems, particularly the propensity of such systems to form inclusion bodies during high-level expression. Using a proteomics approach, we identified promoters that can be induced by simple process parameters or medium compositions in high-density cell culture or shake flasks, respectively. By combining newly developed molecular biological tools with a high-cell-density fermentation process, we were able to produce high levels (>1 g/liter) of soluble, active organophosphohydrolase, a model enzyme prone to inclusion body formation in *E. coli*.

Advances in protein engineering, the completion of numerous bacterial and fungal genome sequencing projects, and the isolation of new genes from extremophiles have led to an increased number of useful proteins. However, to enable recombinant proteins to play a role in applications where larger quantities are required, such as tissue engineering or catalytic materials, production technologies that are more efficient and robust are desirable. Improving protein production is the primary goal of recombinant microbial process development and is a focus of our laboratory. Overall protein productivity can be improved by increasing the product of two variables: (i) the amount of recombinant protein per cell (specific productivity) and (ii) the amount of cell mass per unit of volume and time (cell productivity). In order to improve volumetric productivity in a cost-effective manner, recombinant proteins are often produced in high-cell-density fermentations. High-cell-density fermentations offer many advantages over traditional fermentations in that final product concentrations are higher and downtime and water usage are reduced, yet overall productivity is improved, resulting in lower setup and operating costs (3, 6).

In the absence of specific folding or posttranslational modification requirements, *Escherichia coli* is usually the expression host of choice. *E. coli*-based fermentation systems produce good yields at laboratory scale; however, scale up to industrial scale, where oxygen enrichment, dialysis, and sophisticated feeding algorithms become impractical and cost prohibitive, has been challenging (22). Unlike laboratory-scale fermentors, where the above-mentioned techniques are feasible, large-scale industrial fermentors are limited by mixing constraints and their ability to transfer oxygen and heat. It is well documented that oxygen-limiting conditions in *E. coli* result in the production of reduced carbon metabolites such as acetate, lactate, and formate (1, 20), which accumulate in high-cell-density cultures and ultimately inhibit further microbial growth. Titers of recombinant proteins in *E. coli* are limited by several factors including the final cell density (22), the tendency for inclusion bodies to be formed when strong promoters are used (15, 23), and proteolysis, which adversely affects the quality of the final product (14, 17).

Considerable efforts have been undertaken to overcome the limitations of *E. coli* as a recombinant-protein expression host, and improving the organism’s fermentation performance has been the focus of many biochemical engineering research groups. The accumulation of organic acids during the fermentation process has been reduced by several approaches: (i) installation of inline dialysis membranes (12, 26), (ii) implementation of a controlled feeding regimen imposing a reduced growth rate on the microorganism (28), (iii) enrichment with pure oxygen (7), and (iv) engineering of a heme cofactor into the host organism (11). Inclusion body formation has been reduced by expression of a target protein in frame with a highly soluble protein, thereby creating a more soluble fusion protein, and/or by decreasing the growth rate of the organism by decreasing the temperature of the fermentation (39). Proteolytic activity has been reduced by the generation of protease-deficient mutants (18).

While considerable progress has been made in addressing some of these shortcomings, the performance of *E. coli* as a recombinant-protein expression host still leaves much to be desired. In this paper, we report the development of a novel prokaryotic protein expression system based on a nonpathogenic organism, *Ralstonia eutropha* (formerly *Alcaligenes eutrophus*). The described system permits high-cell-density culture in a defined minimal medium, does not require the addition of antibiotics to maintain plasmid stability, and does not require exogenous addition of inducers such as isopropyl-β-D-thiogalactopyranoside (IPTG) to initiate protein expression. A model protein that has traditionally been difficult to obtain in soluble form in *E. coli* (organophosphohydrolase [OPH] from *Pseudomonas diminuta* MG) was produced at high yield without any measurable formation of inclusion bodies.

*R. eutropha* has been used at a scale of several hundred thousand liters for the production of polyhydroxyalkanoate (PHA), a biodegradable polymer, by ICI/Zeneca and later Monsanto. The genome has been sequenced (http://jgi.doe...
.gov/JGI_microbial/html/ralstonia/ralston_homepage.html), and numerous high-cell-density processes have been reported previously (13, 30). Unlike E. coli and other enterobacteria which preferentially metabolize hexose sugars through the Embden-Meyerhof-Parnas pathway, R. eutropha preferentially uses the Entner-Doudoroff pathway to metabolize hexoses (21, 34). This results in a higher NADPH/NADH ratio, which causes a higher degree of biosynthetic as opposed to respiratory reducing equivalents. This, we believe, positively affects protein formation, since R. eutropha has the ability to balance the reducing equivalents generated from carbon metabolism by using the production of polyhydroxybutyrate (PHB) as a sink for reducing power (i.e., NADPH) in the absence of a final electron acceptor such as oxygen. Both E. coli and Bacillus spp. are forced to synthesize reduced organic acids to balance their redox state under oxygen-limiting conditions, and these acid metabolites have been shown to negatively affect overall fermentation performance. In contrast, PHB is a high-molecular-weight polymer that causes no osmotic stress on the cell and does not adversely affect overall bacterial growth. High-cell-density fermentations of R. eutropha (up to 230 g/liter) in large-scale reactors have been described previously by various groups (31, 37). Most of this work has been aimed at maximizing the PHB content; hence, the real cell mass (real cell mass = total biomass − PHB) was generally below 30 to 40 g/liter.

**OPH, the model enzyme.** OPHs (EC 3.1.8.1) are enzymes that are able to hydrolyze and thereby substantially reduce the toxicity of cholinesterase inhibitors like sarin and VX. OPH is a 72-kDa homodimeric enzyme that requires a divalent cation such as cobalt or zinc (8). The enzyme catalyzes the hydrolysis of the organophosphorus compounds at a remarkable rate; hence, it has found applications in detoxification and decontamination of parathion-containing agricultural fields and chemical weapons stock (41). Other applications include its use as a biosensor for monitoring levels of these compounds and for protection against chemical warfare agents (29). Several attempts to express gram quantities of OPHs in E. coli and other organisms have been hampered by the formation of inclusion bodies and the inability to grow to high cell densities. Attempts to improve production by engineering a fusion protein with highly soluble proteins like green fluorescent protein have resulted in reduced specific productivity and require posttranslational cleavage of the fusion (40, 41). To date, there has been no report of a fermentation process that provides sufficient amounts of OPH for large-scale applications (9). OPH was chosen for this study because it has a well-documented history of forming inclusion bodies in E. coli and thus seemed to be a suitable model protein (32, 33).

**MATERIALS AND METHODS.**

**Strains, plasmids, and oligonucleotides.** The various strains and plasmids that were used in this study are listed in Table 1. The oligonucleotides used in this study were PromUp (dCAGGAATTCCATCGCGCAGCATGC), PromDn (dCTCGAGCTCATGTCGAAATCC), ParUp (dCTCGAGCTCATGTCGAAATCC), and ParDn (dCTCGAGCTCATGTCGAAATCC) (the restriction sites engineered in the oligonucleotides are underlined).

**Growth media and antibiotics.** E. coli strains were grown in Luria-Bertani medium. R. eutropha strains were cultivated in one of the following media depending on the application: NR medium (36), PCT medium (Table 2), and Lee medium (25). NR is a complex medium, while both PCT and Lee media are

<table>
<thead>
<tr>
<th>Component</th>
<th>Concn (g/liter)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose</td>
<td>500</td>
</tr>
</tbody>
</table>

**Table 2. Composition of PCT medium**

<table>
<thead>
<tr>
<th>Salts</th>
<th>Concn (g/liter)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MgSO₄ · 7H₂O</td>
<td>2.2</td>
</tr>
<tr>
<td>K₂SO₄</td>
<td>3.0</td>
</tr>
<tr>
<td>Na₂SO₄</td>
<td>0.18</td>
</tr>
<tr>
<td>FeSO₄ · 7H₂O</td>
<td>0.18</td>
</tr>
<tr>
<td>H₃PO₄ (1.48 M)</td>
<td>9.6*</td>
</tr>
</tbody>
</table>

**Trace elements**

<table>
<thead>
<tr>
<th>Concn (g/liter)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CuSO₄ · 5H₂O</td>
</tr>
<tr>
<td>ZnSO₄ · 6H₂O</td>
</tr>
<tr>
<td>MnSO₄ · 4H₂O</td>
</tr>
<tr>
<td>CaCl₂ · 2H₂O</td>
</tr>
</tbody>
</table>

*Glucose, salts, and trace elements were autoclaved separately, and 40 ml of glucose, 1 liter of salts, and 2.4 ml of trace elements were mixed at room temperature.
*a The pH was adjusted to 6.8 prior to autoclaving with 28% NH₄OH.
*b Milliliters per liter.
null
col based on \textit{R. eutropha} strain NCIMB 40124 that is aimed at maximizing the overall protein content in the reactor. We can routinely obtain cell densities of over 150 g (dry cell weight)/liter in a simple fed-batch mode (data not shown) in a minimal medium containing only inorganic salts and glucose. Previous studies have established that \textit{R. eutropha} produces PHB under phosphate- or nitrogen-limited conditions when supplied with an appropriate carbon source such as glucose or fructose. We conducted a series of fermentation experiments to establish the amount of phosphate required to maximize cell mass formation while minimizing polymer accumulation. We found that by using various carbon/phosphate ratios in the feed, we were able to effectively control the PHB content of the cell in high-cell-density culture (data not shown). By using this feeding strategy, we were able to achieve a cell density of 182 g (dry cell weight)/liter, with low polymer content. \textit{R. eutropha} has been shown to have a comparatively high protein content of typically below 150 mmol/liter protein. When supplied with an appropriate carbon source such as glucose or fructose. We conducted a series of fermentation experiments to establish the amount of phosphate required to maximize cell mass formation while minimizing polymer accumulation. We found that by using various carbon/phosphate ratios in the feed, we were able to effectively control the PHB content of the cell in high-cell-density culture (data not shown). By using this feeding strategy, we were able to achieve a cell density of 182 g (dry cell weight)/liter, with low polymer content. \textit{R. eutropha} has been shown to have a comparatively high protein content of typically below 150 mmol/liter protein. When supplied with an appropriate carbon source such as glucose or fructose. We conducted a series of fermentation experiments to establish the amount of phosphate required to maximize cell mass formation while minimizing polymer accumulation. We found that by using various carbon/phosphate ratios in the feed, we were able to effectively control the PHB content of the cell in high-cell-density culture (data not shown). By using this feeding strategy, we were able to achieve a cell density of 182 g (dry cell weight)/liter, with low polymer content. \textit{R. eutropha} has been shown to have a comparatively high protein content of typically below 150 mmol/liter protein. When supplied with an appropriate carbon source such as glucose or fructose. We conducted a series of fermentation experiments to establish the amount of phosphate required to maximize cell mass formation while minimizing polymer accumulation. We found that by using various carbon/phosphate ratios in the feed, we were able to effectively control the PHB content of the cell in high-cell-density culture (data not shown). By using this feeding strategy, we were able to achieve a cell density of 182 g (dry cell weight)/liter, with low polymer content. 

### Identifying strong inducible promoters.

High-level expression of recombinant proteins requires the availability of a strong and preferably inducible promoter. On the large, commercial scale, the use of antibiotics (to ensure plasmid maintenance) and inducers such as IPTG (to induce expression) is not desirable for environmental and economic reasons. Thus, we sought to systematically identify genes that are up-regulated in \textit{R. eutropha} during the fermentation process itself or are up-regulated in response to the variation of a simple process parameter. The induction events tested were as follows: (i) a change in temperature, (ii) the omission of phosphate in the medium feed, (iii) microaerobic conditions (oxygen limitation), (iv) change in pH, and (v) change in carbon source (glucose to fructose). In order to assess the influence of these changes in the proteome in response to these induction events, we conducted several fermentations. A control fermentation without any induction event was used as the base case. In each of the fermentations, we grew the cells to an OD600 of approximately 300 and then altered one of the above-mentioned parameters and collected cell samples after imposing the specific changes. In three fermentation runs (pH change, temperature change, and oxygen limitation), high cell densities were not obtainable and thus were not considered further. In two of the five fermentations (phosphate limitation and change of glucose to fructose), we were able to achieve cell densities in excess of 150 g (dry cell weight)/liter. Cell samples from these fermentations were collected, and total cell protein was analyzed by 2D SDS-PAGE. By superimposing 2D SDS-PAGE gels containing protein samples obtained pre- and postinduction, we were able to identify two proteins (glucose-to-fructose change [Fig. 1C] and phosphate limitation [Fig. 1D]) that were up-regulated in response to the imposed conditions and one protein that appeared to be expressed at high constitutive levels under all conditions (Fig. 1). Table 3 describes the three proteins denoted in Fig. 1. One protein that was significantly induced by phosphate limitation was found to be \textit{GA24}, a product of the \textit{phaP} gene, a phasin previously described by Wieczorek and coworkers (38). GA24 is a protein found on the surface of PHA granules that regulates the size of the granule. Wieczorek et al. also found that \textit{GA24} was expressed at relatively high levels (5% of the total protein) in \textit{R. eutropha} during PHB production under nitrogen-limiting conditions. Since \textit{phaP} was a promoter, inducible by a simple process parameter (phosphate limitation) and with low-level basal activity, it met our criteria for a suitable recombinant-protein expression promoter for high-cell-density culture. In order to determine whether quorum sensing or high cell density in itself affects a change in the proteome samples, we collected samples at OD600 values of 100 and 600 without changing any process parameters and then analyzed them by 2D SDS-PAGE (Fig. 1A and B).

### OPH production in \textit{R. eutropha}.

Plasmid pJOPPCm, containing the open reading frame of the OPH gene under the control of \textit{phaPp}, was constructed and transformed into \textit{E. coli} by electroporation. This plasmid was integrated into the \textit{phaP} locus of \textit{R. eutropha} by biparental mating, thereby providing a single stable chromosomal copy of the OPH gene. Three individual colonies were selected and analyzed for OPH production. PCR was performed with one internal and one external primer to verify the chromosomal location of integration. All three strains yielded PCR products consistent with a single chromosomal insertion (data not shown). In addition, Southern blotting was performed on one of the strains to confirm that only a single copy of the OPH open reading frame was received and that integration indeed occurred in the \textit{phaP} locus (Fig. 2).

### High-cell-density production of OPH.

Although high OPH-specific activities have been obtained in \textit{E. coli} in shake flask experiments, successful scale-up has failed due to inclusion body formation (33). In order to demonstrate that high levels of the enzyme can be produced in a simple and efficient fermentation process, we conducted a fermentation to produce approximately 100 g of biomass/liter and over 1 g of OPH/liter. The fermentation was conducted as a three-stage process: batch, fed batch, and induction. During the batch phase, the initial inoculum was allowed to grow such that the cells consumed the initial 20 g of glucose/liter. Glucose depletion (14 h after inoculation) was indicated by a sharp increase in the concentration of dissolved oxygen. After depletion of the initial glucose, a feed containing glucose, phosphate, and sulfate at a constant feed rate of 11.7 g of glucose/h was initiated. The cells continued to grow exponentially until a fixed growth rate corresponding to the glucose feed rate was achieved. The feed rate was then further increased to 14.0 g of glucose/h, thereby increasing the growth rate. During this phase, both phosphate and sulfate concentrations increased in the fermentation, whereas glucose as the rate-limiting nutrient remained undetectable due to its immediate consumption in the reactor. During this phase, the amount of PHB in the cell remained less...
than 5% of the total biomass. Despite some PHB production, the basal activity of the \textit{phaP} promoter was low, as determined by enzyme assays (Fig. 3B) and Western blotting (Fig. 4). A biomass concentration of 93.4 g/liter was obtained 38 h after inoculation (24 h after initiating the glucose feed). At this point, the feed was changed to a glucose solution, containing 15 mM cobalt but lacking phosphate, to initiate the induction phase. OPH requires a divalent cation for enzymatic activity.

**TABLE 3. N-terminal sequence and protein similarity**

<table>
<thead>
<tr>
<th>Protein</th>
<th>N-terminal sequence</th>
<th>Protein similarity</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>AAKDVVFGLDA</td>
<td>GroEL (\textit{Burkholderia cepacia})</td>
<td>Chaperon</td>
</tr>
<tr>
<td>II</td>
<td>TOXTAEQCTK</td>
<td>No similarity identified</td>
<td></td>
</tr>
<tr>
<td>III</td>
<td>VILTPQVAAA</td>
<td>GA24 (\textit{R. eutropha}) (also known as PhaP protein)</td>
<td>Surface protein bound to PHB (an intracellular polymer)$^*$</td>
</tr>
</tbody>
</table>

$^*$ GA24 represents 5% of total protein (35, 38).
so cobalt was added to the glucose feed. During the initial
induction phase, the phosphate concentration rapidly de-
creased in the reactor (Fig. 3B), and upon depletion, OPH
production was induced. After 30 h of induction (68 h after
inoculation), the speciﬁc activity of the protein was found to be
145 U/mg (Fig. 3B). In addition to the results of the enzyme
activity assays, the induction of OPH could also be seen in the
appearance of a band corresponding to the MW of OPH (ap-
proximately 36,000) in the Western blot (Fig. 4, lanes corre-
sponding to 44 to 68 h). In this fermentation, we achieved a
concentration of 99.1 g of real biomass/liter. The speciﬁc ac-
tivity of pure OPH (with cobalt as the divalent cation) has been
reported to be 7,250 U/mg (29) and 8,020 U/mg (24) using the
paraoxon enzyme activity assay; thus, the speciﬁc activity of 145
U/mg corresponds to 2.0 or 1.8% of total cellular protein,

FIG. 2. Southern blot analysis of wild-type R. eutropha and R. eu-
tropha SS14. Genomic DNA from the wild type and integrant SS14
were extracted and digested with SacI, PstI, EcoRI, and RsrII. A
400-bp phaP promoter sequence (the FspI/SacI fragment of plasmid
pUCPCm, shown in grey) was used to probe the blot. (A) Results of
Southern blot analysis of genomic DNA of the wild type and the
integrant probed with a horseradish peroxidase-labeled phaP pro-
moter. The sizes of the markers (base pairs) are indicated on the left.
(B) Map of the analyzed genomic region in the wild type and the
integrant, indicating the probe and the various restriction enzymes
used. S, SacI; E, EcoRI; P, PstI; R, RsrII. The open reading frames of
OPH and GA24 (phaP) are also indicated.

FIG. 3. OPH production in high-cell-density fermentation of R. eutropha. (A) The dry cell weight, real biomass, PHB, and glucose feeding
profile for a typical high-cell-density fermentation. The arrow indicates the time of induction. Symbols: open circles, total dry cell weight; closed
triangles, real biomass; crosses, PHB; closed squares, glucose consumed. (B) The oxygen uptake rate (OUR), the carbon dioxide evolution rate
(CER), the phosphate concentration in the reactor, and the speciﬁc activity of OPH produced. Symbols: open squares, OUR; open triangles, CER;
closed diamonds, phosphate concentration; closed circles; speciﬁc activity.

FIG. 4. Western blot analysis of fermentation samples. Total cell
pellets were diluted to approximately 0.2 g (dry cell weight)/liter and
then boiled on SDS-PAGE cracking buffer and resolved on a 12%
polyacrylamide gel. The proteins were transferred to a nitrocellulose
membrane, and blotting was done with anti-OPH antibody. The ﬁgure
shows the time course of OPH production. M, broad-range MW
marker, with MWs indicated on the left.
respectively. As previously noted, the protein content of R. eutropha has been found to be 68% of dry cell weight (15). The product of 99.1 g of biomass/liter, 0.68 g of protein/g of biomass, and 0.018 g of OPH/g of protein yields an OPH concentration of 1.2 g/liter.

**DISCUSSION**

Traditionally, the development of recombinant-protein production systems has focused on improving the fermentation processes of organisms for which molecular biological tools (e.g., transformation protocols, selection markers, inducible promoters, etc.) have already been established. In this study, we used an organism with robust fermentation characteristics and developed the molecular biological tools to produce recombinant proteins at high levels. We achieved cell densities of over 150 g/liter in a simple process that does not require complex medium components or the supplementation of air with pure oxygen. The process can be implemented manually or by a simple programmable logic controller. In the described fermentation process, growth-inhibiting organic acids were not synthesized although the levels of dissolved oxygen remained at 0% throughout most of the process.

Promoter traps have been used previously to identify strong promoters (4). However, the specific dynamic environment of a high-cell-density culture cannot be adequately reproduced on solid media. In particular, differentially expressed genes that respond to subtle environmental stimulants, or growth-phase-dependent genes, are not readily detected on solid media by use of promoter traps. Thus, we decided to isolate promoters that are up-regulated in the environment in which we expect to use these promoters, namely high-cell-density culture. By looking at the entire proteome before and after changing specific environmental conditions, we identified an inducible promoter in R. eutropha that could be regulated with a simple process parameter (i.e., phosphate limitation). Previous work using shake flasks has shown that phaP is induced under PHB production conditions and that expression is controlled by a DNA binding protein, PhaR (43).

In this study, we were able to obtain 1.2 g of soluble active OPH/liter in a simple high-cell-density fermentation process. Although only a single chromosomal copy of the OPH gene was present, it represents the highest OPH titer reported to date (33). In a way very similar to the concept of man-hours, where the product of two variables determines overall productivity, R. eutropha fermentations allow more cells to produce protein at a lower specific rate while achieving higher overall productivities. This reduces the likelihood of inclusion body formation and thus allows for the higher recovery of soluble active protein. However, to further improve expression levels and to test the limits of soluble-protein production, we are currently investigating the influence of gene dosage and artificial promoters.

**ACKNOWLEDGMENTS**

We thank Mikhail Alexeyev, Janet Grimley, Gregory M. York, and Anthony J. Sinskey for providing us with the plasmids and the antibodies for the project. We thank Stefan Wildt and David Wood for productive discussions.

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Production of Recombinant Proteins Using Multiple-Copy Gene Integration in High-Cell-Density Fermentations of Ralstonia eutropha

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Abstract: We have previously reported the development of a novel protein expression system based on Ralstonia eutropha. In this study we report on the influence of gene copy number on recombinant protein expression in R. eutropha. We compare recombinant gene stability and expression levels of chromosomal integration with a plasmid-based expression system. Single, double, and triple copies of a gene encoding organophosphohydrolase (OPH), an enzyme prone to inclusion-body formation in E. coli, were integrated into the R. eutropha chromosome. A linear increase between the concentration of soluble, active OPH and gene copy number was found. Using a triple-copy integrant, we were able to produce approximately 4.3 g/L of OPH in a high-cell-density fermentation. This represents the highest titer reported to date for this enzyme, and is approximately 30 times greater than expression levels reported in E. coli. © 2003 Wiley Periodicals, Inc.

Keywords: protein expression; gene dosage; high cell density; fermentation

INTRODUCTION

High-cell-density fermentations have been used extensively for increasing the productivity and titer of recombinant proteins (Chen et al., 1992; Cutayar and Poillon, 1989; Knorre et al., 1991; Panda et al., 1999). Protein production in fermentation processes depends on several factors, including promoter strength (Wilms et al., 2001), induction time (Wu et al., 2001), gene dosage, and stability of expression construct (Grabherr et al., 2002). Various studies have been conducted to maximize the recombinant protein yield for Escherichia coli-based fermentations (Chae et al., 2000; Grabherr et al., 2002; Portner and Markl, 1998). These have resulted in tremendous improvements in titer and in amount of soluble protein. However, high-cell-density fermentations of E. coli suffer from various drawbacks, including the formation of organic acids (Akesson et al., 1999; Kleman and Strohl, 1994), proteolysis (Han et al., 1999), and inclusion-body formation (Han et al., 1999; Makrides, 1996).

To overcome the shortcomings of E. coli fermentations, a novel high-cell-density fermentation based on Ralstonia eutropha has been developed in our laboratory (Srinivasan et al., 2002). This system has been shown to produce high levels of soluble recombinant protein in a simple, scalable, high-cell-density fermentation. Using this system, >1 g/L of soluble recombinant organophosphohydrolase (OPH) can be produced by a single chromosomal copy of OPH under the control of an inducible phosphate-responsive promoter.

In prokaryotes, high-level protein expression has been achieved by modulating gene dosage through the use of medium- or high-copy number plasmids. However, an increase in plasmid copy number usually increases the metabolic burden on the cell. For example, a 200-copy, 5-kb plasmid represents approximately 1 Mb of DNA, constituting 20% of the bacterial genome. The effect is compounded in a high-cell-density culture and results in unstable and heterogeneous fermentation. This reduces the protein yield and results in inclusion-body formation and proteolysis (Lee, 1996). In lower eukaryotes, especially Pichia pastoris, high levels of protein expression have been achieved by multiple random integration of the gene of interest. Studies have shown that an increase in gene dosage results in an increase in recombinant protein production up to a copy-number of 15 (Werten et al., 1999).

To better understand the effect of gene dosage and its impact on fermentation characteristics, we constructed strains containing single, double, and triple copies of the expression construct integrated into the chromosome. We also constructed a strain containing a multicopy plasmid with the expression construct. In this study, we report the effect of multiple copies on protein expression and stability of the constructs in the genome.
MATERIALS AND METHODS

Strains, Plasmids, and Media

All *E. coli* and *R. eutropha* strains and plasmids used in this study are described in Table I. All pKNOCK series of vectors were transformed in *E. coli* S-17, whereas other vectors were manipulated in *E. coli* TOP10. *E. coli* strains were grown in Luria–Bertani (LB) media. *R. eutropha* strains were cultivated in tryptic soy broth (TSB) media (Difco Laboratories, Detroit, MI) or PCT media (Srinivasan et al., 2002). Antibiotics were added to growth media to the following final concentrations: for *R. eutropha*, gentamicin (10 μg/mL) and chloramphenicol (50 μg/mL); and for *E. coli*, ampicillin (100 μg/mL), gentamicin (10 μg/mL), and chloramphenicol (50 μg/mL). All antibiotics were obtained from Sigma Co. (St. Louis, MO).

DNA Preparation, Manipulation, and Southern Blot Hybridization

Preparation (Miniprep Kit, Qiagen, Inc., Valencia, CA) and manipulation of DNA, genomic DNA preparation (Geno-mic-tip 500, Qiagen), transformation, and hybridization (North2South direct HRP labeling and detection kit; Pierce, Rockford, IL) were carried out using standard procedures (Sambrook and Russell, 2001) or the manufacturer’s instructions. Sequencing was performed at the Molecular Biology Core Facility at Dartmouth College. PCR products were cloned into pCR2.1-TOPO vector (Invitrogen Corp., Carlsbad, CA) and then cut with the appropriate restriction enzymes.

**Table I.** Strains, plasmids, and primers used in this study.

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Description</th>
<th>Reference or source</th>
</tr>
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<tbody>
<tr>
<td><strong>R. eutropha strains</strong></td>
<td></td>
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<tr>
<td>NCIMB 40124</td>
<td>Wild-type</td>
<td>NCIMB</td>
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<td><em>R. eutropha</em> strain containing plasmid pKT230</td>
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<td>TOP10</td>
<td>Single-copy integrant of the OPH expression cassette derived from pKNOCK-Cm and pKNOCK-PPT1</td>
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<td>SS19</td>
<td>Triple-copy integrant of the OPH expression cassette derived from pKNOCK-Cm and pKNOCK-PPT3</td>
<td>This study</td>
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<td><strong>E. coli strains</strong></td>
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<td>TOP10</td>
<td>Strain for ligation/cloning of genes</td>
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<tr>
<td>S-17</td>
<td>Host strain for pKNOCK series of plasmids</td>
<td>Delorenzo et al. (1990)</td>
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<td><strong>Plasmids</strong></td>
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<td>pCR2.1-TOPO</td>
<td>High-copynumber plasmid for cloning PCR products</td>
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<td>pEZSeq</td>
<td>High-copynumber plasmid with strong transcription terminators</td>
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<td>pKNOCK-Cm</td>
<td>Plasmid for recombination conferring chloramphenicol resistance</td>
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<td>pUC19</td>
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<td>pUCPPcm</td>
<td>PhaP-OPH translational fusion and CAT gene cloned into pUC19</td>
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<td>TERMPminus</td>
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<td>mulSPEpplus</td>
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<tr>
<td>mulXHOminus</td>
<td>5'-GCCCAAGGTTATTTGATTTGAGAAGGTTGAA-3'</td>
<td>This study</td>
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</table>

Construction of Plasmids

A list of primers used in the study is shown in Table I. A 100-bp transcription terminator was amplified by PCR from the vector pEZSeq (Lucigen Corp., Middleton, WI) using the primers TERMPplus and TERMPminus. The construct was then cloned into pCR2.1-TOPO yielding pTOPO-Terminator. This vector was then cut with the restriction enzymes BglII/PstI and cloned into the BamHI/PstI fragment of vector pUCPPcm, generating pUCPP2 (contains the PPT expression cassette: GA24 promoter-OPH open reading frame-transcriptional terminator).

Three separate PCRs were performed to amplify the
1600-bp product containing the expression cassette with the following pairs of primers: (a) muiSPIEplus and muiPSSTminus; (b) muiPSPIplus and muiHINDminus; and (c) muiHINDplus and muiXHOminus, using pUCPPT as the template. The products were then cloned into pCR2.1-TOPO vector generating pTOPO-PPTa, pTOPO-PPTb, and pTOPO-PPTc. The insert from pTOPO-PPTc was cut with HindIII and cloned into the pTOPO-PPTb vector, digested with HindIII, and dephosphorylated with calf intestinal phosphatase (CIP), generating the pTOPO-PPT2 vector. pTOPO-PPT1 contains two copies of the expression cassette (PPT).

The pTOPO-PPTa vector was cut with SacI/PstI and the PPT fragment was cloned into the SacI/PstI fragment of vector pKNOCK-Cm, generating pKNOCK-PPT1. Similarly, TOPO-PPT2 was cut with PstI/XhoI and cloned into pKNOCK-Cm and pKNOCK-PPT2 with the same enzymes, generating the vectors pKNOCK-PPT2 and pKNOCK-PPT3. Thus, three vectors, pKNOCK-PPT1, pKNOCK-PPT2, and pKNOCK-PPT3, containing one, two, and three copies of the PPT expression cassette, respectively, were generated. These vectors were then transformed into R. eutropha by biparental mating as described by Srinivasan et al. (2002). Eight colonies from each transformation were selected and tested for the presence of OPH activity. For each copynumber, one positive strain was selected, designated SS17, SS18, or SS19, containing one, two, or three copies of the expression cassette, respectively. (All restriction enzymes and modifying enzymes were obtained from New England Biolabs, Beverly, MA.)

**Fermentation and Enzyme Assay**

Fermentations with R. eutropha strains were performed according to a previously described method (Srinivasan et al., 2002). Fed-batch fermentations were carried out in a 3-L fermentor (Applikon, Foster City, CA) at 30°C, with a 1.5-L/min airflow, 630-rpm initial stirrer speed, and an initial working volume of 1 L (1× PCT media with 5% [v/v] inoculum). An Applikon programmable logic controller (ADI1030) was used for maintaining temperature at 30°C and pH 6.8. Media pH was maintained with aqueous ammonia (28%). Dissolved oxygen concentration was maintained at 30% by controlling the stirrer speed up to a maximum speed of 1250 rpm, at which point the dissolved oxygen concentration dropped below 30% and became a function of the glucose feed rate. Fermentation was carried out in a batch mode until the initial glucose (20 g/L) was consumed.

Following the batch phase, a feed containing glucose, phosphoric acid, CoCl2·7H2O, and MgSO4 (600 g/L, 220 mM, 0.15 mM, and 19 mM, respectively) was used to promote linear growth until a biomass concentration of approximately 100 g/L dry cell weight was achieved. The glucose feed rate was initially maintained at 11.7 g/h and, after 18 h of feeding, was increased to 14.0 g/h. Induction was initiated by changing the feed solution to glucose (600 g/L) containing 15 mM CoCl2. The second glucose feed solution contained no phosphate, which led to a gradual depletion in the medium, which in turn induced OPH expression. Off-gas was analyzed in real time for O2 and CO2 concentrations with a CO2/O2 analyzer (Model 3750, Illinois Instruments, Ingleside, IL).

Fermentation with the plasmid-bearing strain was performed with a supply of chloramphenicol (80 mg/L in the initial media and 400 mg/L in the feed) to maintain selection pressure during the fermentation. Plasmid stability was measured by plating dilutions of the samples on Luria–Bertani (LB) plates with and without chloramphenicol. The plates were incubated at 30°C for 2 days. The stability was measured as the ratio of the number of colonies in the plate containing chloramphenicol to that of the number of colonies in the antibiotic-free plate. Cell viability was also measured by the number of colonies in the antibiotic-free plate.

OPH enzyme assays were performed according to the method of Serdar and Gibson (1985), with modifications (Srinivasan et al., 2002).

**Western Blots**

Whole cell pellets were resuspended in water to a final concentration of 0.2 g (dry cell weight)/L. The cell suspension (20 μL) was added to 20 μL of 2× sodium dodecyl-sulfate (SDS) lysis buffer (100 mM Tris-HCl [pH 6.8], 4% SDS, 0.05% Tween-20 [pH 7.5]) containing 3% bovine serum albumin (BSA; Sigma Co.) and incubated for 2 h at room temperature. The membrane was then exposed to a crude primary rabbit anti-OPH serum (generously supplied by Dr. Janet Grimsley, Texas A&M University) diluted in the TBST buffer. After repeated washing with TBST buffer, the membrane was exposed to a secondary goat anti-rabbit antibody conjugated to horseradish peroxidase (Pierce Co., Rockford, IL), diluted 1:5000 in TBST buffer. After repeated washing with TBST buffer, color development was achieved in a Tris-HCl SDS–12% polyacrylamide gel (Bio-Rad, Hercules, CA) and resolved at 100 V. The proteins were then transferred from the gel to a nitrocellulose membrane (0.2 μm, Schleicher–Schuell, Keene, NH) for 1 h at 100 V/350 mA. The membrane was then blocked in a TBST solution buffer (50 mM Tris base, 188 mM sodium chloride, 0.05% Tween-20 [pH 7.5]) containing 3% bovine serum albumin (BSA; Sigma Co.) and incubated for 2 h at room temperature. The membrane was then exposed to a crude primary rabbit anti-OPH serum (generously supplied by Dr. Janet Grimsley, Texas A&M University) diluted in the TBST buffer. After repeated washing with TBST buffer, the membrane was exposed to a secondary goat anti-rabbit antibody conjugated to horseradish peroxidase (Pierce Co., Rockford, IL), diluted 1:5000 in TBST buffer. After repeated washing with TBST buffer, color development was achieved in a Tris-buffered saline (TBS) buffer containing 500 mg/L dianisobenzinidene (DAB; Pierce) and 100 μL/L of a 30% H2O2 solution (Fisher, Fair Lawn, NJ).

**Quantification of Polyhydroxybutyrate in R. eutropha Cells**

Polyhydroxybutyrate (PHB) was quantified by the sulfuric acid–high-performance liquid chromatography (HPLC) method of Karr et al. (1983), with modifications (York et al., 2001).
RESULTS AND DISCUSSION

High-Cell-Density Fermentation With Strain GS5

A high-cell-density fed-batch fermentation was carried out with the *R. eutropha* strain GS5 containing the plasmid pKTPPCm. This plasmid is a derivative of pKT230, which has been shown to have approximately ten copies per cell in *R. eutropha* (Jackson and Srienc, 1999). The stability of the plasmid, cell viability, and OPH expression levels were monitored during the course of the fermentation (data not shown). During the batch phase approximately 50% of the cells lost the plasmid and only 10% of the cells contained the plasmid at the end of the fermentation (as measured by resistance to chloramphenicol). Cell viability also dropped significantly during the induction phase. However, OPH expression levels increased in the induction phase and reached a maximum specific activity of approximately 240 U/mg. This represents a 50% increase of protein concentration relative to a single chromosomal copy of the OPH gene. We hypothesize that, although the majority of the cells had lost the plasmid, the subpopulation that maintained the plasmid compensated for the loss by expressing a significant amount of OPH. Hence, single-copy gene integration does not saturate the inherent capability of recombinant protein production in *R. eutropha*. To further analyze the extent of transcriptional limitation, we constructed strains containing multiple gene-expression constructs integrated into the chromosome.

Construction of Multiple-Copy Gene-Expression Strains

Multiple gene integrations for recombinant protein production have been used in yeast to increase protein expression levels. However, this approach has not been widely used in prokaryotes, mostly due to the availability of multiple-copynumber plasmids. We constructed single-, double-, and triple-copy integrations of the OPH expression cassette in *R. eutropha* to evaluate protein expression levels. An expression cassette, PPT, was made that contained the open reading frame of OPH under the control of the GA24 promoter and a strong transcriptional terminator. Because the copies were integrated in tandem, the transcriptional terminator sequence was used to reduce the synthesis of polycistronic messages. The expression cassette was cloned into the integration vector pKNOCK-Cm, generating three separate vectors containing one, two, or three copies of the OPH gene. *R. eutropha* wild-type strain was then transformed with these vectors and colonies were selected on a minimal media plate containing chloramphenicol and gentamicin. One colony for each copynumber (SS17, SS18, and SS19) was then selected and Southern blots were performed to confirm the copynumber and region of integration (data not shown). These strains were then evaluated for the OPH expression in a high-cell-density fermentation.

High-Cell-Density Fermentation With Multiple-Copy Integrants

High-cell-density fermentations (Srinivasan et al., 2002) were performed with strains SS17, SS18, and SS19. A typical fermentation involves a batch phase, a growth phase, and an induction phase. During the batch phase, the initial supply of glucose (20 g/L) is consumed. This was followed by a fed-batch growth phase, during which a biomass concentration of approximately 100 g/L (dry cell weight) is achieved. The PHB concentration during this phase remains at <5% of the total biomass (Fig. 1). Induction of the OPH gene is accomplished by limiting the phosphate concentration in the feed. A typical fermentation (SS19, the strain containing three copies of PPT) is shown in Figure 1. In this fermentation, the final concentration in biomass was 130.6 g/L (107.3 g/L real biomass and 23.3 g/L PHB). This indicates that gene dosage does not negatively affect the fermentation capability of *R. eutropha*.

Figure 1. A typical high-cell-density fermentation of *R. eutropha*. (A) Dry cell weight, real biomass, PHB, O2 uptake rate (OUR), and CO2 evolution rate (CER) profile for high-cell-density fermentation with strain SS19 (*R. eutropha* strain with three copies of the expression construct). The arrow indicates the time of induction. Symbols: (■) total dry cell weight (g/L); (●) real biomass (g/L); (▲) PHB (g/L); (○) oxygen uptake rate [OUR, mmol/(L·h)]; (X) carbon dioxide evolution rate [CER, mmol/(L·h)]. (B) Phosphate concentration (g/L) in the reactor and the specific activity of organophosphohydrolase produced (U/mg). Symbols: (▲) phosphate concentration; (○) specific activity.
Stability of Integration Constructs

Recombination of the integration locus during the course of the fermentation is of concern because of the large number of generations (approximately 25 generations). Moreover, direct repeats of DNA loci are known to be genetically unstable. Recombination can be prevented by knocking out recombination genes like recA, recE, etc. (Amundsen et al., 2000; Hou and Hill, 2002). Because transformation in R. eutropha is achieved using homologous recombination, recA-deficient strains would not be suitable for cloning. To evaluate the recombination frequency between the multiple copies of OPH, a Southern blot was performed on samples collected during the initial growth phase and late induction phase (Fig. 2). The results show that multiple copies were stably integrated and recombination during the fermentation was absent. We suspect that multiple-copy integrations can be used successfully in other prokaryotic expression systems to achieve stable protein production in high-cell-density fermentation.

Figure 2. Southern blot analysis of R. eutropha strains SS17, SS18, and SS19. Genomic DNA from strains single-copy (SS17), double-copy (SS18), and triple-copy (SS19) integrants were extracted from samples collected in the initial phase (approximately 25 g/L biomass) and after induction (approximately 125 g/L biomass), and digested with HindIII. A 1-kb OPH open reading frame sequence (the SacI/BamHI fragment of plasmid pUCPBCm) was used to probe the blot. (A) Results of Southern blot analysis of genomic DNA of strains probed with a horseradish peroxidase-labeled OPH open reading frame. Lanes 1, 3, and 5 correspond to genomic DNA before induction and lanes 2, 4, and 6 correspond to genomic DNA after induction, for single-, double-, and triple-copy integrants. The sizes of the markers are indicated on the left. (B) Map of the genomic region analyzed in strains SS17, SS18, and SS19, indicating the expression construct (PPT) and the HindIII restriction enzyme sites. H, HindIII. The open reading frame of organophosphohydrolase (OPH) is also indicated.

Stability of Integration Constructs

Recombination of the integration locus during the course of the fermentation is of concern because of the large number of generations (approximately 25 generations). Moreover, direct repeats of DNA loci are known to be genetically unstable. Recombination can be prevented by knocking out recombination genes like recA, recE, etc. (Amundsen et al., 2000; Hou and Hill, 2002). Because transformation in R. eutropha is achieved using homologous recombination, recA-deficient strains would not be suitable for cloning. To evaluate the recombination frequency between the multiple copies of OPH, a Southern blot was performed on samples collected during the initial growth phase and late induction phase (Fig. 2). The results show that multiple copies were stably integrated and recombination during the fermentation was absent. We suspect that multiple-copy integrations can be used successfully in other prokaryotic expression systems to achieve stable protein production in high-cell-density fermentation.

Comparison of OPH Expression

High-level expression of soluble OPH in E. coli has been unsuccessful due to the formation of inclusion bodies (Serdar et al., 1989; Wu et al., 2000). We investigated the effect of gene dosage to determine if soluble OPH expression can be saturated by multiple chromosomal integrants in R. eutropha. Figure 3A shows the specific activity of OPH produced during the induction phases of the three fermentations with single, double, and triple copies. In addition to enzyme activity assays, OPH expression levels can be observed as a 36-kDa band in a Western blot, with samples from before and after induction for the three fermentations (Fig. 3B). A linear increase in the amount of OPH with gene dosage was observed, whereas basal level expression remained low (maximum specific activities of OPH of 170, 312, and 487 U/mg for one-, two-, and three-copy integrations, respectively). After 30 h of induction (68 h after inoculation) with SS19 (three copies per cell), the specific activity of the protein was found to be 487 U/mg. The specific activity of

Figure 3. Induction profile for fermentations with strains SS17, SS18, and SS19. (A) Specific activity profiles for the strains containing one (SS17), two (SS18), and three (SS19) chromosomal copies of the OPH expression cassette, PPT. Symbols: (●) SS17; (△) SS18; (▲) SS19. (B) Western blot analysis of fermentation samples. Total cell pellets were diluted to approximately 0.2 g/L DCW and then boiled on sodium dodecylsulfate–polyacrylamide gel electrophoresis (SDS-PAGE) lysis buffer and resolved on a 12% polyacrylamide gel. The proteins were transferred to a nitrocellulose membrane and blotting was done with anti-OPH antibody. The figure shows OPH expression levels before (approximately 100 g/L dry cell weight; lanes 2, 4, and 6) and after (approximately 130 g/L dry cell weight; lanes 3, 5, and 7) induction for fermentations with strains SS17, SS18, and SS19, respectively. M, broad-range molecular weight marker.

SRINIVASAN ET AL.: PRODUCTION OF RECOMBINANT PROTEINS IN R. EUTROPHA
purified OPH (with cobalt as the divalent cation) has been reported to be 8020 U/mg, using the paraoxon enzyme activity assay (Omburo, 1992). As previously noted, the protein content of R. eutropha was found to be 68% of dry cell weight (Henderson and Jones, 1997). Thus, the specific activity of 487 U/mg corresponds to 6% of total cellular protein, respectively. The product of 107.3 g/L biomass, 0.68 g protein/g biomass, and 0.06 g OPH/g protein yields an OPH concentration of 4.3 g/L. This is approximately 30 times greater than the levels produced in E. coli and 3 times greater than the previously published data in R. eutropha (Srinivasan et al., 2002).

CONCLUSIONS

In our earlier work (Srinivasan et al., 2002), we reported the development of a simple fermentation process for producing high levels of recombinant proteins in R. eutropha. We showed that plasmids are unstable in R. eutropha, even in the presence of antibiotic. We overcame this difficulty by integrating multiple copies of our gene of interest into the chromosome and thereby increasing the gene dosage while eliminating instability. In E. coli, translational fusions were made with OPH to increase the specific activity of the expressed protein and to reduce inclusion-body formation (Wu et al. 2001).

Our study with R. eutropha has shown that a linear increase in OPH production can be achieved by integrating multiple copies of the gene of interest into the chromosome. Moreover, we have shown that the basal level of induction is not increased substantially, and that multiple copies remain stable in the chromosome. It should be noted that no inclusion bodies were seen, even with such high-level expression of the gene of interest. The levels of protein achieved with three-copy integrant (4.3 g/L) is the highest reported for this protein. We also believe that gene dosage can be further increased by integrating more copies, but it may increase basal expression levels.

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