Regulation of the \( p \)-hydroxybenzoic acid hydroxylase gene (\( pobA \)) in plant-growth-promoting \( Pseudomonas putida \) WCS358

Iris Bertani, Milan Kojic and Vittorio Venturi

The regulation of the \( p \)-hydroxybenzoate hydroxylase gene (\( pobA \)) of \( Pseudomonas putida \) WCS358 involved in the catabolism of \( p \)-hydroxybenzoic acid (PHB) to the central intermediate protocatechuate was studied. Protocatechuic acid (PCA) is then degraded via the \( \beta \)-ketoacid pathway to form tricarboxylic intermediates. In several Gram-negative bacteria \( pobA \) has been found genetically linked to a regulator called \( pobR \) which activates \( pobA \) expression in response to PHB. In this study the identification and characterization of the \( pobC-pobA \) locus of \( P. putida \) WCS358 is presented. The \( p \)-hydroxybenzoate hydroxylase (PobA) is highly identical to other identified PobA proteins, whereas the regulatory protein PobC did not display very high identity to other PobR proteins studied and belonged to the AraC family of regulatory proteins, hence it has been designated PobC. Using the \( pobA \) promoter transcriptionally fused to a promoterless \( lacZ \) gene it was observed that induction via PobC occurred very efficiently when PHB was present and to a lesser but still significant level also in the presence of PCA. This PobC-PCA response was genetically demonstrated by making use of \( pobC::\text{Tn}5 \) and \( pcaH::\text{Tn}5 \) mutants of strain WCS358 constructed in this study. In \( pobC \) mutants both the \( p \)-hydroxybenzoic and PCA response were not observed, whereas in the \( pcaH \) mutant, which lacks a functional protocatechuate 3,4-dioxygenase, the protocatechuic-acid-dependent \( pobA \) activation was still observed. Finally, the activation of \( pobA \) by PHB varied according to the concentration and it was observed that in the \( pcaR::\text{Tn}5 \) regulatory mutant of strain WCS358 the \( pobA \) promoter activity was reduced. PcaR is a regulator involved in the regulation of several loci of the \( \beta \)-ketoacid pathway, one of which is \( pcaK \). It was postulated that the reduction of \( pobA \) activation in \( pcaR::\text{Tn}5 \) mutants was because there was no expression of the \( pcaK \) gene encoding the PHB transport protein resulting in lower levels of PHB present inside the cell.

**Keywords:** protocatechuic acid, \( pobA \), \( pobC \), aromatic acid

**INTRODUCTION**

Pseudomonads have the capacity to catabolize a large number of low-molecular-mass aromatic compounds. Many of these compounds like ferulic acid, vanillic acid, \( p \)-coumaric acid, \( p \)-hydroxybenzoic acid (PHB) and protocatechuic acid (PCA) arise in the environment from the biodegradation of lignin. These compounds are also present in plant cells and consequently are abundantly present in the rhizosphere and have been found to play an important role in signalling gene expression between plants and \( Agrobacterium tumefaciens \) (Bolton et al., 1986; Melchers et al., 1989), demonstrating that these molecules can act as signals for bacteria when in close proximity to the plant. Many strains belonging to the three species of fluorescent pseudomonads, \( Pseudomonas putida \), \( Pseudomonas fluorescens \) and \( Pseudomonas aeruginosa \), are aggressive.

**Abbreviations:** PCA, protocatechuic acid; PHB, \( p \)-hydroxybenzoic acid.

The GenBank/EMBL/DDBJ accession numbers for the \( pcaR \), \( pobC-pobA \) and \( pcaHG \) sequences reported in this paper are AJ252090, AJ251792 and AJ295623, respectively.
rhizosphere colonizers and plant-growth-promoting (O'Sullivan & O'Gara, 1992), thus they have evolved chemotactic and sensing systems to reach and colonize the rhizosphere. Plant phenolic compounds could play a role in the establishment of the symbiosis of plants with plant-growth-promoting bacterial strains, thus the study of catabolic and regulatory genes responding to these compounds could be an approach to investigate this possible role.

In bacteria, diverse aromatic compounds are initially transformed to a limited number of central intermediates, namely catechol (or substituted derivatives) and PCA. These compounds are then channelled into two possible ring fission pathways, either the ortho- or meta-cleavage pathway, funneling these compounds into the tricarboxylic acid cycle (van der Meer et al., 1992). In Gram-negative bacteria, ferulic acid is initially degraded to PCA via vanillic acid, whereas coumaric acid is degraded via PHB (Toms & Wood, 1970; Venturi et al., 1998) (Fig. 1). These catabolic conversion steps require at least three genetic loci (Fig. 1). The transformation of ferulic acid to vanillic acid involves an operon encoding an enoyl-CoA hydratase/aldolase, a vanillin dehydrogenase and another gene encoding feruloyl coenzyme A synthetase (Overhage et al., 1999b; Priefert et al., 1997; Venturi et al., 1998). Vanillic acid is then degraded to PCA by a demethylase encoded by an operon consisting of two genes designated vanA and vanB (Brunel & Davison, 1988; Priefert et al., 1997; Venturi et al., 1998). The degradation of p-coumaric acid to PHB also requires at least one locus that transforms ferulic acid to vanillic acid (Venturi et al., 1998), whereas the conversion of PHB to PCA requires a hydroxylase encoded by the pobA gene (Wong et al., 1994; Parke, 1996; this study). All three loci involved in these conversion steps have been cloned and characterized in plant-growth-promoting P. putida WCS358 (Venturi et al., 1998; this study).

Several regulatory genes and proteins sensing and responding to such aromatic compounds have been identified and characterized (Kok et al., 1998; Parke, 1993; Romero-Steiner et al., 1994). In Acinetobacter sp. ADP1 two transcriptional activators have been identified: PobR, which elicits transcription of the pobA gene in response to PHB, and PcaU, which is triggered by PCA and switches on the expression of the set of genes required for the catabolism of protocatechuate (Gerischer et al., 1998). The two regulators PobR and PcaU are 54% identical belonging to the same family (IclR) and respond to closely related aromatic compounds (Kok et al., 1998). Similarly, a transcriptional activator called PcaR has been described in P. putida and senses and responds to β-ketoadipate, an intermediate in the degradation of PCA, and in turn switches on the transcription of three loci involved in the catabolism of protocatechuate (Romero-Steiner et al., 1994).

The regulation of pobA expression by PobR has been extensively studied in Acinetobacter sp. ADP1 at the genetic and molecular level, and the PHB response and the DNA target have been investigated (DiMarco & Ornston, 1994; Kok et al., 1997). In this study we present genetic data on the regulation of pobA expression in plant-growth-promoting P. putida WCS358. The pobA-pobC locus has been identified. The genetically linked regulator exhibited low similarity to the other studied PobR regulators and belonged to the AraC family of regulators, hence it was designated PobC. PobC activated pobA expression in response to PHB. Interestingly, it also had weak activity in the presence of PCA. Finally, it was observed that the regulator PcaR was important for efficient activation of pobA expression and it was

**Fig. 1.** Biodegradation pathway of ferulic and p-coumaric acids to PCA. Genes involved in each step and genomic mutants having a locus inactivated which have been used or constructed in this study (see text for details) are also shown.
postulated that this effect was mediated via the expression of pcaK, the gene encoding a PHB transporter protein.

METHODS

Bacterial strains, plasmids and media. Strains used in this study include Escherichia coli DH5α (Hanahan, 1983), XL-1 Blue (Bullock et al., 1987), JM101 (Messing, 1983) and HB101::Tn5 (Moore et al., 1984). P. putida strains used are listed in Table 1. P. aeruginosa PAO1 was also used (B. Holloway collection). Plasmids used are listed in Table 1. E. coli was grown in LB medium (Miller, 1972) at 37 °C, whereas Pseudomonas strains were grown in LB medium or M9 minimal medium at 30 °C (Maniatis et al., 1982). The following antibiotic concentrations were used (µg ml⁻¹): tetracycline, 10 (E. coli) and 40 (Pseudomonas); kanamycin, 100; nalidixic acid, 25; ampicillin, 100; gentamicin, 10 (E. coli) and 40 (Pseudomonas). The promoter fusion hybrid plasmid pPPObA was constructed as follows. The promoter of the pobA gene was PCR-amplified from pCOSHB as template using two oligonucleotides, 5′-GGAATTCCGGATGCC-TGTCCGTTAAT-3′ and 5′-GCTCTAGAAGCTTGTGTTTG-TCTTCTAGTCGGG-3′, and cloned into pUC18 to yield pPIBV1. After verification via sequence analysis it was then cloned as a 183 bp EcoRI–XbaI fragment (restriction sites indicated in bold type) into pMP220. The promoter of pcaK was cloned in promoter probe vector pMP220 as follows. Using two oligonucleotides (5′-CTCTAGAGTGTGGTTTATCCAGAAATAG-3′ and 5′-CGAATTCCCCCTTAGC-GAACGCGCCTG-3′) a 298 bp fragment consisting of DNA upstream the ATG start codon of pcaK was PCR-amplified using pCOS272 as template and cloned into pUC18, yielding pPKP1. This fragment was then removed from pPKP1 as an EcoRI–XbaI fragment and cloned into the corresponding sites of pMP220, yielding pPPCAK. The pcaH gene of P. aeruginosa PAO1 was located in contig 1 at position 174773–175492 (www.pseudomonas.com) and was amplified using two oligonucleotides (5′-GGAATTCCATGACAGCGCAGCGAAGC-3′ and 5′-CGGGATCCGTACGGCGGTACCAAGAAA-3′) and PAO1 genomic DNA as template and cloned into pUC18, yielding pPAOH1. The pcaR gene was found in the PAO1 genome (www.pseudomonas.com) located in contig 1 at

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<th>Strain or plasmid</th>
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<td><strong>Strains</strong></td>
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<td>pobA gene promoter in pMP220</td>
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* Ap', Km', Sm', Te', Gm': resistance to ampicillin, kanamycin, streptomycin, tetracycline and gentamicin, respectively.
position 176294–177154 and was PCR-amplified from PA01 genomic DNA using the primers 5′-GTGACCCGAGCCC-GA-3′ and 5′-TCAGTGACAGGGCGG-3′ and cloned as a 860 bp DNA fragment into pUC18 to yield pPAOPCAR.

**Recombinant DNA techniques.** Digestion with restriction enzymes, agarose gel electrophoresis, purification of DNA fragments, ligation with T4 DNA ligase, end-filling with the Klenow fragment of DNA polymerase, hybridizations, radioactive labelling by random priming and transformation of E. coli were performed as described by Maniatis *et al.* (1982). Southern hybridizations were performed using Hybond-N+ membrane (Amersham Pharmacia Biotech). Plasmids were purified as described by Birnboim (1983) and with Qiagen columns. Total DNA from *Pseudomonas* strains was isolated by Sarkosyl/Pronase lysis as described by Better *et al.* (1983). Triparental matings between *E. coli* and *Pseudomonas* strains were performed with the helper strain *E. coli*(pRK2013) (Figursky & Helsinki, 1979). The DNA sequence flanking the transposon insertion in mutant *P. putida* V8FB was determined using arbitrary PCR (Caetano-Annoles, 1993). In this procedure the DNA flanking the Tn5 insertion site is amplified in two rounds using primers specific to the ends of the Tn5 element and primers of random sequence which anneal to chromosomal sequences flanking the transposon. The technique and primers used were as described by O’Toole & Kolter (1998).

**Reporter gene fusion assays and analysis of substrate metabolism.** β-Galactosidase activity was determined essentially as described by Miller (1972) with the modifications of Stachel *et al.* (1985). The biodegradation of aromatic acids by *P. putida* WCS358 and Tn5 mutants was analysed by reverse-phase HPLC (RP-HPLC), using a Varian 9010 solvent delivery system equipped with a Varian 9050 UV detector. *Pseudomonas* was grown either in LB medium supplemented with 0.15% (w/v) of the aromatic acid, or in M9 minimal medium supplemented with 0.1% and/or 0.05% of the aromatic acid. Samples were withdrawn from cultures after growth and centrifuged at 12000 g. The supernatant was diluted 100-fold into methanol and filtered through 0.2 µm filters; 10 µl samples were loaded on a 5 µm spherical C18 reverse-phase column (Supelcosil LC18 150 x 4.6 mm; Supelco) and eluted with 35% methanol and 65% water with 0.1% acetic acid at a flow rate of 0.8 ml min⁻¹. The eluted metabolites were detected at 279 nm. The catabolic intermediates were identified by comparing their elution times with those of pure standards.

**Isolation of mutants unable to use PHB as carbon source and their complementation with a *P. putida* WCS358 gene bank.** Mutants unable to use PHB as carbon source but retaining the ability to use PCA were screened as follows. Colonies from a Tn5 genomic mutant bank (Marugg *et al.*, 1985) were grown at 30 °C in duplicate on minimal M9 plates containing kanamycin and either PHB or PCA as sole carbon source. Mutants were selected which were unable to grow on PHB but retained the ability to grow on PCA. Complementation was performed via triparental matings between a cosmid gene library of *P. putida* WCS358, an *E. coli*(pRK2013) mobilizer (about 4 x 10⁷ cells each) and the WCS358 Tn5 mutant (2 x 10⁸ cells) were set up on a 0.45 µm membrane filter (Millipore) on an LB plate. After 12 h incubation at 30 °C, cells were resuspended and plated on minimal M9 plates containing PHB (0-15%) with tetracycline.

**Cloning of the pcaHG and pcaR loci of *P. putida* WCS358.** The pcaHG genes of strain WCS358 were cloned using the pcaH gene from *P. aeruginosa* PA01 as probe against the cosmID gene library. A 7.36 bp EcoRI–BamHI fragment from pPAOH1 was used as probe and a cosmid designated pCOSH1 was identified that harboured the pcaHG locus on a 5 kb HindIII fragment. The genes were then further localized on a 1.8 kb EcoRI–HindIII subfragment. This fragment was cloned in pluBluescript to yield pBH18. The 5 kb HindIII fragment containing the pcaHG locus was cloned in pLAFR3 to yield pCOSHG5.

The pcaR gene of *P. putida* WCS358 was also cloned using the pcaR gene of *P. aeruginosa* PA01 as probe to screen a cosmid bank of *P. putida* WCS358. An 875 bp EcoRI–HindIII fragment of pPAOPCAR was used as probe and a cosmid, designated pCOS272, was identified which harboured the pcaR gene on a 6.5 kb HindIII fragment. This fragment was cloned in pluBluescript KS to yield p2726.5. The pcaR gene was further localized in a 2.2 Kbp subfragment (Fig. 2b) which was also cloned in pluBluescript KS to yield pBK2.2.

**Transposon Tn5 mutagenesis.** Transposon Tn5 insertions within hybrid plasmids p2726.5 and pCOSHG5, harbouring pcaR and pcaHG, respectively, were obtained as described by Magazin *et al.* (1986) with *E. coli* HB101::Tn5 as the source of the transposon. *E. coli* HB101 cells containing Tn5 insertions within the plasmid pCOSHG5, were mated en masse with *P. putida* WCS358 by using helper strain *E. coli*(pRK2013) as described above. The cells from the conjugation mix were suspended and spread on LB plates containing nalidixic acid, ampicillin, tetracycline and kanamycin, selecting for strains harbouring recombinant plasmids which had received a transposon insertion. About 200 clones were grown and plasmids were purified according to Birnboim (1983). Subsequently, *E. coli* DH5α was transformed and plated on LB tetracycline and kanamycin as described above. DNA was purified from transformants and the Tn5 insertions mapped by restriction analysis and DNA sequencing. One plasmid, designated pCOSHG5::Tn5 had an insertion located in the pcaH gene at position 306 of the submitted sequence (accession no. AJ295623) where position 111 is the ATG of pcaH.

*E. coli* HB101 cells containing Tn5 insertions within the plasmid p2726.5 were identified by purifying plasmid DNA from HB101::Tn5 (p2726.5) which was subsequently used to transform *E. coli* DH5α. Transformants were selected for ampicillin and kanamycin resistance. Transposon insertions in the pcaR gene were then mapped by restriction and Southern analyses and by DNA sequencing. One Tn5 insertion in the pcaR gene in p2726.5 was identified (plasmid designated p2726.5::Tn5) and used in a marker exchange experiment to transfer this Tn5 insertion into the pcaR gene harboured in pCOS272, yielding pCOS272::Tn5. Tn5 was located at position 604 of the sequence (accession no. AJ252090) where position 135 is the ATG of pcaR.

**Site-specific exchange of mutations with the Pseudomonas chromosome.** Plasmids pCOS272::Tn5 and pCOSHG5::Tn5 carrying a Tn5 insertion in the pcaR and pcaH genes, respectively, were homogenized with the corresponding target region of the genome of *P. putida* WCS358 by a marker exchange procedure described by Corbin *et al.* (1982) and Venturi *et al.* (1998). pPH1JI was used as the incoming IncP1 incompatible plasmid and selections were made on LB plates containing nalidixic acid, ampicillin, gentamicin and kanamycin. Putative marker-exchanged mutants were streaked on LB plates containing tetracycline to confirm loss of IncP1
recombinant plasmids. By this method genomic Tn5 mutants were generated, one called P. putida VBPC, harbouring a Tn5 insertion in pcaR, and another designated VBHG, harbouring a Tn5 insertion in the pcaH gene of P. putida WCS3358. The fidelity of each marker exchange event was confirmed by purifying chromosomal DNA of the mutants, which were analysed by digestion with restriction enzymes and via Southern hybridization, verifying that pcaR and pcaH, respectively, were mutated in the chromosome.

DNA sequence determination and analysis. A 2.2 kb KpnI fragment harbouring pcaR (pBKp2.2), a 4.7 kb KpnI–NotI fragment harbouring pobA-pobC (pB4.7KN) and a 1.8 kb EcoRI–HindIII fragment harbouring pcaHG (pBGH18) were subcloned from pCOS272, pCOSH and pCOSHG5, respectively, and utilized for sequencing. The constructs were either encapsidated as single-stranded DNA upon infection with helper phage VCSM13 (Stratagene) or used directly for DNA sequencing. Several oligonucleotides were synthesized and used in sequencing reactions. Nucleotide sequences were determined by the dideoxy chain-termination method (Sanger et al., 1977) using [α-35S]dATP for labelling and 7-deaza-dGTP (Pharmacia) instead of dGTP. The nucleotide sequence was determined in both directions and across all restriction sites.

RESULTS
Isolation and characterization of the pobC-pobA locus of P. putida WCS3358

P. putida WCS3358 can utilize PHB as sole carbon source. The first step in its degradation involves the conversion via hydroxylation of PHB to PCA (Fig. 1). This conversion is catalysed by p-hydroxybenzoate hydroxylase encoded by pobA (DiMarco & Ornston, 1994; Wong et al., 1994). This gene is genetically linked to the pobR regulator which controls its expression in response to PHB. To identify the pobR-pobA locus of strain WCS3358, 5000 genomic Tn5 mutants of strain WCS3358 were screened for their ability to grow on PCA and not on PHB as sole carbon source. One mutant, designated P. putida VBHB, was isolated which had the desired phenotype. A cosmid genomic library of P. putida WCS3358 was introduced in mutant VBHB and transconjugants showing complementation of this mutation for growth on PHB. Restriction analysis revealed that all restriction sites used for subcloning and sequencing are shown above the three physical gene maps. (d) Prosite motifs of the two regulators; PcaR has an ICLR HTH motif (PS01051), and PobC an ARAC HTH motif (PS01124). The amino acids in bold fit the consensus pattern of the motif.

Fig. 2. Genetic organization of the three cloned regions harbouring the three loci. The localization of the transposon Tn5 in each mutant is indicated (see text for details). (a) pobA-pobC, (b) pcaR and pcaK and (c) pcaH-pcaG. Restriction sites used for subcloning and sequencing are shown above the three physical gene maps. (d) Prosite motifs of the two regulators; PcaR has an ICLR HTH motif (PS01051), and PobC an ARAC HTH motif (PS01124). The amino acids in bold fit the consensus pattern of the motif.
calculated molecular mass of 44 kDa (accession no. AJ251792). It exhibited 74% identity with PobA of *Pseudomonas* sp. HR199, 70% identity with *P. fluorescens*, 60% identity with PobA of *Acinetobacter* sp. ADP1 and interestingly the highest identity (80%) was again observed with *Azotobacter chroococcum* (data not shown).

**Gene promoter activity of the pobA promoter**

The promoter of *pobA* was cloned upstream from a promoterless β-galactosidase (*lacZ*) gene in the promoter probe vector pMP220 as described in Methods. The transcriptional fusion, called pPPOBA, was conjugated into *P. putida* WCS358 and mutant derivatives and β-galactosidase activities were determined in response to several phenolic acids (Fig. 3).

As expected the promoter of *pobA* had a strong response to the presence of PHB. When *P. putida* WCS358(pPPOBA) was grown in LB or M9 media supplemented with 0-1% PHB the promoter displayed over 30000 Miller units of β-galactosidase activity, indicating that it is a very strong promoter (Fig. 3a). The same induction level was also observed when the strain was exposed to *p*-coumaric acid. This was most probably due to the fact that *p*-coumaric acid is converted to PHB which would then induce the promoter as confirmed by the absence of promoter activity in the *fca*::Tn5 mutant *P. putida* FA11 (Venturi et al., 1998) when exposed to *p*-coumaric acid (Fig. 3a). This mutant had a Tn5 insertion in a structural gene absolutely necessary for the conversion of *p*-coumaric to PHB. Finally, it was also observed that PCA was involved in the activation of this promoter to a lesser but significant extent (just over 1000 Miller units) (Fig. 3b).

**Phenotype of pobC::Tn5 genomic mutants**

As mentioned above, these mutants could not grow on PHB as sole carbon source but could grow on PCA, thus they were impaired only in the hydroxylation step. Gene promoter studies in the *pobC::Tn5* mutant VBHB are presented in Fig. 3. They showed that the *pobA* promoter, harboured in pPPOBA, in the parent strain was very strong and inducible by PHB, reaching a value of approximately 30000 Miller units; this activity was not observed in the *pobC* mutant VBHB (Fig. 3a). As mentioned above, activation by PCA occurred to a lesser extent in *P. putida* WCS358(pPPOBA) (1100 Miller units). This activity was not observed in the *pobC::Tn5* mutant (Fig. 3b), demonstrating that this PCA induction was occurring via PobC.

**PCA weakly induces pobA gene promoter activity**

It was observed that PCA weakly but significantly induces *pobA* promoter activity (see above). It was possible, however, that this induction was occurring via...
another compound resulting from the stepwise transformation of PCA in the β-ketoadipate pathway (Nichols & Harwood, 1995; Romero-Steiner et al., 1994). To establish that PCA was responsible for the observed pobA promoter activity we determined β-galactosidase levels in a P. putida WCS358 genomic mutant which was blocked in the first transformation step of PCA catabolism. This mutant was constructed via the cloning and characterization of the pcaHG locus, performing transposon mutagenesis on the cloned locus and generating a genomic mutant via a marker exchange technique (see Methods). This led to the construction of a mutant designated P. putida VBHG exhibiting a Tn5 insertion in the pcaH gene in the chromosome of P. putida WCS358. The pcaHG operon encodes two proteins (Fig. 2c) (accession no. AJ295623): PcaH (267 kDa), the β-subunit, and PcaG (22.4 kDa), the α-subunit of protocatechuate 3,4-dioxygenase which transforms PCA to carboxymuconate (Nichols & Harwood, 1995; Romero-Steiner et al., 1994). As expected, these two proteins have very high identities (approx. 80%) with homologues identified in other Pseudomonas spp. (data not shown; Overhage et al., 1999a). It was verified that the P. putida VBHG mutant was unable to transform PCA since when present in the medium after overnight growth, the compound was not transformed. In addition this mutant could not grow in minimal medium when PCA was sole carbon source. This mutant could be complemented for these two phenotypes by pCOSHG5, carrying a 5 kb HindIII fragment with the pcaHG genes.

We determined pobA promoter activity in mutant P. putida VBHG(pPPOBA) in the presence of PCA and it was observed that in this mutant the weak but significant response to PCA was retained (Fig. 3b). Thus, it was concluded that it was PCA that could act as a weak inducer of pobA gene expression via PobC.

Expression of pobA is influenced by PHB concentration

The PHB-induced activity of the pobA promoter via PobC was determined. pobA promoter activity was determined in P. putida WCS358(pPPOBA) grown in the presence of various concentrations of PHB through β-galactosidase assays. As shown in Fig. 4, it was established that pobA gene promoter activity varied according to the amount of PHB present: the activity rose with increasing concentrations of the phenolic compound and the highest level was achieved at 0.05%. At higher concentrations the activity began to decrease and at approximately 0.15% there was a sharp drop in β-galactosidase activity, most probably because higher concentrations of the phenolic compound were bacteriostatic.

Importance of pcaR in pobA gene regulation

A regulator called PcaR has been described in P. putida that regulates several loci involved in the degradation of PCA. Among these genes one called pcaK encoding a transport protein involved in PHB transport has been identified (Nichols & Harwood, 1995; Romero-Steiner et al., 1994). The regulator PcaR is required for the complete degradation of PHB; thus the possible role of this regulator in controlling gene expression of pobA in P. putida WCS358 was investigated via the identification of the gene and creation of a pcaR-deficient mutant. The pcaR gene of P. putida WCS358 was identified in a cosmide gene bank of strain WCS358 maintained in E. coli using the pcaR gene of P. aeruginosa PAO1 as probe. The gene was cloned, mutated and a pcaR-deficient mutant of strain WCS358 was constructed via a marker exchange technique (see accession no. AJ25290; Methods and Fig. 2b). The mutant was designated P. putida VBPC. As expected, this mutant was unable to grow in M9 medium containing PHB and PCA as sole source of carbon, respectively. The PcaR protein of strain WCS358 was 95% identical to PcaR of P. putida PRS2000, 72% identical to PcaR of P. aeruginosa PAO1 and 43% identical to PcaR of Rhodococcus opacus (data not shown). Interestingly, it also displayed 34 and 33% identity with PcaU and PobR of Acinetobacter sp. ADP1, respectively (data not shown). All of these proteins belong to the IcR family of bacterial regulators.

To investigate the possible role of PcaR in pobA gene regulation, promoter fusion pPPOBA was conjugated in mutant VBPC and activation by PHB was determined. In mutant VBPC the promoter had only 15% of promoter activity as compared to the wild-type (Fig. 3a) and it was concluded that pcaR played an important role...
in \textit{pobA} gene expression. This observed effect was probably indirect via the regulation of other gene(s) important for PHB degradation. It was previously observed that in \textit{P. putida}, \textit{pcaR} regulates the PHB transporter gene \textit{pcaK} (Nichols \& Harwood, 1995). We observed that the same was true in strain WCS358. The \textit{pcaK} gene was genetically linked to \textit{pcaR} (Fig. 2b) and contained a putative \textit{pcaR} binding region in its promoter. The \textit{pcaK} promoter of strain WCS358 was also cloned upstream from a promoterless \textit{β} promoter contained a putative \textit{pcaK}; thus in a \textit{pcaR} mutant there is a less efficient transport of PHB, most probably leading to a less efficient \textit{pobA} activation in response to PHB.

**DISCUSSION**

The genetics of the regulation of the \textit{p}-hydroxybenzoate hydroxylase \textit{pobA} gene of \textit{P. putida} involved in the catabolism of PHB to the central intermediate protocatechuate (Fig. 1) was studied. To our knowledge, this is only the second \textit{pobA} regulator studied, the other being \textit{pobA} regulation via \textit{PobR} in \textit{Acinetobacter} (Kok et al., 1997). Promoter studies in strain WCS358 have shown that \textit{pobA} gene expression was activated by PHB and, interestingly, to a lesser extent by PCA. This induction was mediated via the \textit{PobC} transcriptional activator, whose corresponding gene was identified and characterized. Like all hitherto identified \textit{pobR} genes, the \textit{pobC} gene of \textit{P. putida} WCS358 was in close proximity to the \textit{pobA} structural gene. The protein of strain WCS358, however, was not so closely related to the other \textit{pobR} regulators as expected as revealed by analysis of the primary structure. \textit{PocB} of \textit{P. putida} WCS358 only exhibited identities below 50% with corresponding proteins of other \textit{Pseudomonas} strains and only 37 and 10% identity with \textit{PobR} of \textit{R. leguminosarum} and \textit{Acinetobacter} sp. ADP1, respectively. This difference in the primary structure most probably also reflects a functional difference. Thus the further study of this protein could be of great interest. The WCS358 \textit{PobC} protein had 58% identity with the uncharacterized \textit{PobR} of \textit{Azotobacter chroococcum} and this \textit{PobR} has an \textit{AraC} DNA binding motif at a similar position; thus it appears that the \textit{PobR} proteins belong to either the \textit{IclR} or the \textit{AraC} family, showing that divergent evolution has taken place. Overhage et al. (1999a) have depicted a relationship between the different \textit{PobR} proteins identified. It appears that \textit{PobR} of \textit{Acinetobacter calcoaceticus} is evolutionarily distant from the other proteins and it is the only one studied. The designation of \textit{PobC} for the protein in \textit{P. putida} WCS358 was chosen since it belongs to the \textit{AraC} family.

The \textit{pobA} promoter was regulated by \textit{PobC} and it was activated very efficiently by PHB; the levels of \textit{β}-galactosidase activity obtained using the \textit{pobA} promoter \textit{lacZ} fusion indicated that this promoter is very strong, considerably stronger than the \textit{pobA} promoter of \textit{Acinetobacter} sp. ADP1 (DiMarco et al., 1993). A weak but significant level of \textit{pobA} promoter activity was also observed in response to PCA and this was confirmed to be most probably due to a \textit{PobC}-PCA interaction since in \textit{pobC::Tn5} mutants (VBHB) this protocatechuate-dependent activity was not observed (Fig. 3b). It was verified that it was PCA which was responsible for this weak activation and not another intermediate in its catabolism since in a \textit{pcaH::Tn5} mutant, which cannot
A regulatory role of PcaR has been identified in Pseudomonas putida strain WCS358. This protein responds to protocatechuate and to 3-hydroxybenzoate, but not to phenylacetic acid or 4-hydroxybenzoate. PcaR binds to the pcaK promoter region, located in the pcaIJ operon, and activates its transcription. PcaK is a member of the multidrug resistance family and it is involved in the transport of phenolics.

This study provides data on the regulation of pcaK expression in P. putida WCS358 via PobC and PcaR, with PHB and PCA being identified as effectors. Interestingly, this demonstrated that P. putida the genetically linked regulator was different in primary structure, that it responded efficiently and strongly to PHB, weakly to PCA and that PcaR was important via pcaK gene expression for complete pcaK activation. Future work will more precisely define the mode of action of these regulatory responses which are summarized in Fig. 5 and the role that these genes and proteins might play in signalling gene expression in the rhizosphere in this plant-growth-promoting Pseudomonas strain.

**ACKNOWLEDGEMENTS**

I. Bertani is beneficiary of a fellowship from the ‘Fondazione Adriano Buzzati-Traverso’. M. Košic is a scientist on leave from the Institute of Molecular Genetics and Genetic Engineering, Belgrade, and is beneficiary of an ICGEB fellowship.

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