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Nitrogen regulation of the xyl genes of *Pseudomonas putida* mt-2 propagates into a significant effect of nitrate on *m*-xylene mineralization in soil

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Hence, for nitrogen sources, regulatory patterns that emerge in soil reflect those observed in liquid cultures. The current study shows how distinct regulatory traits can lead to discrete environmental consequences; and it underpins that attempts to improve bioremediation by nitrogen amendment should integrate knowledge on their effects on growth and on catabolic gene regulation under natural conditions.

**Introduction**

Approaches used in environmental biotechnology to bring about pollutant degradation, i.e. bioremediation, rely on the activities of catabolic microorganisms in complex environments. In their natural habitat, these microorganisms encounter numerous exogenous factors that can affect their growth and general metabolic activity, and even their ability to express specific genes involved in pollutant degradation (de Lorenzo, 2008). Hence, the impact of environmental factors on catabolic microorganisms is of paramount significance for the optimal exploitation of specific degrader microorganisms in bioaugmentation, where microorganisms selected for catabolic performance under laboratory conditions are brought back into their natural habitat.

However, how these properties are regulated by microorganism in the environment is at present not clear (Meckenstock *et al.*, 2015).

*Pseudomonas putida* mt-2, which carries the catabolic TOL plasmid, pWW0, enabling *m*-xylene and toluene degradation is a safe and well-studied paradigm organism for applications in bioaugmentation (de Lorenzo *et al.*, 2013). The catabolic *xyl* genes on pWW0, which are involved in *m*-xylene and toluene degradation, are organized in the upper and lower/meta TOL pathway operons (Fig. 1). The significance of environmental factors for *xyl* gene expression has been intensively studied in pure culture model systems (Velázquez *et al.*, 2006; Del Castillo and Ramos, 2007). Some of these studies have revealed that nitrogen sources, e.g. *NH₄⁺* and *NO₃⁻*, influence *xyl* gene expression in mt-2 (Velázquez *et al.*, 2006; Huang *et al.*, 2008). Expression of *xyl* genes of the upper TOL pathway is regulated by the sigma factor, *σ^54*, which was initially identified as a...
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Fig. 1. Degradation of m-xylene and organization of the xyl structural and regulatory genes of the TOL pathway on pWW0. Enzymes of the upper pathway catalyse the sequential oxidation of one methyl group of m-xylene resulting in 3-methyl benzoate (3MB), which is further converted to tricarboxylic acid cycle intermediates by enzymes encoded in the meta pathway operon. Six promoters are involved in the expression of the two catabolic gene clusters. Transcription of the upper pathway is initiated from the $\sigma^{54}$-dependent promoter $Pu$, while the meta pathway is transcribed from $Pm$ that requires either $\sigma^{32}$ ($\sigma^{n}$) or $\sigma^{38}$ ($\sigma^{b}$). Furthermore, two regulatory proteins, XylR and XylS, are involved in the tightly controlled expression of the entire TOL pathway that additionally requires the presence of specific effector molecules, m-xylene and 3MB, and the chromosomal-encoded HU and IHF proteins. The master regulator XylR, encoded by the xylR gene, is transcribed from two $\sigma^{70}$-dependent tandem promoters, and is involved in activation of $Pu$ and the $\sigma^{54}$-dependent $Ps1$ promoter of xylS, encoding the meta pathway regulator, XylS. In addition, xylS is constitutively expressed from the $\sigma^{70}$-dependent promoter $Ps2$. The two catabolic genes employed as proxies of TOL pathway expression in this study, xylM and xylE from the upper and meta pathway, respectively, are shown in bold.

Nitrogen specific sigma factor (Ramos et al., 1997; Cases et al., 2003). Hence, this global regulator might modulate substrate-specific induction of the TOL pathway in response to altered environmental conditions caused by the nitrogen supplements (Commichau et al., 2006; Hervás et al., 2009).

Nitrogen is an important limiting element for bacterial growth in many environments, in particular at hydrocarbon contaminated sites (van Veen et al., 1997; Jensen and Nybroe, 1999; Walecka-Hutchison and Walworth, 2006), and several studies on bioremediation of hydrocarbon contaminated soils and sediments have shown the significance of inorganic nitrogen amendments for in situ pollutant biodegradation (Lindstrom et al., 1991; Davis and Madsen, 1996; Aislabie et al., 2012). The chosen source of nitrogen to add in bioremediation studies is NH$_4^+$ that can be taken up and assimilated directly by the bacterial degraders (Walecka-Hutchison and Walworth, 2006; Komilis et al., 2010). Hence, it becomes of interest whether the different effects of NH$_4^+$ and NO$_3^-$ on catabolic gene expression by $P$. putida mt-2, which have been revealed by well-controlled pure culture conditions, where typically one parameter was changed at a time (Velázquez et al., 2006; Hervás et al., 2008) manifest also in a complex environmental context (de Lorenzo, 2008). An additional, unsettled issue is how tightly changes in xyl gene expression are coupled to the functional outcome of the pathway, i.e. changes in m-xylene biodegradation in a soil system.

The objective of current study was to address whether the test tube effects of nitrogen on catabolic gene expression by $P$. putida mt-2 propagate into an actual environmental scenario. To this end we established an experimental model system allowing us to compare the effect of specific nitrogen sources (NH$_4^+$ vs. NO$_3^-$) on the transcriptional dynamics of $P$. putida mt-2 catabolic xyl genes in pure culture and after introduction to natural soil with different nitrogen regimes. In either systems, we focused on expression of xylM and xylE of the upper and lower TOL pathway, respectively, as the enzyme products of these two genes are regarded as key enzymes in the biodegradation of toluene and m-xylene (Hendrickx et al., 2006; Martinez-Lavanchy et al., 2010). In addition, sensing of the nitrogen status by $P$. putida mt-2 cells was compared for pure culture and soil systems through expression of the $amtB$ and $gdhA$ genes signalling NH$_4^+$ deficiency and surplus respectively (Hervás et al., 2008). The system further allowed us to examine whether changes in gene expression in soil were translated into actual variations in biodegradation performance.

Results

Nitrogen source impact on expression of xylM and xylE in pure culture

Initially, we performed a detailed analysis of the temporal dynamics of xylM and xylE expression for exponentially growing $P$. putida mt-2 incubated with m-xylene and either NH$_4^+$ or NO$_3^-$ as nitrogen source. NH$_4^+$ had an initial stimulating effect on xylM expression compared with NO$_3^-$ ($P = 0.006$) within the first hour after shifting the nitrogen source (Fig. 2). However after 3–5 h, the expression pattern shifted, and while xylM expression in
NH₄⁺ medium decreased, a delayed expression peak in NO₃⁻ medium was observed. Hence after 5 h, expression of \textit{xylM} in NO₃⁻ medium was significantly higher than expression in NH₄⁺ medium (\( P = 0.027 \)). In contrast, we observed no difference in \textit{xyle} expression between the two treatments until after 3 h (Fig. 2). At this time, NO₃⁻ stimulated \textit{xyle} expression compared with NH₄⁺, and after 5 h the difference to expression in NH₄⁺ medium was statistically significant (\( P = 0.015 \)). Cultures in NH₄⁺ medium as well as cultures in NO₃⁻ medium reached stationary phase after 1–3 h according to qPCR quantification of \textit{xylM} and \textit{xyle} copy numbers (data not shown). Hence, the differences in expression levels were not related to differences in growth phase between cultures.

Expression of the nitrogen-regulated genes \textit{amtB} and \textit{gdhA}, encoding a high-affinity NH₄⁺ transporter expressed during NH₄⁺ limitation, and glutamate dehydrogenase, reported to be highly expressed in the presence of NH₄⁺, respectively (Hervás \textit{et al.}, 2008), was measured to determine whether the two nitrogen sources were perceived differentially by the cells (Fig. 3). In cultures incubated with NO₃⁻, \textit{amtB} expression was initially more than 100-fold higher than in cultures incubated with NH₄⁺ as nitrogen source. The \textit{amtB} expression then declined but remained significantly higher than for cells incubated in NH₄⁺ medium for at least 7 h (Fig. 3, insert). In contrast, \textit{gdhA} expression initially peaked for cells shifted from a spent to a fresh NH₄⁺ medium, but remained low for cells grown with NO₃⁻. The expression of \textit{gdhA} hereafter decreased to a low and steady level that remained highest (\( P < 0.05 \)) for cells cultured with NH₄⁺ throughout the entire sampling period.

In conclusion, the nitrogen sources impact \textit{xyl} gene expression in this pure culture system with NO₃⁻ having
a delayed, but overall stimulating effect compared with NH₄⁺. Furthermore, the expression of amtB and gdhA provided information on the NH₄⁺ availability to P. putida mt-2, and we consequently transferred this monitoring system for use in subsequent soil experiments.

Response of P. putida mt-2 to changing nitrogen-conditions in soil microcosm

A soil microcosm was established in which nitrogen limitation was brought about by pre-incubation with ground barley straw (Jensen and Nybroe, 1999) so that the influence of added nitrogen sources could be addressed with minimal interference from indigenous nitrogen pools. After incubation with straw for 7 days, the soil contained ~0.1 mmol kg⁻¹ soil of water soluble NO₃⁻ and NH₄⁺ as determined by chemical analyses. This soil is referred to as N-limited soil hereafter. P. putida mt-2 was then introduced to the N-limited soil and exposed to m-xylene. Nitrogen in the form of NaNO₃ or NH₄Cl was added to reach a concentration of 10 mmol kg⁻¹ soil respectively. The pH of the NH₄⁺-amended soil (pH 6.5) at the end of the 46-h incubation period.

Addition of NO₃⁻ to the N-limited soil gave rise to an increase in expression of amtB compared with that seen for the N-limited soil supplemented with NH₄⁺ (Fig. 4). Expression peaked at 8–10 h incubation, i.e. later than in liquid culture (Fig. 3), and after 12 h, amtB expression was again downregulated; nonetheless, the expression lasted longer than in liquid culture. In contrast, gdhA expression was strongly upregulated in the N-limited soil receiving NH₄⁺, but only increased slightly from the background level in NO₃⁻-amended soil (Fig. 4). Downregulation of gdhA in NH₄⁺-amended soil also appeared, but the downregulation occurred slightly later than the downregulation of amtB in NO₃⁻-amended soil. The levels of amtB and gdhA expression were comparable, which contrast the ~20-fold higher expression of amtB than gdhA in pure culture (compare Figs 3 and 4).

In conclusion, sources of inorganic nitrogen in the soil directly affect expression of the selected indicator genes involved in nitrogen uptake and transformations. Although the expression patterns were not identical to those recorded for P. putida mt-2 in liquid culture, they reveal that soil amended with NO₃⁻, unlike soil amended with NH₄⁺, is perceived as being NH₄⁺ deficient by the introduced cells.

Nitrogen source impact on expression of xylM and xylE and on m-xylene mineralization in soil

In soils receiving NO₃⁻, expression of xylM and xylE peaked after 10 h of incubation, while the expression peaks in NH₄⁺-amended soils appeared slightly delayed after 12 h (Fig. 5). The NO₃⁻ amendment resulted in higher expression of both xyl genes in the ascending part of the expression curves. For xylM the expression was significantly (P = 0.044) higher (approximately two-fold) in NO₃⁻-amended soil when comparing the peak after 10 h with the peak after 12 h in the NH₄⁺-amended counterpart. For xylE, there was nevertheless only a tendency towards a higher expression peak in the NO₃⁻-amended soil (P = 0.30).

Compared with observations made for pure cultures, the initial stimulatory effect of NH₄⁺ on xylM expression was not seen in soil, and there was a delay in the stimulatory effect on xylM and xylE expression exerted by NO₃⁻ (compare Figs 3 and 5). Importantly, the higher xyl gene expression in NO₃⁻-amended soils was reflected in a significantly (P = 0.047) higher mineralization of m-xylene after 21 h and onwards when compared with soils amended with NH₄⁺ (Fig. 5). In N-limited soil

Fig. 4. Dynamics of expression of the N-regulated genes gdhA and amtB by P. putida mt-2 inoculated into N-limited soil amended with 10 mmol kg⁻¹ soil NH₄⁺ or NO₃⁻. Data are mean values of mRNA normalized to DNA copies of the corresponding genes from triplicate soil setups, and error bars represent standard error of mean.

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that did not receive NO$_3^-$ or NH$_4^+$, the mineralization did not differ from mineralization in NH$_4^+$-amended microcosms (data not shown).

In the current experiment, P. putida mt-2 was introduced to a natural soil that may contain indigenous xylene mineralizing populations carrying xyl genes. To determine the extent to which these populations contributed to our expression and mineralization analyses, we showed that the soil contained less than $10^3$ copies g$^{-1}$ soil of xyl genes. Finally, mineralization analysis in soil microcosm without inoculated mt-2 cells revealed that mineralization by indigenous m-xylene-degrading soil bacteria accounted for a minor part (~10%) of $^{14}$C-CO$_2$ build up (data not shown). Consequently, m-xylene mineralization could be ascribed to the inoculated P. putida mt-2 cells.

In conclusion, xyl gene expression by P. putida mt-2 in soil was stimulated more by NO$_3^-$ than by NH$_4^+$. The same was observed for liquid cultures, however with a different temporal expression pattern. Importantly, the changes in xyl gene expression in response to the different nitrogen sources served as descriptors of corresponding changes in m-xylene mineralization in the soil system.

**Discussion**

Environmental conditions affecting xyl gene expression by P. putida mt-2 introduced to soil has to the best of our knowledge not previously been clarified. In complex soil environments, introduced degrader bacteria are exposed to a variety of biotic and abiotic stress factors, which might not resemble situations tested individually under standard liquid culture conditions. At the current time, it remains obscure how bacterial metabolism is regulated in their natural habitat (Meckenstock *et al.*, 2015), and whether regulatory concepts derived from liquid culture studies (Duetz *et al.*, 1996; Commichau *et al.*, 2006; Hervás *et al.*, 2008; Pflüger-Grau and Görke, 2010) are valid for catabolic bacteria exposed to the plethora of challenging conditions in their natural environment. Hence, the current study integrates experiments in a pure culture system and a soil model system. Importantly, our analyses couples changes in xylM and xylE gene expression to changes in the output of the catabolic pathway in question, m-xylene biodegradation, as transcript abundance and their cognate processes is often not correlated under environmental conditions (Rocca *et al.*, 2014).

Our results on xyl gene regulation by nitrogen sources in pure culture expand the results of Velázquez and colleagues (Velázquez *et al.*, 2006), who determined xyl gene expression by microarray technology and by Huang and coworkers (Huang *et al.*, 2008), who detected increased Pu promoter activity with NO$_3^-$ as nitrogen source at single time points. Interestingly, the stimulation of xyl gene expression by NO$_3^-$ observed in the current study occurred later than in previous studies emphasizing the importance of monitoring temporal dynamics of gene expression.

NH$_4^+$ is considered the preferred nitrogen source for bacteria, as its assimilation is less energy-expensive as...
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To monitor the availability of NH$_4^+$ hydrogen peroxide (Svenningsen et al., 2015 and Leigh and Edwards, 1995; Leigh and Dodsworth, 2007). The physiological change following substitution of NH$_4^+$ with NO$_3^-$ might consequently be due to introduction of a poor nitrogen source, although Velázquez et al. (2006) noted a weak induction of indicator genes for nitrogen starvation stress in _P. putida_ mt-2 exposed to NO$_3^-$

To monitor the availability of NH$_4^+$ to mt-2 cells, we quantified the expression of two genes, _amtB_ and _gdhA_ that are under control of the major nitrogen-associated transcriptional regulator, NtrC. The _amtB_ gene encodes a high-affinity NH$_4^+$ transporter. It belongs to the NH$_4^+$ transport family of proteins ubiquitous to all bacteria, and is blocked under conditions of nitrogen excess (Coutts et al., 2002; Javelle and Merrick, 2005; Leigh and Dodsworth, 2007). Expression of _amtB_ in _P. putida_ is stimulated under nitrogen limiting conditions established, e.g. during growth on serine (Hervás et al., 2008; Yeom et al., 2010). The glutamate dehydrogenase gene, _gdhA_, on the other hand is reported to be expressed under conditions of normal nitrogen access and is actively repressed by nitrogen limitation in _P. putida_ (Hervás et al., 2010). Our observation of high _amtB_ and very low _gdhA_ expression in NO$_3^-$-amended cultures over the entire time-course examined here indicates that mt-2 sensed this medium as being NH$_4^+$ deficient. The opposite expression pattern recorded during growth with NH$_4^+$ demonstrates that, in concert, _amtB_ and _gdhA_ function as indicators for the cellular nitrogen status. Interestingly, the expression of _amtB_ and _gdhA_ is highly dynamic within 1–3 h where after expression is downregulated to a steady level likely because the nitrogen fluxes have reached balance. Peaks in expression have previously been observed, e.g. for the _Cupriavidus pinatubonensis_ _tfdA_ gene involved in herbicide catabolism just after exposure to the substrate, and for the _P. putida_ catalase gene _katA_ just after exposure to hydrogen peroxide (Svenningsen et al., 2015 and unpublished observations). We speculate that a pool of enzymes is produced during the burst in gene expression that is able to carry out the requested function for an extended time period. Again, our data underline that data obtained from sampling at single timepoints in gene expression studies might lead to incorrect conclusions.

To be able to assess the nitrogen source impact on _m-xylene_ biodegradation in soil, we reduced the readily accessible soil nitrogen pool through incubation with barley straw. Due to a C:N ratio higher than the average bacterial C:N ratio, this treatment immobilizes nitrogen in non-sterile soil (Geisseler et al., 2010). The expression of the two nitrogen-regulated genes _amtB_ and _gdhA_ showed initial peaks as discussed above for liquid cultures. However, the response was slower and we also noted subtle differences in induction levels between pure cultures and soil that could be explained by the NH$_4^+$ levels in the two systems. Hence, the weaker induction of _amtB_ in NO$_3^-$-amended soil than in liquid NO$_3^-$-amended medium as well as the weak induction of _gdhA_ in NO$_3^-$-amended soil suggest that small amounts of an easily available nitrogen source were available in the soil. Indeed, chemical analysis showed that the nitrogen-limited soil still contained 0.1 mmol kg$^{-1}$ of water soluble NH$_4^+$ after the straw pre-treatment. This NH$_4^+$ pool has been available even to the cells introduced to NO$_3^-$-amended soils. Hence, our results indicate that mt-2 cells are able to sense and respond to indigenous nitrogen pools in the soil, and they demonstrate that the _amtB_ and _gdhA_ genes are valid indicator genes for studying the bioavailability of NO$_3^-$ versus NH$_4^+$ to _P. putida_ mt-2 in natural soil.

The higher expression of _xyl_ genes in response to _m-xylene_ in NO$_3^-$-amended than NH$_4^+$-amended soil was in general agreement with observations made for pure cultures. Obviously, _xyl_ gene induction in the soil was slower than in liquid culture. This might be caused by sorption of _m-xylene_ to soil organic matter. However, the slower response was even recorded for expression of genes involved in nitrogen metabolism as discussed above. Hence, the delay might be ascribed to the downshift that the cells experience upon transfer to the oligotrophic soil environment (van Veen et al., 1997; Koch et al., 2001) with a high complexity of potential stressors (including the _m-xylene_ carrier hexane) that the cells need to deal with (Daurabas and Chakrabarty, 1992; Velázquez et al., 2006). Importantly, the robustness of our gene expression system permitted us to relate small differences in gene expression in soil under the two nitrogen regimes to a significant difference in total mineralization of the added _m-xylene_. This is important because discrepancy between the amounts of transcripts and their corresponding protein abundance and functional activity is occasionally observed (Poblete-Castro et al., 2012). Regulation of gene expression is the first and most direct cellular response to changed environmental conditions in prokaryotes. We indeed observed that _xyl_ gene induction preceded _m-xylene_ mineralization in soil, probably reflecting the time required for establishing a pool of catabolic enzymes in the cells. Comparable time-courses have been observed for _tfdA_ gene expression and MCPA herbicide mineralization by _C. pinatubonensis_ introduced to soil (Nicolaisen et al., 2008). When combined with $^{14}$C-mineralization assays, we suggest that _xyl_ transcript analysis provides robust insight into factors controlling _m-xylene_ biodegradation, but for future studies proteome analyses of the catabolic enzymes could be of considerable interest.

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It remains to be clarified exactly how nitrogen status affect xyl gene expression. The upper TOL pathway promoter Pu as well as the Ps1 promoter of the meta pathway transcriptional regulator XylS are controlled by the sigma factor, $\sigma^{54}$, encoded by the rpoN gene (Ramos et al., 1997; Cases et al., 2003; Shingler, 2003) (Fig. 1). Velázquez and coworkers (Velázquez et al., 2006) proposed that NO$_3^-$ could increase xyl gene expression by a mechanism involving stimulation of the two $\sigma^{54}$ dependent TOL pathway promoters by increasing the amount of $\sigma^{54}$-bound core RNA polymerases; a condition that might occur during assimilation of NO$_3^-$-derived NH$_4^+$ through glutamine synthetase–glutamate synthase (Moreno-Vivián et al., 1999; Velázquez et al., 2006). An alternative mechanism suggested by Aranda-Olmedo et al. (2005) is that the nitrogen phosphotransferase system, PTS$^{NH_4}$, involved in nitrogen metabolism (Pflüger-Grau and Görke, 2010), also interferes with activation of the $\sigma^{54}$-dependent TOL pathway promoters via their effector molecules; hence, this mechanism is more related to the interplay between nitrogen starvation/metabolism and carbon metabolism. The observation that xylene mineralization was comparable in natural soil and nitrogen-depleted soil amended with NH$_4^+$ might suggest that the higher mineralization in NO$_3^-$-amended soils is a direct response to NO$_3^-$$. However, to the best of our knowledge, a NO$_3^-$-sensing mechanism has not been described for P. putida.

The current methodological approach allowed us to gain insight into regulation of catabolic gene expression of P. putida mt-2 by environmental factors under close-to-natural soil conditions. Although temperature and water content were kept constant, the mt-2 cells introduced to a natural soil would be confronted with some spatial heterogeneity, with possible competition or collaboration from indigenous microorganisms, and with realistic indigenous pools of carbon sources and nutrients. Our study underscores that global regulation of catabolic genes acts beyond direct substrate induction. Furthermore, regulatory patterns emerge in our soil model systems that are comparable to those observed in liquid cultures. Nevertheless, we even observe noteworthy differences in terms of temporal dynamics and induction levels. Interestingly, we have seen that environmental regulation of xyl genes in pure culture does not correspond to regulation in soil, when changing the available carbon sources (NB Svenningsen, unpublished results). Hence, more effort could be devoted to deciphering the environmental factors that affect expression of these genes in the soil.

With the current model system in hand, we have a good basis for investigating the ‘behaviour’ of P. putida mt-2 under realistic conditions in different soils and considering other stressors that could influence the potential for biodegradation. From both a basic and an applied perspective, it is a key issue to understand the in situ environmental conditions able to stimulate the biodegradative potential of a particular organism (Cases and de Lorenzo, 2005). Although the specific nitrogen sources available for inoculated degrader bacteria will influence their growth potential, and therefore the potential for pollutant degradation on the long run, our data show that specific nitrogen sources in soil also affect the expression of catabolic genes of degrader bacteria. Hence, we suggest that attempts to improve bioremediation of pollutants from contaminated sites should integrate knowledge on environmental effects on growth as well as on catabolic gene regulation under natural conditions.

**Experimental procedures**

*Bacterial strain and growth conditions*

*Pseudomonas putida* mt-2 harbouring the TOL plasmid, pWW0 (Greated et al., 2002) that enables it to degrade among others toluene, m- and p-xylene, was obtained from Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany (DSM-6125). For all experiments, the strain was pre-cultured over night at 28°C with agitation at 150 r.p.m. in M9 minimal medium (6.0 g L$^{-1}$ Na$_2$HPO$_4$, 3.0 g L$^{-1}$ KH$_2$PO$_4$, 0.5 g L$^{-1}$ NaCl, 1.0 g L$^{-1}$ NH$_4$Cl, 0.25 g L$^{-1}$ MgSO$_4$$\cdot$7 H$_2$O, 0.015 g L$^{-1}$ CaCl$_2$$\cdot$2 H$_2$O) supplemented with 5 mM Na-succinate. For pure culture experiments, the overnight cultures were diluted in fresh M9 medium as specified in following section. For soil experiments, cultures were harvested by centrifugation (5000 g, 5 min, 21°C), and cells were subsequently washed twice and re-suspended in 1× phosphate-buffered saline (PBS). Cell densities were calculated based on measurements of optical density at 600 nm with OD = 1 corresponding to 10$^9$ cells ml$^{-1}$ measured by standard CFU counting on LB agar.

*Liquid culture experiment and sampling for nucleic acid extraction*

Overnight cultures of P. putida mt-2 in M9 medium (OD$_{600nm}$ ~0.8) were diluted 100 times in fresh medium and exposed to vapours of m-xylene (Sigma-Aldrich, St. Louis, MO, USA) stemming from a 1:5 dilution in dibutyl phthalate (Sigma-Aldrich) in sealed flasks, basically as described in Velázquez et al. (2006). At OD$_{600nm}$ ~0.5, cells were washed twice in PBS before resuspending them in N-free M9 medium supplemented with either 10 mM NO$_3^-$ or NH$_4^+$ as nitrogen source and incubated in the presence of m-xylene at 28°C with agitation at 150 r.p.m. The bottles were sealed and kept closed during the incubation. At 15 min, 30 min, 1, 3, 5 and 7 h
after the shift in nitrogen sources, samples were withdrawn with a sterile syringe through a septum in the cap. Cells were pelleted by centrifugation at 4°C (10,000 g, 2 min), frozen in liquid N2 and immediately stored at −70°C until nucleic acid extraction.

Soil characteristics and soil model set-up

Agricultural soil was collected from the Ap horizon (0–34 cm) of a soil profile located 20 km west of Copenhagen at 55°40’ N and 12°18’ E on the experimental farm Rørrendegård of Copenhagen University. The soil was stored in closed containers at 4°C until use. A subsample of soil was used for soil characterization. The soil pH was 6.8, determined in a 1:1 soil–water suspension. The particle size distribution was 22% clay, 13% silt, 29% course sand and 36% sand. The total carbon content was 1.1% (w/w) and total nitrogen was determined by Kjeldahl digestion. Determination of total soil carbon was carried out by dry combustion, and total nitrogen was determined by Kjeldahl digestion. The total carbon content was 1.1% (w/w) and total nitrogen was 0.13% (w/w).

Prior to the experiment, the moist soil was passed through a 2 mm mesh sieve, and a subsample of soil was heated at 105°C for 24 h to determine the water content. To obtain depletion of nitrogen, ground barley straw (2.5% w/w) was mixed into the soil, which was subsequently incubated at 20°C for 1 week in order to immobilize soil nitrogen (Jensen and Nybroe, 1999). Straw residues were then removed by passing the soil through the 2 mm mesh sieve again. Next the moisture content was adjusted to 18% of soil dry weight with sterile water suspensions. The particle size distribution was 22% clay, 13% silt, 29% course sand and 36% fine sand, and was determined by sieving and sedimentation. Determination of total soil carbon was carried out by dry combustion, and total nitrogen was determined by Kjeldahl digestion. The total carbon content was 1.1% (w/w) and total nitrogen was 0.13% (w/w).

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In addition to the treatments described above, a control soil microcosm without inoculation of mt-2 cells, plus addition of m-xylene was prepared to test for background mineralization of m-xylene and direct capture of 14C m-xylene in NaOH traps. Furthermore, a control with inoculation of mt-2 cells but without addition of m-xylene was set up to test for if the soil itself stimulates induction of the xyl genes in soil.

Additionally, at the beginning and in the end of incubation, soil water samples were collected for determination of pH and concentrations of NH4+ and NO3− associated to soil water (i.e. the directly bioavailable part). This was done by vortexing 0.15 g soil with 1.5 ml MilliQ water, followed by 1 h of shaking at 200 r.p.m. Finally, samples were centrifuged (10,000 g, 5 min) and analyses of pH and concentrations of NO3− and NH4+ were conducted on the supernatants.

Nucleic acid extraction and quantitative PCR

For extraction of nucleic acids from pure culture samples, the AllPrep DNA/RNA Mini Kit (Qiagen, Manchester, UK) was used according to the manufacturer’s protocol with addition of a lysozyme pre-treatment step at room temperature for 20 min (100 μl of 1 mg ml−1 in 10 mM Tris-Cl buffer, pH 8, per sample of 100 μl) as the only modification. From soil samples, DNA and RNA were co-extracted by the phenol–chloroform method as formerly described (Nicolaersen et al., 2008). Subsequent to extraction DNA was eliminated from RNA samples by treating aliquots of each nucleic acid sample with RQ1 RNase-free DNase 1 (Promega, Nacka, Sweden) according to the manufacturer’s protocol. cDNA was synthesized immediately thereafter by using 2 μl subsamples of each DNase-treated extract as template for reverse transcription (RT) with the Omniscript RT Kit (Qiagen). DNase-treated control reactions were prepared in parallel for RNA samples without addition of the reverse transcriptase (RT) to ensure the absence of DNA contamination. RT reactions were prepared with 400 ng of random hexamer primers (Promega), 4 U of SUPER RNase inhibitor (Ambion, Austin, TX, USA) and reagents provided in the kit for a final volume of 20 μl. Incubation conditions were followed as recommended by...
the manufacturer. Resulting cDNA samples were stored at –20°C until use in qPCR.

Previously published primers were used to quantify the expression of xylM, xyle (Martinez-Lavanchy et al., 2010), amtB and gdhA (Hervás et al., 2008). qPCR reactions were prepared in 20 µl with 10 µl Brilliant II SYBR Green QPCR Master mix (Stratagene, La Jolla, CA, USA), 0.3 µM of each primer and 1 mg ml−1 BSA. Thermal cycling conditions were following: an initial cycle of 95°C for 10 min, followed by 40 cycles of 95°C for 30 s, primer annealing at the temperatures stated in (Hervás et al., 2008; Martínez-Lavanchy et al., 2010) for 45 s and an elongation step at 72°C for 1 min. Subsequently a melting curve was run. All cDNA and DNA samples were diluted 1:10 before the qPCR. To check for possible contamination of RNA samples by genomic DNA, diluted samples of RNA were analysed by qPCR as well. Ct values for pure culture samples were related to a standard curve prepared by inoculation of 101–109 P. putida mt-2 cells per gram soil and subsequently extracting the DNA. Soil without inoculation of mt-2 cell had a natural background of xyl genes; hence, the standard curve was not linear below 103 gene copies per gram of soil. From the slope of the standard curves, the amplification efficiencies of the qPCRs were calculated using the formula E = 10−(1/slope)−1; for all four gene amplified, the efficiencies were in the range 98–106%. Gene expression was calculated as mRNA normalized per DNA copy numbers as previously described (Nicolaisen et al., 2008), taking dilution steps from the DNase-treatment and RT into consideration when calculating mRNA numbers from the cDNA numbers. DNA and cDNA samples from the soil qPCRs were randomly chosen for Sanger sequencing to verify that the primers only targeted specific products in the soil.

Statistical analysis
All experiments were repeated independently at least twice, with each independent experiment involving triplicate samples. Mean values of such triplicates from one representative experiment are reported ± standard error of mean. Statistical significance was tested with Student’s t-test using the software PAST3.10 (University of Oslo, Norway). Data were considered significant when P < 0.05.

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Conflict of interest
The authors have no conflict of interest.

References

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