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Functional identification in *Lactobacillus reuteri* of a PocR-like transcription factor regulating glycerol utilization and vitamin B<sub>12</sub> synthesis

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Abstract

**Background:** *Lactobacillus reuteri* harbors the genes responsible for glycerol utilization and vitamin B<sub>12</sub> synthesis within a genetic island phylogenetically related to gamma-Proteobacteria. Within this island, resides a gene (*lreu_1750*) that based on its genomic context has been suggested to encode the regulatory protein PocR and presumably control the expression of the neighboring loci. However, this functional assignment is not fully supported by sequence homology, and hitherto, completely lacks experimental confirmation.

**Results:** In this contribution, we have overexpressed and inactivated the gene encoding the putative PocR in *L. reuteri*. The comparison of these strains provided metabolic and transcriptional evidence that this regulatory protein controls the expression of the operons encoding glycerol utilization and vitamin B<sub>12</sub> synthesis.

**Conclusions:** We provide clear experimental evidence for assigning *Lreu_1750* as PocR in *Lactobacillus reuteri*. Our genome-wide transcriptional analysis further identifies the loci contained in the PocR regulon. The findings reported here could be used to improve the production-yield of vitamin B<sub>12</sub>, 1,3-propanediol and reuterin, all industrially relevant compounds.

**Background**

*Lactobacillus reuteri* is a heterofermentative lactic acid bacterium colonizing the gastrointestinal tract (GI tract) of various mammals, including humans [1]. It is able to convert glycerol to 1,3-propanediol in a two-step enzymatic conversion, yielding NAD<sup>+</sup> [2]. In the first reaction, glycerol dehydratase (EC 4.1.2.30), converts glycerol to 3-hydroxypropionaldehyde requiring the presence of vitamin B<sub>12</sub> as a coenzyme [3]. Reuterin, a mixture of 3-hydroxypropionaldehyde isomers [4], is a potent antimicrobial, bestowing *L. reuteri* with an important growth advantage over other residents of the GI tract, such as Gram-negative enteric bacteria [5,6].

We have shown previously that *L. reuteri* CRL1098 encodes the complete machinery necessary for de novo synthesis of vitamin B<sub>12</sub> in a single chromosomal gene cluster [7]. This cluster was shown to be very similar to that present in various representatives of γ-Proteobacteria, standing out against canonical phylogeny. Complete genome sequence analysis of the type strain of *L. reuteri* revealed that the region immediately upstream of the vitamin B<sub>12</sub> biosynthesis cluster maintains a gene order similar to that of *Salmonella* [8]. The functionality of this upstream region was demonstrated to also match *Salmonella* where the *pdu* gene cluster is located. The latter encodes the assembly machinery of metabolosomes and the several subunits of a large diol dehydratase that can metabolize both glycerol and 1,2-propanediol [9].

Also within this cluster resides a gene (*lreu_1750*) predicted to encode a 359 amino acid long putative transcription factor of the AraC type family, containing a typical helix-turn-helix domain. Based strictly on its conserved genomic context, this gene has been suggested to encode PocR, a regulatory protein that modulates propanediol utilization (*pdu*) and vitamin B<sub>12</sub> synthesis.
biosynthesis in enteric bacteria [8-10]. This functional annotation, however, does not seem to be fully supported by sequence homology. And more importantly, to the best of our knowledge, it completely lacks experimental confirmation.

Here we provide the first experimental evidence to support the functional assignment of Lreu_1750. This was achieved by overexpression and inactivation of Lreu_1750, assessing its impact on central carbon and energy metabolism, and on reuterin and vitamin B₃₂ synthesis. In addition, we characterized the genome-wide transcriptional response of both constructs in comparison to their parent strains leading to the identification of the genes comprised in the PocR regulon of Lactobacillus reuteri.

Results and Discussion
Phylogenetic analysis of Lreu_1750
Phylogenetic comparisons between Lreu_1750 and other PocR sequences raise serious doubts about its functional annotation (Figure 1). When compared to the PocR found in enteric bacteria, Lreu_1750 reveals limited amino acid sequence identity (19.1%) and a large percentage of gaps (40.1%). The sequence identity and percentage of gaps (20.5% and 38.8%, respectively) of the PocR-like regulatory proteins of other vitamin B₃₂-producing Firmicutes, such as

Figure 1 Amino acid sequence alignment of Lreu_1750 and putatively related sequences. Alignments were obtained using ClustalW with default settings [20] and visualized in CLC Sequence Viewer 6.5. Abbreviations stand for: LRE, Lactobacillus reuteri; LAR, Lactobacillus acidophilus; LBR, Lactobacillus brevis; MLSK, Lactobacillus plantarum; LPL, Lactococcus lactis; LST, Lactococcus lactis subsp. lactis; STL, Staphylococcus aureus; YEN, Yersinia enterocolitica; KPN, Kitasatospora sp. Ty2; SEN, Senegalia senegalensis; SMI, Saccharomyces cerevisiae; FNF, Fusarium oxysporum; CLC, Complete Linkage Clustering; ECL, Empty Cloning Loop; TLR, Toll-Like Receptors; GTP, Guanosine triphosphate; MAF, Multiple Alignment File; PDB, Protein Data Bank; B or T, Bacteria or Taxa; CIV, Center for In Vivo Navigation; FPR, False Positive Rate; ROC, Receiver Operating Characteristic; 10-50, 10-60, 10-70, 20-50, 20-60, 20-70, 20-80, 20-90, 20-100, 50-60, 50-70, 50-80, 50-90, 50-100, 60-70, 60-80, 60-90, 70-80, 70-90, 80-90, 90-90, 90-100, 100-100. Darker blue background stands for higher percentage conservation of respective residue.
as *Listeria monocytogenes*, suggest that it is slightly more related. The closest homolog of Lreu_1750 present in the complete genomes available is found in *L. brevis* ATCC 367 (GI:116334199) with 36.1% identity and only 1.4% gaps. *L. brevis* is also able to produce 1,3-propanediol [3], but it cannot synthesize vitamin B₁₂ [7]. The predicted products of *lreu_1750* and its homolog in *L. brevis* are approximately 60 amino acid residues longer in the C-terminus in comparison to PocR from *S. typhimurium* LT2. This could additionally affect its functionality and further urges the experimental confirmation of its tentative annotation. The putative PocR of two different wild type *L. reuteri* strains, JCM1112 and ATCC PTA 6475, have also been aligned and found to display 100% sequence identity and 0% gaps (Figure 1). Subsequent experiments have been carried out using derivatives of both strains predominantly for technical convenience. Nevertheless, this choice is also important to further substantiate the generality of our findings regarding the role of this PocR-like protein in *L. reuteri* strains.

**Physiological effects**

The functional assignment of *lreu_1750* was initiated by characterizing the impacts of its overexpression on central carbon and energy metabolism. Since functionally active glycerol metabolizing enzymes are encoded in the vicinity of *lreu_1750*, the experimental focus was on glycerol metabolism. In the absence of glycerol, except for a slight impairment (< 10%) of *μ*ₘₐₓ (Figure 2), no metabolic effects were observed related to the overexpression of *lreu_1750* (Figure 3, panels a. and c.). In the presence of glycerol, however, the overexpressing strain in comparison with JCM1112 transformed with pNZ7021 (empty plasmid), displays a drop in the final ethanol concentration from 13.7 to 6.2 mM while acetate increased approximately 4 mM. This enhancement of the shift from ethanol to acetate formation (*p*-value < 0.025, paired two-tailed *t*-test) is accompanied by a 22.5% increase of 1,3-propanediol production, which is produced on a 2:1 molar ratio with acetate, assuring the regeneration of reducing equivalents (Figure 3, panels b. and d.).

Overexpressing *Lreu_1750* does not lead to significant changes (*p*-value = 0.07, paired two-tailed *t*-test) in reuterin production (Figure 4). This is not totally unexpected, since changes in the level of enzymes involved in central carbon metabolism often do not result in drastic changes in fluxes [11]. In contrast, the disruption of the *lreu_1750* gene leads to an abrupt decrease in

![Figure 2 Biomass formation and sampling scheme in pH-controlled batch fermentations](image-url)
reuterin production from 25 mM in the parent strain to undetectable levels (< 0.1 mM) in the mutant. When this strain is complemented with a plasmid harboring \textit{lreu\_1750} under control of its native promoter (pJKS101), reuterin production is restored to levels in the same order of magnitude as \textit{L. reuteri} 6475 (11 mM). Mostly human-derived \textit{L. reuteri} strains can produce reuterin, and therefore, it is thought that this may be important for their survival in the human GI tract [1]. The observed reduction by more than 250-fold in reuterin production most likely debilitates the probiotic functionality of the PocR mutant strain [1,12]. Furthermore, it will condition the potential utilization of glycerol for the regeneration of NAD+, limiting its biomass yield on carbon substrate [10].

The regulatory role of \textit{lreu\_1750} on vitamin B\textsubscript{12} synthesis is clearly illustrated by the drastic inhibitory effect that its inactivation exerts over vitamin B\textsubscript{12} production (Figure 5). In contrast to the parent strain, the deletion mutant of the putative PocR did not produce detectable levels of B\textsubscript{12} (6.09 and less than 0.01 μg.L\textsuperscript{-1}.OD\textsubscript{600}\textsuperscript{-1}, respectively). Furthermore, the complementation of the mutant with pJKS101 (harboring the putative pocR) leads to the reestablishment of B\textsubscript{12} production (5.36 μg.L\textsuperscript{-1}.OD\textsubscript{600}\textsuperscript{-1}). Additionally, in the strain overexpressing \textit{lreu\_1750} (JCM1112 pNZ7748) we observe a significant increase (\textit{p}-value < 0.016, paired two-tailed \textit{t}-test) of more than 25% in vitamin B\textsubscript{12} production in comparison to JCM1112 transformed with the empty plasmid (pNZ7021). This increase was obtained regardless of the addition of glycerol, and was observed in all the media and conditions tested including the pH-controlled batch fermentations using CDM (data not shown).

The physiological effects observed for the overexpression and inactivation of \textit{lreu\_1750} are all in agreement with its functional assignment as the regulatory protein PocR.

\textbf{Transcriptomic response}

In order to probe the global regulatory role of the putative PocR of \textit{L. reuteri}, we compared the transcriptomes...
of the deficient and overexpressing strains relative to their parent strains. Considering that (i) glycerol has been shown to induce the expression of \textit{lreu\_1750} [10], masking the effect of its overexpression; (ii) consequently the differentiating phenotype of the PocR deficient strain can be best observed under conditions in which its growth kinetics are hampered (such as in the presence of glycerol - Figure 2); and (iii) there is a large redundancy between the different transcriptome analyses carried out; most emphasis in this report has been put on the data related to the \textit{lreu\_1750} overexpression in the absence of glycerol. The complete list of differentially regulated genes under all conditions assayed is available in Additional file 1: Transcriptome analysis data.

Upon overexpressing \textit{lreu\_1750} only 120 genes (approximately 6\% of the genome) are differentially regulated, of which, all but two are up-regulated. Three functional classes were represented with 10\% or more of its members in the list of differentially expressed loci, namely the ones related to coenzymes, secondary metabolites and energy production (Additional file 1, Table S2). A closer inspection of the list of differentially regulated genes shows that \textit{lreu\_1750} is clearly involved in the regulation of the same processes that have been linked to PocR in \textit{Salmonella} [13]. These genes include the \textit{pdu} cluster flanking \textit{lreu\_1750}, encoding the several subunits of the diol dehydratase and the metabolosome-assembly proteins [9], along with the two operons of the \textit{B12} biosynthesis cluster [7] (Figure 6). The lack of statistical significance observed for some of the expression data of the \textit{B12} synthesis cluster is easily explained. This cluster is divided into two multicistronic operons with a relatively low abundance and a remarkably large size. This raises great technical difficulties during mRNA purification as reported in the past [7,14].

Besides these genes stretching from \textit{lreu\_1695} to \textit{lreu\_1752}, which are expected to be regulated by PocR by homology with \textit{Salmonella} [2], we found two genes (\textit{lreu\_0429} and \textit{lreu\_0430}) predicted to be co-transcribed and annotated with unknown function in GenBank, that are up-regulated ~3.5-fold (Table 1). A closer look at their sequence indicates that these are most likely two subunits of an ATPase transporter [15], which
have been tentatively associated with copper transport in ERGO [16]. We speculate that these are cobalt- rather than copper-transporters, based on the fact that cobalt availability is essential for the synthesis of vitamin B$_{12}$. We also found regulated a few genes related to sugar uptake and carbon metabolism. These are presumably related to the up-regulation of \textit{lreu}_1750 (transcription factor of LacI family), which is most likely a consequence of a slight drop in growth rate caused by the extra burden of the \textit{lreu}_1750 overexpression (Figure 2).

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**Figure 5** Vitamin B$_{12}$ production by \textit{L. reuteri} strains in commercial Vitamin B$_{12}$-assay medium supplemented with glycerol. Bars represent average values along with standard deviation (error bars) of at least two independent biological replicates measured in triplicate using strains 6475 (parent strain), 6475::pocR (PocR deficient mutant), 6475::pocR pJKS100 (PocR deficient mutant transformed with empty plasmid), 6475::pocR pJKS101 (PocR deficient mutant complemented with putative pocR of 6475 under control of its native promoter), JCM1112 pNZ7021 (type strain transformed with empty plasmid) and JCM1112 pNZ7748 (type strain carrying the \textit{lreu}_1750 overexpression).

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**Figure 6** Relative expression levels of the loci situated within the genetic island that harbors PocR. Color-scale plot of the relative expression levels of the loci situated between \textit{lreu}_1690 and \textit{lreu}_1757 (not to scale). All genes situated within the genetic island are up-regulated when \textit{lreu}_1750 is overexpressed with the exception of the transposase. The lack of statistical significance observed for some of the loci is discussed in the text. Abbreviations stand for: M, log$_2$(intensity of signal of \textit{L. reuteri} pNZ7748/intensity of signal of \textit{L. reuteri} pNZ7021); ***, p-value $\leq$ 0.05.
A considerable number of enzymes involved in recombination and DNA repair were also up-regulated. This is probably a consequence of the homologous region to the genome of L. reuteri present in plasmid pNZ7748 (harboring lreu_1750) and not in pNZ7021 (empty vector), as previously observed [17,18].

The transcriptome studies carried out for the PocR insertion mutant were consistent with the results obtained through the overexpression of lreu_1750. We mainly observed in the PocR mutant compared to the wild-type strain, a down-regulation of the genes located within the genetic island that comprises the pdu and vitamin B_{12} operons (Additional file 1, Table S3). Again due to the rarity and fragility of these transcripts [7,14] only 30 out of 58 loci are differentially expressed significantly (p-value ≤ 0.05) even though the whole region, excluding the transposase, appears co-regulated.

There is strong phylogenetic evidence supporting that the pdu and vitamin B_{12} synthesis gene clusters have been acquired by L. reuteri through distant horizontal gene transfer [7,8]. The confinement of the PocR regulon to mostly one continuous stretch of the chromosome (Figure 6), with exception of the putative cobalt transporter, further substantiates this hypothesis.

Conclusions
In this study, we have provided experimental evidence that lreu_1750 encodes a PocR-like regulatory protein, despite its lack of sequence homology to PocR from enteric bacteria. This was achieved by overexpression and inactivation of lreu_1750, and assessment of its impact on central carbon and energy metabolism, and on reuterin, 1,3-propanediol and vitamin B_{12} biosynthesis. In addition, we characterized the genome-wide transcriptional response of both constructs in comparison to the wild-type leading to the identification of the genes encompassed in the PocR-like regulon of L. reuteri. The latter were found to be similar to the ones present in some representatives of γ-Proteobacteria. Ultimately, the demonstrated stimulatory effects of PocR on vitamin B_{12}, 1,3-propanediol and reuterin synthesis could be applied to improving the production yield of these industrially relevant compounds.

Methods
Phylogenetic analysis of Lreu_1750
The sequence of Lreu_1750 (GI:148544956) was entered as a string to search for closely related homologs within available microbial genomes using the protein-protein BLAST algorithm [19]. Relevant sequences were retrieved and aligned using ClustalW with default settings [20] and visualized in CLC Sequence Viewer 6.5.

Strains, plasmids, primers and cultivation conditions
The bacterial strains, plasmids and primers used in this study are listed in Table 2. L. reuteri strains were cultivated at 37°C in undefined MRS broth [21], in Vitamin B_{12} assay medium (Sigma-Aldrich, Zwijndrecht, The Netherlands) enriched with 0.5% glycerol (v/v), in the semi-defined medium LDMIIIG [12] and in a chemically defined medium (CDM) previously used to study vitamin B_{12} production in L. reuteri [14]. When appropriate, erythromycin and/or chloroamphenicol were added to a final concentration of 10 μg/mL.

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Table 1 Relative expression levels of loci associated to PocR and not within its flanking regiona

| Locus     | Function                                                                 | M^b | p^c | Accession number |
|-----------|--------------------------------------------------------------------------|-----|-----|------------------|
| Lreu_0088 | Transcriptional regulator, LacI family                                   | 1.11| 0.03| gi|148543330 |
| Lreu_0103 | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)                       | 0.89| 0.03| gi|148543342 |
| Lreu_0429 | Putative cobalt-transporting ATPase^d                                | 1.85| 0.00| gi|148543665 |
| Lreu_0430 | Putative cobalt-transporting ATPase^d                                | 1.76| 0.00| gi|148543666 |
| Lreu_0479 | Arabinose-proton symporter                                            | 1.67| 0.00| gi|148543714 |
| Lreu_0631 | Pyruvate dehydrogenase alpha subunit (EC 1.2.4.1)                       | 0.88| 0.02| gi|148543863 |
| Lreu_0632 | Pyruvate dehydrogenase beta subunit (EC 1.2.4.1)                       | 0.86| 0.04| gi|148543864 |
| Lreu_0633 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | 0.81| 0.03| gi|148543865 |
| Lreu_0910 | Alpha-galactosidase (EC 3.2.1.22)                                       | 0.90| 0.03| gi|148544139 |
| Lreu_1007 | Transcription regulator, Crp family                                    | -0.82| 0.04| gi|148544234 |
| Lreu_1531 | Fumarate hydratase (EC 4.2.1.2)                                        | 1.09| 0.05| gi|148544743 |
| Lreu_1768 | Lactose permease                                                        | 0.97| 0.05| gi|148544974 |
| Lreu_1832 | Histidine decarboxylase (EC 4.1.1.22)                                   | -1.67| 0.03| gi|148545038 |

^a Genes predicted to encode phage-related proteins, recombinases, mobile elements, DNA repair and general or unknown functions were omitted (for full list, please see Additional file 1, Table S1)
^b M, log_{2}(intensity of signal of L. reuteri pNZ7748/intensity of signal of L. reuteri pNZ7021).
^c p, p-value.
^d Annotated as hypothetical protein in GenBank and as copper-transporting ATPase (EC 3.6.3.10) in ERGO database [16].
Construction of putative pocR overexpression and deletion mutants

Gene \textit{ireu\_1750}, encoding the putative PocR in \textit{L. reuteri} JCM1112\(^2\), was overexpressed constitutively under control of the \textit{pepN} promoter in a similar fashion as previously described [22]. A fragment containing \textit{ireu\_1750} was amplified from chromosomal DNA of \textit{L. reuteri} using Herculase II DNA polymerase (Stratagene, La Jolla, USA), and primers P180 and P181 (Table 2). After digestion with \textit{KpnI}, the modified amplicon was purified and cloned in pNZ7021 making use of the \textit{KpnI} and \textit{PmlI} restriction sites directly downstream of the \textit{pepN} promoter. The resulting plasmid, termed pNZ7748, was used directly from the ligation reactions to transform \textit{Lactococcus lactis} NZ9000 by electroporation [23]. Subsequently, pNZ7748 was purified from \textit{Lc. lactis} MG1363 pepN:nisRK, cloning host. NIZO culture collection (Ede, The Netherlands) and used to transform \textit{L. reuteri} also by electroporation [25].

The disruption of the putative pocR gene was carried out in \textit{L. reuteri} ATCC PTA 6475, which shares an identical sequence with the type strain (JCM1112) for this region of the chromosome [1]. This was achieved by site-specific integration of plasmid pORIpocR as described previously [26] using the temperature-sensitive plasmid pVE6007 [27] as the helper plasmid. The internal fragment of the target gene was amplified by PCR using primers LR0062F-BHI and LR0062R-ERI (Table 2) to construct pJKS100.

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**Table 2 Strains, plasmids and primers used in this study**

| Materials | Relevant features | Source or reference |
|-----------|-------------------|---------------------|
| **Strains** | | |
| \textit{L. reuteri} JCM1112 | Type strain, synonymous to ATCC 23272, DSM 20016 and F275. Human isolate. | Japanese Collection of Microorganisms (Riken, Japan) |
| \textit{L. reuteri} ATCC PTA 6475 | Synonymous to MM4-1A. Finnish mother's milk isolate. | Biogaia AB (Stockholm, Sweden) |
| \textit{L. delbrueckii} subsp. lactis ATCC 7830 | Vitamin B\(_1\) assay indicator strain. | NIZO culture collection (Ede, The Netherlands) |
| \textit{L. delbrueckii} NIZO235 | | |
| \textit{L. delbrueckii} NIZO235 | | |
| **Plasmids** | | |
| pCR\(^\circ\)2.1 | Used in routine cloning and to construct pJKS100 | Invitrogen (Carlsbad, CA) |
| pLEM5 | \textit{L. reuteri} replication origin used to construct pJKS100 | [28] |
| pNZ7021 | \textit{Cm}\(^R\), pNZB148 derivative with the nisin promoter replaced by the \textit{pepN} promoter | [23] |
| pNZ7748 | \textit{Cm}\(^R\), pNZ7021 derivative harboring \textit{ireu\_1750} downstream of the \textit{pepN} promoter. | This study |
| pVE6007 | \textit{Cm}\(^R\), repA-positive temperature-sensitive derivative of pWV01 | [27] |
| pORI28 | \textit{Em}\(^R\), repA-negative derivative of pWV01 | [35] |
| pORIpocR | \textit{Em}\(^R\), pORI28 derivative harboring internal fragment of gene encoding putative PocR | This study |
| pJKS100 | \textit{Cm}\(^R\), E. coli-\textit{L. reuteri} shuttle vector | This study |
| pJKS101 | \textit{Cm}\(^R\), pJKS100 derivative expressing 6475 pocR gene under control of its natural promoter | This study |
| **Primers** | 5\('\) - 3\('\)’ | Application |
| P180 | AAAAGGTACCGTAGGCGAAATTCAAATGTACG | Amplification of \textit{ireu\_1750} and addition of \textit{KpnI} site |
| P181 | GATATAAAATCGAGCTGGGCAC | Amplification of \textit{ireu\_1750} |
| P182 | ATGACTCTATTCAAGGGAATTG | Control of pNZ7748 |
| LR0062F-BHI | TGACGGATCTAACACACAATCAGCGAGCAATTG | Amplification of internal fragment of putative pocR, addition of \textit{BamHI} site and translational stop codon |
| LR0062R-ERI | TGACGAATTCGCGTCTGATTCTATATGTGATTC | Amplification of internal fragment of putative pocR and addition of \textit{EcoRI} site |
| LR0062 FL F | CGCTTTATCCCTAATTTGGTACG | Amplification of wild-type pocR gene and natural promoter |
| LR0062 FL R | GCTTTATCCCAATTTTCGAGCA | Amplification of wild-type pocR gene and natural promoter |

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\(^2\)L. \textit{reuteri} JCM1112 was previously described in 2011 [22]. Indeed, it was identified as a human isolate [1].
and inserted into pORI28 by directional cloning using standard techniques [24]. The resulting insertion mutant was designated 6475::pocR.

**Complementation of L. reuteri 6475::pocR**

An E. coli–L. reuteri shuttle vector (pJKS100) was constructed by combining an L. reuteri replicon from pLEM5 [28], the chloramphenicol resistance gene (Cmr) from pVE6007 [27], the L. lactis promoter (P23) [29], and the pUC origin and multiple cloning site (MCS) from pCR®2.1 (Invitrogen, Carlsbad, CA). Each fragment was PCR amplified from their respective template, restriction enzyme digested and subsequently ligated to generate the final shuttle-vector, pJKS100. To create the complementation vector for 6475::pocR, the L. reuteri 6475 pocR gene with its natural promoter was PCR-amplified from genomic DNA using LR0062 FL F and LR0062 FL R primers and cloned into pJKS100 using standard techniques [24]. Both constructs, pJKS100 and pJKS101, were electroporated separately into L. reuteri 6475::pocR as previously described [25].

**Fermentation conditions and substrate and product analysis**

The physiological effects of the overexpression of lur_1750 were studied in pH-controlled batch cultivations of L. reuteri pNZ7748 (lreu_1750 overexpression) and L. reuteri pNZ7021 (empty plasmid) in CDM in the presence or absence of glycerol carried out as described previously [14]. At different time points, samples were taken for transcriptome, supernatant and vitamin B12 analysis (Figure 2). We determined the extracellular concentration of main fermentation substrates and products by HPLC, as described elsewhere [6,30].

The comparison between the insertion mutant, 6475::pocR, and its parent strain was established in batch fermentations of LDMIIIG or MRS carried out in an anaerobic chamber (80% N2, 10% H2, and 10% CO2; Microbiology International). Transcriptome comparisons were carried out at the end of the fermentation when biomass concentration became stable.

**Vitamin B12 and reuterin determination**

Vitamin B12 levels were determined as described in the Official methods of analysis of AOAC International [31], using a bioassay with L. delbrueckii subsp. lactis ATCC 7830 as the indicator strain. Reuterin production was measured with a bioassay and carried out as previously described [5].

**Transcriptome analyses**

- **Transcriptional analysis of the putative PocR overexpression mutant**

  The transcriptome of cells transformed with pNZ7748 (lreu_1750 overexpression) and pNZ7021 (empty plasmid) were compared using cDNA microarrays as previously detailed [14] using a hybridization scheme comprising 17 arrays in a loop-design. The following samples were hybridized per array labeled with cyanine3 and cyanine5, respectively: sta-F6 and sta-F5, sta-F7 and sta-F8, sta-F5 and sta-F7, sta-F8 and sta-F6, sta-F4 and sta-F1 and sta-F3, sta-F2 and sta-F1, sta-F4 and sta-F2, exp-F3 and exp-F4, exp-F1 and exp-F3, exp-F2 and exp-F1, exp-F4 and exp-F2, exp-F4 and sta-F4, sta-F3 and exp-F3, sta-F2 and sta-F8, sta-F4 and sta-F6, exp-F2 and sta-F2. Here, F1 and F5 represent completely independent biological duplicates of L. reuteri pNZ7021 cultured in the absence of glycerol; F2 and F6 represent completely independent biological duplicates of L. reuteri pNZ7748 cultured in the absence of glycerol; F3 and F7 represent completely independent biological duplicates of L. reuteri pNZ7021 cultured in the presence of glycerol; and F4 and F8 represent completely independent biological duplicates of L. reuteri pNZ7748 cultured in the presence of glycerol. The prefix exp- and sta- stand for cells harvested at mid-logarithmic and early-stationary growth phases, respectively. The custom probe design of the Agilent 11 K microarray platform (Agilent Technologies, Santa Clara, CA, USA) used is available at the Gene Expression Omnibus http://www.ncbi.nlm.nih.gov/geo under accession number GPL6856, and the data obtained were deposited in the same repository under accession number GSE13289.

- **Transcriptional analysis of the putative PocR insertion mutant**

  The transcriptome of the insertion mutant, 6475::pocR, and its parent strain were compared using two-color microarrays as previously detailed [32]. Briefly, oligonucleotides (60-mers) were designed and synthesized for 1,966 open reading frames from a draft genome sequence of L. reuteri ATCC PTA 6475 [1]. For expression analyses, three biological replicates of the insertion mutant and parent strain were compared. Moreover, dye-swap hybridization was performed for each comparison. Following mRNA isolation [32], cDNA synthesis, labeling, and hybridization were performed as previously described [32]. Information regarding the microarray platform and data obtained is deposited at NCBI Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo) under GPL7541 and GSE22926, respectively.

  GenePix Pro 4.0.12 software was utilized for image analysis of the 6475 microarrays. Normalization within arrays and between arrays was performed by applying the Loess algorithm [33] using the Limma package [34] in R http://www.r-project.org. Normalized intensities were used for further analysis. The average signal intensities of three biological replicates were calculated in order to compare the relative gene expression of mutant and wild type strains. The statistical significance of
differences was calculated based on variation in biological duplicates, using the ebayes function in Limma (cross-probe variance estimation) and false discovery rate (FDR) adjustment of the \( p \)-values. Only genes that were differentially expressed by least 1.5-fold with FDR-adjusted \( p \)-values lower than 0.05 were considered significant.

**Additional material**

**Additional file 1: Transcriptome analysis data** Single PDF containing three tables with additional transcriptome analysis data: Additional file 1, Table S1, Complete list of transcripts from *L. reuteri* that are differentially expressed by the overexpression of *lreul_1750*; Additional file 1, Table S2, Distinct distribution of transcripts listed in Additional file 1, Table S1 throughout categories of clusters of orthologous groups (COG, [35]); Additional file 1, Table S3, Complete list of loci from *L. reuteri* ATCC PTA 6475 that are differentially expressed by the disruption of the putative PocR.

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**Authors’ contributions**

FS performed the phylogenetic analysis and all experiments related to the overexpression of PocR and measurement of vitamin B12 production, and wrote the first draft of the manuscript. JS constructed the PocR mutant and measured reuterin production and helped to draft the manuscript. DS performed the purification and cDNA microarrays related to the PocR mutant and helped to draft the manuscript. DM supervised the statistical analysis and interpretation of the cDNA microarrays related to the PocR overexpression. BT supervised the interpretation of the fermentation data. WW helped in the design and supervision of the PocR overexpression experiments and helped to draft the manuscript. JV helped in the design and supervision of the PocR deletion experiments and helped to draft the manuscript. JH conceived the study, participated in its coordination and supervision of the PocR deletion experiments and helped to draft the manuscript. All authors read and approved the final manuscript.

**Competing interests**

The authors declare that they have no competing interests.

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