Type III secretion system expression in oxygen-limited 
Pseudomonas aeruginosa cultures is stimulated by isocitrate lyase activity

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1. Summary

Pseudomonas aeruginosa is an opportunistic human pathogen and a common cause of chronic infections in individuals with cystic fibrosis (CF). Oxygen limitation was recently reported to regulate the expression of a major virulence determinant in P. aeruginosa, the type III secretion system (T3SS). Here, we show that expression of the T3SS in oxygen-limited growth conditions is strongly dependent on the glyoxylate shunt enzyme, isocitrate lyase (ICL; encoded by aceA), which was previously shown to be highly expressed in CF isolates. ICL-dependent regulation of the T3SS did not alter the expression level of the master transcriptional regulator, ExsA, but did affect expression of the T3 structural proteins, effectors and regulators (ExsC, ExsD and ExsE). An aceA mutant displayed enhanced biofilm formation during anaerobic growth, which suggested that AceA-dependent modulation of type III secretion might impinge upon the RetS/LadS signalling pathways. Indeed, our data suggest that RetS is able to mediate some of its effects through AceA, as expression of aceA in trans partially restored T3SS expression in a retS mutant. Our findings indicate that AceA is a key player in the metabolic regulation of T3SS expression during oxygen-limited growth of P. aeruginosa. To the best of our knowledge, this is the first demonstration that the T3SS can be regulated by factors that do not affect ExsA expression levels.

2. Introduction

Pseudomonas aeruginosa is an opportunistic human pathogen and a major cause of chronic infections in individuals with cystic fibrosis (CF). P. aeruginosa expresses a highly regulated protein secretion machinery called the type III secretion system (T3SS), which translocates a specific subset of exotoxin effector proteins (ExoS or ExoU, ExoT and ExoY) directly into the host cell cytosol where they mediate their pathogenic effects [1–5]. The T3SS regulon consists of approximately 40 coordinately regulated genes which are arranged into five operons, encoding the needle complex, translocation apparatus and regulator proteins; the effectors and chaperones are encoded elsewhere on the genome [6]. Transcription of the regulon is directly coupled to secretion through a cascade of interactions involving ExsC, ExsD and ExsE, which ultimately impinge upon the master transcriptional activator of T3SS gene expression,
ExxS [6–10]. When the T3SS is inactive, ExxS and ExxC form a complex, allowing ExxD to bind to and sequester ExxS. When type III secretion (T3S) is induced (e.g. by host cell contact or low Ca²⁺ concentration, established triggers of secretion [6,11]), ExxS is exported through the secretion machinery. This allows ExxC to bind ExxD, liberating ExxS to initiate transcription of the T3SS genes [9,10,12–14].

In recent years, metabolism has been implicated in the regulation of exsA-dependent T3SS expression. Rietts & Mekalanos [15] showed that in metabolically unfavourable conditions, low Ca²⁺-induced exsS expression was disrupted in an aceE mutant (aceE encodes the E1 subunit of pyruvate dehydrogenase (PDH), which controls the flux of glycolytic carbon entering the tricarboxylic acid (TCA) cycle). The opposite effect was observed in mutants in the citrate synthases (gltA and prpC). Similarly, Dacheux and colleagues [16] showed that PDH mutants in the P. aeruginosa clinical CF isolate, CHA, were no longer able to induce exsA-dependent T3S or cytotoxicity against polymorphonuclear neutrophils in low Ca²⁺ conditions. (Note that in these early papers describing aceE mutants, the PDH-encoding gene was often denoted ‘aceA’. However, in the intervening years, the gene annotation has changed and this is not the same as the isocitrate lyase (ICL)-encoding aceA gene described in this work, which has not previously been reported to regulate T3S.)

Our previous work suggested that anaerobiosis plays a role in regulating T3SS expression in P. aeruginosa, which may be relevant in the oxygen-limited environment of chronic CF lung infections [17]. In support for this, T3SS expression and activity were recently shown to be upregulated when planktonic cultures were grown in low oxygen conditions [18]. Microaerobic (or ‘oxygen-limited’) respiration has been proposed as the dominant growth mode of P. aeruginosa in the CF lung and involves the use of three terminal oxidases: two cytochrome chb-type oxidases (Cbb3-1 and Cbb3-2) and a cyanide-insensitive oxidase, CI0 [19–21]. Denitrification, involving the use of alternative electron acceptors such as nitrate, has also been demonstrated to occur in these conditions [22]. Given the known link between metabolism and T3S in aerobic growth conditions [15,23], we hypothesized that the re-wiring of central metabolic fluxes during the transition from aerobic to oxygen-limited growth might also impact on T3SS expression in P. aeruginosa. In this report, we describe a major new metabolic input regulating oxygen-limited T3SS expression which may play a role in chronic CF lung infections.

3. Results

3.1. Type III secretion system expression and the glyoxylate shunt pathway in oxygen-limited conditions

One of the most significant central metabolic changes that accompany the onset of low oxygen conditions is the re-routing of carbon skeletons through the glyoxylate shunt pathway. This bypasses the CO₂-producing steps of the TCA cycle and therefore conserves carbon skeletons for anabolic consumption (figure 1a). In the glyoxylate shunt, isocitrate is cleaved by ICL into glyoxylate and succinate. The glyoxylate is condensed with acetyl-CoA to yield malate in a reaction catalysed by malate synthase (MS). This pathway is known to be strongly induced in P. aeruginosa during anaerobic growth and during growth on C₃-sources, such as acetate or fatty acids, as the sole carbon source [24–26]. The alternative catabolic fate of isocitrate is oxidative decarboxylation to yield α-ketoglutarate, a reaction catalysed by isocitrate dehydrogenase. Unlike most Gram-negative bacteria, P. aeruginosa contains two divergently transcribed isocitrate dehydrogenase-encoding genes; icd (PA2623) and idh (PA2624). Both genes are simultaneously expressed in P. aeruginosa in AGSY medium (H. G. Stickland & M. Welch 2009, unpublished data). The decision as to whether isocitrate is routed through the glyoxylate shunt or the oxidative decarboxylation steps of the TCA cycle is partly determined by AceK-dependent phosphorylation (and consequent inhibition) of isocitrate dehydrogenase [27].

In our previous work [9,10], we showed that aceA mutants disrupt T3S expression during aerobic growth [15,16]. We found that this was also the case during growth in oxygen-limited conditions (figure 1b). Interestingly, a mutant in aceS also showed greatly diminished PcrV expression, whereas a mutant in glcB (the next
enzyme along the glyoxylate shunt pathway) displayed essentially wild-type levels of expression. The aceK mutant also had lower PcrV expression (figure 1b). In Escherichia coli, aceK mutants are unable to grow on acetate as a sole carbon source, indicating that phosphorylation of isocitrate dehydrogenase is a prerequisite for redirection of flux through the glyoxylate shunt pathway [27]. Conversely, the icd–idh double mutant, in which isocitrate is forced through the glyoxylate shunt, displayed wild-type levels of PcrV expression. To further confirm this observation, we also analysed the transcriptional activity of pG (the T3SS operon encoding perGVH-popBD) in the icd–idh double mutant and found that it was comparable with wild-type (see the electronic supplementary material, figure S2a). Together, these data indicate that the branch point at which carbon skeletons are routed through either the oxidative decarboxylation steps of the TCA cycle or through the glyoxylate shunt plays a key role in regulating T3S during oxygen-limited growth.

3.2. Isocitrate lyase activity is necessary for optimal type III secretion system expression under oxygen-limited conditions

We next examined the link between T3S expression and the branchpoint of the TCA and glyoxylate cycles by assaying for aceA-encoded ICL and aceE-encoded PDH enzyme activities in the oxygen-limited cultures of the wild-type and each mutant (figure 2a,b, respectively). The aceE mutant exhibited low ICL activity, which was comparable with that assayed in the aceA mutant (figure 2a). Conversely, although PDH activity was negligible in the aceE mutant as expected, it was essentially unaffected (relative to the wild-type) in the aceA mutant (figure 2b). In addition, glcB-encoded MS activities in the aceA and aceE mutants were comparable with that of the wild-type (data not shown). It therefore seems possible that the diminished T3SS expression observed in the aceE mutant may in fact be because of its lower ICL activity in these growth conditions. The measured ICL activity in the aceK mutant was comparable with that in the wild-type, which was expected since ICL activity is not affected by AceK.

To verify that this effect was associated with the ICL (i.e. enzymatic) activity of the AceA protein, we examined whether the ICL inhibitors itaconic acid and 3-nitropropionic acid could phenotypically mimic the effects of an aceA mutation on the transcription of pS (encoding exoS, a T3 effector) and pG (the T3SS operon encoding perGVH-popBD) in the wild-type background. Indeed, addition of these compounds to oxygen-limited wild-type cultures resulted in a reduction in transcription of both pS (figure 2c(i)) and pG (figure 2c(ii)). In conclusion, these data suggest that in oxygen-limited growth conditions, aceA-encoded ICL activity is required for optimal T3S expression.

**Figure 2. Effect of ICL activity on T3SS expression.** Oxygen-limited planktonic cultures of PAO1 and the indicated TCA or glyoxylate cycle mutants (sampled at PE and PS) were analysed for (a) total isocitrate lyase (ICL) activity, and (b) total pyruvate dehydrogenase (PDH) activity. The ICL inhibitors itaconic acid (ITA) or 1 mM 3-nitropropionic acid (3NP); pMP220 acted as an empty plasmid control. *p < 0.05.
3.3. Type III secretion system expression in an aceA mutant under oxygen-limited conditions

We next analysed the expression of other T3SS-related gene products in an aceA mutant. In addition to PcrV, the expression of PopN (a regulator of the T3SS translocation process), ExoS (a T3 effector protein) and ExsD (a T3S regulator) was also greatly reduced in the aceA mutant (figure 3a).

Interestingly, although all of these proteins showed a diminished expression in the aceA mutant, some were affected more than others, suggesting that the loss of AceA differentially impacts on these T3SS components. Consistent with these observations, transcription of pS (encoding exoS) and pG (the T3SS operon encoding pcrGVH-popBD) was lower in the aceA mutant (figure 3b). We were also able to show that expression of aceA from a plasmid in trans could restore PcrV expression and ICL activity in the aceA mutant (figure 3c).

Given that the enzymatic activity of AceA was important for expression of the T3SS, we also tested whether the products of ICL activity might be accountable. However, when we supplemented oxygen-limited cultures of the aceA, aceE and aceK mutants with succinate or glyoxylate (or indeed with other TCA cycle intermediates, including citrate, isocitrate, α-ketoglutarate, fumarate and glycine (the transamination product of glyoxylate)), PcrV expression was not restored to wild-type levels (see the electronic supplementary material, figure S2b) despite (in some cases) improved growth in the presence of the additive.

3.4. Effect of an aceA mutation on exsA, exsC, exsD and exsE expression

Since the activity of more than one unlinked T3SS gene was depressed in an aceA mutant (figure 3a), it seemed probable that the master transcriptional regulator of T3SS expression, ExsA, might be involved. However, ExsA protein levels in the aceA mutant were found to be similar to wild-type (figure 4a). Furthermore, when exsA transcript levels were measured by reverse transcriptase (RT)–PCR in the oxygen-limited wild-type and aceA mutant cultures, they were found to be comparable (figure 4b(i)). Conversely, and in agreement with protein expression and transcriptional activity (figure 3ab, respectively), pcrV transcript levels were much lower in the aceA mutant at the exponential (PE) and stationary (PS) growth phases relative to wild-type (figure 4b(ii)). Note that T3 transcript levels were higher during PE oxygen-limited growth compared with PS, whereas the opposite was observed for protein expression. We speculate that
this may be because of the (as yet uncharacterized) post-transcriptional regulatory processes that impact upon the expression levels of T3SS proteins in the different growth phases.

The levels of ‘free’ ExsA in the cell are tightly controlled by a series of regulatory proteins, namely ExsC, ExsD and ExsE. RT–PCR revealed that the transcript levels for all three regulators were reduced in the aceA mutant at both growth phases relative to wild-type (figure 4(b)(i)). Notably, although ExsA levels remained unchanged in the aceA mutant, levels of exsD (which encodes an anti-activator of ExsA) mRNA (figure 4(b)(i)) and protein (figure 3(a)) were much lower in the mutant. Based on the current model in which expression of the T3SS is solely controlled by the level of free ExsA, a reduction in ExsD expression should give rise to enhanced expression of the T3SS proteins [9,10,12–14]. However, the opposite was observed. Clearly, the existing model is an over-simplification that does not account for the regulation of T3SS expression by metabolic inputs during oxygen-limited growth.

Consistent with the notion that oxygen limitation stimulates T3S, pcrV transcript levels were significantly higher in wild-type cultures grown under oxygen-limited conditions (figure 4(b)(ii)) than under aerobic conditions (figure 4(b)(i)) at both growth phases. Furthermore, no differences in T3 transcript levels were observed between the wild-type and aceA mutant under aerobic conditions (figure 4(b)(ii)), despite comparable growth (see the electronic supplementary material, figure S1b), suggesting that regulation by aceA is specific to oxygen-limited conditions.

3.5. Biofilm formation is enhanced in an aceA mutant and can be complemented by expression of aceA in trans

The CF lung has been demonstrated to be an oxygen-limited environment, where P. aeruginosa is thought to grow as biofilm-like aggregates [28]. Given our earlier findings suggesting that anaerobiosis-mediated T3SS expression occurred in biofilms [17], we next examined whether biofilm formation might be affected in the aceA, aceE, aceK, icd–idh and glcB mutants. Biofilm formation under anaerobic conditions was significantly enhanced in the aceA mutant as well as in the other mutants that showed reduced PcrV expression (figure 5a). Furthermore, the enhanced biofilm formation by the aceA mutant could be restored towards the wild-type situation by expression of aceA in trans from a plasmid (figure 5b). RT–PCR analysis of a transcript (pslA) encoding an enzyme involved in the biosynthesis of an extracellular polysaccharide associated with biofilm matrix formation, Psl, showed that the levels of pslA were increased in an aceA mutant at the exponential growth phase relative to wild-type (figure 5c). These results suggest that aceA can regulate biofilm formation by influencing psl expression.

Figure 4. Expression of the master T3 transcriptional regulator (exsA) and other T3S regulators (exsC, exsD and exsE) in an aceA mutant. The origin of diminished T3SS expression in the aceA mutant was investigated: (a) ExsA protein expression in PAO1 and an aceA mutant in oxygen-limited conditions (sampled at PE and PS), as determined by Western blot analysis; (b) RT–PCR analysis of T3SS gene transcripts in PAO1 and aceA: total RNA was isolated from cultures grown under (i) oxygen-limited or (ii) aerobic conditions at PE and PS. 16S rRNA (16S) transcript levels indicate equal loading. Samples lacking RT show that no DNA contamination was present.
3.6. Expression of aceA partially bypasses the type III secretion defect in a retS mutant

The inverse relationship between biofilm formation and T3S in the aceA mutant was reminiscent of the phenotype associated with a retS mutation. Furthermore, Hagins et al. [29] previously reported that aceA transcription is repressed in a retS mutant. We therefore investigated whether AceA might contribute towards the retS phenotype.

As a first step, we confirmed that the RetS signalling pathway was also necessary for the reciprocal regulation of T3SS expression and biofilm formation in oxygen-limited conditions (see the electronic supplementary material, figure S3a,b). This was indeed the case. Note that in contrast to the situation in the aceA mutant, cyaA transcript levels (as well as the transcript levels for cysC, cysD and cysE) were lower in a retS mutant relative to wild-type (see the electronic supplementary material, figure S3b; cf. figure 4b(i)).

ICL activity was found to be depressed in a retS mutant (figure 6a). Furthermore, expression of aceA from a plasmid in trans led to partial complementation of ICL activity and PcrV expression in the retS mutant (figure 6b). These observations indicate that the T3S defect associated with a retS mutant could be at least in part attributed to the lower aceA activity. To determine if retS may affect T3SS by modulating aceA expression, RT–PCR analysis was carried out. However, and in contrast to the results of Hagins et al. [29], who studied aceA expression levels in aerobically grown cultures, aceA transcript levels in oxygen-limited cultures of the retS mutant were found to be similar to those in the wild-type (figure 6c). Therefore, the depressed ICL activity associated with the retS mutant in oxygen-limited conditions is because of post-transcriptional effects.

T3SS expression and biofilm formation are reciprocally regulated by the RetS/LadS signalling pathways through a complex mechanism involving the GacS/GacA two-component system, the small regulator RNAs RsmZ and RsmY, and the translational repressor RsmA [30–34]. Activation of LadS (or reduced expression of RetS) results in the formation of GacS
homodimers, which leads to the phosphorylation and activation of GacA and concomitant production of rsmZ and rsmY. These small RNAs bind to and sequester RsmA, which in turn leads to the activation of biofilm formation [32,33]. Conversely, when RetS is activated, it forms heterodimers with GacS, thus preventing stimulation of the GacA/GacS signalling pathways. Free RsmA binds to and influences the stability of specific mRNA targets, which indirectly leads to the activation of exsA-dependent T3SS expression [33].

RT–PCR was used to assess whether the expression level of retS, or other components of the signalling pathway were affected in the aceA mutant (figure 7). Transcript levels for gacA, gacS and rsmA were all similar between the wild-type and the aceA mutant. Transcript levels for retS and ladS appeared to be higher in the aceA mutant during the exponential phase (PE) of growth. This may indicate that some sort of feedback mechanism is in action, perhaps compensating for the lower T3SS expression in the aceA mutant. However, it is also possible that the increased expression of retS in this mutant may be cancelled out by the concomitantly increased expression of ladS.

Consistent with the central role played by RsmA in regulating T3S, an rsmA mutant displayed reduced PcrV expression relative to the wild-type (see the electronic supplementary material, figure S3a(iii)). However, and unlike the retS mutant, when aceA was expressed in trans in the rsmA mutant, only a marginal increase in PcrV expression was observed (figure 7b(i)). In contrast, the low level of PcrV expression in the aceA mutant could be complemented by expressing rsmA from a plasmid in trans (figure 7b(ii)). Taken together, these data indicate that AceA primarily exerts its effect(s) on T3S downstream of RetS but upstream of RsmA.

### 4. Discussion

Recent studies indicate that T3SS expression in *P. aeruginosa* is activated upon exposure to low oxygen conditions [17,18]. In the present report, we show that an enzyme involved in anaerobic metabolism, ICL (encoded by aceA), plays an important role in ensuring optimal T3SS expression under these growth conditions. Loss of aceA function had no effect during aerobic growth. An aceA mutant also displayed enhanced biofilm formation during anaerobic growth, which suggested that AceA might modulate these activities through the RetS/LadS signalling pathways. Indeed, expression of aceA in trans was able to partially complement T3SS expression in a retS mutant. In contrast, expression of aceA in trans did not substantially restore PcrV expression in an rsmA mutant. This suggests that AceA primarily impinges upon T3S upstream of RsmA, and is necessary for maximal T3SS expression when the RetS signalling pathway is activated in oxygen-limited conditions.

Our results provide further insight into the link between central carbon metabolism and T3SS expression, as previously reported by Rietisch & Mekalanos [15]. However, the mainstream model for T3SS regulation posits that control is primarily achieved through modulation of exsA expression (ExsA is the master T3 transcriptional regulator). In contradiction with this model, we found that protein and transcript levels of ExsA were unaffected in the aceA mutant, in spite of the severely reduced level of T3SS protein expression. Moreover, the expression of ExsD (an anti-activator of T3SS expression) was decreased in the aceA mutant. ExsD is thought to act by binding/sequestering ExsA, so this lower expression of ExsD should increase the level of ‘free’ ExsA and concomitantly increase T3SS expression. Since the opposite was observed, it seems that under oxygen-limiting growth conditions, metabolic regulation of the T3SS involves more than simple modulation of free ExsA levels.

aceA (PA2634) is a monocistronic gene of the glyoxylate shunt pathway and is the only ICL-encoding gene in *P. aeruginosa* PAO1 [35,36]. ICL expression is stimulated during growth in oxygen-limiting conditions, and, consistent with the anaerobic nature of the CF lung, the enzyme was found to be highly expressed in *P. aeruginosa* isolates from
chronically infected CF individuals [24,25,29,37]. Although its primary function in *P. aeruginosa* is carbon catabolism, recent evidence suggests that ICL can also have an impact on pathogenesis [36–38]. For example, in the mucoid *P. aeruginosa* CF isolate, FRD1, increased ICL activity was directly linked to the production of a precursor metabolite (glycine) of hydrogen cyanide (HCN), a poison and potent inhibitor of cytochrome c oxidase and other metalloenzymes, including nitrite reductase and superoxide dismutase [38,39]. However, as far as we are aware, no previous workers have reported that ICL impinges upon T3SS expression in any organism. Moreover, and unlike many other known modulators of T3SS expression, the regulatory effect of AceA was not routed through the control of *exsA* expression levels. Concomitant with the diminished T3SS expression in the *aceA* mutant, we also observed that this strain exhibited enhanced biofilm formation in oxygen-limited conditions. We previously reported that the T3SS is expressed in PA01 biofilms, and that this expression correlated with the expression of genes involved in anaerobic respiration [17,40]. We therefore speculate that ICL may play a role in regulating T3SS expression during the development of oxygen-limited conditions inside biofilms.

Our data indicate that regulation by *aceA* may be mediated through the RetS/LadS signalling pathways. O'Callaghan *et al*. [18] recently presented data showing that the T3SS was activated during oxygen-limited growth in LB medium, and suggested a model implicating components of the same signalling pathways. These authors proposed that oxygen limitation is sensed by Anr (anaerobic regulator), which stimulates the expression of narL of the NarL/NarX two-component system regulating denitrification and arginine fermentation. In turn, NarL represses expression of the RsmA-antagonistic RNAs, rsmY and rsmZ. The lower levels of rsmY/Z lead to a higher concentration of free RsmA, which indirectly leads to the stimulation of *exsA*-dependent T3SS expression. However, we found that AceA-dependent regulation of T3S did not involve changes in ExsA transcript or protein levels. Furthermore, in oxygen-limited AGSY media, PcrV expression in a *narL* mutant was comparable with that in the wild-type (J. C. S. Chung & M. Welch, unpublished data). Lastly, in oxygen-limited conditions, the T3S defect associated with a *retS* mutant could be at least partially attributed to the lower ICL activity in this genetic background, since the *retS* T3S phenotype could be bypassed (in proportion with the degree of restoration of ICL activity) by expression of *aceA* in trans. Interestingly, in spite of the expression of *aceA* from a multicopy plasmid, we were never able to completely restore PcrV expression or ICL activity to wild-type levels in the *retS* mutant. In addition, and considering that *aceA* transcript levels were unaffected (relative to the wild-type) in the *retS* mutant, these data indicate either that ICL activity is silenced in the absence of RetS signalling, or that translation of the *aceA* transcript is suppressed.

At this stage, we can only speculate on the mechanism(s) by which AceA might impact upon T3SS expression. Some possibilities are outlined in figure 8. Our data indicate that during anaerobic growth conditions, AceA impinges on the signalling pathway at some point between RetS and RsmA, so these proteins (and/or GacA/GacS or the small RNAs, rsmY/Z) could directly interact with AceA. However, and mitigating against a direct protein–protein or protein–RNA interaction is the observation that it is ICL activity (rather than the presence of the AceA protein *per se*) that is necessary for optimal T3SS expression. Another possibility is that ICL activity may directly or indirectly alter the abundance of one or more metabolites which affect T3SS expression (e.g. through allosteric interactions). If so, the identity of these low molecular weight effectors remains unknown. Alternatively, mutation of *aceA* could lead to large-scale metabolic perturbations that indirectly impact on the T3SS. We feel that this is unlikely because the *aceA* mutant did not display a growth defect (compared with the wild-type) as might be expected if its fitness was impaired by global metabolic ‘rewiring’. Consistent with this, gas chromatography–mass spectrometry profiling of the *aceA* mutant and the wild-type failed to reveal any significant differences in the resolved metabolites (data not shown). Finally, and although ExsA expression was unaffected in the *aceA* mutant, it remains formally possible that AceA (or an AceA-dependent metabolite) may modulate ExsA activity (i.e. its ability to bind T3S promoters or regulatory proteins) through post-translational effects. Post-translational modification of ExsA may be a means to temporally modulate T3S activity such that it becomes integrally linked to the metabolic state of the cell. In this regard, we note that enzyme-catalysed lysine acetylation has recently been shown to regulate the activity of many bacterial proteins, including ICL [41]. Moreover, an activated acetate metabolite (acetyl phosphate) has been implicated in regulation of the T3SS-encoding SPI-1 pathogenicity island in *Salmonella* [42].

In summary, we have demonstrated that the re-routing of metabolic flux through the glyoxylate shunt plays a key role in regulating T3SS expression in oxygen-limited growth conditions. Notably, ICL-dependent metabolic control was found to key into the RetS signalling pathway. This T3S induction by ICL probably contributes to the T3S observed in *P. aeruginosa* biofilms [17,40] and, furthermore, may play an important role during chronic *P. aeruginosa* infections in the CF lung. Future work will focus on understanding the detailed mechanism by which AceA affects T3SS expression during oxygen limitation.

### 5. Material and methods

#### 5.1. Bacterial strains, plasmids and growth conditions

Bacterial strains and plasmids used in this study are listed in the electronic supplementary material, table S1. *Pseudomonas*
**5.2. Strain and plasmid construction**

The \( \Delta icd-\Delta idh \) mutant was generated by marker exchange in PAO1. The marker exchange construct was produced by overlap PCR, fusing the 500 bp region upstream of \( icd \) (icd500) with the 500 bp region downstream of \( idh \) (idh500). The resulting construct was digested with BamHI and EcoRI and cloned into pUCP20 to generate pJC3. Ndel–SpeI restriction sites were incorporated between the two fragments to allow the insertion of a gentamicin resistance cassette (a 1 kb fragment containing the disrupted icd–idh operons, \( 15 \mu g \text{ ml}^{-1} \) Tc, \( 50 \mu g \text{ ml}^{-1} \) Cb, \( 10 \mu g \text{ ml}^{-1} \) Gm or \( 50 \mu g \text{ ml}^{-1} \) kanamycin) for \( E. coli \).

**5.3. Western blot analysis**

Whole-cell lysates from planktonic cultures were prepared by normalizing cell pellets to the same OD\text{600} using TE lysis buffer (50 mM Tris, 4 mM EDTA, pH 8.3) and vortexing vigorously. This method was found to yield equivalent protein concentrations across different samples. Whole-cell lysates (20 \( \mu l \)) were separated on 12 per cent sodium dodecyl sulfate–polyacrylamide gels, transferred to polyvinylidene fluoride membrane and analysed by Western blotting. Enhanced chemiluminescence peroxidase labelled anti-rabbit or anti-guinea pig antibodies (Sigma) were used as secondary antibodies. Blots were developed using Immobilon Western Chemiluminescent HRP Substrate (Millipore). All Western analyses were repeated on independent cultures at least three times. Representative results are shown.

**5.4. β-Galactosidase assay**

β-Galactosidase activity was measured essentially as described by Miller [46]. Briefly, cells were permeabilized by treatment with toluene in Z-buffer (60 mM Na\(_2\)HPO\(_4\), 40 mM NaH\(_2\)PO\(_4\), 10 mM KCl, 1 mM MgSO\(_4\), 7H\(_2\)O, 50 mM \( \beta \)-mercaptoethanol), β-Galactosidase activity was measured by incubating diluted toluenized cell suspension with 4 mg ml\(^{-1} \) O-nitrophenyl-β-galactoside (ONPG) at 37°C and monitoring the change in absorbance at 420 nm. Miller units are defined as \( \Delta OD_{420} \text{ min}^{-1} \text{ ml}^{-1} \text{ OD}_{660} \). All β-galactosidase assays were repeated on independent cultures at least thrice.

**5.5. Isocitrate lyase activity**

ICL activity was assayed based on the method of Diehl & McFadden [47]. Total intracellular proteins were prepared by resuspending cell pellets in TE lysis buffer (50 mM Tris–HCl, 4 mM EDTA, pH 8.3) followed by sonication of the cell suspension and centrifugation at 10,000g for 15 min at 4°C to remove cell debris. ICL activity was determined by incubating 50 \( \mu g \) protein extract in ICL buffer (50 mM MOPS, 5 mM MgCl\(_2\), 1 mM DTT, 0.1% (v/v) phenyl-hydrazine, 1 mM isocitrate, pH 7.3) for 10 min at 37°C. The reaction was stopped by adding 0.45 ml of concentrated HCl. Potassium ferricyanide (0.25% w/v) was then added to the mixture and incubated at room temperature for 10 min. Glyoxylate production was measured as a colorimetric change at 520 nm, which occurs because of the reaction of ferricyanide with the phenylhydrazone of glyoxylate.

**5.6. Pyruvate dehydrogenase activity**

PDH activity was assayed according to Bourguignon et al. [48]. Briefly, 100 \( \mu g \) protein extract was incubated at 30°C in PDH buffer (5 mM MgCl\(_2\), 0.2 mM CoASH, 0.5 mM thiamine pyrophosphate, 2 mM \( 3\text{-acetylpyridine} \text{ adenine dinucleotide (APADH) } \), 2 mM DTT, 15 mM sodium pyruvate, 30 mM potassium phosphate, pH 7) and the formation of APADH (the reduced form) was measured by monitoring the absorbance at 366 nm.

**5.7. Biofilm attachment assay**

For biofilm attachment in aerobic conditions, cells seeded in static 96-well polystyrene microtitre plates were incubated at 37°C for 24 h. For biofilm attachment in anaerobic
conditions, plates were incubated in an Anaerogen jar (Oxoid) at 37 °C for 3 days. Following incubation, culture supernatant and non-adherent cells were removed and the wells were washed once with 300 μL water. Attached cells were stained for 30 min with 0.1% (w/v) crystal violet. The stained plates were rinsed thrice with water and the adsorbed dye was released by adding 50% (v/v) ethanol. Attachment was quantified by measuring absorbance at 595 nm.

5.8. Total RNA isolation and reverse transcriptase–PCR

Cells were collected in RNAlater solution (Ambion) and incubated on ice for 1 h before sedimentation by centrifugation at 3200g for 15 min, 4 °C. Cell pellets were incubated in 1 mg ml⁻¹ lysosome for 15 min at room temperature and total RNA was extracted using the RNeasy Mini kit (Qiagen) according to the manufacturer’s instructions. The resulting RNA (200 ng) was used as a template for reverse transcription and conversion into cDNA. PCR reactions were prepared with 5 μl of diluted cDNA (1:5 in water) as a template and primers specific to the specified genes. All RT–PCR analyses were carried out on samples from at least three independent cultures. Representative results are shown.

5.9. Statistical analysis

Statistical analyses were performed using the Student’s t-test based on three independent replicates. A p-value <0.05 was considered as statistically significant.

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