Mini-Review

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A pivotal role for the response regulator DegU in controlling multicellular behaviour

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Bacteria control multicellular behavioural responses, including biofilm formation and swarming motility, by integrating environmental cues through a complex regulatory network. Heterogeneous gene expression within an otherwise isogenic cell population allows for differentiation of cell fate and adds to the complexity of multicellular behaviour. This review focuses on recent data about how DegU, a pleiotropic response regulator, co-ordinates multicellular behaviour in Bacillus subtilis. We review studies that challenge the conventional understanding of the molecular mechanisms underpinning the DegU regulatory system and others that describe novel targets of DegU during activation of biofilm formation by B. subtilis. We also discuss a novel role for DegU in regulating multicellular processes in the food-borne pathogen Listeria monocytogenes.

Multicellular behaviour in single-celled prokaryotes

It is easy to forget that when bacteria are grown in the laboratory the conditions used to generate such rapidly dividing free-living cells are very different from those in the natural environment. Most bacteria exist in their natural habitats as sessile multicellular communities called biofilms in which the bacterial population differentiates as part of the development process (Costerton et al., 1995; Vlamakis et al., 2008). That most bacterial species can live and grow within a shared habitat, and co-ordinate complex group behaviour that benefits the whole community, is still a relatively new concept (Shapiro, 1998). Examples of such behaviour leading to the propagation of bacterial spores include fruiting body formation in Myxococcus xanthus (Kaplan, 2003), biofilm formation and fruiting-body-like assembly in Bacillus subtilis (Branda et al., 2001) and aerial hyphae development in Streptomyces coelicolor (Claessen et al., 2006).

Experimental advances provide insight into multicellular behaviour

B. subtilis, like other bacterial species, is capable of manifesting different multicellular processes. Studies have focussed on understanding how this species is able to co-ordinate processes that include sporulation (Piggot & Hilbert, 2004), the uptake of exogenous DNA (genetic competence) (Hamoen et al., 2003), social motility (swarming) (Kearns & Losick, 2003), extracellular protease production (Dahl et al., 1992), and biofilm formation/complex colony development (Branda et al., 2001; Hamon & Lazazzera, 2001). Investigations on multicellular behaviour in B. subtilis have advanced through three main approaches. First, investigations using ‘wild’ isolates led to the discovery that laboratory strains had lost their ability to express some of the multicellular behaviours described above (Branda et al., 2001; Kearns & Losick, 2003; Stanley & Lazazzera, 2005). B. subtilis laboratory isolates such as 168 (Spizizen, 1958) were derived from a progenitor strain that was treated with X-rays or chemical mutagens to make the cells more tractable (Srivatsan et al., 2008; Zeigler et al., 2008). The genes in which the mutations were introduced are now recognized as important for social behaviour and their identification helped to elucidate the genetic circuitry underpinning multicellular responses to the environment (Kearns & Losick, 2003, 2005; Kearns et al., 2004; Stanley & Lazazzera, 2005). Second, developments in the use of fluorescent reporter fusions enabled gene expression to be monitored readily within the single cell by flow cytometry. Third, advances in microscopy techniques allow the detection of cell differentiation in an otherwise isogenic bacterial population (Veening et al., 2004, 2005; Vlamakis et al., 2008).

Co-ordination of multicellular behaviour processes by DegS–DegU

Two-component signal transduction systems are the major family of signalling proteins by which bacteria sense and respond to changes in the environment. They typically consist of a membrane-associated histidine kinase (DegS) and a cytoplasmic response regulator (DegU). The former detects the signal or stress, whereas the latter controls cellular response, predominantly through gene transcription (Mascher et al., 2006). DegU plays a key role in
regulating post-exponential-phase processes in *B. subtilis*, including activation and inhibition of genetic competence (Dubnau *et al.*, 1994; Kunst *et al.*, 1994; Ogura & Tanaka, 1996), activation and inhibition of motility (Amati *et al.*, 2004; Kobayashi, 2007; Verhamme *et al.*, 2007), activation of degradative enzyme production (Dahl *et al.*, 1992; Msadek *et al.*, 1990), activation of poly-γ-glutamic acid production (Stanley & Lazazzera, 2005) and also the activation and inhibition of biofilm formation (Kobayashi, 2007; Verhamme *et al.*, 2007). DegU has regulatory activity in both its unphosphorylated and phosphorylated states. This initially led to its designation as a ‘molecular switch’ dependent on DegU phosphorylation by DegS (Dahl *et al.*, 1992). However, recent studies using wild isolates of *B. subtilis* indicate that DegU~P functions as a ‘rheostat’ that senses and responds to changes in the environment. This, in turn, enables the integration of genetic competence, swarming motility, biofilm formation and exoprotease production along an increasing gradient of DegU phosphorylation (Kobayashi, 2007; Verhamme *et al.*, 2007).

**Mechanism of DegU and DegU~P in response to signalling**

In its unphosphorylated state DegU activates genetic competence through the recruitment of ComK (Hamoen *et al.*, 2000). ComK functions as an anti-repressor for the transcriptional repressors Rok and CodY, and thereby allows the expression of its own gene. This permits the establishment of the bistable system pre-required for competence development (Albano *et al.*, 2005; Smits *et al.*, 2007). In contrast, DegU~P recruits RNA polymerase at promoter regions of genes such as *yveA* and *aprE* to activate biofilm formation and exoprotease production respectively (Ogura *et al.*, 2003; Verhamme *et al.*, 2007). Recent genome-wide transcription and proteomic studies have identified over 170 genes (~4% of the *B. subtilis* genome) that are regulated by DegU~P under various growth conditions (Kobayashi, 2007; Mader *et al.*, 2002; Ogura *et al.*, 2001). Therefore the mechanism by which DegU~P coordinates multicellular behaviour processes in response to signal perception is challenging. One simple model supported by *in vitro* data indicates that DegU~P has specific affinities for different promoter regions. For example, the *flgB* promoter has a higher affinity for DegU~P than the *sacB* promoter. This provides the molecular basis by which swarming motility could be activated prior to other multicellular processes (Kobayashi, 2007; Tsukahara & Ogura, 2008). Variations in promoter binding affinities by transcription factors may represent a common mechanism mediating control over multicellular behaviour responses. High- and low-affinity binding sites in *B. subtilis* are used within the promoter regions of genes controlled by Spo0A. At low levels of Spo0A phosphorylation, biofilm formation and cannibalism are regulated. In contrast, the activation of sporulation occurs at high levels of Spo0A phosphorylation (Fujita *et al.*, 2005). However, the question arises: Why does a process that is activated at lower levels of signal perception not occur in the presence of a high level of the signal? The first possibility is that when low-affinity promoters are triggered, a negative feedback loop blocks the process that is controlled by the high-affinity promoters. Second, the promoter regions contain multiple binding sites, with specific affinities, that result in the activation of transcription at low levels of signal perception but inhibition of transcription at high levels of signal. Third, multiple environmental conditions need to be sensed and integrated by the cell to activate a physiological response.

**A three-tiered regulatory system controls DegS–DegU activity**

Given the central role that DegS and DegU have in coordinating multicellular responses in *B. subtilis* it is not surprising that the DegS–DegU regulatory system is finely controlled at the following three stages within the cell: *degU* transcription, DegU phosphorylation and DegU~P activity.

**degU transcription**

The *degSU* operon contains three promoters (Veening *et al.*, 2008a; Yasumura *et al.*, 2008). The first is upstream of *degS* and drives the expression of *degS* and *degU*. The second is located within the coding region of *degS* and increases the level of *degU* under nitrogen-limiting conditions. The third is located in the *degS–degU* intergen region and increases the level of *degU* in response to DegU~P. In laboratory isolates, the positive auto-regulation of *degU* transcription (Fig. 1) by DegU~P leads to the heterogeneous expression of *degU* within the population (Veening *et al.*, 2008a, b).

**DegU phosphorylation**

DegS is a cytoplasmic bifunctional protein that exhibits kinase and phosphatase activities (Tanaka *et al.*, 1991). DegS interacts with the SMC–ScpA–ScpB complex, which controls DNA condensation and repair. The interaction of DegS with ScpA inhibits its kinase activity and results in a decrease in the pool of DegU~P within the cell. As the level of SMC–ScpA–ScpB complex decreases during stationary phase there is an increase in the level of DegU~P in that growth phase (Dervyn *et al.*, 2004). Transfer of the phosphate moiety from DegS to DegU (Fig. 1) is enhanced in the presence of DegQ, a small protein of 46 amino acids (Kobayashi, 2007). Some laboratory isolates of *B. subtilis* contain a point mutation within the promoter of *degQ* that reduces the level of DegQ synthesized (Stanley & Lazazzera, 2005); this in turn, reduces the level of DegU~P in the cell (Kobayashi, 2007; Stanley & Lazazzera, 2005; Verhamme *et al.*, 2007). This single point mutation highlights one of the key genomic differences between wild and laboratory isolates of *B. subtilis* that influences multicellular behaviour (Kears *et al.*, 2004; Kobayashi, 2008; Stanley & Lazazzera, 2005). Transcription of *degQ* is regulated by the quorum-sensing-responsive transcription factor ComA (Msadek *et al.*, 1991). This ensures that DegU~P in the cell increases alongside an increase in cell density and is maximal at
DegU~P activity

The response regulator aspartyl phosphatase (Rap) RapG binds to DegU, without affecting the latter’s phosphorylation status. This suggests that RapG inhibits the ability of DegU to bind to target promoter DNA (Ogura et al., 2003). RapG is encoded in an operon with PhrG, a phosphatase regulator (Phr). Although rapG and phrG share a common promoter upstream of rapG, the transcription of phrG is also activated by a σH-dependent promoter on entry to stationary phase (Britton et al., 2002). At high levels of PhrG production, PhrG interacts with RapG, lessening RapG inhibition of DegU activity. As the RapG–PhrG system functions as a quorum-sensing system (Fig. 1), DegU~P activity increases in parallel with an increase in cell density (Lazazzera et al., 1999; Ogura et al., 2003).

New roles for DegU activity in *B. subtilis* during biofilm formation

DegU was first identified as a positive regulator of biofilm formation in a study using *B. subtilis* isolate RO-FF1.
are activated by DegU~P are known. The first is poly-
(Stanley & Lazazzera, 2005). Currently, three targets that
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population of cells in which
the same study it also was demonstrated that a small
matrix production or sporulation (Chai et al., 2008; Verhamme et al., 2009). YvcA is a putative membrane-bound lipoprotein
required for complex colony development in NCIB 3610 but not for pellicle formation in ATCC 6051 (Kobayashi, 2007; Verhamme et al., 2008). A complex genetic circuit that is dependent on activation of DegU and Spo0A ensuring yvcA and yuaB transcription during complex colony development in B. subtilis NCIB 3610 has recently been described (Verhamme et al., 2008).

**Heterogeneous degU expression and exoprotease production**

During biofilm formation by B. subtilis, cells differentiate into specific subpopulations that become responsible for matrix production or sporulation (Chai et al., 2008; Vlamakis et al., 2008). This finding suggests that biofilm matrix production altruistically benefits the entire population/community, not just the producer cells. During heterogeneous gene expression, threshold levels of a key regulator controlling cell state need to be attained. This can be mediated by a positive feedback loop at the transcription stage (Losick & Desplan, 2008). Intriguingly it was recently reported that while degU transcription is auto-activated it is not sufficient to generate heterogeneous expression in wild-type laboratory isolates. However, when genetic manipulations are used to increase the level of DegU~P, a distinct bistable population was observed (Veening et al., 2008a). In the same study it also was demonstrated that a small population of cells in which aprE, the gene encoding the major exoprotease of B. subtilis, is copiously transcribed can be established (Veening et al., 2008a). Two criteria must be met for this to happen in the small subset of cells. First, Spo0A~P levels must increase to a threshold that stimulates derepression of aprE transcription (but not to such a level that the cells sporulate). Second, the levels of DegU~P in the cell must be high. This dual requirement of DegU and Spo0A activation as part of a genetic logic-AND network might represent a common mechanism for co-ordinating entry into the different multicellular behavioural processes of B. subtilis (Veening et al., 2008a, b; Verhamme et al., 2008). It remains to be seen whether intracellular fluctuations of phosphorylated DegU and Spo0A combined with intrinsic differences in promoter binding affinities coordinate the different multicellular behavioural processes manifested by B. subtilis.

**Motility and biofilm formation regulation by DegU in L. monocytogenes**

The role of DegU in co-ordinating multicellular behaviour is not restricted to B. subtilis. *Listeria monocytogenes* is a Gram-positive facultative intracellular pathogen that causes listeriosis. DegU (encoded by *Imo2515*) regulates motility, biofilm formation and virulence in *Listeria* species (Guerriri et al., 2008b; Knudsen et al., 2004; Williams et al., 2005a, b). The genome sequences of the pathogenic strain *L. monocytogenes* EGD-e and non-pathogenic strain *L. innoca* are remarkably similar to that of *B. subtilis* (Glaser et al., 2001). However, in the region surrounding degU, the degS homologue is conspicuously absent despite other major genome features being maintained (Guerriri et al., 2008b; Knudsen et al., 2004). The absence of degS appears to be specific to the *Listeria* species (Fig. 2), although further evolutionary analyses are needed to establish whether degS has been lost from *Listeria* or gained by *Bacillus* (Guerriri et al., 2008b).

Biofilm formation by *L. monocytogenes* is dependent on flagellar motility to propel the cells towards a surface prior to attachment (Lemon et al., 2007). DegU was recently identified as a positive activator of flagellum biosynthesis (Knudsen et al., 2004; Williams et al., 2005a, b). When grown at ≤30 °C *L. monocytogenes* has four to six simple peritrichous glycosylated flagella. The flagellum is glycosylated at multiple sites on the flagellin protein FlaA, with up to six glycosylation moieties per monomer. The glycosylation moiety is transferred to FlaA post-translationally by the bifunctional O-GlcNac transferase GmaR (Shen et al., 2006). The physiological significance of the glycosylation is not yet fully understood but it is proposed that it may be an important factor for environmental adaptation outside the host. At temperatures ≥37 °C *L. monocytogenes* is typically non-motile. Inhibition of motility at high temperatures occurs through the tightly controlled repression of flaA transcription by the protein MogR, which binds to the flaA upstream promoter region (Shen & Higgins, 2006). It was initially proposed that DegU served as a direct activator of flaA transcription at low temperature, although later work showed that this role is indirect (Shen & Higgins, 2006). At low temperatures DegU activates transcription of gmaR, which encodes GmaR, the transcriptional activator of flaA. How DegU activates gmaR transcription at low temperatures but not at high temperatures remains unknown. GmaR is a bifunctional protein that first binds to MogR, removes it from the flaA promoter, and then glycosylates the FlaA protein. DegU also controls flagellin levels post-transcription, as transcription of flaA in a mogR degU strain background per se is not sufficient to restore motility (Shen & Higgins, 2006). This unique regulatory mechanism ensures that flagella of *L. monocytogenes* are only synthesized at low temperatures and that the flagella are fully glycosylated.
DegU regulates virulence in *L. monocytogenes*

Although the mechanism for DegU-dependent motility is relatively well known, how DegU affects virulence is not yet understood. DegU mutant strains are still able to enter host cells with an efficiency that is comparable to, or even better than, that of wild-type cells (Williams et al., 2005a). However, the bacterial load maintained within the spleen and other organs of the host is lower (Knudsen et al., 2004). DegU-dependent control of virulence is not due to the non-motile phenotype because flagella-minus strains of *L. monocytogenes* remain virulent (Shen & Higgins, 2006). It will be exciting to understand how DegU contributes to virulence and how this is co-ordinated with its other roles in controlling motility and activation of biofilm formation (Gueriri et al., 2008b).

DegU is an orphan response regulator in *L. monocytogenes*

The absence of degS in *L. monocytogenes* raises questions about whether DegU can be phosphorylated, and if so, whether DegU–P is required to activate flagella-based motility and/or virulence. Although DegU is an orphan response regulator in *L. monocytogenes*, importantly there are no orphan sensor kinases encoded in its genome (Williams et al., 2005a). It is possible that in the absence of a cognate or orphan sensor kinase, DegU could be phosphorylated by a non-cognate sensor kinase. However, this is very unlikely due to the inbuilt specificity mechanisms in a two-component regulatory system (Laub & Goulian, 2007). Alternatively, phosphorylation of DegU could be mediated via a small molecular phosphate donor such as acetyl phosphate. This is becoming increasingly important to understand.
recognized as a global regulator of gene transcription (Wolfe et al., 2003, 2008). The presence of an ‘orphan’ response regulator, or sensor kinase that also has phosphatase activity, suggests that acetyl phosphate may play a role in the signal transduction system (Wolfe, 2005). A study on motility and ethanol resistance by L. monocytogenes investigated whether DegU is required to be phosphorylated in order to carry out its regulatory function (Mauder et al., 2008). These authors constructed a strain of L. monocytogenes carrying a variant of degU with a point mutation in the proposed phosphorylation site. They demonstrated a partial restoration of swimming motility in comparison with the degU mutant, though motility was less than that observed in the wild-type. These findings indicate that DegU retains some functionality in its unphosphorylated state, but do not rule out the possibility that DegU~P has some physiological role. Consistent with this suggestion, DegU of L. monocytogenes can be phosphorylated by acetyl phosphate in vitro and alterations in the level of acetyl phosphate in vivo control motility and biofilm formation (Guerri et al., 2008a). As the level of acetyl phosphate varies with both growth condition and growth phase (Klein et al., 2007; Wolfe, 2005) it is possible that DegU functions as a read-out of the metabolic status of L. monocytogenes.

Future studies
Since the advent of single-cell analyses and the observation of multicellular behaviour, the full potential of DegU as a central regulator in both L. monocytogenes and B. subtilis is becoming apparent. There remain many unanswered questions about how DegU functions in both Bacillus and Listeria species. A recent phosphoproteome screening of B. subtilis found that DegS can be phosphorylated on amino acid serine 79. This is outside the HisKA_3 domain containing histidine 189, which is the site (Fig. 1) of autophosphorylation (Macek et al., 2007). This raises questions about whether phosphorylation on serine 79 has any physiological role in B. subtilis. For example, is the phosphorylation of serine 79 and histidine 189 responsible for controlling separate multicellular behaviour processes that are dependent on DegU~P in the face of different environmental stimuli? Additionally, growing evidence indicates that the function of DegU in laboratory isolates differs from that of wild isolates of B. subtilis (Kobayashi, 2007; Stanley & Lazazzera, 2005; Veening et al., 2008a; Verhamme et al., 2007). Therefore it remains to be established whether heterogeneous expression of degU occurs in wild isolates (e.g. NCIB 3160) of B. subtilis. If heterogeneous expression is observed, what influence does this have over the capacity to integrate multicellular behaviour responses? For L. monocytogenes, which lacks degS, it is important to establish whether a heterogeneous population dependent on DegU can be formed. If so, does the differentiation of tasks within the cell population confer any survival advantage to the bacterium both within and outside the host?

Concluding remarks
It is likely that the DegS–DegU regulatory system will continue to provide an excellent model of a ‘systems biology’ approach. Thus objectives will be to understand how bacteria co-ordinate the decision-making processes that occur within the cell to ensure that the desired physiological response occurs in the face of different environmental conditions. Our ability to study multicellular behaviour in B. subtilis, and other closely related species, will be enhanced upon completion of genome sequences of natural isolates collected from a variety of geographical locations (http://www.bacillusgenomics.org/bsubtilis/index.html) (Erl et al., 2007, 2008; Srivatsan et al., 2008). Such data could be used to determine the impacts of genome polymorphisms on behaviour and adaptation.

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