

# Increased phosphorylation of the RcsB regulator of the RcsCDB phosphorelay in strains of Dickeya dadantii devoid of osmoregulated periplasmic glucans revealed by Phos-tag gel analysis

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1	Increased phosphorylation of the RcsB regulator of the RcsCDB	
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4	analysis.	
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#### 18 Abstract

19 Osmoregulated periplasmic glucans (OPGs) are general constituents of many 20 Proteobacteria. OPGs are important factors required for full virulence in many pathogens 21 including Dickeya dadantii. D. dadantii causes the soft-rot disease on a wide range of plant 22 species. The total loss of virulence and motility of *opg*-negative strains of *D. dadantii* is 23 linked to the constitutive activation of the RcsCDB phosphorelay deduced from expression 24 analysis of genes of the RcsCDB regulon. Here, the *in vivo* level of constitutive activation of 25 the RcsCDB phosphorelay opg-negative strain was demonstrated by direct analysis of the 26 phosphorylation level of the RcsB regulator protein by using a Phos-tag<sup>TM</sup> retardation gel 27 approach and was correlated with the phenotype and the expression of gene of motility. 28

29 Keywords : Osmoregulated periplasmic glucans, RcsCDB phosphorelay, Dickeya dadantii,

30 phosphorylation

#### 33 **1. Introduction**

Osmoregulated periplasmic glucans (OPGs) are oligosaccharides found in the envelope of most Proteobacteria (Bohin and Lacroix, 2006). The backbone is synthesized by the two products of the *opgGH* operon and consists of  $\beta$ ,1-2 linked glucose units to which the branches are attached by  $\beta$ ,1-6 linkages. These glucans belong to the common virulence factors of many Proteobacteria zoopathogens and phytopathogens such as *Pseudomonas aeruginosa* (Mahajan-Miklos *et al.*, 1999), *Brucella abortus* (Arellano-Reynoso *et al.*, 2005) or *Dickeya dadantii* (Page *et al.*, 2001).

41 *Dickeya dadantii* is a phytopathogen Enterobacteria that causes soft rot disease in a wide 42 range of plant species (Perombelon, 2002). This opportunistic pathogen devastates 43 economically important crops in storage facilities or in growing plants. In D. dadantii, opgG 44 or *opgH* mutant, completely devoid of OPGs, show a pleiotropic phenotype including loss of 45 motility (Page *et al.*, 2001), induction of a general stress response (Bouchart *et al.*, 2007) 46 and complete loss of virulence on potato tubers and chicory leaves (Page *et al.*, 2001). All 47 these phenotypes suggest an impairment in the perception of the environment. This 48 hypothesis was confirmed by the restoration of motility and virulence on potato tubers by 49 inactivation of the RcsCDB phosphorelay regulatory system in strains devoid of OPGs.

50 Phosphorelays (also called two component systems) are the key of gene expression 51 plasticity in response to environmental variations. The RcsC sensor has both kinase and 52 phosphatase activities (Clarke, 2010). Under various stimuli, the transmembrane RcsC 53 sensor activates, its kinase activity increased, RcsC autophosphorylates and transfers its 54 phosphate group to its cognate cytoplasmic response regulator, RcsB, via the intermediate 55 transmembrane protein RcsD. In turn, RcsB regulates the expression of numerous target 56 genes affecting various cellular processes including repression of virulence and motility 57 (Cano et al., 2002, Majdalani and Gottesman, 2005). In contrast, when the RcsC sensor 58 phosphatase activates and dephosphorylates the RcsB regulator, virulence and motility 59 occurs.

Loss of OPGs leads to a constitutive activation of the RcsCDB phosphorelay system.
Restoration of virulence and motility was obtained in the *opgG* by secondary mutations
decreasing the activation level of the RcsCDB phosphorelay. This was the case for the *opgG*

63 rcsC2, the opgG rcsC or the opgG  $rcsB_{D56N}$  double mutant strains. In these strains, the 64 secondary mutation encoded a mutated RcsC2 protein with an increased phosphatase 65 activity, no RcsC protein or a non phosphorylatable RcsB<sub>D56N</sub> protein respectively (Bouchart 66 et al., 2010, Bontemps-Gallo et al. 2013). The phosphorylation of the  $RcsB_{D56N}$  protein is 67 impossible since its phosphorylatable aspartic acid residue at position 56 was changed in 68 an asparagine residue. These conclusions about the activation level of the RcsCDB 69 phosphorelay system in the wild-type and the different mutant strains were classically 70 deduced from expression analysis of genes regulated by this phosphorelay.

In the present study, we showed the variation of activation level of the RcsCDB phosphorelay system in different genetic background by direct observation of the RcsB phosphorylated and non phosphorylated protein forms separated with a Phos-tag<sup>™</sup> acrylamide gel retardation approach(ref phos tag). We demonstrated that the loss of OPGs severely increases the phosphorylation level of the RcsB protein and this constitutive phosphorylation repress motility.

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#### 78 2. Materials and Methods

79 2.1 Bacterial strains, media and growth conditions

Bacterial strains and plasmids are described in Table 1. Bacteria were grown in Lysogeny
broth (LB) (Bertani, 2004) at 30°C (*D. dadantii*) or 37°C (*Escherichia coli*). Antibiotics were
used at the following concentrations for *D. dadantii*: gentamicin at 2 µg.ml<sup>-1</sup>,
chloramphenicol at 12.5 µg ml<sup>-1</sup>, and kanamycin at 25 µg ml<sup>-1</sup>, spectinomycin at 50 µg ml<sup>-1</sup>.

84 Ampicillin was used at 50  $\mu$ g ml<sup>-1</sup> for *E. coli*.

85

86 2.2 Plasmid constructs and protein purification

Plasmid used for the expression of the His tagged-RcsB, pNF410, was previously described in Bontemps-Gallo *et al.*, 2013. For the construction of the His tagged-RcsB<sub>D56N</sub>, a DNA fragment encoding the mutated *rcsB*<sub>D56N</sub> gene was amplified by PCR using pNFW374 as template, with the rcsBacf (CACCATGAGCAATCTAAACGTAATTATTGCAG) and rcsBacr (CGCCGGCAAGAGCATTACTC) primers, cloned into the His-tag expression vector pET100/D-Topo<sup>®</sup> (Invitrogen Life Technologies) to give pNFW491. The His-tagged RcsB
and RcsB<sub>D56N</sub> proteins were expressed in *E. coli* BL21(DE3) and purified according to
Bontemps-Gallo *et al.*, 2013.

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96 2.3 Production of the phosphoramidate

97 The phosphoramidate (PA) used to phosphorylate the RcsB Protein *in vitro* was synthesized
98 by reaction of phosphoryl chloride with ammonium as described by Sheridan (Sheridan *et al.*, 1972).

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#### 101 2.4 Analysis of RcsB phosphorylation in vitro

102 Phosphorylation reactions of purified RcsB or RcsB<sub>D56N</sub> were performed with 5 µg of 103 proteins in 50 mM Tris-HCl, pH7.5, 100 mM NaCl, 10 mM MgCl<sub>2</sub> and 2 mM  $\beta$ -104 mercaptoethanol. PA was added to a final concentration of 15 mM to initiate the reaction. 105 After 0, 15 or 30 minutes of incubation at room temperature, the reactions were stopped by 106 addition of SDS-PAGE loading buffer (final concentration: 50 mM Tris-HCl pH6.8, 2% (w/v) 107 SDS, 10% (w/v) glycerol, 20 mM DTT, 0.02% bromophenol blue). The mixtures were 108 resolved using phosphoprotein affinity gel electrophoresis as described in Barbieri and 109 Stock, 2008, with minor modifications. Briefly, Phos-tag<sup>™</sup> acrylamide gels were composed 110 of a 10% resolving solution [10% (w/v) 37.5:1 acrylamide/N,N'methylenebisacrylamide, 375 mM Tris (pH8.8) and 0.1% (w/v) SDS, 125µM Phos-tag<sup>™</sup> acrylamide and 250 µM 111 112 MnCl<sub>2</sub>] and 4% stacking solution [4% 37.5:1 а (w/v)113 acrylamide/N,N'methylenebisacrylamide, 125 mM Tris (pH6.8) and 0.1% (w/v) SDS]. The 114 gels were run at 4 °C under constant voltage (150 V) with standard running buffer (0.1% 115 (w/v) SDS, 25 mM Tris and 192 mM glycine) and stained with Coomassie Blue.

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#### 117 2.5 Analysis of RcsB phosphorylation in vivo

118 At mid-log phase, equivalent of 1 ml of  $0.15 \text{ OD}_{620\text{nm}}$  of *D. datantii* cells was harvested by 119 centrifugation and pellets were immediately lysed with 12.7 µl of 1M formic acid, 120 solubilised by 5 µl of 4X SDS-PAGE loading buffer and neutralized by 2.8 µl 5 N NaOH. 121 Samples were quickly loaded onto gels containing 35 µM Phos-tag<sup>TM</sup> acrylamide and 70 µM 122 MnCl<sub>2</sub> prepared and run as described before. After 10 min wash with transfer buffer (25 mM Tris and 192 mM glycine) supplied with 1 mM EDTA, followed by 10 min wash with transfer buffer without EDTA, gels were transferred to nitrocellulose membranes using a Trans-Blot<sup>®</sup> Turbo<sup>TM</sup> Blotting system (Bio-Rad) with a pre-programmed protocol (2.5 A, up to 25 V, 7 min). Western blotting against RcsB were performed as described in Bontemps-Gallo *et al.*, 2013. When required, purified RcsB or RcsB<sub>D56N</sub> protein (2.5 µg) were phosphorylated by a 30 min incubation at room temperature with PA, as described previously. RcsB or phosphorylated RcsB proteins were added to bacteria prior lysis.

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#### 131 2.6 Quantification of the phosphorylated RcsB protein amount.

Phosphorylated RcsB and RcsB were quantified by determination of the area intensity of each band with the software Quantity One (Bio Rad) after staining with coomassie blue or detection by Western blot. Quantification of phosphorylated RcsB was expressed as the ratio of the phosphorylated RcsB amount divided by the sum of the RcsB and the phosphorylated RcsB amounts as described elsewhere (Barbieri and Stock, 2008).

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138 2.7 Dosage fusion

- 139 ...
- 140 2.8 Analyse motility nage et fliC antibodies
- 141

#### 142 **3. Results and Discussion**

143 3.1 Phosphorylated RcsB (RcsB-P) migrate slower than RcsB

The method to observe the phosphorylated form of cytoplasmic regulators proteins is available when the phosphate group is linked to a serine, threonine or tyrosine because the linkage is relatively stable. In the case of bacterial phosphorelays, the phosphate group is linked to an aspartate residue for the cytoplasmic regulator. Unfortunately, in this last case, linkage is highly unstable and since recently, observation of the kind of phosphorylated proteins was impossible.

In 2008, Stock's lab published a method allowing separation of the phosphorylated and the non-phosphorylated forms of phosphorelay regulators (Barbieri and Stock, 2008). This method relies on Phos-tag<sup>TM</sup>: a dinuclear metal complex acts as a specific phosphatebinding agent. In a Phos-tag<sup>TM</sup> acrylamide gel, the Phos-tag<sup>TM</sup> linked to acrylamide 154 molecules interact with the phosphorylated form of the protein which migrates slower than 155 the non-phosphorylated protein allowing the separation of both forms of the protein. The 156 method was first applied *in vitro* on RcsB since method must be adapted to each regulator 157 (dixit Stock ref). Purified RcsB was phosphorylated in vitro by the phosphodonor 158 phosphoramidate (PA) (Lukat *et al.*, 1992). 5 µg of RcsB was incubated different times with 159 or without PA (see materials and methods), samples were loaded onto a Phos-tag<sup>™</sup> 160 acrylamide gel and RcsB was revealed with coomassie blue after migration. Without PA 161 added, a single band, corresponding to the non-phosphorylated RcsB form (called RcsB) 162 was observed (lanes 1 and 2, Fig. 1A). In contrast, a retardation of migration of 57% and 163 61% of the band was observed (lanes 3 and 4, Fig. 1A) when PA was added during 15 min 164 and 30 min respectively. This strongly suggests that the shifted band corresponds to the 165 phosphorylated RcsB form (called RcsB-P) but indicating that in our conditions, PA was 166 unable to phosphorylate all RcsB. The same experiment was performed with the non 167 phosphorylatable RcsB<sub>D56N</sub> protein (lanes 5 to 8, Fig. 1A). In these lanes, a single band 168 migrating as the single band of lanes 1 and 2 was observed. These data indicate that the 169 lower band corresponded to RcsB, that the upper band corresponded to RcsB-P and that PA 170 phosphorylates the proper aspartic residue of RcsB. These conditions allowed us to analyze 171 the stability of the phosphorylation of RcsB in vivo.

172 Fin de la correction

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#### 175 3.2 The lysis with formic acid had no effect on the RcsB-P amount

176 The *in vivo* analysis required rapid lyse of bacteria with formic acid before loading onto the 177 gel (Barbieri and Stock, 2008). Because the phospho-aspartate bond is very unstable, it was 178 important to check both the effect of the formic acid and the lysis of cell on the stability of 179 RcsB and of the RcsB-P phospho-aspartate bond. To do this, 5 µg of purified RcsB or RcsB-P, 180 phosphorylated by PA, was added to an *rcsB* null mutant strain of *D. dadantii* (NFB7279) 181 prior lysis with formic acid. Lysates were then loaded onto a Phos-tag<sup>TM</sup> gel. As controls, the 182 same amount of RcsB and RcsB-P without bacteria were loaded onto the same gel. The same 183 experiments and controls were performed with the RcsB<sub>D56N</sub>. After run, RcsB was revealed 184 by Western blot. When the lysate of the NFB7279 strain was loaded onto the gel alone, RcsB 185 was not detected (lane 1, Fig. 1B). A similar amount of RcsB was revealed when RcsB was 186 added to the NFB7279 strain before lysis (lane 2, Fig. 1B) or when RcsB was loaded alone 187 onto the gel (lane 6, Fig. 1B). The same two bands in similar amount, corresponding to RcsB (53%, lower band) and RcsB-P (47%, upper band), were revealed when RcsB 188 189 phosphorylated by PA was added to the NFB7279 strain before lysis (lane 3, Fig. 1B). The 190 same two bands in similar amount, corresponding to RcsB (52%, lower band) and RcsB-P 191 (48%, upper band), were revealed when RcsB phosphorylated by PA was loaded alone on 192 the gel (lane 7, Fig. 1B). The same conclusions can be drawn when  $RcsB_{D56N}$  was used 193 instead of RcsB except that only one band was observed corresponding to the non 194 phosphorylated form of RcsB (lane 4, 5, 8, 9, Fig. 1B). Taken together, these results indicate 195 that neither cell lysate nor formic acid affect the RcsB stability or the RcsB-P phospho-196 aspartate bond stability and that the two forms of RcsB are separated within a cell lysate. 197 These results allowed us to analyse the RcsB phosphorylation *in vivo*.

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#### 199 3.3 The phosphorylation of RcsB is increased in a strain devoid of OPGs

200 We previously showed that the RcsCDB phosphorelay was constitutively activated in an 201 opgG strain devoid of OPGs and constitutive activation was resumed by secondary 202 mutations reducing the activity of the RcsCDB phosphorelay (see introduction). These 203 conclusions were deduced from expression analysis of genes regulated by the RcsCDB 204 phosphorelay. To confirm these results, the level of *in vivo* phosphorylation of RcsB was 205 performed using the Phos-tag<sup>™</sup> approach in the same strains (Fig. 1C). As expected, no 206 RcsB was detected in the *rcsB* strain (lane 7, Fig. 1C). As expected, in the *rcsB*<sub>D56N</sub>, only one 207 band was observed corresponding to the RcsB form (lane 6, Fig. 1C). In the wild-type strain 208 (lane 1, Fig. 1C), a low amount of RcsB-P (11% upper band) was observed as compared to 209 the RcsB amount (89%, lower band). In the opgG strain (lane 2, Fig. 1C), an increased 210 amount of RcsB-P (23%, upper band) as compared to RcsB (77%, lower band) was 211 observed as compared to the wild-type but RcsB remained more important. In the opgG 212 *rcsC2* (lane 3, Fig. 1C), in the *rcsC2* (lane 4, Fig. 1C), in the *rcsC* null mutant (lane 5, Fig. 1C), 213 and in the rcsB<sub>D56N</sub> (lane 6, Fig. 1C) strains, RcsB-P cannot be detected. These data 214 confirmed the results observed by Bouchart et al. (2010). In addition, they showed that in 215 wild-type cells, the RcsB-P form is present in very limited amount and that a moderate increase in RcsB-P (*opgG* strain) is sufficient to confer the pleiotropic phenotype observed in *D. dadantii*. The direct analysis of phosphorylation level of regulators of phosphorelays is of a great interest particularly for determination of the phosphorylated to non phosphorylated ratio of regulator imposible to do with analysis of gene expression but remains difficult to use systematically because adaptation of the method is required for each new phosphorelay studied is time consuming.

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regulator aspartate phosphorylation both *in vitro* and *in vivo* using Phos-tag<sup>™</sup> -based
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272 Legends to figures

Figure 1: Separation of RcsB and RcsB-P by Phos-tag<sup>™</sup> polyacrylamide gel electrophoresis
and detection *in vivo* by Western analysis.

A. Phosphorylation of RcsB *in vitro*. Each lane contains 5µg of either purified wild-type
RcsB (lanes 1 to 4) or RcsB<sub>D56N</sub> (lanes 5 to 8) incubated in presence of 15mM PA, during
0 min (lanes 2, 6), 15 min (lanes 3, 7) and 30 min (lanes 4, 8) or in absence of PA (lanes
1, 5) before loading onto the gel. After migration, RcsB and RcsB-P proteins were
visualized by coomassie-stained Phos-tag<sup>TM</sup> gel.

B. Stability of RcsB and phospho-aspartate of RcsB-P during cell lysate processing. Purified
RcsB (lane 2), RcsB-P (lane 3) or unphosphorylatable RcsB<sub>D56N</sub> (lanes 4-5) were mixed
with *rcsB* mutant strain before treatment with formic acid as described in Materials and
Methods. As controls, *rcsB* cell lysate (lane 1), RcsB protein (lanes 6) RcsB-P (lane 7)
and RcsB<sub>D56N</sub> protein (lanes 8, 9) were also loaded on the gel. Revelation of RcsB was
performed by Western blot analysis after electrophoresis on Phos-tag<sup>™</sup> gel. Lanes were
PA is noted indicated that RcsB (or RcsB<sub>D56N</sub>) was treated 30 min with PA prior to lysis.

C. Phosphorylation of RcsB *in vivo*. Cell lysates of wild-type (lane 1), opgG (lane 2), opgGrcsC2 (lane 3), rcsC2 (lane 4), and rcsC (lane 5), rcsB<sub>D56N</sub> (lane 6) and rcsB (lane 7) mutant strains of *D. dadantii* were subjected to Phos-tag<sup>TM</sup> acrylamide gel electrophoresis and Western blot analysis.

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303 Table 1

Strain	Genotype <sup>a, b</sup>	Source or Reference	
Dickeya dadantii			
EC3937	Wild-type	Laboratory collection	
NFB3591	opgG::uidA-Kan <sup>r</sup> rcsC2	Bouchart <i>et al.</i> , 2010	
NFB3611	rcsC2	Bouchart <i>et al.</i> , 2010	
NFB3682	<i>rcsC</i> ::Cml <sup>r</sup>	Bouchart <i>et al.</i> , 2010	
NFB3723	<i>opgG</i> ::Cml <sup>r</sup>	Laboratory collection	
NFB7112	rcsB::Cml <sup>r</sup> rcsCB <sub>D56N</sub> D-Spe <sup>r</sup>	Bontemps-Gallo et al., 2013	
NFB7279	<i>rcsB</i> ::Gm <sup>r</sup>	Bontemps-Gallo et al., 2013	
Escherichia coli			
BL21(DE3)	ompT, hsdSB, gal, dcm	Invitrogen	
Plasmids			
pNFW374	pUC18Not- rcsCB <sub>D56N</sub> D, Amp <sup>r</sup>	Bontemps-Gallo et al., 2013	
pNFW410	pET100/D-topo <i>rcsB, Amp<sup>r</sup></i>	Bontemps-Gallo et al., 2013	
pNFW491	pET100/D-topo <i>rcsB<sub>D56N</sub>, Amp<sup>r</sup></i>	This study	

304 arcsCB<sub>D56N</sub>D is carried by a Spe<sup>r</sup> mini-Tn5

<sup>305</sup> <sup>b</sup>Cml<sup>r</sup>, chloramphenicol resistance; Amp<sup>r</sup>, ampicillin resistance, Kan<sup>r</sup>, kanamycin resistance,

306 Spe<sup>r</sup>, spectinomycin resistance, Gm<sup>r</sup>, gentamicin resistance.