A CsrA/RsmA translational regulator gene encoded in the replication region of a Sinorhizobium meliloti cryptic plasmid complements Pseudomonas fluorescens rsmA/E mutants

Betina Agaras,† Patricio Sobrero† and Claudio Valverde

Members of the CsrA/RsmA family are global regulatory proteins that bind to mRNAs, usually at the ribosome-binding site, to control mRNA translation and stability. Their activity is counteracted by small non-coding RNAs (sRNAs), which offer several binding sites to compete with mRNA binding. The csrA/rsmA genes are widespread in prokaryotic chromosomes, although certain phylogenetic groups such as Alphaproteobacteria lack this type of global regulator. Interestingly, a csrA/rsmA-like sequence was identified in the replication region of plasmid pMBA19a from the alphaproteobacterium Sinorhizobium meliloti. This rsmA-like allele (rsmASm) is 58% identical to Xanthomonas axonopodis pv. citri chromosomal rsmA and bears an unusual C-terminal extension that may fold into an extra α-helix. Homology-based modelling of RsmASm suggests that all key mRNA-binding residues are conserved and correctly positioned in the RNA-binding pocket. In fact, a 1.6 kb fragment from pMBA19a encompassing the rsmASm locus restored rsmA/E-dependent phenotypes of rsmA/E P. fluorescens mutants expressing RsmX/Y/Z RNAs indicated that RsmASm is able to bind these antagonistic sRNAs. In agreement with the latter observation, it was also found that the sRNA RsmY was stabilized by RsmASm. Deletion of the C-terminal extra α-helix of RsmASm affected its cellular concentration, but increased its relative RNA-binding activity. This is believed to be the first report of the presence and characterization of a functional csrA/rsmA homologue in a mobile genetic element.

INTRODUCTION

Post-transcriptional regulatory mechanisms usually exert a fine-tuning control of gene expression, being in most cases dependent on RNA-binding proteins that impose translational control on target mRNAs (Kaberdin & Blasi, 2006). This is the case for members of the CsrA/RsmA protein family. CsrA (carbon storage regulator A) was first identified and characterized in Escherichia coli (Romeo et al., 1993), whereas RsmA (repressor of secondary metabolites A) was discovered later in Erwinia carotovora (Chatterjee et al., 1995) and a few years later in Pseudomonas fluorescens (Blumer et al., 1999). These are small dimeric proteins that bind to RNA sequence motifs typically (but not exclusively) present around the ribosome-binding site of target mRNAs. As a consequence of mRNA binding, CsrA/RsmA competes for ribosome access and/or influences mRNA stability, thus affecting the translation rate of the bound mRNAs (Romeo et al., 2012). This regulatory mechanism is reversed by small non-coding RNA molecules (sRNAs), which bear a number of RNA motifs equivalent to those present in target mRNAs (Liu et al., 1997). These RNA motifs contain conserved GGA triplets that are critical for the activity and stability of antagonistic sRNAs (Dubey et al., 2005; Valverde et al., 2004). Thus, the antagonistic sRNAs are able to outcompete bound mRNAs and release the translational control exerted by CsrA/RsmA proteins (Romeo et al., 2012). As expected, the intracellular level of
the antagonistic sRNAs is itself regulated by cellular and extracellular cues (Valverde & Haas, 2008). As CsrA/RsmA proteins bind to a number of mRNAs, induction of the competing mimic sRNAs results in global control of gene and operon expression (Romeo et al., 2012).

Inspection of the large number of prokaryotic genome sequences available led to the conclusion that csrA/rsmA genes are heterogeneously present in a wide variety of eubacteria (see Table S1 available with the online version of this paper), in single or multiple copies. E. coli and Bacillus subtilis, for instance, have one csrA gene (Romeo & Gong, 1993; Yakhnin et al., 2007), whereas P. fluorescens strain CHA0 encodes two homologue proteins, RsmA and RsmE (Reimmann et al., 2005), and some Pseudomonas species, such as Pseudomonas syringae and Pseudomonas putida, have up to four CsrA/RsmA-like homologues (Lapouge et al., 2008). In all cases, the csrA/rsmA-like genes are encoded in chromosomes. On the other hand, certain eubacterial divisions lack chromosomal CsrA/

RsmA homologue genes, as is the case of sequenced Alphaproteobacteria (Table S1). Functional studies of CsrA/RsmA homologues have only been carried out in a few taxa other than Gammaproteobacteria, for example B. subtilis, Helicobacter pylori and Borrelia burgdorferi (Barnard et al., 2004; Sze et al., 2011; Yakhnin et al., 2007). Interestingly, a csrA/rsmA homologue sequence has been detected in the replication region of the alphaproteobacterium Sinorhizobium meliloti cryptic plasmid pMBA19a, although it has not been further characterized (Watson & Heys, 2006). This work reports for what is believed to be the first time the functional characterization of a csrA/rsmA gene encoded in a mobile genetic element.

**METHODS**

**Bacterial strains and culture conditions.** The bacterial strains and plasmids used in this study are listed in Table 1. P. fluorescens strain CHA0 has been recently taxonomically reassigned to the novel species

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*P. fluorescens strain CHA0 has been recently reassigned to Pseudomonas protegens (Ramette et al., 2011).*
**Pseudomonas protegens** (Ramette et al., 2011). In this work, we keep the former taxonomic designation, which appears in all the literature related to genetics of the Gac/Rsm cascade. *Pseudomonas* spp. and *E. coli* were usually grown on nutrient agar (NA) and in nutrient yeast broth (NYB) (Valverde et al., 2003), whereas *S. meliloti* was grown in agarized or liquid TY medium (Sobero & Valverde, 2011). When required, tetracycline was added to the growth medium at 125 μg ml⁻¹ for *P. fluorescens* strains and 5 μg ml⁻¹ for *S. meliloti* strains. Routine incubation temperature was 28 °C. *P. fluorescens* strains were grown at 35 °C to improve their capacity to accept heterologous DNA in electroporation with plasmids.

**DNA manipulation and cloning procedures.** DNA preparations were obtained and cloning steps were carried out according to standard protocols (Sambrook et al., 1989). Small-scale plasmid preparations were obtained with the one-tube cetyltrimethylammonium bromide (CTAB) method (Del Sal et al., 1988) and high-quality plasmid preparations with the Jet-Quick miniprep spin kit (Genomed). PCRs were carried out as reported previously (Valverde, 2009). DNA fragments were purified from agarose gels with Qiagen II (Qiagen). All cloned PCR products were verified by sequencing from both ends by Macrogen.

### Construction of plasmids.
A 1.6 kb fragment from pBB84 encoding the *rsmASm* allelic was subcloned as an EcoRI–PstI insert into pME6000 to generate plasmid pSM1 (Fig. 1). Vector pSM2 was generated by PCR-amplifying the *rsmASm* locus with primers rsmAR (5′-TGTACGCGATGTAATCCCGAGCAGC-3′) and rsmAF1 (5′-TCTGAACTTTACGGAGGAGGAACC-3′), which introduced PstI and EcoRI sites (underlined) at the borders of the amplicon. The 0.5 kb PCR product was treated with EcoRI/PstI and cloned into pME6000 to give pSM2 (Fig. 1). Vector pSMAC was generated by PCR-amplifying the *rsmASm* locus with primers rsmAR and rsmAF2 (5′-AATGATTCTTACGGAGGAGGAGG-3′), thus introducing a C-terminal deletion of 48 bp (residues 62–77). The 0.45 kb PCR product was treated with EcoRI/PstI and cloned into pME6000 to give pSMACt. In all three constructs the *rsmASm* gene and its own promoter region lay in the opposite orientation from that of the pME6000 vector *P. fluorescens* cells by electrotransformation.

### Detection of RsmA-like proteins by Western blotting.
Erlenmeyer flasks containing 20 ml NYB amended with 0.05 % (w/v) Triton X-100 were inoculated at 1 : 100 from overnight saturated cultures and grown with shaking for 200 r.p.m. Cells equivalent to an OD₆₆₀ of 0.4 U ml⁻¹ were centrifuged, washed with 0.9 % (w/v) NaCl, resuspended in 20 μl loading buffer (50 mM Tris/HCl, pH 6.8, 2 % (w/v) SDS, 0.1 % (w/v) bromophenol blue, 15 % (v/v) glycerol, 5 % (v/v) β-mercaptoethanol) and immediately treated at 100 °C for 10 min. Samples (15 μl) were electrophoresed in a 12 % (w/v) acrylamide-bisacrylamide gel (Laemmli, 1970) and electrotransferred onto PVDF membranes (Immobilon P; Millipore). Immunodetection of RsmA-like proteins was carried out as reported elsewhere using monoclonal antibodies raised against purified *Yersinia enterocolitica* RsmA (Reimann et al., 2005).

### Modelling of RsmAₘₙ structure.
Sequence alignments were generated with CLUSTAL W (Larkin et al., 2007). The 3D-PSSM algorithm was used for secondary structure prediction (Cuff et al., 1998). A model of RsmAₘₙ tertiary structure was generated by a homology-based procedure using RmE from *P. fluorescens* CHA0 (PDB 2JPP) as a template (Schubert et al., 2007). Models were obtained with the program MODELLER (Sali et al., 1995), run in the TITO server (Labesse & Mornon, 1998), and structures were validated by calculating geometric (RAMPAGE – Ramachandran plot assessment) or energetic (PROSAII) parameters (Lovell et al., 2003; Wiederstein & Sippl, 2007). Surface potential was calculated with APBS (Adaptive Poisson–Boltzmann Solver) (Baker et al., 2001) and visualized with PyMol (http://www.pymol.org/).

### Detection of HCN, exoprotease and antagonism against *Pythium ultimum* in *P. fluorescens*.
For quantitative hydrogen cyanide (HCN) determinations, *P. fluorescens* cultures were grown in Paraflim-sealed 15 ml tubes containing 5 ml NYB, with shaking (200 r.p.m.). Cyanide production was quantified colorimetrically in overnight cultures (Gewitz et al., 1976). Exoprotease activity was detected on skimmed milk agar plates (Sacherer et al., 1994). Antagonism against *Pythium ultimum* isolate Pu-67 was assessed as hyphal growth inhibition in dual plate assays (Ongena et al., 1999).

### Detection of pyocyanin in *Pseudomonas aeruginosa*.
Pyocyanin production was estimated from overnight cultures in King’s A agar plates (Olivas et al., 2012). Equal square pieces of agarized medium with bacterial lawn (approx. 2 cm²) were excised from plates and bacterial cells were removed by repeated pipetting of 1 ml of 0.9 % (w/v) NaCl. Pyocyanin was then extracted from homogenized agar with 3 ml chloroform followed by re-extraction into 1 ml of 0.2 M HCl. Pyocyanin concentration was estimated by measuring absorbance at 520 nm. Measurements were normalized to cell density measured as the OD₆₆₀ of cell suspensions in 0.9 % (w/v) NaCl.

**Glycogen production and motility assay in *E. coli*.** Glycogen content of *E. coli* strains was estimated by anthrone colorimetry, as reported previously (Valverde et al., 2004). One millilitre of culture was centrifuged, and cells were washed with 0.9 % (w/v) NaCl. Then, 100 μl of 1 M NaOH was added, and the cell suspension was incubated for 30 min at 55 °C to promote cell lysis. Lysates were neutralized with 100 μl of 1 M HCl. The content of hexoses was determined by mixing an aliquot of the lysates with anthrone reagent [Sigma; 0.2 % (w/v) in 98 % sulfuric acid] and incubating in a boiling water bath for 10 min. After cooling the tubes on ice, absorption was measured at 620 nm. The standard curve was prepared with glucose (1 mg glucose equals 0.9 mg glycogen). The protein content of cell lysates was determined with the Bradford method. Glycogen content was expressed as milligrams of glycogen per milligram of protein. Spreading of *E. coli* strains by swimming motility was assessed on semi-solid agar plates [0.5 % (w/v) yeast extract, 2.5 % (w/v) nutrient broth, 0.3 % (w/v) agar]. Freshly isolated colonies were spotted onto swimming plates with a toothpick and incubated overnight in sealed plastic bags at 30 °C (Valverde et al., 2004).

**β-Galactosidase assays.** Strains were grown in 20 ml NYB (in 125 ml Erlenmeyer flasks) with shaking at 200 r.p.m. Triton X-100 was routinely added at 0.05 % (w/v) to avoid cell aggregation. β-Galactosidase activities were quantified by the Miller method (Miller, 1972), with cells permeabilized with 5 % (w/v) toluene.

**RNA preparation and Northern blots.** RNA preparations from *P. fluorescens* strains and Northern blotting were done as described previously (Valverde et al., 2004). RsmY stability was estimated after addition of rifampicin (200 μg ml⁻¹) to near-stationary cultures and analysed by Northern blotting (Reimann et al., 2005).

### RESULTS

**The rsmASₘₙ locus in the *S. meliloti* cryptic plasmid pMBA19a**

The *S. meliloti* isolate MBA19 contains the 36 kb plasmid pMBA19a, whose encoded functions are dispensable for the
host (i.e. pMBA19a is a cryptic plasmid) (Watson & Heys, 2006). In addition to genes required for plasmid replication and maintenance, the 4.5 kb replication region of pMBA19a contains a small ORF in the vicinity of the repA gene that is 82 % identical to the Xanthomonas axonopodis carbon storage regulator CsrA (NCBI reference sequence NP_642074.1) (Fig. 1). The coding sequence of this csrA/rsmA homologue (hereafter rsmASm) is preceded by a typical AG-rich Shine–Dalgarno motif and by a putative σ^70^-dependent promoter identified by the Bprom algorithm (http://linux1.softberry.com/berry.phtml), which may drive rsmASm expression (Fig. 1). A second divergent σ^70^-dependent promoter was identified in the same region, which may control transcription of the ORF II–repA operon (Fig. 1). ORFs IV and V resemble the transcriptional repressor protein KorA and the IncC regulatory protein from the broad-host-range plasmid RK2, respectively (Fig. 1). Members of the CsrA/RsmA family, although widespread in the eubacterial domain, had not previously been found as part of mobile elements, nor identified in alphaproteobacterial species. This finding prompted us to study the functionality of this CsrA/RsmA homologue gene.
The RsmA<sub>Sm</sub> homologue present in the pMBA19a <i>rep</i> region has 77 residues and a predicted molecular mass of 8.4 kDa. It is an unusual member of the CsrA/RsmA family in that the first 50 residues are strongly conserved among other bacterial species (Fig. 2a), but the last 27 residues form a C-terminal extension that resembles that of Gram-positive species (Yakhnin <i>et al.</i>, 2007) (Fig. 2b). Overall, the predicted secondary structure is similar to other CsrA/RsmA partners with a $\beta_1 - \beta_2 - \beta_3 - \beta_4 - \alpha$ arrangement, and the extra $\alpha$-helix (Fig. 2b). The high level of amino acid identity found between the first 53 residues of RsmA<sub>Sm</sub> and those of the <i>P. fluorescens</i> RsmE homologue (Fig. 2c) served as a basis for the structural homology modelling of the RsmA<sub>Sm</sub> dimer excluding the C-terminal $\alpha$-helix. The modelled RsmA<sub>Sm</sub> dimer showed almost perfect overlap with the crystal structures determined for <i>P. fluorescens</i> RsmE (Schubert <i>et al.</i>, 2007), <i>P. aeruginosa</i> RsmA (Rife <i>et al.</i>, 2005) and <i>Y. enterocolitica</i> RsmA (Heeb <i>et al.</i>, 2006) (Fig. 2d). Moreover, both the position of critical residues for CsrA/RsmA activity and a...
similar surface charge distribution are conserved in the RsmA Sm RNA-binding pocket (Fig. 2e, f). Together, this in silico evidence strongly suggests that, if expressed, RsmA Sm may be a functional post-transcriptional repressor of the CsrA/RsmA family.

**The rsmA Sm gene negatively controls Gac/Rsm-dependent phenotypes in *P. fluorescens***

In *P. fluorescens* strain CHA0, the membrane-bound GacS sensor and the cytoplasmic transcriptional regulator GacA constitute a two-component system that, upon entry into early stationary phase, induces expression of *rsmX/Y/Z* genes, which encode RsmA/E-antagonistic sRNAs (Laville et al., 1992; Zuber et al., 2003). Thus, the simultaneous deletion of *rsmX/Y/Z* genes or of those encoding the GacS/A system allows RsmA and RsmE proteins to fully repress translation of mRNAs encoding proteins for the synthesis of several extracellular products (e.g. exoprotease AprA, HCN, antifungal compounds) (Kay et al., 2005; Laville et al., 1992; Zuber et al., 2003). In this background, genetic inactivation of *rsmA* and *rsmE* results in maximal expression of target mRNAs (Reimmann et al., 2005). Thus, *gacS rsmA rsmE* triple mutants are suitable hosts to test the functionality of heterologous members of the CsrA/RsmA family, because introduction of a foreign *csrA/rsmA*-like gene should restore translational control of target genes and reveal a negative effect on the production of extracellular metabolites. As *gacS rsmA rsmE* triple mutants are unable to express the RsmA/E-antagonistic *rsmX/Y/Z* genes (Reimmann et al., 2005), introduction of a foreign *csrA/rsmA*-like gene in this background would reveal its full repressive potential towards RsmA/E mRNA targets. In turn, *P. fluorescens rsmA/rsmE* double mutants with a wild-type and functional *gacS* gene (Reimmann et al., 2005) serve to study the ability of heterologous CsrA/RsmA proteins to interact with, and to be counteracted by, the small regulatory RNAs RsmX/Y/Z.

With this in mind, the 1.6 kb *EcoRI–PstI* fragment from pBB84 was subcloned into pME6000 to give vector pSM1, in which *rsmA Sm* would be expressed from its own promoter (Fig. 1), and used to transform *P. fluorescens rsmA rsmE* mutant strains (Table 1). As the *rep* region identified for pMBA19a (Fig. 1) resembled that of the broad-host-range plasmid pVS1 (Watson & Heys, 2006), strains were also transformed with pBB84. Next, we studied the impact of *rsmA Sm* expression on Gac/Rsm-dependent phenotypes such as antagonism of *Pythium ultimum*, AprA activity and HCN production (Fig. 3). Wild-type strain CHA0 produces the antibiotic DAPG (2,4-diacetylphloroglucinol) and inhibits growth of the oomycete *Pythium ultimum* in dual culture plates, whereas the *gacS* mutant CHA19 no longer expresses the DAPG biosynthetic genes due to repression of the *phi* operon by RsmA and RsmE proteins (Fig. 3a). Expression of *rsmA Sm* from vector pSM1 in strain CHA1008 (*rsmA rsmE gacS*) resulted in reduced antagonism of *Pythium ultimum* (Fig. 3a), and in a drastic reduction in AprA activity (Fig. 3b) and HCN production (Fig. 3c). Surprisingly, the *rsmA Sm* allele in pBB84 did not result in a reduction of antagonism of *Pythium ultimum*, of AprA activity or of HCN production (Fig. 3).

**The rsmA Sm gene acts as a repressor of Gac/Rsm-dependent genes in *P. fluorescens***

The results described above suggest strongly that RsmA Sm imposed a negative control on AprA activity and HCN production at the translational level. Thus, we followed the expression pattern of chromosomal *hcnA–lacZ* and *aprA–lacZ* translational fusions in *P. fluorescens rsmA rsmE gacS* mutant strains. For both reporter genes, *rsmA Sm* in pSM1 resulted in a strong repression (Fig. 4). However, as observed for the corresponding phenotypes (Fig. 3b, c), the presence of plasmid pBB84 did not significantly affect *hcnA–lacZ* or *aprA–lacZ* expression (Fig. 4). Thus, *rsmA Sm* is not expressed or is expressed at a very low level in *P. fluorescens* strains bearing pBB84.

**RsmA Sm function is antagonized by *P. fluorescens* RsmX/Y/Z sRNAs***

Repression of HCN, AprA and antibiotic production by RsmA Sm indirectly suggests that this protein is able to bind to the recognition motifs present in the vicinity of the ribosome-binding site of the corresponding mRNAs (Lapouge et al., 2007). In *P. fluorescens rsmA rsmE gacS* mutants, the RsmA Sm repressive activity is maximal because expression of the antagonistic sRNAs RsmX/Y/Z is abolished (Kay et al., 2005). We therefore wondered if the natural *P. fluorescens* Rsm sRNAs would be able to bind to and counteract RsmA Sm. To this end, the effect of the *rsmA Sm* gene was studied in *P. fluorescens rsmA rsmE* mutants bearing a functional *gacS* gene. As shown in Fig. 3, the strong negative effect of RsmA Sm on Gac/Rsm-dependent phenotypes was clearly attenuated in these *rsmA rsmE* mutants. As expected, the strong repression exerted by RsmA Sm on target genes was also counteracted in these strains (Fig. 4). These results suggest that RsmA Sm would recognize and bind to the *P. fluorescens* RsmX/Y/Z sRNAs. In *P. fluorescens* CHA0, RsmY and RsmZ sRNAs bind to RsmA and RsmE proteins to form a series of ribonucleoprotein complexes (Reimmann et al., 2005). RsmA/E binding strongly stabilizes the antagonistic Rsm sRNAs (Valverde et al., 2004). Thus, in the absence of RsmA/E proteins, RsmY and RsmZ sRNAs become strongly destabilized (Reimmann et al., 2005). We then hypothesized that binding of RsmA Sm to RsmX/Y/Z sRNAs should increase sRNA half-lives in an *rsmA/rsmE* mutant background. As shown in Fig. 5, expression of *rsmA Sm* (from either pSM1 or pSM2 vectors; see Fig. 1) restored the wild-type stability to RsmY sRNA in the *rsmA rsmE* background. On the other hand, the low RsmY half-life displayed by the *rsmA rsmE* mutant bearing pBB84 confirmed that *rsmA Sm* is expressed at such a low level.
from the plasmid rep region that it cannot confer full protection from degradation to RsmY (Fig. 5).

The C-terminal α-helix of RsmASm is not essential for its function

Comparison of the deduced sequence of RsmASm with CsrA/RsmA proteins from other Gram-negative bacterial lineages revealed a C-terminal extension that may fold into an extra α-helix (Fig. 2b). To test if the C-terminal extension is required for RsmASm function, we removed the last 48 coding nucleotides of rsmASm (Fig. 2c) and cloned this allele in pME6000 to generate pSMDCt. The cellular level of the C-terminal-truncated polypeptide was about threefold lower than that of the full-length protein in Western blots (Fig. 6a). However, the RsmASmCt variant was still able to strongly repress Gac/Rsm-dependent phenotypes in the heterologous test strains (Fig. S1). The results of quantitative expression of target mRNA reporters showed that the repressive activity of the RsmASmCt variant was more effectively counteracted by RsmX/Y/Z sRNAs, as the expression level of both translational reporter fusions was significantly higher than in cells expressing the full-length version (Table 2). Moreover, the RsmASmCt variant was able to restore wild-type RsmY sRNA stability in an rsmAE mutant background (Fig. 5). Together, these results indicate that the extra C-terminal sequence of RsmASm is not essential for its function as a repressor of mRNA genes or for interaction with the RsmAE-antagonistic sRNAs in the heterologous host P. fluorescens. Removal of the C-terminal extra α-helix is associated with lower cellular levels of the RsmASm repressor protein.

Negative control of rsmASm expression in the rep region of cryptic plasmid pMB19a

The results above indicate that the rsmASm allele is expressed and functional in P. fluorescens strains (Figs 3–5, Table 2). However, the expression level seems to depend on the genetic context of the rsmASm allele. For instance, rsmASm seems to be expressed at very low levels from vector pBB84, which contains the replication region of the rhizobial cryptic plasmid pMBA19a (Fig. 1). The expression level is so low that it was only evidenced by the slight stabilization of RsmY RNA (Fig. 5) and the slight
repression of aprA’–lacZ expression (Table 2) in strains bearing pBB84; however, the same construct failed to complement RsmA/E-controlled phenotypes (Fig. 3). In contrast, rsmASm is expressed at levels similar to those of P. fluorescens RsmA/E proteins from either pSM1 or pSM2 constructs (Figs 3–5, Table 2). In agreement with these observations, the RsmASm polypeptide was immunodetected in P. fluorescens cells bearing vectors pSM1 or pSM2, but not in cells transformed with pBB84 (Fig. 6a). That is, rsmASm expression appears to be negatively controlled when the allele is present in the genetic context of the cryptic plasmid rep region (Fig. 1). This negative control seems to be relieved when the rsmASm allele is disentangled from the plasmid copy control region (Fig. 6a).

Expression of rsmASm is host strain-dependent

The rsmASm allele was originally identified in a cryptic plasmid from an S. meliloti soil-dwelling isolate (Watson & Heys, 2006). Here, we have demonstrated that this allele is functional in the heterologous host P. fluorescens. We then tested if the repressor gene was expressed in the natural host S. meliloti. As shown in Fig. 6(b), the RsmA Sm polypeptide could not be detected by Western blotting in S. meliloti strains bearing the rsmASm allele in the rep region of the cryptic plasmid pMBA19a or pBB84. The protein was not detected in strains carrying pSM1 or pSM2 constructs, in which the rsmASm allele was disentangled from the copy number control mechanisms (Fig. 1). Strain-specific effects were discounted because the RsmA Sm polypeptide was not detected in two different S. meliloti host strains (Fig. 6b). The presence of genomic copies of KorA-like sequences in S. meliloti replicons was ruled out because BLASTN searches did not identify genes with significant homology to these transcriptional repressors.

Next, we studied rsmASm expression in two other heterologous hosts for which csrA/rsmA mutants were

![Fig. 4](image_url)

**Fig. 4.** Translational control of Gac/Rsm-dependent genes by RsmASm in P. fluorescens. β-Galactosidase activity of P. fluorescens strains carrying a chromosomal hcnA’–lacZ (a) or an aprA’–lacZ (b) fusion. Each value represents the mean of three replicate cultures ± sd. The growth curves of the tested strains are shown in the right-hand panels. Strain genetic features: rsmA rsmE gacS/pME6000 (○); rsmA rsmE gacS/pBB84 (●); rsmA rsmE gacS/pSM1 (▲); rsmA rsmE/pSM1 (△). MU, Miller units.

![Fig. 5](image_url)

**Fig. 5.** RsmASm protects RsmY sRNA from degradation. RsmY transcript decay in the wild-type strain P. fluorescens CHA0 and in the rsmA rsmE double mutant bearing different vectors was determined by Northern blotting after blocking transcription with rifampicin. The amount of RNA loaded was 5 μg for the wild-type, 10 μg for the rsmA rsmE double mutant bearing pME6000 or pBB84, and 3 μg for the rsmA rsmE double mutant bearing pSM1, pSM2 or pSMΔCt.
available. In the *P. aeruginosa* *rsmA* background, the *rsmASm* allele in pSM2 partially complemented pyocyanin production and the RsmA<sub>Sm</sub> polypeptide was detected by Western blotting (Fig. S2). In contrast, in the *E. coli* background, *rsmASm* in pSM2 was not able to repress glycogen production or activate the flagellar swimming

**Fig. 6.** Western blot detection of RsmA<sub>Sm</sub>. Western blots of total cellular proteins from *P. fluorescens* (a) and *S. meliloti* (b) strains probed with polyclonal antibodies against *Y. enterocolitica* RsmA protein. The Coomassie blue-stained portion of the SDS-PAGE gels corresponding to the RsmA migration zone is shown under the blots to visualize protein loading. (a) Expression of *rsmASm* alleles in *P. fluorescens* rsmAE mutant strain CHA1009 bearing different plasmid constructs (as detailed in Table 1). Under the utilized electrophoretic conditions, RsmA and RsmE from wild-type strain *P. fluorescens* CHA0 migrated as a single band. (b) Expression of *rsmASm* alleles in *S. meliloti* strains bearing different plasmid constructs (as detailed in Table 1). 2011 and JJ1c10, wild-type reference strains that do not contain cryptic plasmids; MBA19, wild-type isolate bearing cryptic plasmid pMBA19a, which encodes *rsmASm*. The arrow points to RsmA/E and RsmA<sub>Sm</sub> bands.

**Table 2.** Translational control of target mRNA reporters by the full-length R<sub>Sm</sub>A<sub>Sm</sub> and its C-terminal-truncated variant

<table>
<thead>
<tr>
<th>Reporter</th>
<th>Genetic background (strain)</th>
<th>Complementing plasmid*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>pME6000</td>
<td>pBB84</td>
</tr>
<tr>
<td>hcaA&lt;sup&gt;−&lt;/sup&gt;−lacZ</td>
<td><em>rsmA</em> <em>rsmE</em> <em>gacS</em> (CHA1028)</td>
<td>7209 ± 562</td>
</tr>
<tr>
<td></td>
<td><em>rsmA</em> <em>rsmE</em> (CHA1027)</td>
<td>10 271 ± 1157</td>
</tr>
<tr>
<td>aprA&lt;sup&gt;−&lt;/sup&gt;−lacZ</td>
<td><em>rsmA</em> <em>rsmE</em> <em>gacS</em> (CHA1007)</td>
<td>1962 ± 159</td>
</tr>
<tr>
<td></td>
<td><em>rsmA</em> <em>rsmE</em> (CHA1021)</td>
<td>2169 ± 306</td>
</tr>
</tbody>
</table>

*Values shown are in Miller units. The translational repression factor exerted by the corresponding RsmA<sub>Sm</sub> version is indicated in parentheses. The data correspond to the mean of three replicate cultures ± SD.*
motility of the csrA mutant (Fig. S2). Expression of rsmASm in E. coli could not be confirmed by Western blotting due to the strong cross-reactivity of the antibody towards other cellular proteins of similar size (data not shown). To summarize, the rsmASm allele is expressed and functional in P. fluorescens and P. aeruginosa, but it is not expressed or functional in E. coli and S. meliloti.

**DISCUSSION**

The eubacterial Csr/Rsm post-transcriptional regulatory circuits control diverse and unrelated cellular processes such as central carbon metabolism, motility, biofilm formation, extracellular metabolite synthesis, virulence and pathogenesis, quorum sensing and oxidative stress response (Lapouge et al., 2008; Romeo et al., 2012; Timmermans & Van Melderen, 2010). The circuits depend on RNA-binding proteins of the CsrA/RsmA family that control mRNA expression at the translational level, and on cognate sRNAs that titrate away CsrA/RsmA proteins to relieve bound mRNAs (Romeo et al., 2012). Members of the CsrA/RsmA translational regulatory protein family can be found encoded exclusively in the chromosomes of a number of eubacterial divisions, although remarkably some lineages such as Alphaproteobacteria lack csrA/rsmA chromosomal homologues (Table S1). In this context, the identification of a csrA/rsmA gene in the replication region of a cryptic plasmid from the alphaproteobacterium S. meliloti (Watson & Heys, 2006) motivated us to further characterize this plasmid-encoded allele. The gene, here referred to as rsmASm, is highly similar to the rsmA allele of X. axonopodis pv. citri, but it differs from typical CsrA/RsmA proteins of Gram-negative bacteria in that it has an extended C terminus with a predicted additional α-helix with a predicted C-terminal α-helix (Fig. 2). All other sequence and structural features strongly suggest that rsmASm is a translational regulator functionally related to CsrA/RsmA proteins (Fig. 2). In fact, the results presented here show that: (1) the rsmASm allele present in pSM1 is expressed and encodes a functional repressor in the heterologous host P. fluorescens; (2) the activity of the RsmASm protein is antagonized by the P. fluorescens antagonistic sRNAs RsmX/Y/Z; (3) the RsmASm protein protects RsmY from degradation; and (4) the RsmASm C-terminal extra α-helix is dispensable for the protein to function as a repressor of target mRNA genes and to be counteracted by Rsm sRNAs in P. fluorescens, although it is necessary to achieve a proper cellular level.

Interestingly, the rsmASm gene was poorly expressed in the heterologous host P. fluorescens from vector pBB84 unless the genes required for plasmid pMB19a replication initiation and control were removed (as in pSM1 or pSM2 constructs). As the rsmASm gene is encoded divergently to the plasmid replica operon, it may be speculated that rsmASm transcription is coincidentally subject to the negative control of replica expression typical of IncC plasmids (Fig. 1). Although the perfect KorA-binding motif GTTGTAGCTAAAC (Kostelidou & Thomas, 2002) is not present in the ORF II–rsmASm intergenic region, a less perfect repeat may serve as a negative regulatory site that directly affects rsmASm expression. This would explain the very low expression of rsmASm from the pBB84 vector in the heterologous P. fluorescens cells, and the gain of expression when removed from the original genetic context. As the gene was not expressed in the natural background in S. meliloti strains (either in pBB84 or in pSM2), we cannot speculate on the operation of the postulated negative control of rsmASm expression by the plasmid copy control mechanism in the original S. meliloti host.

The fact that expression of the rsmASm allele depended on the host strain (Figs 6 and S2) suggests that there might be specific transcriptional and/or translational requirements for proper rsmASm expression. Transcriptional signals and transcriptional regulation of csrA/rsmA genes have been characterized only in E. coli (Yakhnin et al., 2011). In this enterobacterium, the promoter region spans 250 bp and csrA transcription is driven by five different promoters, two of which are dependent on the RpoS sigma factor (Yakhnin et al., 2011). In other bacterial taxa, csrA/rsmA transcription has not yet been characterized. As the wild-type rsmASm alleles present in pSM1 and pSM2 were not expressed from the cloning vector lac promoter, we could delimit a minimal 250 bp region that allows expression of rsmASm in P. fluorescens and that may serve to further characterize the transcriptional regulation of the rsmASm gene. Sequence inspection of the 250 bp region containing the rsmASm promoter (Fig. 1) did not reveal an obvious DNA motif closely resembling the σ70 consensus of E. coli (TTGACA-N17-TATAAT) (Harley & Reynolds, 1987) or that of rhizobial promoters (CTTGAC-N17-CTATATc) (MacLellan et al., 2006). Instead, a putative bacterial σ70-dependent promoter was recognized in silico (GTGCCG-N17-TATTTC) (Fig. 1), whose −10 and −35 motifs deviate markedly from the canonical enterobacterial, rhizobial and xanthomonad (Katzen et al., 1996) consensus sequences. These observations might explain the lack of rsmASm expression in S. meliloti (Figs 6 and S2). In E. coli, we could not rule out that the protein is expressed but not able to functionally complement the csrA mutation (Fig. S2). It has been recently reported that the Campylobacter jejuni CsrA protein, expressed from an inducible araBAD promoter, does not repress glycogen production in E. coli (Fields & Thompson, 2012).

To our knowledge, this study constitutes the first functional characterization of a member of the CsrA/RsmA family that is encoded in a mobile genetic element. It could be speculated that the rsmASm gene was mobilized from the chromosome of a gammaproteobacterium to a broad-host-range plasmid that has been fortuitously detected in an S. meliloti soil isolate (Watson & Heys, 2006). A further transfer event from this mobile platform to the chromosome of a bacterium lacking csrA/rsmA genes, such as S. meliloti, might introduce unexpected global regulation and pleiotropy (Mukherjee et al., 2011).
As we could not identify sequences that would encode sRNAs antagonistic to RsmA, the 4.5 kb sequenced portion of the cryptic plasmid pMBA19a, it would be interesting to explore the whole 36 kb sequence of pMBA19a to search for putative accompanying sRNA genes that may constitute the mobilization of a complete Csr/Rsm circuit. However, the activity of CsrA/RsmA proteins may also be controlled by molecules other than sRNAs; the post-transcriptional regulatory activity of the B. subtilis CsrA protein is negatively controlled by direct interaction with the FliW protein (Mukherjee et al., 2011). Moreover, the FliW protein is an ancestral element often encoded adjacent to csrA and flagellar genes in Firmicutes, thus suggesting an evolutionary and functional link to the control of flagellar motility (Mukherjee et al., 2011). In this regard, the RsmA protein is atypical in that its sequence bears features of both Gram-negative and Gram-positive CsrA/RsmA homologues: its conserved core resembles that of Alphaproteobacteria (particularly of xanthomonads) and the extended C terminus that may fold into an extra z-helix more likely resembles the CsrA/RsmA proteins of Gram-positive bacteria (Fig. 1). The evolutionary path of this apparently chimeric rsmA gene is intriguing.

The heterogeneous phyletic distribution of csrA/rsmA genes among bacterial species could be due to horizontal gene transfer of this kind of global regulator (Table S1). A recent phylogenetic analysis of members of the CsrA/RsmA family indicates that these regulatory elements were lost from the Alphaproteobacteria and Betaproteobacteria but reappeared in the Gammaproteobacteria branch adjacent to tRNA genes, which are commonly implicated as sites of horizontal gene transfer (Mukherjee et al., 2011). Thus, it would be worth extending the search for and characterization of csrA/rsmA genes in other mobile genetic elements such as plages, plasmids and genomic islands, in order to contribute to the understanding of the evolutionary history of this family of post-transcriptional regulators of mRNA expression.

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