Prediction of Sinorhizobium Meliloti sRNA Genes and Experimental Detection in Strain 2011

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Abstract

Background: Small non-coding RNAs (sRNAs) have emerged as ubiquitous regulatory elements in bacteria and other life domains. However, few sRNAs have been identified outside several well-studied species of gamma-proteobacteria and thus relatively little is known about the role of RNA-mediated regulation in most other bacterial genera. Here we have conducted a computational prediction of putative sRNA genes in intergenic regions (IgRs) of the symbiotic α-proteobacterium S. meliloti 1021 and experimentally confirmed the expression of dozens of these candidate loci in the closely related strain S. meliloti 2011.

Results: Our first sRNA candidate compilation was based mainly on the output of the sRNAPredictHT algorithm. A thorough manual sequence analysis of the curated list rendered an initial set of 18 IgRs of interest, from which 14 candidates were detected in strain 2011 by Northern blot and/or microarray analysis. Interestingly, the intracellular transcript levels varied in response to various stress conditions. We developed an alternative computational method to more sensitively predict sRNA-encoding genes and score these predicted genes based on several features to allow identification of the strongest candidates. With this novel strategy, we predicted 60 chromosomal independent transcriptional units that, according to our annotation, represent strong candidates for sRNA-encoding genes, including most of the sRNAs experimentally verified in this work and in two other contemporary studies. Additionally, we predicted numerous candidate sRNA genes encoded in megaplasmids pSymA and pSymB. A significant proportion of the chromosomal- and megaplasmid-borne putative sRNA genes were validated by microarray analysis in strain 2011.

Conclusion: Our data extend the number of experimentally detected S. meliloti sRNAs and significantly expand the list of putative sRNA-encoding IgRs in this and closely related α-proteobacteria. In addition, we have developed a computational method that proved useful to predict sRNA-encoding genes in S. meliloti. We anticipate that this predictive approach can be flexibly implemented in many other bacterial species.
Background

In bacteria, small, non-coding RNA molecules that influence the expression of other genes are collectively referred to as sRNAs [1]. Significant experimental and theoretical evidence suggests sRNA-based regulation of gene expression is a paradigm common to all domains of life [2,3]. To date, two main mechanisms of sRNA activity have been described, both of which result in a modification of target mRNA translation and/or stability. The most common mechanism involves antisense pairing between the regulatory sRNA and the mRNA target [4]. In some cases, a single sRNA can mediate disparate regulatory effects on different mRNA targets. For instance, binding of the E. coli RyhB to the 5'-untranslated region of shiA mRNA activates shiA translation [5] whereas RhyB binding to sodB mRNA promotes its degradation [6]. In many cases the sRNA:mRNA interaction occurs over short regions of imperfect sequence complementarity and thus requires stabilization by the RNA chaperone Hfq [7]. The second sRNA-based mechanism is molecular mimicry, in which sRNAs offer multiple binding sites to RNA binding proteins of the CsrA/RsmA family, thus competitively relieving protein-mediated regulation of target mRNAs [8]. Most sRNAs characterized to date act as intermediate genetic elements of signal transduction cascades that are themselves initiated by a variety of external stimuli [9].

The number of putative and physically confirmed prokaryotic sRNAs has grown significantly in recent years, due in large part to the development and utilization of computational methods for predicting sRNA-encoding loci [10,11]. The pioneering predictive studies were initiated a few years ago when several groups discovered dozens of sRNAs in the intergenic regions of E. coli [12-14]. In these seminal studies, putative sRNAs were identified based on their association with genetic features common to several previously known sRNAs [15], such as their transcription from DNA regions between protein coding genes, their association with Rho-independent transcriptional terminator and/or promoter signals, the conservation of their primary sequence among closely related species, and their potential for encoding conserved secondary structure [16].

Sinorhizobium meliloti is an α-proteobacterium able to establish an intimate symbiosis with the roots of legumes belonging to the genera Medicago, Melilotus and Trigonella [17]. Upon an intricate chemical dialog and cross-recognition between bacterium and roots, S. meliloti colonizes the interior of de novo root organs, the nodules, in which it differentiates into bacteroids committed to biological fixation of atmospheric nitrogen [18]. The genome of the sequenced strain S. meliloti 1021 is organized into three replicons, the "chromosome" (3.65 Mb) and two megaplasmids, pSymA (1.35 Mb) and pSymB (1.68 Mb), that were most likely acquired through horizontally transfer. Sequence analysis indicates that pSymA, the giant plasmid devoted to nodulation and nitrogen fixation functions, was acquired later in the evolution of the host bacterium than pSymB [19-21]. The chromosome of S. meliloti encodes an hfq homolog, suggesting that it also encodes sRNAs. However, prior to the initiation of this study, no screens for sRNAs had been conducted in Sinorhizobium and only the conserved chromosomal tmRNA homolog (ssrA) and an antisense countertranscript involved in control of pSymA and pSymB replication had been functionally characterized in S. meliloti [22-25]. While this work was in preparation, two groups reported the identification of a total of 15 chromosomally encoded sRNAs (including the widely conserved 6S RNA) and one pSymB-derived sRNA in S. meliloti strain 1021 [26,27]. These two studies employed similar predictive criteria, ones that were significantly different from the one utilized in this work. Here we report the prediction of dozens of putative sRNA genes encoded in the three replications of S. meliloti and the experimental detection of many transcripts under different stress conditions in the closely related strain S. meliloti 2011. Our first sRNA candidate compilation was based mainly on the output of the sRNAPredictHT algorithm. A thorough manual sequence analysis of the curated list rendered an initial set of 18 IgRs of interest, from which 14 candidates were detected by Northern blot and/or microarray analysis. As we suspected that S. meliloti would encode more sRNA transcripts, we developed an alternative computational method to more sensitively predict sRNA-encoding genes, which introduces a novel cumulative scoring procedure to identify the strongest candidates. This scheme takes into account the location of predicted transcription signatures (promoters and terminators), their relative orientations and proximity to flanking protein coding genes, and their association with regions of conserved primary sequence and secondary structure. A novel scoring algorithm was integrated into this approach to allow the strongest candidate loci to be readily identified. Using this prediction and scoring approach we detected most of the S. meliloti small transcripts revealed by our first screening and in two recent studies [26,27] as well as numerous strong candidates for novel sRNA-encoding genes in IgRs of S. meliloti chromosome and megaplasmids. A significant proportion of these chromosomal- and megaplasmid-borne putative sRNA genes were validated by microarray analysis.

Methods

First set of predicted sRNA-encoding genes in S. meliloti chromosomal intergenic regions

Among the 2920 chromosomal IgRs of S. meliloti 1021 [28], a first set of IgRs potentially encoding sRNAs (Table 1) was compiled by: 1) selection of IgRs with annotated orphan transcriptional terminators [28]; 2) selection of
Table 1: First compilation of *S. meliloti* chromosomal IgRs predicted to encode sRNAs.

| IgR# | Found by | Adjacent genes | sRNA strand | Prom.? | Term.? | Blast hits in | Expected size | Band size in Northern blot | Microarray detection | Gene* | Reference |
|------|----------|----------------|-------------|---------|--------|---------------|---------------|----------------------------|---------------------|--------|-----------|
|      |          |                |             |         |        |               |               |                            |                     |        |           |
| 1    | Rfam     | SMc03975<      | s70         | n       | eubacteria | ~160 nt     | ~155 nt       | <, H, C, S, A, B, O       | (2972187–2972236) | 6S RNA (sraC22 = sra56) [26,27,62,67] |
| 2    | OT       | SMc04042<      | NN–s70      | y       | Sm Ri Re At | ~80 nt       | duplet < 100 nt | -                           | sm8 = suhB           | [65,67], this work |
| 3    | SP       | SMc01933<      | NN–s70      | y       | Sm Re RI At Ml | ~150 nt     | ~165 nt       | <, A, C, H, S (1398340–1398389) snc9 = sra32 [26,27] |
| 4    | tR       | Gln-tRNA<      | <           | -       | y       | Sm Re RI     | ?             | multiple ~150 nt & ~80 nt | -                   | sm137 | this work |
| 5    | tR       | SMc02151<      | NN–s70      | y       | -       | ~240 nt      | no bands detected | >, S (*) (560802–560753) | srl2                | [27] |
| 6    | OT       | gltB<          | NN          | y       | Sm Re RI | ~100–200 nt | not done 4   | >, A, C (3031662–3031711) | -                   | this work |
| 7    | OT       | SMc04453<      | NN          | y       | Sm Re RI | ~390 nt      | duplet, ~135 & ~200 nt | <, A, C, O, S (2321429–2321478) | sm26               | this work |
| 8    | OT       | SMc01257<      | NN–s70–PhoB | y       | Sm At Oa Msp | ~170 nt     | not done 4   | -                           | sm30                | this work |
| 9    | OT       | thdF<          | s70         | y       | Sm       | ~180 nt      | not done 4   | -                           | sm130               | this work |
| 10   | SP       | SMc00034<      | s70         | y       | Sm Re RI | ~190 nt      | ~175 nt      | -                           | sra25               | [27] |
| #  | SP | sRNA Accession | Orientation | Strand | Sequence | Sense | Methylase | Length | M-value | Stress Conditions | smRNA Name | Reference(s) |
|----|----|----------------|-------------|--------|----------|-------|-----------|--------|---------|-----------------|------------|--------------|
| 11 | SP | SMc00108<SMc00109< |  > | < | s70 | y | Sm Rl Re At | ~100–120 nt | ~100–120 nt | - | sm145 | this work |
| 12 | SP | celR2>rpmG< | > | < | s70 | y | Sm Rl Re At, Mi Msp Ac | ~150 nt | not done 6 | >, A, B, C, H, O, S | smrC10 = sra33 | [26,27] |
| 13 | SP | polA<SMc02851> |  > | > | NN–s70 | y | Sm Rl Re At | ~150 nt | duplet, ~140 & ~90 nt | - | smrC7 = sra03 | [26,27] |
| 14 | SP | SMc02910<SMc02911< | > | < | s70 | y | Sm Rl Re At, Mi Bo Oa | ~60–150 nt | multiple, ~90–100 & ~180–210 | >, B, C, O | sm76 | this work |
| 15 | SP | SMc03988<SMc03989> | > | < | s70 | y | Sm Rl Re At | ~110 nt | ~80 nt | >, A, B, C, H, O, S | sm84 | this work |
| 16 | SP | atpH<SMc02497< | > | < | s70 | y | Sm Rl Re At | ~110 nt | ~100 nt | - | sm270 | this work |
| 17 | SP | dapF<ffh> | > | < | s70 | y | Sm Rl Re At | ~120 nt | not done | >, A, B, O, S | sm5 | this work |
| 18 | OT | SMc00821<SMc00822> | > | - | - | y | Sm Re Rl | ~80 nt | not done | >, A, C, H, O, S | sml90 | this work |

1. Rfam, RNA families database [33,67]; OT, IgR with annotated orphan terminator; tR, IgR flanking tRNAs; SP, sRNAPredictHT.
2. The transcribed strand is indicated (>, forward; <, reverse).
3. Putative promoter sequence detected by conservation in sequence alignment, search of consensus sequences or neural network promoter prediction. s70, sequence highly similar to the S. meliloti constitutive promoter consensus sequence [49]; NN, neural network promoter prediction [47]; PhoB, sequence detected with homology to the PhoB transcriptional regulator binding consensus [51].
4. Sm, Sinorhizobium medicae WSM419; Rl, Rhizobium leguminosarum biovar viciae 3841; Re, Rhizobium etli CFN42; At, Aegobacterium tumefaciens C58; Mi, Mesorhizobium loti MAFF303099; Oa, Ochrobactrum anthropi ATCC49188; Msp, Mesorhizobium sp. BNC1; Bo, Brucella ovis ATCC25840.
5. Approximate length of sRNA based on putative 5’ and 3’ ends.
6. PCR failed to amplify the IgR.
7. Detection on the oligonucleotide microarray Sm14kOLI. > and < denote the orientation of the detected signal (absolute M-value ≥ 2.5 represents an enrichment of small RNA transcripts). A, B, C, H, O and S denote the stress condition under which the signal was detected (A, acidic; B, basic; C, cold shock; H, heat shock; O, oxidative, S, saline). The coordinates of the oligonucleotide probes that gave positive signals are indicated in brackets. -, not detected under the conditions studied. (*), M-value ≥ 2.
8. Gene name as designated in the literature (smrC#, sra#) [26,27] or according to our predictive scheme (sm#).

Table 1: First compilation of S. meliloti chromosomal IgRs predicted to encode sRNAs. (Continued)
IgRs in the vicinity of tRNAs [29,30]; 3) application of sRNApredictHT (I. Livny; unpublished data), an improved version of the program sRNApredict2 developed by Livny and co-workers [31]. Using default parameters, sRNApredictHT identified 186 sequence elements as putative sRNAs (Additional file 1). However, almost 60% of the hits corresponded to annotated [19,28,32] or non-annotated sequence repeats. Each IgR was used to query Rfam database [33] to identify previously annotated RNA regulatory elements and then inspected for the presence of transcriptional signals (promoters and Rho-independent terminators; see below). We retained 17 chromosomal IgRs that were likely to encode sRNAs and an additional IgR encoding a putative 6S RNA homologue (Table 1).

**Northern blot detection of the first set of sRNA candidates**

*Sinorhizobium meliloti* strain 2011 [34] was maintained on TY agar plates [35] with streptomycin (400 μg/ml). We chose the *Rhizobium* defined medium (RDM) [36] with shaking (120 rpm) at 28°C as the referential growth condition. For preparation of RNA extracts, 125-ml flasks containing 20 ml of RDM were inoculated with 0.2 ml of a saturated RDM pre-culture and incubated at 120 rpm until cell harvest. To introduce stress conditions, the RDM basal medium or growth conditions were modified as follows: high salt RDM (0.3 M NaCl), low phosphate RDM (0.1 mM phosphate, 10 mM MOPS pH 7.0), RDM with ethanol (2% v/v), RDM with SDS (0.1% w/v) and RDM with H₂O₂ (0.1 mM). High temperature stress was applied by growing cells at 37°C. For acid stress, exponential phase cells growing in 20 ml of RDM (OD₆₀₀ = 0.5) were collected by low speed centrifugation, washed and resuspended in 20 ml of RDM containing 20 mM MES and equilibrated at pH 5.5, and incubated 90 min at 28°C with shaking before harvesting cells for RNA extraction.

Total RNA was extracted immediately after cell harvest by low speed centrifugation (1800 g, 10 min, and 20°C). The cell pellet was resuspended in Trizol® (Invitrogen; 1.5 ml for cultures with OD₆₀₀ < 1.5 or 3.0 ml for cultures with OD₆₀₀ > 1.5) and treated 1 min at 60°C. Upon addition of 0.2 vols of chloroform and vigorous shaking during 15 secs, the RNA present in the aqueous supernatant was precipitated with 0.5 vol of isopropanol. The pellet was washed in 70% ethanol, air dried and resuspended in 20 μl of DEPC-treated deionized water. RNA samples were conserved at -130°C. The purity and integrity of RNA preparations were assessed by denaturing PAGE electrophoresis followed by silver staining [37] and the RNA concentration was estimated by UV spectrometry [38]. For Northern blots, 1–3 μg RNA present in 1 μl of each sample were fractionated on denaturing polyacrylamide gels (60 × 80 × 0.75 mm containing 8.3 M urea, 8% acrylamide and 0.2% bisacrylamide in 1× TBE buffer). The lane corresponding to the molecular weight markers (low range RNA ladder; Fermentas) was cut out, stained with 5 μg ml⁻¹ ethidium bromide and photographed under UV light. The rest of the gel was electrophorized at 150 mA (15–25 V) onto a Hybond-N membrane in 1× TBE buffer for 20 min. Membranes were washed with 2× SSC (0.3 M NaCl and 30 mM sodium citrate) before nucleic acids were cross-linked by exposure to UV light for 5 min [38]. Northern hybridizations were done with digoxigenin (DIG)-labeled DNA probes generated by PCR covering entirely or partially each IgR (Additional file 2). The IgR amplicons of detected candidate sRNAs were cloned in the pCR®2.1-TOPO vector and sequenced to confirm the identity of the PCR products. Hybridized membranes were developed following the protocol recommended by the manufacturer (Roche Diagnostics GmbH). The detected RNA bands were quantified by densitometry with Imagej v1.38 [39] and standardized by the amount of loaded RNA visualized by silver staining.

**Microarray detection of sRNA candidates**

Pre-cultures of *S. meliloti* strain 2011 were grown at 30°C in TY [35] or GMS [40] media. For RNA isolation, 100 ml flasks with 50 ml TY or GMS medium, supplemented with 8 μg/ml nalidixic acid, were inoculated with 200 μl of pre-culture and incubated in a rotary shaker (175 rpm) at 30°C to an OD₆₀₀ = 0.6. To induce stress, the medium and growth conditions were modified as follows. High salt stress: addition of NaCl to a final concentration of 0.4 M in GMS medium. Oxidative stress: addition of H₂O₂ to a final concentration of 10 mM in GMS medium. Cold shock stress: temperature shift of the culture in TY medium from 30°C to 20°C. Heat shock stress: temperature shift of the culture in TY medium from 30°C to 40°C. Acid or alkaline stress: cultures grown in GMS to an OD₆₀₀ = 0.6 were centrifuged and then re-suspended in GMS modified by adding HCl to pH 5.8, or by adding NaOH to pH 8.5. In all cases, cells were harvested 15 and 45 min after exposure to stress conditions.

RNA was isolated and separated into small RNA (< 200 nt) and long RNA (> 200 nt) fractions using the miRNeasy Mini Kit (Qiagen) or Ambion mirVana miRNA Isolation Kit (Ambion) according to the manufacturers’ instructions. Quality of RNA was analyzed applying the Agilent RNA 6000 Pico Kit on the Agilent 2100 Bioanalyzer (Agilent Technologies). To consider both orientations, aliquots from the same fractions of small and long RNA pools were sense labelled using the mirVana miRNA Labeling Kit (Ambion) and antisense labelled as described [41]. Differing from the cDNA labelling procedure [41], small RNA fractions were first tailed with PolyA polymerase (Ambion). Oligo dT and amino-allyl random hexamer primers were used for the synthesis of cDNA.
Hybridization of the small RNA fraction (Cy3-fluorescent marker) was compared to that of the long RNA fraction (Cy5-fluorescent marker). Three combinations were performed: 1. the small RNA fraction with the long RNA fraction, both of which were sense labelled, 2. the same fractions in which both were antisense labelled, and 3. a combination of the sense labelled small RNA fraction and the antisense labelled long RNA fraction. Slide processing, sample hybridization, and scanning procedures were performed as described [41] applying the Sm14kOLI microarray that carries 50 mer to 70 mer oligonucleotide probed directed against coding regions and intergenic regions [42]. Analysis of microarray images was carried out applying the ImaGene 6.0 software (BioDiscoveries) [41]. Lowess normalization and significance test (fdr) were performed with the EMMA software [43]. The M-Value represents the logarithmic ratio between both channels. The A-Value represents the logarithm of the combined intensities of both channels. Positive M-values ≥ 2.5 represent an enrichment of small RNA fragments (< = 200 nt) and therefore were classified as sRNA candidates.

**Novel method for in silico identification of sRNA candidate genes**

From the original 2920 chromosomal IgRs, all the annotated repetitive elements of 1021 chromosome (Sm-repeats, RIMEs and AB, C motifs) [19,28,32] were removed and the flanking IgR segments were treated as new IgRs. 1720 chromosomal IgRs free of annotated repeats and longer than 150 nt were retained for further analysis. Certain IgRs were also removed if they gave Blast hits with E-value < 10^-3 when queried against themselves, reducing the number of IgRs to 778. With the help of open source algorithms and web based tools, the 778 chromosomal IgRs were subjected to the following sequence analyses: prediction of Rho-independent transcription terminators and of promoter signals, sequence conservation (BlastN, [44]) and secondary structure conservation (QRNA analysis) [45].

For prediction of Rho-independent transcription terminators, the web based TranstermHP server [46] was queried to generate a list of putative terminator sequences in chromosomal IgRs of strain 1021, having a stem length of 4–23 bases, a hairpin score ≤ -1.5, a tail score ≤ -2.0 and ≥ 80% of confidence. Orphan terminators (i.e., those that do not correspond to flanking CDS) were scored 3. Predicted terminators co-oriented with flanking ORFs were scored according to their relative distance to the 3’-end of the corresponding annotated gene so that a score of 2 was assigned if the terminator was farther than 200 bp, 1 if the distance was 100–200 nt, and 0 if it was closer than 100 bp.

Promoter signals were predicted with three alternative methods. A first set of putative promoters was generated with a web based neural network based routine [47] set up for bacterial sequences in both DNA strands with a minimum score of 0.8. A second set of putative promoters was compiled by querying IgRs with Fuzznuc [48] using available *S. meliloti* consensus sequences as input. For σ^54^-dependent promoters the query was CITGAC(N_{17})CTATAT [49] with up to 4 mismatches allowed. For σ^70^-dependent promoters the query was TGCCACG(N_{4})ITGCW [50] with up to 2 mismatches allowed. For putative PhoB-binding sites the results of two queries were pooled, CTGTCT(A_N)CTGTCT [51] with up to 4 mismatches allowed and TGWCA(N_{4})CYKTCAK [52] with up to 2 mismatches allowed. A third group of promoters was predicted with the help of the matrix-scan tool available at the Rsat web server [53], upon introduction of available scoring matrices for *S. meliloti* σ^54-, σ^70-, and PhoB-dependent promoters [49-52] and with default parameters. A similar scoring criterion to that used for terminators was applied to predicted promoters. Orphan promoters were scored 3. Putative promoters were rated 2 if the 5’-end of the co-oriented flanking CDS was farther than 300 bp, 1 if this distance was 200–300 bp and 0, if they were closer than 200 bp.

Similarity searches performed with BlastN were done using default parameter values. IgRs were used to query against a database of 559 complete eubacterial genomes [54] and we defined a Blast score (#BlastN) that for each input IgR sequence consists in the sum of all the hits with E-values below 10^-3. We used QRNA [45] to analyze the sequence alignments generated for each IgR and a score was derived summing all the positive hits detected (#QRNA).

Finally, the individual scores for predicted terminators (#T), promoters (#P), BlastN (#BlastN) and QRNA analysis (#QRNA) were combined to generate a Global Score (GS). If a putative promoter and a terminator lay co-oriented and separated from each other by 40–500 bp, suggesting the presence of a single and independent transcriptional unit, the IgR is scored 10 and the individual scores for promoter and terminator are no longer considered. The GS for those IgRs containing such putative elements indicative of sRNAs was calculated as (10 + #BlastN + #QRNA). For those IgRs lacking putative independent transcriptional units, the GS was calculated as (#T + #P + #BlastN + #QRNA).

**Results & Discussion**

**A first selection of chromosomal intergenic regions potentially encoding sRNAs**

At the time we initiated this study, the only chromosomal non-coding RNA gene that had been characterized in the
α-proteobacterium *S. meliloti* was the tmRNA homolog *ssrA* [23]. However, several findings suggested that other sRNAs might be expressed in this α-proteobacterium. The electrophoretic fractionation in denaturing polyacrylamide gels of total RNA from strain 2011 cells grown under different conditions (Additional file 3) revealed several RNA bands of < 300 nt other than the conserved and abundant 5S RNA, 4.5S RNA and tRNAs [27]. Another indirect evidence of the existence of sRNAs in *S. meliloti* comes from the pleiotropic phenotype of the *S. meliloti* 2011 *hfq* mutant (Sobrero & Valverde, unpublished). These observations suggest that the product of the *hfq* gene (Smco01048 = *nrfA*) may be required to assist diverse regulatory interactions between mRNAs and sRNAs, as reported for other bacterial species [7,55]. We thus decided to perform a bioinformatic search of sRNA genes using the genomic information of the sequenced strain *S. meliloti* 1021.

Although there are reports of sRNAs transcribed from coding regions in other bacteria [56,57], we focused our search in the regions between annotated ORFs (hereafter IgRs) of the *S. meliloti* chromosome [19]. We first identified in the *S. meliloti* annotated database [28] chromosomal IgRs containing transcriptional terminators unlikely to be associated with flanking ORFs as well as regions of sequence conservation in the vicinity of annotated tRNA genes, which may represent horizontally transferred genetic elements [29,30]. This “manual” procedure resulted in the identification of a few interesting IgRs (tagged OT and tR in Table 1). Next, we applied sRNApredictHT, an improved version of the systematic and integrative tool sRNAPredict2 already used for the prediction of sRNA genes in several bacterial species [31]. sRNApredictHT identifies sRNA-encoding loci based on the colocalization of transcriptional terminators and IgR sequence conservation [31]. Among the 186 candidate loci identified by sRNApredictHT (Additional file 1), 56% were identified in IgRs containing at least one repetitive DNA element, either the annotated *Rhizobium*-specific intergenic mosaic elements (RIMEs) [19,32], Sm-repeats [19,28], AB, C palindromes [19,28], or in some cases, even non-annotated repeats. Rhizobial genomes are characterized for the presence of dozens of these intergenic sequences of unknown function that typically share significant primary sequence and secondary structure conservation [58]. Upon elimination of IgRs containing repeats, the sRNApredictHT output was narrowed down to a list of 76 candidate IgRs (Additional file 4). To further reduce the number of IgRs for experimental verification, we looked for candidates associated with putative promoters. This stringent filtering yielded a list of 17 interesting IgRs (Table 1). In fact, 15 candidate IgRs have both potential 5’ and 3’ transcriptional signals and are conserved in related species (Table 1), suggesting that they correspond to bona fide sRNA-encoding genes. Table 1 also includes a putative homolog of the widely conserved 6S RNA (IgR#1; [33]) which was not picked up by sRNApredictHT because it lacks a typical Rho-independent terminator (Table 1). With the exception of IgR#5, all the candidates in Table 1 are conserved in at least one related α-proteobacterium. All IgRs but the aforementioned IgR#1 (6S RNA) are associated with a predicted Rho-independent terminator.

**Experimental verification of selected sRNA candidates in S. meliloti strain 2011**

For experimental verification of most putative sRNA genes listed in Table 1, we performed Northern hybridizations and microarray analysis of RNA from *S. meliloti* strain 2011 that, like the sequenced strain 1021, is a streptomycin-resistant mutant derived from the isolate SU47. Although the separate and parallel continuous manipulation of these isogenic strains gave origin to subtle differences in their symbiotic behaviour and gene expression [52,59], the overall high degree of sequence similarity between both strains permits the use of strain 2011 to test predictions based on 1021 sequence. As many characterized sRNAs are involved in regulatory processes induced by a variety of external stimuli [9], RNA extracts were prepared from cells grown both under standard culture conditions and under a variety of stressful conditions.

Of the 12 candidate IgRs from our initial compilation that were subjected to experimental verification by Northern analysis of *S. meliloti* 2011 RNA, 11 were detected (Table 1, Figure 1, Additional file 5). For the majority, the transcript size was consistent with our predictions (Table 1). In some cases (e.g., IgR#10, IgR#11 or IgR#13), multiple bands were observed. Two IgRs (#4 and #14) revealed a complex banding pattern (Table 1; Additional file 5) and further experiments are required to elucidate the origin of the detected RNA bands. Microarray analysis of strain 2011 RNA detected enrichment of RNA molecules < 200 nt corresponding to the predicted DNA regions for IgR#1, IgR#3, IgR#6, IgR#7, IgR#12, IgR#14, IgR#15, IgR#17 and IgR#18 (M-value > 2.5; Table 1). For the rest of the IgRs for which no signals were detected in Northern blot or microarray analysis, it may be that the transcript level is below our threshold of detection or that this candidate sRNA has a very specific inducing signal different from those included in our assays. This may be the case for IgR#5 with no detected bands in Northern blot (Figure 1) and a slightly lower enrichment detected in the microarray experiment (M-value = 2.15 under 45 min of saline stress; Table 2). In fact, two transcripts of different polarity (*sra12a* and *sra12b*) were reported for the same IgR in strain 1021 [27]. During the preparation of this manuscript, transcripts were reported in total RNA from strain 1021 for IgR#1, IgR#3, IgR#5, IgR#10, IgR#12 and IgR#13 [26,27]. Thus, our data independently confirmed the
Table 2: Top 20 highest-scoring putative sRNA genes predicted by the global scoring procedure as independent transcriptional units in chromosomal IgRs of *S. meliloti* 1021.

| Gene or Designation | IgR length | Upstream ORF | Orientation | Promoter$^3$ | Predicted 5'-end$^3$ | Predicted 3'-end$^4$ | Blast score | Qrna score | Global score | Length (nt)$^5$ | SP$^4$ | Microarray detection$^7$ |
|---------------------|------------|--------------|-------------|--------------|------------------|------------------|-------------|-------------|--------------|----------------|-------|-----------------------------|
| *smrC15* (sm3)     | 652        | SMc01226     | <           | <           | NN, s70          | 1698732          | 1698618     | 6           | 2           | 98            | 114   | 151 (1698954-1698905)       |
| *smrC16* (sm3')    | 922        | SMc02051     | <           | <           | NN, s70          | 1667614          | 1667488     | 3           | 5           | 58            | 126   | 214 (1667516-1667467)       |
| *sm4*              | 541        | SMc01844     | >           | >           | NN, s70          | 2371490, 2371606 | 2371852     | 1           | 1           | 82            | 256-362 | n                  |
| *sm5*              | 384        | SMc03856     | <           | >           | s70              | 3522121, 3522271 | 3522379     | 12          | 8           | 80            | 108-258 | y                  |
| *sm6*              | 491        | SMc01202     | <           | <           | NN, s70          | 1728153, 1728196, 1728269 | 1728021     | 1           | 1           | 62            | 120-248 | n                  |
| *sm8*              | 301        | SMc04042     | <           | >           | NN, s70          | 3046713          | 3046789     | 9           | 4           | 53            | 76     | y                  |
| *sm9*              | 470        | SMc02080     | >           | <           | NN, s70          | 1635343, 1635411, 1635564 | 1635217     | 1           | 1           | 52            | 126-347 | n                  |
| *sm10*             | 405        | SMc00057     | >           | >           | NN, s70          | 1091047, 1091106 | 1091343     | 1           | 1           | 52            | 237-296 | n                  |
| *smrC9* (sm12)     | 710        | SMc01933     | <           | <           | NN, s70          | 1398427, 1398584 | 1398279     | 4           | 3           | 47            | 148-305 | y                  |
Table 2: Top 20 highest-scoring putative sRNA genes predicted by the global scoring procedure as independent transcriptional units in chromosomal IgRs of *S. meliloti* 1021.

| sRNA candidate | Global score (GS) | NN, σ70 | sRNA length | m54, RpoN | PhoB | σ70-dependent promoter (range of possible lengths) | σ54-dependent promoter (range of possible lengths) |
|----------------|-------------------|---------|-------------|-----------|------|-----------------------------------------------|-----------------------------------------------|
| smrC7 (sm13)   | 472               | < > >  | NN, σ70    | 201682    | 201829 | 4 3 47 147 y                                 | -                                             |
| sm14           | 410               | < > <  | NN, PhoB   | 573816, 573830 | 574040 | 4 1 45 210 y                                 | -                                             |
| sra12 (sm17)   | 829               | < > <  | NN, σ70    | 560780, 560916, 561000 | 561258 | 1 1 42 258–478 n >, S (*) (560802–560753) | -                                             |
| sm16           | 902               | > < >  | NN, σ70    | 1198309, 1198440, 1198508 | 1198093 | 1 1 42 212–416 n                             | -                                             |
| sm18           | 277               | < > >  | σ70        | 2270996, 2271068 | 2271224 | 1 1 42 156–228 n                             | -                                             |
| sm23           | 292               | < > <  | NN         | 1706863, 1706715 | 1706715 | 1 3 34 148 n                                 | -                                             |
| sm25           | 396               | < > >  | σ70, PhoB  | 2210185, 2210260 * | 2210322 | 1 2 33 62–137 n                              | -                                             |
| sm26           | 1270              | < < >  | NN         | 2321447, 2321055 | 2321055 | 2 1 33 392 y                                 | <, A, C, O, S (2321429–2321478)              |
| sm28           | 826               | > < >  | NN, σ70    | 713461, 713680, 713763 | 713290 | 1 1 32 170–463 n                             | -                                             |
| sm30           | 644               | < > >  | NN, σ70, PhoB | 1518613, 1518748 * | 1518988 | 1 1 32 234–375 n                             | -                                             |

1 sRNA candidates reported in contemporary studies retain their original notation (smrC# or sra#) [26,27]. Otherwise, the designation smt# corresponds to the full list of sRNA predictions obtained in this work by the global scoring procedure (Additional file 17). Candidate IgRs are sorted according to its descending global score (GS). Bolded candidates have been verified experimentally ([26,27]; this work).

2 NN, neural network promoter prediction; σ70, σ70-dependent promoter; s54, RpoN (σ54)-dependent promoter promoter; PhoB, putative PhoB binding site.

3 The coordinates of all putative promoters and/or transcription factor binding sites within an IgR are presented. The position given for NN is the 3' end of the identified sequence. For σ54 the position given is 7 bases downstream of the 3' end of the -10 hexamer. The 3' end of the predicted binding site for σ54 and PhoB is indicated with an asterisk.

4 Given is the position of the last uridine at the end of the terminator sequence.

5 Range of possible lengths based on putative 5' and 3' ends.

6 y, candidate present in sRNApredictHT search (Additional file 4); n, candidate absent in sRNApredictHT output.

7 As described in Table 1.
Figure 1 (see legend on next page)
expression of those putative sRNAs under different experimental conditions and in a different but closely related strain, so we assume that the corresponding IgRs of strain 2011 encode the sRNA homologues of 6S RNA (smrC9 = sra03), smrC10 ( = sla25), smrC22 (= sra33) and smrC7 (= sla03), respectively [26,27]. To summarize, through this first compilation of putative sRNA-encoding IgRs, we obtained experimental evidence by Northern and/or microarray hybridization for eight novel S. meliloti RNA transcripts corresponding to candidates IgR#2, IgR#6, IgR#7, IgR#11, IgR#15, IgR#16, IgR#17 and IgR#18 (Table 1, Figure 1). Figure 2 shows the genomic context of these putative sRNA-encoding genes. The sequence alignments and associated transcriptional signals of these confirmed candidate loci are presented in Additional files 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16.

Growth phase and stress conditions influence accumulation of detected transcripts
For several of the sRNA transcripts detected by Northern analysis, we observed differential abundances under the various growth conditions tested (Figure 1). Transcripts originating from IgR#1, IgR#2, IgR#10 and IgR#13 were more abundant in stationary phase cells (> 2×), whereas those from IgR#7 and IgR#11 seemed to be downregulated in saturated cultures. The only RNA species that was clearly upregulated under high salt conditions was the one coded in IgR#11 (> 6×). Agents that alter membrane fluidity, as SDS or ethanol, induced accumulation (> 2×) of transcripts from IgR#1, IgR#2, IgR#7, IgR#10, IgR#11 and IgR#13. In E. coli, several sRNAs participate in the control of porin levels upon membrane stress [9]. An increase in growth temperature from 28 to 37°C resulted in upregulation (> 2×) of transcripts from IgR#2 and IgR#11. Upon phosphate starvation, the transcripts from IgR#1, IgR#7, IgR#15 and IgR#16 were upregulated. A conserved PhoB binding site [51] is not evident upstream the predicted promoter for these sRNA candidates, suggesting that the positive regulation may be indirect or PhoB-independent. Finally, exposure of S. meliloti 2011 to pH 5.5 for 90 minutes, an acid stress condition that does not support growth [60], resulted in accumulation of RNAs from IgR#1, IgR#7, IgR#10 and IgR#13. For IgR#6, IgR#12, IgR#17 and IgR#18, for which no Northern hybridization data was available, we could observe an enrichment of short transcripts upon 45 min of stress conditions using microarray analysis (Table 1).

The observed expression pattern for IgR#1 is consistent with that observed for 6S RNA homologues in other bacteria. The transcript accumulated in stationary phase cells, in the presence of SDS, under phosphate deprivation and more markedly under conditions of acid stress. The level of 6S RNA increases along the growth curve being maximal in stationary phase in E. coli [61] and B. subtilis cells [62]. This correlates with a reduced utilization of the vegetative σ70 subunit by the RNA polymerase complex in favour of alternative sigma subunits [63,64]. The abundance of the sRNA from IgR#2 detected in strain 2011 was upregulated both in response to increased cell density as well as to several different stress conditions (Figure 1). This sRNA had previously been annotated as SuhB [65] but had not been subjected to experimental verification.

While the abundance of a significant number of the sRNAs identified in this study appears to be significantly affected by growth phase and/or environmental stress conditions (Figure 1, Table 1), it is still unclear how this regulation is affected. Conserved sequences suggestive of upstream regulatory sites were not detected for any of the sRNA loci confirmed in this study (Additional files 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16). Time course studies of transcript levels upon stress application together with the study of promoter expression in vitro and in planta are currently being undertaken to elucidate the regulatory mecha-
Figure 2 (see legend on next page)
Improvement of the bioinformatic predictive method and application to *S. meliloti* chromosome

Our initial computational screen proved quite accurate in identifying both previously identified and novel sRNAs (Table 1, Figures 1 and 2). However, the parameters used in this screen were quite stringent, requiring nearly all candidate loci to be associated with a putative promoter, a predicted terminator, and conserved intergenic sequence. We therefore postulated that a significant number of predicted terminator, and conserved intergenic sequence. Bioinformatic searches using similar algorithms [13,66] have often yielded a large proportion of false predictions, significantly decreasing the efficiency in which putative sRNA loci could be experimentally confirmed. Based on these previous studies, we were concerned that increasing the sensitivity of our predictive approach would result in a significant decrease in its accuracy. To address this concern, we incorporated a novel scoring algorithm that allows predicted loci to be ranked based on their likelihood of encoding a *bona fide* sRNAs (Figures 3 and 4). This allows stronger candidates to be readily identified and prioritized for experimental verification and characterization.

In our improved computational approach, IgRs are analyzed for the presence of transcriptional signals (promoters and terminators), sequence conservation (BlastN) and secondary structure conservation (QRNA) (Figure 3), and receive a corresponding score for each item (Figure 4). Thus, prediction of a promoter and a terminator co-oriented but separated for > 40 bp and < 500 bp, determines a score = 10 for this pair of signals for a given IgR (Figure 4). Instead, if only one of the signals is present (terminator or promoter) or both are predicted but not co-oriented, the maximum score for each signal would be 3 (Figure 4). Similarly, a score is assigned to each IgR based on the presence of sequence and/or secondary structure conservation (see Methods). These different scoring analyses are integrated by the assignment of a global score (GS) calculated as the sum of the individual scores (Figure 4).

We first applied our improved predictive approach to the *S. meliloti* 1021 chromosome (Figure 3 illustrates the pipeline for the chromosome). We limited our searches to IgRs 150 bp or longer that do not contain annotated or non-annotated repetitive sequences. We found that *S. meliloti* IgRs containing experimentally verified sRNA transcripts were assigned a GS of 6 (IgR#16) or higher (up to GS = 168, for the RNAse P RNA) ([26,27]; Table 3); thus we established GS = 6 as the cut-off for sRNA prediction. Our predictive scheme identified and ranked 271 IgRs with GS ≥ 6 (Additional file 17). We designated the candidate RNA elements as sm# (sm1 to sm271). SsrA, RNAse P RNA, 4.5S RNA and 6S RNA were ranked within the top 32 hits (Additional file 17). All 18 of the IgRs initially selected for experimental verification (Table 1) are contained within the list of candidate sRNA genes (Additional file 17). From the entire set, we extracted a subset of 58 IgRs predicted to contain 60 transcriptional units (i.e., a predicted promoter co-oriented with a predicted terminator separated at 40–500 bp; Figure 4) (Additional file 18). Eleven of the 18 IgRs initially compiled were included in the subset of predicted transcriptional units; the other 7 IgRs were missing from this subset because either they lack typical transcription signatures (IgR#1, IgR#4 and IgR#18; Table 1) or they differ significantly from the queried consensus and only became evident as conserved regions in sequence alignments with IgRs of related α-proteobacteria (IgR#6, IgR#10, IgR#12 and IgR#16; Table 1). On the other hand, 42 of the 60 listed candidate transcriptional units in this list (Additional file 18) had not been identified previously by sRNAPredictHT (Additional file 4).
Figure 3
Improvement of the predictive strategy of chromosomal *S. meliloti* sRNAs. From the initial list of 2920 chromosomal IgRs, we retained 778 IgRs longer than 150 bp than did not contain annotated or non-annotated repeats. Next, we introduced a global scoring criterion for each IgR to assign a numerical score taking into account the presence of putative independent transcriptional units or transcriptional signals and their relative distance to flanking ORFs, sequence conservation (BlastN analysis) and secondary structure conservation (QRNA analysis). See text for further details.
The 20 top-scoring candidate IgRs with predicted transcriptional units consistent with putative sRNAs are listed in Table 2. For 8 of these IgRs we observed microarray signals from exponential phase cells of strain 2011 RNA upon introduction of various stress conditions (Table 2). Thus, there is experimental evidence to date for 10 candidate sRNA loci among those top 20 IgRs (Table 2); i.e. smrC15 and smrC16 [26] (= sra41; [27]), sm4 (this work), sm5 (this work), smrC14 [26] (= sm7; this work), sm8 (this work), sm9 (this work), smrC9 [26] (= sra32; [27], = sm12; this work), smrC7 [26] (= sra03; [27], = sm13; this work), sra12 [27] (= sm17; this work) and sm26 (this work). The high proportion of confirmed sRNAs among these high-scoring loci suggests many of the 10 still unidentified candidates in this cohort correspond to bona fide sRNA-encoding genes. Another remarkable feature of our predictive method is that it was able to locate quite precisely the limits of the transcriptional units. The predicted transcription start site and the last uridine of smrC15 (sm3 in Table 2), smrC14 (sm7 in Table 2), smrC9 (sm12 in Table 2) and smrC7 (sm13 in Table 2), differ by only 1–3 bp from the experimentally determined 5'- and 3'-termini [26]. This is also an important validation of the in silico prediction of IgR transcriptional units. It is noteworthy that the IgR with
the highest global score is predicted to encode two independent sRNAs (Table 2). This region has recently been shown to encode two sRNA loci, *smrC15* and *smrC16* [26], with remarkably similar sizes to those predicted in this study (*sm3* and *sm3'*) (Table 2) one of which has been experimentally verified (*smrC14 = sm7*) and the second of which awaits experimental detection [26].

Our predictive method also identified sequence elements that correspond to highly conserved small non-coding RNAs (Table 3). These predictions include the RNAseP RNA component (GS = 168), the SRP RNA component (4.5S RNA; GS = 41), 16S RNA (GS = 19), and cobalamin (GS 11–16) riboswitches and two cis-regulatory RNA elements (GS = 27) [23, 27, 67], as well as cis-regulatory RNA elements [26].

**Table 3: Other small RNAs and cis-regulatory RNA elements detected in the chromosome of *S. meliloti* 1021 by the global scoring procedure.**

| Prediction          | Rfam1 | IgR coordinates | upstream ORF2 | RNA element2 | downstream ORF2 | GS3 | Ref. |
|---------------------|-------|----------------|---------------|--------------|-----------------|-----|------|
| RNAseP RNA          | y     | 2356367–2357249| Smc01857<     |              | Smc01856<       | 168 | [73] |
| FMN riboswitch      | y     | 2398059–2398737| Smc01608>     |              | RibH2 (SMc01609)> | 127 | [67] |
| 4.5S RNA (SRP)      | y     | 259823–260123  | Smc02904<     |              | Smc01242>       | 41  | [67] |
| Glycine riboswitch  | y     | 1674762–167635 | geoT<         |              | Smc01449<       | 37  | [67] |
| srrA (tmRNA)        | n     | 2290955–2291142| Smc01449<     |              | Smc01450>       | 33  | [23] |
| smrC45 (speF)       | y     | 3105052–3105637| Smc02983<     |              | Smc02984>       | 27  | [65] |
| Thiamine riboswitch | n     | 3532759–3533026| Smc03868<     |              | Smc03869>       | 19  | [67] |
| ilvIH cis regulatory| n     | 2276530–2276876| Smc01431 (ilvIH)< |              | Smc01432>       | 16  | [74] |
| Cobalamin riboswitch| n     | 1999510–1999806| Smc00166<     |              | Smc00165<       | 16  | [67] |
| Cobalamin riboswitch| n     | 2122378–2123250| Smc04305 (cobPW)< |              | Smc04306>       | 14  | [67] |
| Cobalamin riboswitch| n     | 954445–955076  | Smc00983<     |              | Smc00982>       | 11  | [67] |
| ybhL cis regulatory | n     | 3505880–3506125| Smc03838>     |              | Smc03839>       | 3   | [65] |
| serC cis regulatory  | y     | 2938993–2939230| serC<         |              | Smc00639<       | 2   | [65] |
| Methionine riboswitch| y     | 3461713–3461838| Smc03796<     |              | Meta>           | -   | [65] |
| Methionine riboswitch| y     | 580068–580264  | metZ<         |              | Smc02218>       | -   | [65] |

1 RNA gene or element present (y) or absent (n) in Rfam database.  
2 The transcribed strand is indicated.  
3 Global score (GS) calculated for the element in our predictive procedure (Figure 3).

Putative sRNA-encoding genes in *S. meliloti* megaplasmids

We next applied our improved predictive approach to the *S. meliloti* 1021 megaplasmids pSymA and pSymB. The list of independent transcriptional units that may represent novel sRNA-encoding genes in pSymA and pSymB is presented in Table 4. A significantly lower density of independent transcriptional units was identified in megaplasmids (an average of 8–9 sRNA genes per Mb) than in the chromosome (ca. 16 sRNA genes per Mb). It is noteworthy that most of the candidate transcripts were validated in our microarray screen (Table 4), strongly supporting the predictive methodology. Most of the transcripts were enriched > 5.5-fold (M-value > 2.5) in RNA from strain 2011 subjected to various stress stimuli, and two others (*smA1* and *smB7*) showed a > 4-fold induction (M-value > 2) (Table 4).

One of the candidates identified in pSymB and detected in strain 2011 (*smB5b*; Table 4) seems to be a second copy of the strain 1021 transcript *smrB35* [26] (*smB6*; Table 4). Interestingly, the plasmid-encoded candidate *smB5b* that lies in an IgR only 3 kb upstream *smrB35* was found to share 64% sequence identity with *smrB35* (*smB6*) (Additional file 19). Finally, the pSymA candidate *smA4b* was found to share sequence similarity with both chromosomally-encoded candidates *smrC15* and *smrC16* [26] (60% and 67%, respectively; Additional file 19). The putative sRNA *smA4b* is encoded within an IgR flanked by two transposable elements, ISRm5 and ISRm25, both containing their corresponding transposase genes SMA0995 and SMA0997 (Additional file 19), suggesting *smA4b* may have been acquired through horizontal transfer. The incompatibility-related pSymA and pSymB *incA* sRNAs were not detected as transcriptional units because they bear atypical terminators [25], but their σ70-dependent promoters were precisely predicted (data not shown).
Table 4: Putative sRNA genes predicted as independent transcriptional units in IgRs of *S. meliloti* 1021 megaplasmids pSymA (smA#) and pSymB (smB#).

| Gene or Designation | IgR length | Upstream ORF | Orientation Up sRNA Dn | Promoter | Predicted 5' end | Predicted 3' end | Length (nt) | Microarray detection |
|---------------------|------------|--------------|------------------------|----------|-------------------|-------------------|-------------|----------------------|
| smA1                | 719        | SMa0450      | > > >                  | s70      | 241667            | 241961            | 294         | >, C, O (*)          |
| smA2a               | 817        | SMa0585      | < < >                  | s54      | 313672            | 313529            | 143–243     | >, A, B, C, H, S     |
| smA2b               | < < >      | s70          |                        | 313772   | 313529            | 143–243          | 444         | (314210–314161 313991–314040 314162–314211 313784–313833) |
| smA2c               | < > <      | NN           |                        | 313667   | 314181            |                   |             |                      |
| smA3a               | 1007       | SMa0922      | > < <                  | s70      | 512362            | 512439            | 208–285     | <, A, C              |
| smA3b               |            |              |                        |          |                   |                   |             | (512371–512420)     |
| smA4a               | 714        | SMa0995      | < > >                  | NN       | 552600            | 552980            | 127–280     | >, A, B, C, H, O, S |
| smA4b               | < > >      | NN           |                        | 552853   | 552980            |                   |             | (552880–552929 552801–552752 552954–552905) |
| smA5                | 292        | SMa1024      | < > >                  | PhoB     | 567336            | 567465            | 129         | >, H, S              |
| smA6                | 624        | SMa1245      | < < <                  | NN       | 682304            | 682237            | 67          | <, O                 |
| smA7                | 879        | SMa1644      | > > <                  | s70      | 916928            | 917238            | 93–310      | -                    |
| smA8                | 1124       | SMa2165      | > > >                  | NN       | 1220442           | 1220807           | 365         | >, A, H, O, S        |
| smB1                | 282        | SMb20203     | > > >                  | NN       | 213506            | 213617            | 111         | -                    |
| smB2                | 495        | SMb20366     | > > <                  | NN       | 379143            | 379269            | 126         | >, H, S              |
| smB3a               | 750        | SMb20516     | > < <                  | NN       | 541963            | 541769            | 64–194      | <, H                 |
| smB3b               | > < <      | NN           |                        | 541911   |                   |                   |             | (541835–541884)     |
| smB3c               | > > <      | s70          |                        | 541833   |                   |                   |             |                      |
| smB4a               | 592        | SMb20543     | < < <                  | NN, s70  | 571374            | 571217            | 123–157     | <, A, C              |
| smB4b               | < < <      | NN, s70      |                        | 571340   | 571217            |                   |             | (571271–571222 571222–571271) |
| smB5a               | 1623       | SMb20548     | > > >                  | NN       | 574477            | 574763            | 142–286     | >, A, B, C, H, O, S |
| smB5b               | > > >      | NN, s70      |                        | 574621   |                   |                   |             | (574671–574622)     |
Table 4: Putative sRNA genes predicted as independent transcriptional units in IgRs of *S. meliloti* 1021 megaplasmids pSymA (*smA*#) and pSymB (*smB*#). (Continued)

| smrB35 (smB6) | 751 | SMb20551 | < | > | > | s70 | 577731 | 577869 | 138 | >, O, S (577781–577732) |
|--------------|-----|----------|---|---|---|-----|-------|-------|----|-------------------------|
| smB7 | 196 | SMb21316 | < | > | > | s70 | 983786 | 983878 | 92 | >, S (*) (983845–983796) |
| smB8 | 767 | SMb20872 | < | < | < | NN, s70 | 1279964 | 1279836 | 128–274 | <, A, O (1279979–1280028 1280182-1280231) |
| smB9 | 1014 | SMb20916 | < | > | > | s70 | 1325140 | 1325588 | 448 | >, H (1325459–1325508) |
| smB10 | 506 | SMb20748 | < | < | > | NN | 1325794 | 1327673 | 121 | - |

1 sRNA candidates verified experimentally retain their original notation [26].
2 NN, neural network promoter prediction; s70, σ70-dependent promoter; s54, RpoN (σ54)-dependent promoter promoter; PhoB, putative PhoB binding site.
3 The coordinates of all putative promoters and/or transcription factor binding sites within an IgR are presented. The position given for NN is the 3′ end of the identified sequence. For σ70 the position given is 7 bases downstream of the 3′ end of the -10 hexamer. The 3′ end of the predicted binding site for σ54 and PhoB is indicated with an asterisk.
4 Given is the position of the last uridine at the end of the terminator sequence.
5 Range of possible lengths based on putative 5′ and 3′ ends.
6 As described in Table 1.
Comments on the global scoring procedure

Our findings suggest that the GS method is effective in identifying both known and novel sRNA genes. Half of the chromosomal and 80% of the megaplasmid IgRs predicted to contain transcriptional units suggestive of sRNA genes have been validated experimentally in this (Tables 2 and 4) and other works [26,27]. However, it is yet unclear what proportion of all candidate predictions correspond to false positives. On the other hand, the number of potential sRNA loci may be underestimated in this study as we have ignored protein coding DNA sequences as a source of sRNA transcripts [56,57,68]. Another underestimation comes from the possibility that certain sRNA genes may require RNA polymerase sigma factors different from those screened here or may have atypical terminator sequences (as the aforementioned incA genes from pSymA and pSymB). As consensus sequences for additional S. meliloti transcription factors are determined, the modular design of our predictive protocol will allow these motifs to be readily incorporated into future searches. It is important to note that our method does not exclude the possibility that the identified putative sRNA loci, if expressed, do translate into short peptides [69] or are integral parts of mRNAs such as 5′-UTR leader regions. In fact, there are reports of sRNAs that are generated by post-transcriptional processing of mRNAs [70] including self-cleavage of riboswitch elements [71]. Our systematic procedure for IgR sorting is largely dependent on the utilization of open source tools (e.g., TranstermHP, Fuzznuc, Rsat, NNPP, BlastN, Rfam, QRNA) Thus, this methodology could be readily applied to any annotated DNA sequence for which appropriate BLAST partners and promoter consensus sequences are available. One key feature of our GS methodology is that the relative weighing of individual scores for transcriptional signatures and conservation features may be modified to generate different priority listings of candidate IgRs. We therefore anticipate that our predictive approach can be flexibly implemented in identifying sRNAs in many other bacterial species.

Conclusion

We have utilized the chromosomal DNA information of the sequenced strain S. meliloti 1021 to compile a first list of candidate sRNA genes (Table 1). By a combination of Northern hybridization and microarray analysis of RNA from the highly similar strain 2011, we here report eight novel sRNA loci (Table 1, Figures 1 and 2). Significant variation of transcript abundance was observed for many of the confirmed sRNAs of our first compilation under different growth conditions (Figure 1 and Table 1), providing important clues into their regulation and potential regulatory function.

The experimentally verified non-coding RNAs of S. meliloti, other than ssrA, 4.5S RNA, 6S RNA and RNAse P RNA ([26,27], this work), may encode regulatory sRNAs of the base-pairing mechanism. Two lines of sequence-based evidence suggest that S. meliloti and probably other α-proteobacteria as well, does not encode sRNAs of the molecular mimic type. First, no homologues of the translational regulator RNA-binding proteins of the RsmA/CsrA family could be detected by aminoacid sequence similarity (PSI-BLAST) in α-proteobacteria. Second, when we applied the CSRNA_FIND algorithm [72] to S. meliloti 1021 chromosomal and pSym IgRs, it did not detect a significantly higher density over the average of A(R)GGA sequence motifs, the hallmark of the molecular mimic sRNAs of the RsmZ/CsrB family [8]. Thus, most likely, S. meliloti only contains regulatory sRNA genes of the antisense trans-acting type [4].

To identify additional S. meliloti sRNA genes, we conducted a bioinformatic screen with a novel algorithm designed to more sensitively detect previously unannotated genes. The results of these screens significantly expand the list of putative sRNA-encoding IgRs in the three replications of S. meliloti 1021 and in closely related α-proteobacteria. Importantly, microarray data provided a strong support to our GS approach for prediction of putative sRNA-encoding genes (Tables 2 and 4). One advantage of the scoring criterion used here is that allows the strongest candidate loci to be prioritized for experimental verification and characterization. Thus, as bioinformatic screens continue to identify putative sRNA-encoding genes at rates that far exceed the throughput of existing experimental tools for sRNA confirmation and characterization, this prioritization of candidate genes should be very helpful in confirming and unravelling the diverse biological roles of these important and ubiquitous riboregulators.

Authors’ contributions

CV conceived of the study, coordinated the research, carried out Northern blot analysis and wrote the manuscript; JL executed the bioinformatics search with sRNApredictHT; JPS carried out microarray hybridization experiments and microarray data analysis; IR contributed to the analysis of microarray data; AB designed the transcriptomic experiments and produced the microarrays; GP participated in the design, programming and execution of the Global Score algorithm. All authors revised and approved the final version of the manuscript.
Additional file 1
Crude sRNApredictHT predictions on S. melliloti 1021 genome. Direct output of the sRNApredictHT algorithm applied to the complete set of S. melliloti 1021 chromosomal IgRs.
Click here for file
[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S1.xls]

Additional file 2
Oligonucleotides used for synthesis of Northern blot probes. Oligonucleotides used to PCR amplify the IgR sequences encompassing sRNA candidates.
Click here for file
[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S2.xls]

Additional file 3
Denaturing PAGE fractionation of S. melliloti 2011 total RNA. Electrophoretic pattern of S. melliloti 2011 total RNA in a denaturing polyacrylamide gel (8.3 M urea, 8% acrylamide and 0.2% bisacrylamide in 1× TBE buffer; 25 cm-long). Approximately 20–60 μg of total RNA, corresponding to all cells present in 20 ml of RDM cultures, were loaded in each lane. The gel was stained with ethidium bromide and visualized on an UV transilluminator. Under these conditions, effective fractionation of RNAs < 600 nt was achieved. RNA bands of varying intensity in different samples are indicated with arrowheads. Stat, stationary phase cells; log, exponential phase cells; NaCl 0.3 M, saline stress, H2O2, oxidative stress; pH 4.0, acid stress; SDS and EtOH, membrane stress; -P, phosphate starvation; 0°C, cold shock; 45°C, heat shock.
Click here for file
[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S3.jpeg]

Additional file 4
Curated sRNApredictHT predictions. The sRNApredictHT output listed in Additional file 1 was curated upon elimination of IgRs containing annotated and non annotated repeats.
Click here for file
[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S4.xls]

Additional file 5
Expression of putative sRNAs in IgR#4 and IgR#14. Northern blot analysis of putative sRNAs encoded in IgR#4 and IgR#14. See legend to Figure 1 for details.
Click here for file
[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S5.jpeg]

Additional file 6
Novel candidate sRNA gene sm8 in IgR#2. Conservation of the novel candidate sRNA gene sm8 (IgR#2) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of S. melliloti 1021 (1021), Sinorhizobium medicae WSM419 (Smed), Agrobacterium tumefaciens C58 (At), Rhizobium etli CFN42 (Retli) and Rhizobium leguminosarum bv viciae 3841 (Rleg). The Rho-independent terminator was predicted for S. melliloti 1021 (see text) and confirmed from conserved positions in the alignment. The putative sigma 70-dependent promoter (-10 and -35 hexamers) and transcription start site (+1) were deduced from conserved positions in the alignment. The secondary structure presented for S. melliloti Sm8 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy.
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[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S6.jpeg]

Additional file 7
Novel candidate sRNA gene sm137 in IgR#4. Conservation of the novel candidate sRNA gene sm137 (IgR#4) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of S. melliloti 1021 (1021), S. medicae WSM419 (Smed), R. etli CFN42 (Retli) and R. leguminosarum bv viciae 3841 (Rleg). The Rho-independent terminator was predicted for S. melliloti 1021 (see text) and confirmed from conserved positions in the alignment, but there was no prediction of a promoter in this IgR.
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[http://www.biomedcentral.com/content-supplementary/1471-2164-9-416-S7.jpeg]

Additional file 8
Novel candidate sRNA gene smIgR69. Conservation of the novel candidate sRNA gene smIgR69 in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of S. melliloti 1021 (1021), R. etli CFN42 (Retli) and R. leguminosarum bv viciae 3841 (Rleg). Two putative sigma 70-dependent promoters (-10 and -35 hexamers), transcription start sites (+1) and a single Rho-independent terminator were predicted for S. melliloti 1021 (see text). The secondary structure presented for both possible S. melliloti sRNAs from IgR#6 were calculated with the Mfold server [75] and correspond to the predicted structures with lower free energy.
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Additional file 9
Novel candidate sRNA gene sm26 in IgR#7. Conservation of the novel candidate sRNA gene sm26 (IgR#7) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of S. melliloti 1021 (1021), S. medicae WSM419 (Smed), R. etli CFN42 (Retli) and R. leguminosarum bv viciae 3841 (Rleg). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and Rho-independent terminator were predicted for S. melliloti 1021 (see text). The secondary structure presented for S. melliloti Sm26 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy.
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Additional file 10

**Candidate sRNA gene sm64 (sra25) in IgR#10.** Conservation of the candidate sRNA gene sm64 (IgR#10; sra25, [27]) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of *S. meliloti* 1021 (1021), *S. medicae* WSM419 (Smed), *R. etli* CFN42 (Retli) and *R. leguminosarum* bv *viciae* 3841 (Rleg). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and Rho-independent terminator were predicted for *S. meliloti* 1021 (see text) and confirmed from conserved positions in the alignment. The secondary structure presented for *S. meliloti* Sm64 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy. Click here for file [http://www.biomedcentral.com/content/supplementary/1471-2164-9-416-S10.jpeg]

Additional file 11

**Novel candidate sRNA gene sm145 in IgR#11.** Conservation of the novel candidate sRNA gene sm145 (IgR#11) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of *S. meliloti* 1021 (1021), *S. medicae* WSM419 (Smed), *A. tumefaciens* CS8 (At), *R. etli* CFN42 (Retli) and *R. leguminosarum* bv *viciae* 3841 (Rleg). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and Rho-independent terminator were predicted for *S. meliloti* 1021 (see text) and confirmed from conserved positions in the alignment. The secondary structure presented for *S. meliloti* Sm145 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy. Click here for file [http://www.biomedcentral.com/content/supplementary/1471-2164-9-416-S11.jpeg]

Additional file 12

**Novel candidate sRNA gene sm76 in IgR#14.** Conservation of the novel candidate sRNA gene sm76 (IgR#14) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of *S. meliloti* 1021 (1021), *S. medicae* WSM419 (Smed), *A. tumefaciens* CS8 (At), *R. etli* CFN42 (Retli), *R. leguminosarum* bv *viciae* 3841 (Rleg), *Mesorhizobium loti* MAFF303099 (Mloti), *Ochrobactrum anthropi* ATCC49188 (Oa) and *Brucella ovis* ATCC25840 (Bo). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and Rho-independent terminator were predicted for *S. meliloti* 1021 (see text) and confirmed from conserved positions in the alignment. A second putative promoter was predicted for *S. meliloti* upstream then conserved one, but it seems to be specific for *Sinorhizobium*. The alternative secondary structures presented for *S. meliloti* Sm76 RNA were calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy for the two possible transcripts. Click here for file [http://www.biomedcentral.com/content/supplementary/1471-2164-9-416-S12.jpeg]

Additional file 13

**Novel candidate sRNA gene sm84 in IgR#15.** Conservation of the novel candidate sRNA gene sm84 (IgR#15) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of *S. meliloti* 1021 (1021), *S. medicae* WSM419 (Smed), *A. tumefaciens* CS8 (At), *R. etli* CFN42 (Retli) and *R. leguminosarum* bv *viciae* 3841 (Rleg). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and Rho-independent terminator were predicted for *S. meliloti* 1021 (see text) and confirmed from conserved positions in the alignment. The secondary structure presented for *S. meliloti* Sm84 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy. Click here for file [http://www.biomedcentral.com/content/supplementary/1471-2164-9-416-S13.jpeg]

Additional file 14

**Novel candidate sRNA gene sm270 in IgR#16.** Conservation of the novel candidate sRNA gene sm270 (IgR#16) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of *S. meliloti* 1021 (1021), *S. medicae* WSM419 (Smed), *A. tumefaciens* CS8 (At), *R. etli* CFN42 (Retli) and *R. leguminosarum* bv *viciae* 3841 (Rleg). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and the putative Rho-independent terminator were predicted for *S. meliloti* 1021 (see text) and confirmed from conserved positions in the alignment. The secondary structure presented for *S. meliloti* Sm270 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy. Click here for file [http://www.biomedcentral.com/content/supplementary/1471-2164-9-416-S14.jpeg]

Additional file 15

**Novel candidate sRNA gene sm5 in IgR#17.** Conservation of the novel candidate sRNA gene sm5 (IgR#17) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of *S. meliloti* 1021 (1021), *R. etli* CFN42 (Retli) and *R. leguminosarum* bv *viciae* 3841 (Rleg). The putative sigma 70-dependent promoter (-10 and -35 hexamers), transcription start site (+1) and the putative Rho-independent terminator were predicted for *S. meliloti* 1021 (see text) and confirmed from conserved positions in the alignment. The secondary structure presented for *S. meliloti* Sm5 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy. Click here for file [http://www.biomedcentral.com/content/supplementary/1471-2164-9-416-S15.jpeg]
Additional file 16

Novel candidate sRNA gene sm190 in IgR#18. Conservation of the novel candidate sRNA gene sm190 (IgR#18) in α-proteobacteria. Sequence alignment generated with ClustalW for the corresponding IgRs of S. meliloti 1021 (1021), R. etli CFE42 (Retli) and R. leguminosarum bv vicieae 3841 (Rleg). The putative Rho-independent terminator was predicted for S. meliloti 1021 (see text) and confirmed from conserved positions in the alignment. The secondary structure presented for S. meliloti Sm190 RNA was calculated with the Mfold server [75] and corresponds to the predicted structure with lower free energy assuming that the sRNA extends along the conserved sequence upstream the terminator and includes the terminator itself.

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Additional file 17

List of S. meliloti sRNA gene predictions based on the GS method. Complete list of S. meliloti 1021 chromosomal IgRs predicted to encode sRNAs according to the global scoring procedure (summarized in Figure 3).

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Additional file 18

Predicted transcriptional units in S. meliloti 1021 chromosomal IgRs. sRNA candidates identified as putative transcriptional units in intergenic regions of S. meliloti 1021 chromosome.

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Additional file 19

Homologs of sRNA genes smrC14-smrC15 and smrB35 are present in pSymA and pSymB IgRs. Identification of extra copies of sRNA genes smrC14-smrC15 and smrB35 in pSymA and pSymB IgRs. Genetic surroundings and sequence alignments generated with ClustalW for the sRNA genes of S. meliloti 1021 smrC14, smrC15 [26] and the corresponding identified homolog in pSymA (smmAaB; Table 4), and for the sRNA gene smrB35 [26] and the corresponding identified homolog in pSymB (smmB5b; Table 4). The putative sigma 70-dependent promoters, transcription start sites (+1) and Rho-independent terminators were predicted for S. meliloti 1021 pSymA and pSymB (Table 4) and confirmed from conserved positions in the alignment.

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References

1. Storz G, Haas D: A guide to small RNAs in microorganisms. Curr Opin Microbiol 2007, 10(2):93-95.
2. Gottesman S: Micros for microbes: non-coding regulatory RNAs in bacteria. Trends Genet 2003, 21(7):399-404.
3. Chapman EJ, Carrington JC: Specialization and evolution of endogenous small RNA pathways. Nat Rev Genet 2007, 8(11):884-896.
4. Aiba H: Mechanism of RNA silencing by Hfq-binding small RNAs. Curr Opin Microbiol 2007, 10(2):134-139.
5. Prevost K, Salva H, Desnoyers G, Jacques JF, Phaneuf E, Masse E: The small RNA RyhB activates the translation of shiA mRNA encoding a permease of shikimate, a compound involved in siderophore synthesis. Mol Microbiol 2007, 61(4):1260-1273.
6. Masse E, Escoria FE, Gottesman S: Coupled degradation of a small regulatory RNA and its mRNA targets in Escherichia coli. Genes Dev 2003, 17(19):2374-2383.
7. Brennan RG, Link TM: Hfq structure, function and ligand binding. Curr Opin Microbiol 2007, 10(2):125-133.
8. Babitzke P, Romeo T: CsrB sRNA family: sequestration of RNA-binding regulatory proteins. Curr Opin Microbiol 2007, 10(2):156-163.
9. Ulverde C, Haas D: Small RNAs controlled by two component systems. Adv Exp Med Biol 2008, 631:54-79.
10. Vogel J, Sharma CM: How to find small non-coding RNAs in bacteria. Biochimie 2005, 87(12):1219-1238.
11. Limy J, Walder MK: Identification of small RNAs in diverse bacterial species. Curr Opin Microbiol 2007, 10(2):96-101.
12. Argaman L, Hershberg R, Vogel J, Bejerano G, Wagner EG, Margalit H, Altuvia S: Novel small RNA-encoding genes in the intergenic regions of Escherichia coli. Curr Opin Microbiol 2001, 11(12):941-950.
13. Rivas E, Klein RJ, Jones TA, Eddy SR: Computational identification of noncoding RNAs in E. coli by comparative genomics. Curr Opin Microbiol 2001, 11(17):1369-1373.
14. Wassarman KM, Repolla F, Rosenow C, Storz G, Gottesman S: Identification of novel small RNAs using comparative genomics and microarrays. Genes Dev 2001, 15(13):1637-1651.
15. Gottesman S: The small RNA regulators of Escherichia coli: roles and mechanisms*. Annu Rev Microbiol 2004, 58:303-328.
16. Storz G, Altuvia S, Wassarman KM: An abundance of RNA regulators. Annu Rev Biochem 2005, 74:199-217.
17. Blondi EG, Pilli E, Giuntini E, Roumiantseva ML, Andronov EE, Onichchouk OP, Kurchak ON, Simarov BV, Dzyubenko NI, Mengoni A, Bazzicalupo M: Genetic relationship of Sinorhizobium mellioti and Sinorhizobium medicae strains isolated from Caucasian region. FEMS Microbiol Lett 2003, 220(2):207-213.
18. Gage DJ: Infection and invasion of roots by symbiotic, nitrogen-fixing rhizobia during nodulation of temperate legumes. Microbiol Mol Biol Rev 2004, 68(2):280-300.
19. Galibert F, Finan TM, Long SR, Puhler A, Abola P, Ampe F, Barloy-Huber F, Barnett MJ, Becker A, Boistard P, Boutry G, Bowser L, Buhrmester J, Cadieu E, Capela D, Chain P, Cowie A, Davis RW, Federspiel NA, Long MH, Vorholter FJ, Weidner S, Wells DH, Wong K, Yeh KC, Bautj J: The composite genome of the legume symbiont Sinorhizobium meliloti. Science 2001, 293(5530):668-672.
20. Barnett MJ, Fisher RF, Jones T, Komp C, Abola APA, Barloy-Huber F, Bowser L, Capela D, Galibert F, Gouzy J, Gurtul M, Haas D, Huizlar L, Hyman RW, Jones T, Komp C, Komp D, Komp M, Komp S, Keating DH, Kiss E, Kompa C, Lealirve V, Masuy D, Palm C, Peck MC, Pohi TM, Porte-telle D, Purnelle B, Rasmusperger U, Surzycyki R, Thebault P, Vandenbol M, Vorholter FJ, Weidner S, Wells DH, Wong K, Yeh KC, Bautj J: The composite genome of the legume symbiont Sinorhizobium meliloti. Science 2001, 293(5530):668-672.
21. Finan TM, Weidner S, Wong K, Buhrmester J, Chain P, Vorholter FJ, Hernandez-Lucas I, Becker A, Coullie A, Gouzy J, Golding B, Puhler A: The complete sequence of the 1,683-kb pSymB megaplasmid from the NF-fixing endosymbiont Sinorhizobium meliloti. Proc Natl Acad Sci USA 2001, 98(17):9889-9894.
22. Ebeling S, Kundig C, Hennecke H: Discovery of a rhizobial RNA that is essential for symbiotic root nodule development. J Bacteriol 1991, 173(20):6373-6382.
23. Ulve VM, Cheron A, Trautwetter A, Fontenelle C, Barloy-Hubler F: Characterization and expression patterns of Sinorhizobium meliloti tmRNA (srrA). FEMS Microbiol Lett 2007, 269(1):117-123.

24. Keiler KC, Shapiro L, Williams KP: tmRNAs that encode protolyis-inducing tags are found in all known bacterial genomes: A two-piece tmRNA functions in Caulobacter. Proc Natl Acad Sci USA 2000, 97(14):7778-7783.

25. MacLellan SR, Smallbone LA, Sibley CD, Finan TM: The expression of a novel anti-sense gene mediates incompatibility within the large repABC family of alpha-proteobacterial plasmids. Mol Microbiol 2005, 55(2):611-623.

26. Del Val C, Rivas E, Torres-Quesada O, Toro N, Jimenez-Zurdo JI: Identification of differentially expressed small non-coding RNAs in the legume endosymbiont Sinorhizobium meliloti by comparative genomics. Mol Microbiol 2007, 65(5):1080-1091.

27. Ulve VM, Cheron A, Barloy-Hubler F: Identification of cis-encoded small non-coding RNAs in Sinorhizobium meliloti strain 1021. BMC Genomics 2007, 8:467.

28. Sinorhizobium meliloti strain 1021 Genome Project [http://jgi.doe.gov/sequenced-bacteria.html].

29. Sridhar J, Raft ZA: Identification of novel genomic islands associated with small RNAs. In Silico Biology 2007, 7:53.

30. Lung B, Zemann A, Madej MJ, Schuelke M, Techritz S, Ruf S, Bock R, Huttenhofer A: Identification of small non-coding RNAs from mitochondria and chloroplasts. Nucleic Acids Res 2006, 34(14):3842-3852.

31. Livny J, Brencic A, Lory S, Waldor MK: Identification of 17 Pseudomonas aeruginosa sRNAs and prediction of sRNA-encoding genes in 10 diverse pathogens using the bioinformatic tool sRNApredict2. Nucleic Acids Res 2006, 34(12):3484-3493.

32. Cossart M, Stanley I, Finan TM: Identification of Rhizobium-specific intergenic molaric elements within an essential two-component regulatory system of Rhizobium species. J Bacteriol 1995, 177(19):5485-5494.

33. Griffiths-Jones S, Moxon E, Marshall M, Kanna A, Eddy SR, Bateman A: Rfam: annotating non-coding RNAs in complete genomes. Nucleic Acids Res 2005, 33(suppl 1):D121-124.

34. Meade HM, Signer ER: Genetic mapping of Rhizobium meliloti. Proc Natl Acad Sci USA 1977, 74(5):2076-2078.

35. MacLellan SR, MacLean AM, Finan TM: Identification of Rhizobium-leguminosarum small RNAs in the legume endosymbiont Sinorhizobium meliloti strains 1021 and 2011. Mol Genet Genomics 2004, 272(1):11-17.

36. Regulatory Sequence Analysis Tools [http://rast.cbs.msu.edu/].

37. Blum H, Beier H, Gross HJ: Identification of regulatory sequence analysis tools in cyanobacterial non-coding RNAs by comparative genome analysis. Genome Biol 2005, 6(9):R73.

38. Kawano M, Reynolds AA, Miranda-Rios J, Storz G: Detection of 5' and 3'-UTR-derived small RNAs and cis-encoded antisense RNAs in Escherichia coli. Nucleic Acids Res 2005, 33(suppl 1):O40-1050.

39. Alamgir M, Barloy-Hubler F, Pouy J, Botte G, Ampe F, Batut J, Boisard P, Becker A, Bouter M, Cadieu E, Dreano S, Gloux S, Godrie T, Goueffe A, Kahn D, Kess E, Lelaure Y, Masuy D, Pohl T, Portetelle D, Puhler A, Ramsperger U, Renard C, Thebault P, Vandenbom M, Weidner S, Gilbert F: Analysis of the chromosome sequence of the legume symbiont Rhizobium meliloti strain 1021. Proc Natl Acad Sci USA 2001, 98(17):9877-9882.

40. Wais RJ, Wells DH, Long SR: Analysis of differences between Sinorhizobium meliloti 1021 and 2011 strains using the host calcium spiking response. Mol Plant Microbe Interact 2002, 15(12):1245-1252.

41. del Pino MF, Balague J, Sowinski SC, Wegener C, Segundo E, Abarca FM, Toro N, Niehaus K, A Ph, Aguilar OM, Martinez-Drets G, Lagares A: Isolation and characterization of alfalfa nodulating rhizobia present in alder soils of central Argentina and uruguay. Appl Environ Microbiol 1999, 65(4):1420-1427.

42. Wasserman KM, Storz G: 6S RNA regulates E. coli RNA polymerase activity. Cell 2000, 101(6):613-623.

43. Tourski P, Alm EE, Medvedev P, Salzberg SL: SPPS: a dual function for a bacterial small RNA. Nucleic Acids Res 2005, 33(12):3592-3600.

44. Cherevko I, Eddy SR, Ruzzo WL: Prediction of sRNA species and indicates parallel transcriptional output in bacteria. Nucleic Acids Res 2003, 31(22):6435-6443.
71. Barrick JE, Corbino KA, Winkler WC, Nahvi A, Mandal M, Collins J, Lee M, Roth A, Sudarsan N, Jona I, Wickiser JK, Breaker RR: New RNA motifs suggest an expanded scope for riboswitches in bacterial genetic control. Proc Natl Acad Sci USA 2004, 101(17):6421-6426.

72. Kulkarni PR, Cui X, Williams JW, Stevens AM, Kulkarni RV: Prediction of CsrA-regulating small RNAs in bacteria and their experimental verification in Vibrio fischeri. Nucleic Acids Res 2006, 34(11):3361-3369.

73. Li Y, Altman S: In search of RNase P RNA from microbial genomes. Rna 2004, 10(10):1533-1540.

74. Vitreschak AG, Lyubetskaya EV, Shirshin MA, Gelfand MS, Lyubetsky VA: Attenuation regulation of amino acid biosynthetic operons in proteobacteria: comparative genomics analysis. FEMS Microbiol Lett 2004, 234(2):357-370.

75. Zuker M: Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Res 2003, 31(13):3406-3415.