Role of RpoS in virulence and stress tolerance of the plant pathogen *Erwinia carotovora* subsp. *carotovora*

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The plant-pathogenic bacterium *Erwinia carotovora* subsp. *carotovora* causes soft rot on many economically important plants. The pathogen produces a number of plant-cell-wall-degrading enzymes, cellulases (Cel), pectate lyases (Pel), pectin lyase (Pnl), polygalacturonase (Peh) and proteases (Prt). The production and secretion of these enzymes is tightly regulated by several regulatory genes that have been identified and characterized in a number of studies (Andersson et al., 1999; Chatterjee et al., 1995; Cui et al., 1995, 1996; Eriksson et al., 1998; Frederick et al., 1997; Harris et al., 1998; Jones et al., 1993; Liu et al., 1993, 1998, 1999; Mukherjee et al., 1996; Murata et al., 1991, 1994; Pirhonen et al., 1991, 1993; Thomson et al., 1997, 1999). These genes encode various types of regulators (both positive and negative) that act on transcription, transcript stability and secretion of virulence factors.

During recent years, the function of the alternative sigma factor RpoS (σ<sup>R</sup>) has been extensively studied in *Escherichia coli* and other Gram-negative bacteria. RpoS is a regulator of stationary-phase-induced genes and is required for survival during stress and starvation (for reviews, see Hengge-Aronis, 1996; Loewen & Hengge-Aronis, 1994; Loewen et al., 1998). Recently, the rpoS gene from *Er. carotovora* subsp. *carotovora* strain 71 was cloned and an rpoS mutant strain was constructed and characterized (Calcutt et al., 1998; Mukherjee et al., 1998). It was shown that RpoS is needed to withstand various environmental stresses in *vitro*, and that the rpoS mutant had increased maceration capability and produced increased amounts of extracellular enzymes in...
vitro. This effect was found to be mediated by lower expression of the negative regulator *rsmA* in the *rpoS* mutant (Mukherjee et al., 1998). We have previously found that a mutant that overproduces RpoS due to a mutation in a gene designated *expM* has reduced virulence and is affected in extracellular enzyme production and secretion (Andersson et al., 1999). The overproduction of RpoS was found to partly cause the phenotype of the *expM* mutant. The *ExpM* protein is a response regulator homologous to RssB/SprE in *Es. coli* and MviA in *Salmonella typhimurium*. These proteins belong to a new group of response regulators that are involved in the control of the stability of RpoS (Andersson et al., 1999; Pearson et al., 1996; Muffler et al., 1996; Pratt & Silhavy, 1996). In this study we set out to characterize the phenotype of an *rpoS* mutant of *Er. carotovora* subsp. *carotovora* strain SCC3193, especially with regard to its virulence on tobacco plants. The mutant caused more severe symptoms than the wild-type strain on tobacco, presumably due to higher *in planta* production of extracellular enzymes, although it did not grow to higher cell densities on these plants. However, we show that the mutant was not able to infect tobacco with reduced catalase levels as efficiently as the wild-type strain, and that the growth of the mutant was impaired on these plants. Furthermore, we found that the *rpoS* mutant was outcompeted by the wild-type strain *in planta and in vitro*. As expected, we found that the *rpoS* mutant was more sensitive than the wild-type strain to osmotic and oxidative stress *in vitro.*

**METHODS**

**Strains, plasmids, basic techniques and chemicals.** The bacterial strains, plasmids and phages used in this study are listed in Table I. *Er. carotovora* subsp. *carotovora* and *Es. coli* were grown in L medium at 28 °C and 37 °C, respectively. Plasmids were isolated with Qiagen plasmid purification kits according to the instructions given by the manufacturer. Transfer of plasmids to *Er. carotovora* subsp. *carotovora* was done by electroporation using a Bio-Rad gene pulser and transfer to *Es. coli* by electroporation or standard transformation techniques. Samples for Northern and Western blot analysis were collected from cells grown in L medium supplemented with 0.4% polygalacturonic acid (PGA; P-1879, Sigma). Assays for enzymes in *in vitro* cultures were performed on cells grown both with and without PGA. Ampicillin (Amp; 150 µg ml⁻¹) or kanamycin (Km; 25 µg ml⁻¹) were added when appropriate. Km was not used during the collection of samples for Northern blots and enzyme assays in order to avoid negative antibiotic effects. Transduction in *Er. carotovora* subsp. *carotovora* was performed as described by Pirhonen et al. (1991) using T4GT7. Transduction in *Es. coli* was performed with P1 using standard procedures (Miller, 1972). *β*-Galactosidase assays were performed essentially as described by Miller (1972) and plasmid pMMKatF₅ was used as a positive control in these experiments. The PCR reactions were performed with the proof-reading polymerase *Pfu* (Stratagene). Absorbance and optical density were measured with a DU-70 spectrophotometer from Beckman.

**Construction of the *Er. carotovora* subsp. *carotovora rpoS* mutant strain.** The alignment of nucleotide sequences from *Es. coli* and *S. typhimurium* *rpoS* genes enabled us to design an oligonucleotide primer pair, RAPSIG (5'-ATTTGGGTTAC-AGGGGAATCCGTA) and VIKSIGMA (5'-TTTACATGC- GTACTTGGGTGTATCTT), which was used for PCR analysis of genomic *Er. carotovora* subsp. *carotovora* DNA. The PCR-generated product of predicted size, 870 bp, was subsequently cloned into *pBluescript* II to make pBSIG and checked by sequencing. Next, the Km' interposon from pHP452-Km (Fellay et al., 1987) was inserted into the DraII site of the internal region of *rpoS* in the plasmid pBSIG. To generate a homologous exchange mutant of the *Er. carotovora* subsp. *carotovora rpoS* gene, the suicide vector pUT mini-Tn5 Cm was used. pUT mini-Tn5 Cm carries the *zip*-dependent R6K ori, which does not replicate in bacteria that lack *zip*, such as *Er. carotovora* subsp. *carotovora* (de Lorenzo & Timmis, 1994). The mobile unit of pUT mini-Tn5 Cm was cut out with EcoRI and XbaI and replaced with the fragment carrying the *rpoS* gene interrupted by the Km' gene from pBSIG digested with EcoRI/XbaI. This construction, pUSIG, was mobilized by conjugation from *Es. coli* S17-1 *zip* into *Er. carotovora* subsp. *carotovora* SCC3193 as described by de Lorenzo & Timmis (1994). Transconjugants were selected for the Km' gene used for gene inactivation on minimal medium (M9) with glycerol (0.4%) and then tested for the loss of the vector marker (Amp). The potential marker-exchange mutants were verified by PCR using primers RAPSIG and VIKSIGMA. We transduced the mutated allele back to the wild-type strain SCC3193; all transductants were found to have the same phenotype on indicator plates for extracellular enzymes. We chose one of the transductants for further studies. The transductant was named SCC8002 and a Southern blot showed that it had a single Km' insertion in *rpoS*. A Western blot using an *Es. coli* RpoS antiserum (Jishage & Ishihama, 1995) showed that SCC8002 did not produce any RpoS protein. The mutated *rpoS* allele from SCC8002 was then cloned by cutting chromosomal DNA from SCC8002 with *SacI/SacII* and ligating these fragments to *pBluescript* II. The ligation was transformed into *Es. coli* and the mutated allele was isolated by direct selection for the Km' gene of the interposon. The DNA flanking the interposon was sequenced and the sequence obtained was used to generate oligonucleotides that were used to amplify the *rpoS* gene from the wild-type strain SCC3193. The resulting PCR fragment of about 1.5 kb was cloned into the Smal site of the low-copy vector pACYC177 to generate pRA910.

**Nucleotide sequencing.** Nucleotide sequence of both strands of the *Er. carotovora* subsp. *carotovora rpoS* gene was determined by the dideoxy chain-termination method (Sanger et al., 1977) using customized synthetic primers (15- to 22-mers; GENSET OLIGOS) and Sequenase system (version II) from US Biochemicals with [*α-³²P*]-JATP (Amerham Life Sciences). A *Blast* search was used to compare the deduced amino acid sequence from the *Er. carotovora* subsp. *carotovora rpoS* gene and RpoS proteins from other bacteria.

**Glycogen production, catalase assays and Erwinia auto-inducer (EAI) measurement.** Accumulation of glycogen was tested by growing cells overnight on agar plates containing 1% glucose and then staining with iodine vapour (Laftila, 1956). Catalase activity was assayed by measuring hydrogen peroxide decomposition in a spectrophotometer at 240 nm (Beers & Sizer, 1952). The amount of EAI was determined by a bioassay; *Er. carotovora* subsp. *carotovora* strain SCC3065 (Pirhonen et al., 1991, 1993), unable to produce EAI and harbouring the pHV2001 plasmid, was mixed with various dilutions of supernatant from SCC3193 and SCC8002. Light production, and hence the concentration of EAI, was then measured in a luminometer.
Table 1. Strains, plasmids and phages used in this study

<table>
<thead>
<tr>
<th>Strain/plasmid/phage</th>
<th>Relevant genotype/property</th>
<th>Reference/source</th>
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<tr>
<td><strong>Strains</strong></td>
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<tr>
<td><em>Erwinia carotovora</em> subsp. <em>carotovora</em></td>
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<tr>
<td>SCC3193</td>
<td>Wild-type</td>
<td>Pirhonen et al. (1988)</td>
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<tr>
<td>SCC8002</td>
<td>SCC3193 rpoS Km'</td>
<td>This study</td>
</tr>
<tr>
<td>SCC3065</td>
<td>SCC3193 expl Km'</td>
<td>Pirhonen et al. (1993)</td>
</tr>
<tr>
<td>SCC3032</td>
<td>SCC3193 explM Km'</td>
<td>Andersson et al. (1999)</td>
</tr>
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<td><strong>Escherichia coli</strong></td>
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<tr>
<td>DH5α</td>
<td>Strain for cloning and plasmid preparations</td>
<td>Hanahan (1983)</td>
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<td>MC4100</td>
<td>rpoS'</td>
<td>Laboratory stock</td>
</tr>
<tr>
<td>FF1112</td>
<td>MC4100 φ(otsB–lacZ) (p-placMu55)</td>
<td>Giaever et al. (1988)</td>
</tr>
<tr>
<td>RH90</td>
<td>MC4100 rpoS359::Tn10</td>
<td>Lange &amp; Hengge-Aronis (1991)</td>
</tr>
<tr>
<td>RA100</td>
<td>FF1112 rpoS359::Tn10</td>
<td>This study</td>
</tr>
<tr>
<td><strong>Plasmids</strong></td>
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<td>Cloning vector, Amp'</td>
<td>Stratagene</td>
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<td>Cloning vector, Amp' Km'</td>
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<td>pUS101</td>
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<td>This study</td>
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<tr>
<td>pRA910</td>
<td>rpoS' (Er. carotovora subsp. carotovora), Amp'</td>
<td>This study</td>
</tr>
<tr>
<td>pMMKatF</td>
<td>rpoS' (Es. coli), Amp'</td>
<td>Mulvey et al. (1988)</td>
</tr>
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<td>pUT mini-Tn5 Cm</td>
<td>Cm' Amp' R6K ori</td>
<td>de Lorenzo &amp; Timmis (1994)</td>
</tr>
<tr>
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<td>luxI Amp'</td>
<td>Pearson et al. (1994)</td>
</tr>
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<td>pH45Ω-Km</td>
<td>Km' interposon</td>
<td>Fellay et al. (1987)</td>
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<td><strong>Phage</strong></td>
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<tr>
<td>P1</td>
<td>Transducing phage</td>
<td>Laboratory stock</td>
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<tr>
<td>T4GT7</td>
<td>Transducing phage</td>
<td>Wilson et al. (1979)</td>
</tr>
</tbody>
</table>

Enzyme assays and virulence tests. The activities of Peh, Pel, Prt and Cel in vitro were assayed as described previously (Pirhonen et al., 1991). The levels of Peh, Pel and Prt in planta were measured as follows. Twenty-four plants (*Nicotiana tabacum* cv. Xanthi) were infected for each strain (about $2 \times 10^6$ c.f.u. per plant). After 48 h incubation plants were pooled in groups of six and the fresh weight was determined. Plants were then homogenized in 1 ml water. Plant material and bacteria were removed by centrifugation and the extra- cellular enzyme activities were determined. The results are expressed as activity per gram fresh weight (units for Peh, 0.1 μmol glucose equivalent min$^{-1}$; for Prt, increase in $A_{450}$ h$^{-1}$ (ml sample)$^{-1}$; and for Pel, $A_{543}$). As a control, the enzyme activities in uninfected plants were determined. Symptom development and bacterial growth in planta were determined in wild-type plants (*N. tabacum* cv. Xanthi) and antisense catalase (*Asca*1 no. 17) plants (Takahashi et al., 1997). The plants were grown for 4 weeks at 22 °C in a growth chamber [16 h light regime, 150 μE s$^{-1}$ m$^{-2}$ (167 mls)]. Plants were then infected and bacteria extracted essentially as described by Vidal et al. (1998) with the exception that 2–3 × 10$^6$ c.f.u. per plant (equal numbers for SCC3193 and SCC8002) were used to infect plants. After infection, plants were incubated for 48 h under the same conditions as above, but at 100% humidity to allow efficient infection. The results were analysed statistically by means of the Student’s t-test for which P-values are reported. Symptom levels were determined according to the following scale: 0 = no symptoms, 1 = clear infection of one leaf, 2 = one leaf macerated, 3 = infection spread to more than one leaf, 4 = several leaves macerated, 5 = only a few leaves uninfected. The mean symptom level was then calculated by adding the symptom levels of the infected plants and dividing by the number of plants used in each experiment. Salicylic acid (SA) treatment was done by adding SA to a final concentration of 1 mM to the plant growth medium 24 h before infection. When competition between SCC3193 and SCC8002 was studied in planta, 15 plants (*N. tabacum* cv. Xanthi) were infected with a mixture of equal numbers of both strains (a total of $2 \times 10^6$ c.f.u. per plant). After incubation for 48 h, bacteria were extracted and serial dilutions were plated on L medium with and without Km. The total c.f.u. and the c.f.u. on Km plates (SCC8002) were calculated as c.f.u. per infected plant. As a control, 30 plants were infected by SCC3193 and SCC8002 alone ($2 \times 10^6$ and $2 \times 10^6$ c.f.u. per plant, respectively). Virulence tests on potato stems were performed on greenhouse-grown potato (*Solanum tuberosum* cv. Bintje), using a toothpick to infect the plants directly into the stem as described by McMillan et al. (1993).

RNA isolation, Northern and Western blot analysis. RNA for Northern blot analysis was isolated by the Qiagen RNA isolation kit. Samples were collected during 24 h of growth and Northern blots were performed as described previously (Andersson et al., 1999). Western blots with *Es. coli* RpoS antisera (Jishage & Ishihama, 1995) were performed according to Andersson et al. (1999).

Stress experiments and competition in vitro. Stress exper-
RESULTS AND DISCUSSION

Cloning of the rpoS allele of strain SCC3193 and construction of an rpoS mutant

The rpoS gene encodes a subunit of the RNA polymerase which is involved in the control of a number of genes required for stress tolerance and survival during starvation (for reviews, see Hengge-Aronis, 1993, 1996; Loewen & Hengge-Aronis, 1994; Loewen et al., 1998). To characterize the rpoS allele in the Er. carotovora subsp. carotovora strain SCC3193 and construct an rpoS mutant strain we first cloned a part of the rpoS gene by PCR. We constructed an rpoS mutant by marker exchange mutagenesis and then transduced the mutated allele to a clean background (SCC3193). One of the transductants, SCC8002, was chosen for further studies. A Southern blot analysis showed that SCC8002 had a single Ω-Km insertion in rpoS. We also performed a Western blot with antisera to the previously reported RpoS protein (Calcutt et al., 1998) from Er. carotovora subsp. carotovora strain 71 (data not shown). To investigate whether the Er. carotovora subsp. carotovora rpoS gene was expressed from pRA910 and whether the RpoS protein encoded by the plasmid was functional in Es. coli, we performed complementation experiments. For this purpose we constructed the Es. coli strain RA100 by P1 transduction of the rpoS359::Tn10 allele from RH90 to FF1112, which carries a chromosomal osB-lacZ fusion. The osB gene in Es. coli encodes trehalose-6-phosphate phosphatase, which is known to be regulated by RpoS (Kaasen et al., 1992). We transformed FF1112 and RA100 with pRA910 and control plasmids and assayed the β-galactosidase activity during growth in L medium. The results showed that the β-galactosidase activity in RA100 carrying the empty vector pACYC177 was almost undetectable, whilst the introduction of pRA910 into RA100 activated the osB-lacZ fusion (data not shown). We also tested the ability of pRA910 to complement the salt-stress-sensitive and the catalase- and glycogen-deficient phenotypes of the Es. coli rpoS mutant RH90. We found that pRA910 complemented all these phenotypes (data not shown). The rpoS gene encoded by pRA910 is driven by its own promoter but does not contain the major promoter region which was found between nt −561 and −525 upstream of the rpoS gene in strain 71 (Mukherjee et al., 1998). However, it was found in this study that a weak promoter exists between nt −166 and +19. Since the DNA sequence in this region is almost perfectly conserved between the two strains, it is likely that this minor promoter region drives the expression of rpoS in pRA910. Similar to the results from strain 71 (Mukherjee et al., 1998), we did not detect any rpoS transcript smaller than about 1600 bp by Northern blot using RNA from the wild-type strain (Andersson et al., 1999; data not shown) indicating that the region between nt −561 and −525 is also the major rpoS promoter in SCC3193.

Characterization of the stress tolerance of the Er. carotovora subsp. carotovora rpoS mutant in vitro

The sigma factor RpoS has been shown to be involved in the production of secondary metabolites, virulence and/or stress survival in many bacterial species, including plant and animal pathogens (Anderson et al., 1998; Fang et al., 1992; Flavier et al., 1998; Loewen et al., 1998; Sarniguet et al., 1995; Swords et al., 1997; Wilmes-Riesenberg et al., 1997). We therefore decided to investigate whether RpoS has similar functions in the Er. carotovora subsp. carotovora strain SCC3193. To determine whether RpoS is needed for stress tolerance in SCC3193 during stationary phase, we analysed the phenotype of SCC8002 under osmotic and oxidative stress in L medium (Table 2). We found that SCC8002 was sensitive to these kinds of stresses as the survival of the rpoS mutant was significantly lower than for the wild-type strain. Es. coli rpoS mutants are deficient in the production of glycogen (Lange & Hengge-Aronis, 1991). We therefore performed a glycogen plate assay and found that SCC8002 was affected in the production of glycogen (data not shown). We also performed a
complementation test with pRA910 and found that the plasmid complemented the stress sensitivity of the mutant as well as the deficiency in glycogen accumulation (data not shown). The complementation of these phenotypes was not complete, but nevertheless evident, perhaps due to the low expression from the minor rpoS promoter. We also tested stress sensitivity during exponential growth (OD_600_1.0; 3.3-4.5 x 10^8 c.f.u. ml^{-1}). No significant difference in tolerance towards 2.5 mM H_2O_2 between SCC3193 and SCC8002 was shown as 14% of the cells survived for both strains. However, we found that the expM mutant strain SCC3032, which overproduces RpoS during exponential growth (Andersson et al., 1999), had enhanced tolerance as 29% of the cells survived. The fact that the rpoS mutant did not show higher sensitivity than the wild-type might be explained by the low levels of RpoS found in the wild-type during exponential growth (Andersson et al., 1999).

**Production of extracellular enzymes by the rpoS mutant**

The ability of the rpoS mutant strain SCC8002 to produce extracellular cell-wall-degrading enzymes in vitro was characterized by growing the cells in L medium containing 0.4% PGA and determining the Peh and Pel activity in the culture supernatant. As shown in Fig. 1(a), we found these enzyme activities to be similar in SCC3193 and SCC8002. We also analysed the accumulation of transcripts from the pehA and pelC genes by Northern blot analysis; as shown in Fig. 1(b), these transcripts accumulated to similar levels in both strains. In addition, we found that the amounts of Cel and Prt in the supernatant from SCC8002 were similar to SCC3193 (data not shown). We also assayed the basal level of Peh and Pel in L medium without PGA and found similar activities from both strains (data not shown). These results were somewhat surprising since Mukherjee et al. (1998) found increased extracellular enzyme activities in the supernatant of an rpoS mutant of strain 71. They showed that RpoS acts positively on the expression of rsmA, which encodes a negative regulator of extracellular enzyme production. RsmA has been shown to be an RNA-binding protein that most likely binds various transcripts encoding virulence determinants and expedites their degradation (Liu et al., 1998). We performed a Northern blot and found that, during stationary phase, the accumulation of rsmA transcript was lower in our rpoS mutant, whilst the levels were more similar to the wild-type during exponential phase. This is to be expected since rsmA seems to be controlled by both σ^32 and RpoS (Mukherjee et al., 1998). Since the amount of RpoS protein is low during exponential growth (Andersson et al., 1999), an rpoS mutation is not likely to affect rsmA levels until the cells reach stationary phase and RpoS starts to accumulate. This is supported by the finding that rsmA transcript accumulates to a higher level during exponential growth in an expM mutant strain which overproduces RpoS (Andersson et al., 1999). Taken together, our data strongly suggest that RpoS also acts as a positive regulator of rsmA in SCC3193.

We also analysed the amount of the diffusible signal molecule EAI but could not find any significant difference in its production in SCC8002 compared to SCC3193 (data not shown).

**Virulence of the rpoS mutant**

To characterize the virulence of SCC8002 on plants, we performed an assay on in-vitro-grown tobacco. The rpoS mutant was found to cause more severe symptoms than the wild-type strain (see Fig. 2). This is in agreement with Mukherjee et al. (1998) who showed that an rpoS mutant strain caused increased maceration of celery petioles. We also performed a virulence test on potato stems as described by McMillan et al. (1993). The virulence of SCC8002 was found to be similar to SCC3193 (data not shown). The reason why the rpoS mutant appears to be more virulent on tobacco but not on potato is not known, but it may be due to the infection starting in different parts of the host plants.
Fig. 1. Enzyme activities and mRNA accumulation in the rpoS mutant strain SCC8002 and wild-type strain SCC3193. (a) Cell growth and activities of Peh and Pel in culture supernatants. Cells were grown in L medium containing 0.4% PGA. ■, SCC3193; ▲, SCC8002. (b) Northern blot showing the accumulation of pehA and pelC transcripts. Five micrograms of RNA was loaded in each lane. The results are from a representative experiment.

The increased virulence of SCC8002 on tobacco seedlings prompted us to investigate the growth of the rpoS mutant on tobacco in more detail. We therefore performed a number of experiments on in-vitro-grown tobacco plants in order to investigate if the enhanced symptoms caused by the rpoS mutant strain SCC8002 allowed it to grow better on tobacco when compared to the wild-type strain. Since the rpoS mutant was found to be more sensitive to oxidative stress in vitro we also tested the growth and the symptom development on transgenic tobacco (Ascat plants) with severely reduced catalase activity (about 90%) due to an antisense construction (Takahashi et al., 1997). It has been postulated by Takahashi et al. (1997) that this reduction in catalase activity results in higher levels of reactive oxygen species in these plants. The results (Fig. 2), showed that SCC8002 caused more severe symptoms than the wild-type strain on control plants although the amount of bacteria extracted from the plants infected by the mutant was slightly, but not significantly, lower after 48 h incubation as compared to control plants infected by SCC3193. Interestingly, we found that the rpoS mutant caused significantly lower levels of symptoms on transgenic Ascat plants compared to control plants. Similarly, significantly lower numbers of bacteria could be extracted from the Ascat plants infected by the mutant strain as compared to control plants (P-value = 0.064). This is in contrast to the growth of the wild-type strain, which was not affected on Ascat plants as compared to control plants. These results suggest that the rpoS mutant strain is more sensitive to the higher levels of reactive oxygen species produced in Ascat plants. However, since 3 × 10^6 cells were used to inoculate the plants, multiplication clearly occurred in both hosts, showing that the Ascat plants only partially restricted the growth of the rpoS mutant. Interestingly, Hassouni et al. (1999) recently reported that an Erwinia chrysanthemi msaR (methionine sulfoxide reductase) mutant exhibited reduced virulence. The msaR gene, which is not RpoS-regulated in Es. coli (Moskovitz et al., 1995), encodes a protein which repairs oxidized proteins. The Er. chrysanthemi msaR mutant was found to have increased sensitivity to oxidative stress (Hassouni et al., 1999). This study indicates, as in our work, that resistance to oxidative stress may be important for the virulence of soft-rot erwinias.

It has previously been shown that Ascat plants, as used
in this study, are more resistant to tobacco mosaic virus (TMV) infection and that this effect is mediated through SA (Du & Klessig, 1997; Takahashi et al., 1997). In tobacco, SA has been shown to induce resistance towards Er. carotovora subsp. carotovora (Palva et al., 1994; Vidal et al., 1998). To find out if SCC8002 was more sensitive to plant defence responses induced by SA and to rule out the possibility that the results obtained with the transgenic Ascat plants were due to higher levels of SA, we infected SA-treated tobacco plants with SCC3193 and SCC8002. On the control plants we found similar results as shown in Fig. 2, whilst the SA-treated plants showed increased resistance at the level of both symptom development and bacterial growth in planta.

**Table 3.** Extracellular enzyme activities in plants infected with rpoS mutant strain SCC8002 and wild-type strain SCC3193

<table>
<thead>
<tr>
<th>Strain</th>
<th>Peh</th>
<th>Pel</th>
<th>Prt</th>
</tr>
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<tbody>
<tr>
<td>SCC3193</td>
<td>0.77 ± 0.21</td>
<td>1.1 ± 0.32</td>
<td>0.16 ± 0.057</td>
</tr>
<tr>
<td>SCC8002</td>
<td>1.7 ± 0.44</td>
<td>1.2 ± 0.28</td>
<td>1.1 ± 0.50</td>
</tr>
<tr>
<td>Uninfected</td>
<td>0.35</td>
<td>0.028</td>
<td>ND</td>
</tr>
</tbody>
</table>

Enzyme activities were determined and are expressed as indicated in Methods. The results shown are means ± SD of four samples per strain. P-values for the difference between SCC8002 and SCC3193 are 0.011 for Peh, 0.73 for Pel and 0.0086 for Prt. Six pooled uninfected plants were used as a control in order to estimate the background levels. ND, Not detectable.

We were not able to detect any significant difference in the growth of SCC3193 and SCC8002 on the SA-treated plants (data not shown). Taken together, our results suggest that SCC8002 is more sensitive to reactive oxygen species not only in vitro but also in planta. The results also suggest that the rpoS mutant is not affected in its ability to infect wild-type tobacco. On the contrary, it causes more severe symptoms than SCC3193 on wild-type tobacco plants. This suggests that the rpoS mutant produces more extracellular enzymes in planta. To investigate this, we performed enzyme assays by using macerated plant tissue to determine the in planta levels of Peh, Pel and Prt (Table 3). We found that the level of Peh and Prt was significantly higher (twofold for Peh and sevenfold for Prt) in tobacco plants infected with the rpoS mutant as compared to plants infected with the wild-type strain, whilst the production of Pel did not differ between the two strains. It is therefore likely that the increased symptoms caused by the rpoS mutant strain are due to increased extracellular enzyme production in planta and not to higher cell density. This is in contrast with the in vitro results, as we could not find any difference in the levels of extracellular enzymes in vitro when the cells were grown in L medium with or without PGA. Whilst our work indicates that RpoS is a positive regulator of rsmA in SCC3193, it appears that the level of rsmA is more important in planta than during growth in L medium. This is supported by our previous results showing that the expM mutant strain SCC3032, which overproduces RpoS and thereby shows enhanced rsmA expression, has significantly lower virulence on tobacco than the wild-type strain (Andersson et al., 1999). Introduction of an rpoS mutation in the expM mutant background caused an rsmA expression similar to that seen in an rpoS mutant and the expM rpoS double mutant was found to have almost fully restored virulence (Andersson et al., 1999). In addition, the expM mutant is also affected in production and secretion of the extracellular enzymes in vitro (L medium plus PGA), but this phenotype seems not to be rsmA-dependent as the expM rpoS double

![Fig. 2. Symptom development and bacterial growth in wild-type and transgenic Ascat tobacco plants. The rpoS mutant strain SCC8002 causes lower symptom levels on tobacco plants carrying an antisense construction to catalase (Ascat) when compared to control plants (Xanthi), whilst the wild-type strain SCC3193 is not affected. (a) Symptom development. Symptom levels were determined on a scale of 0–5 as described in Methods and mean values are shown above the bar diagrams. (b) Numbers of bacteria extracted from these plants. Results are means ± SD of 18 infected plants incubated for 48 h.](image-url)
mutant is similar to the expM mutant in this respect (Andersson et al., 1999).

The rpoS mutant is unable to compete with the wild-type strain in vitro and in planta

It has previously been reported that an Es. coli strain with a null mutation in rpoS is unable to compete with an rpoS+ strain when grown in vitro (Zambrano et al., 1993). Similarly, we found that the Er. carotovora subsp. carotovora rpoS mutant SCC8002 was unable to compete with SCC3193 when grown for 48 h in L. medium. In these experiments, about $3 \times 10^8$ c.f.u. of the mutant and the wild-type strains were inoculated either together or separately. After incubation, only 0.3–10% of the total number of bacteria (about $1.5 \times 10^6$ c.f.u. ml$^{-1}$) were SCC8002. When the strains were grown separately under the same conditions the rpoS mutant and the wild-type strain grew to about $8.0 \times 10^8$ c.f.u. ml$^{-1}$ and $1.5 \times 10^9$ c.f.u. ml$^{-1}$, respectively. This indicates that the growth of the wild-type is not affected by the presence of the rpoS mutant, whilst the mutant is severely affected in growth in the presence of the wild-type strain. The competition experiments in vitro prompted us to test if the rpoS mutant is able to compete with the wild-type strain in planta. We infected tobacco plants with a mixture of equal numbers of bacteria of both strains (total c.f.u. $2.1 \times 10^6$ per plant) and incubated the plants for 48 h. We then extracted the bacteria and plated serial dilutions on L medium with and without Km. In plants infected by the mixture, approximately 25% of the cells (total c.f.u. $2.4 \times 10^8$ per plant) were SCC8002, whilst both strains grew similarly in control plants infected with SCC3193 and SCC8002 separately (means of $2.6 \times 10^8$ and $2.9 \times 10^8$ c.f.u. per plant, respectively). This indicates that the rpoS mutant is not able to compete with the wild-type strain SCC3193 in planta. When we examined the symptom levels, we found that the plants infected by the mixture showed symptoms very similar to the plants infected by the wild-type strain alone (mean symptom levels of 1.9 for the mixture and 2.1 for SCC3193), whilst plants infected by the rpoS mutant alone showed more severe symptoms (mean symptom level 3.3). This indicates that the rpoS mutant does not contribute to the development of the symptoms when a mixture of the two strains is used to infect tobacco. Taken together, our results indicate that a functional rpoS gene is needed mainly for survival in a competitive environment and in the long term. This is supported by the fact that Mukherjee et al. (1998) found that an Er. carotovora subsp. carotovora rpoS mutant of strain 71 is sensitive to carbon starvation.

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