

IAA Synthesis in *Azospirillum brasilense* Sp6: Analysis of a Mutant Impaired in IAM-Hydrolase

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Abstract

A. brasilense SpM7918, a previously isolated *A. brasilense* Sp6 Tn5 mutant, is shown to produce high amounts of indoleacetamide, which is a precursor of indole-3-acetic acid in the indoleacetamide pathway, and to excrete very low amounts of indole-3-acetic acid. From genomic DNA of the mutant, the Tn5 containing restriction fragment was cloned in pUC19 and used as a hybridization probe to screen a genomic library of *A. brasilense* Sp245. Seven positive clones were isolated and conjugated into the original mutant restoring IAA production. One transconjugant was further analyzed for indoleacetamide and indole-3-acetic acid production by HPLC.

Keywords: *A. brasilense*, indole-3-acetic acid mutant, IAM pathway

1. Introduction

Bacteria of the genus *Azospirillum* are diazotrophs associated with the roots of grasses and cereals (reviewed by Bashan et al., 1990). The capacity of

azospirilla to promote plant growth, although not fully understood, is presumed to depend on several bacterial properties. One of these factors could well be the production of phytohormones, e.g. indole-3-acetic acid (IAA), (Barbieri et al., 1986). In order to elaborate further on this property, more knowledge on IAA biosynthesis by *Azospirillum* is needed, especially on the biochemical pathway(s) and the determining genes.

The best investigated pathway for IAA biosynthesis is described for the phytopathogen *Pseudomonas syringae*. Tryptophan-2-monooxygenase converts tryptophan to indoleacetamide (IAM) and then indolacetamide-hydrolase catalyzes the conversion of IAM to IAA. *iaaM* and *iaaH*, and *tms-1* and *tms-2*, the genetic determinants for these enzymatic conversions, respectively in *Pseudomonas syringae* and *Agrobacterium tumefaciens*, have been cloned and sequenced (Yamada et al., 1985; Klee et al., 1984; Gielen et al., 1984). Also in *Bradyrhizobium japonicum* the *bam* gene, which encodes for the indolacetamide-hydrolase has been cloned (Sekine, 1989), but there is no evidence that in this bacterium the IAM pathway operates in symbiotic conditions.

In *A. lipoferum* only the presence of the transamination pathway has been reported, while the excretion of IAM in the supernatants of bacterial cultures was not detected (Ruckdaschel, et al., 1990). Recently genes involved in the IAA synthesis have been localized on the 85 MDa plasmid of *A. brasilense* Sp245, by isolating a Tn5-*mob* insertion mutant with less IAA production and accumulation of anthranilic acid (Katzy et al., 1990). A possible regulation role of anthranilic acid on IAA biosynthesis in *Azospirillum brasilense* has been proposed (Zimmer and Elmerich, 1991). Since no mutant completely unable to synthesize IAA was isolated after Tn5 mutagenesis in *A. lipoferum* (Abdel-Salam and Klingmuller, 1987) and *A. brasilense* (Barbieri et al., 1990), it was suggested that *Azospirillum* possesses more than one pathway for IAA synthesis.

The biosynthetic pathway to indole-3-acetic acid in *Azospirillum* is still unclarified. Here we present data consistent with the existence of the IAM pathway in *A. brasilense*.

2. Materials and Methods

Bacterial strains

Strains used in this study are listed in Table 1.

Table 1. Bacterial strains

Strains	Relevant properties	Source/Reference
<i>E. coli</i> HB101	F ⁻ <i>hsd20</i> (r_B^- m_B^-), <i>recA13</i> <i>ara</i> ⁻¹⁴ , <i>proA2</i> , <i>lacY1</i> , <i>galK2</i> <i>rpsL20</i> , (<i>Sm</i> ^r) <i>xyt</i> ⁻⁵ , <i>mtl</i> ⁻¹ <i>supE44</i> ⁻	Boyer et al. (1969)
<i>E. coli</i> S17-1	<i>pro</i> , <i>thi</i> , <i>hsdR</i> , <i>hsdM</i> ⁺ , <i>recA</i> , Tp ^r , Sm ^r , (RP4-2-Tc::Mu::Km::Tn7)	Simon et al. (1983)
<i>A. brasilense</i> Sp7 (ATCC29145)		Tarrand et al. (1978)
<i>A. brasilense</i> Sp245		Baldani et al. (1987)
<i>A. brasilense</i> Sp6		Bani et al. (1980)
<i>A. brasilense</i> SpM7918	Tn5-induced IAA mutant of Sp6	Barbieri et al. (1990)
<i>A. lipoferum</i> Sp59		Tarrand et al. (1978)
<i>A. lipoferum</i> Br17		Tarrand et al. (1978)
<i>A. irakense</i> KBC1		Khammas et al. (1989)
<i>A. halopraeferens</i> Au4		Rheinhold et al. (1987)

Growth media

Azospirillum strains were grown at 30°C in L*, which is LB supplemented with 2.5 mM CaCl₂ and 2.5 mM MgSO₄ or in MMAB medium (Vanstockem et al., 1987). For screening the IAA synthesis, growth medium was supplemented with 0.1 mg/ml of tryptophan. *Escherichia coli* strains were maintained on M9 glucose agar plates or LB agar plates and grown in LB broth at 37°C (Sambrook et al., 1989). When required, antibiotics were added in the following concentrations (µg/ml): tetracycline (Tc), 10; kanamycin (Km), 30; ampicillin (Ap), 100.

DNA manipulation

Isolation of total DNA and plasmid DNA, DNA ligations, Southern hybridizations, and transformations were performed using standard techniques (Sambrook et al., 1989). Plasmid profiles of *A. brasilense* were visualized by gel electrophoresis according to Kado and Liu (1981).

DNA restriction fragments for cloning and for ³²P-labelling were isolated from agarose gel pieces, after electrophoresis, by a freeze and thaw method (Sambrook et al., 1989).

Bacterial conjugations

One ml portions of log phase cultures of donor, recipient, and when necessary, helper strain, were centrifuged and cells were resuspended in 100 μ l LB broth. Thirty μ l of the appropriate suspensions were then mixed and spread as a patch on D agar plates, which contained per liter: 8 g Bacto Nutrient Broth (Difco Laboratories, MI, USA), 0.25 g MgSO₄·7H₂O, 1 g KCl, 0.01 g MnCl₂. After overnight incubation at 30°C in a humid atmosphere, bacteria were scraped from the agar surface, suspended in 1 ml sterile 0.85% NaCl, and plated on selective media.

Detection of indole-3-acetic acid

IAA was colorimetrically determined with the Salkowsky reagent in supernatants of *Azospirillum* cultures grown for 72 hr in MMAB with 0.1 mg/ml tryptophan (Kaper and Veldstra, 1958).

3. Results and Discussion

From a collection of Tn5-induced mutants of *A. brasilense* Sp6, a particular mutant SpM7918 with reduced IAA production was previously isolated (Barbieri et al., 1990) using a screening with Salkowsky reagent (Kaper and Veldstra, 1958). Lower IAA production by this mutant was confirmed and IAM accumulation was found by H.P.L.C. analysis (Table 2), suggesting that the IAM pathway is present and the IAM-hydrolase is impaired.

Table 2. H.P.L.C.-analysis^a of *A. brasilense* strains for tryptophan (TRP), indolacetamide (IAM), and indole-3-acetic acid (IAA)

Strains	Minimal medium without tryptophan			Minimal medium with tryptophan	
	TRP	IAM	IAA	IAM	IAA
Sp6	12549	28.6	86882	15696	1392379
SpM7918	46943	408.6	1946	59388	80812
SpM7918(p0.2)	ND	ND	ND	787	465906

Data are given in picomol per 10 ml culture supernatant. Values are averages obtained from samples taken at the 2nd, 3rd, 4th day of growth. Sp6 is an *A. brasilense* wild type, SpM7918, a Tn5 insertional mutant, and SpM7918(p0.2) an exconjugant with a positive hybridizing clone.

^aAnalyses were carried out as described by Prinsen et al. (1991)

From *Sal* I digested genomic DNA of the mutant SpM7918, a 13.5 Kb *Sal* I fragment containing a Tn5 flanking region of 11 Kb and the kanamycine resistance half of Tn5 was cloned in pUC19.

Other *Azospirillum* spp. were analysed for the presence of the sequence which had been mutated in SpM7918 (Fig. 1). Total DNA was isolated from *A. brasilense* Sp7, *A. brasilense* Sp245, *A. lipoferum* Sp59, *A. lipoferum* Br17, *A. irakense* KBC1 and *A. halopraeferens* Au4, and digested with *Sal* I. The fragments were separated by gel electrophoresis and blotted onto nitrocellulose filters. These were hybridized against the 13.5 Kb *Sal* I fragment, cut from agarose gel and ³²P-labelled. Two positive signals, ca. 13.5 and 7 Kb were detected, with the Tn5 insertional mutant SpM7918, representing, as expected, the right and left flanking sequences of the inserted Tn5 (since this transposon has one unique central *Sal* I site). Hybridization signals were found for all the strains tested except *A. irakense*, indicating that this sequence is generally present among *Azospirillum* spp.

The same 13.5 Kb *Sal* I fragment hybridized also with the chromosomal DNA band on plasmid profiles obtained by the protocol of Kado and Liu (Kado and Liu, 1981) showing its localization in the chromosome (data not shown).

In order to clone the corresponding sequences, a pLAFR1 cosmid genomic library of *A. brasilense* Sp245 was screened by colony hybridization with the 13.5 Kb fragment cloned from the mutant SpM7918. Seven pLAFR1 clones, all containing a 6.5 Kb *Eco*RI fragment, were identified and subsequently transferred into *E. coli* S17-1 strain. Plasmids were subsequently mobilized into *A. brasilense* SpM7918 in a biparental mating with the *E. coli* S17-1 transformants. Exconjugants were selected on minimal medium plates that contained tetracycline and kanamycine. To determine if the IAA production was restored, the seven exconjugants were grown on minimal medium with the appropriate antibiotics and 0.1 mg/ml tryptophan. After 3 days, IAA production was colorimetrically demonstrated with Salkowsky reagent in the supernatants of all the exconjugants. As a control, an exconjugant, where only the cosmid pLAFR1 was mobilized, did not show any positive reaction (data not shown).

One of the exconjugants, named SpM7918(po.2), was further investigated by H.P.L.C. analysis. Samples of culture supernatant were analyzed at the 2nd, 4rd, and 4th day of growth. Data indicate that the IAA production of the complemented clone increased five times compared with the mutant, abolishing the accumulation of IAM. The fact that IAA production was not fully restored to the wild type level might be due to the presence of other genes, structural as well as regulatory, involved in the IAA biosynthesis, on the multicopy plasmid used for complementation.

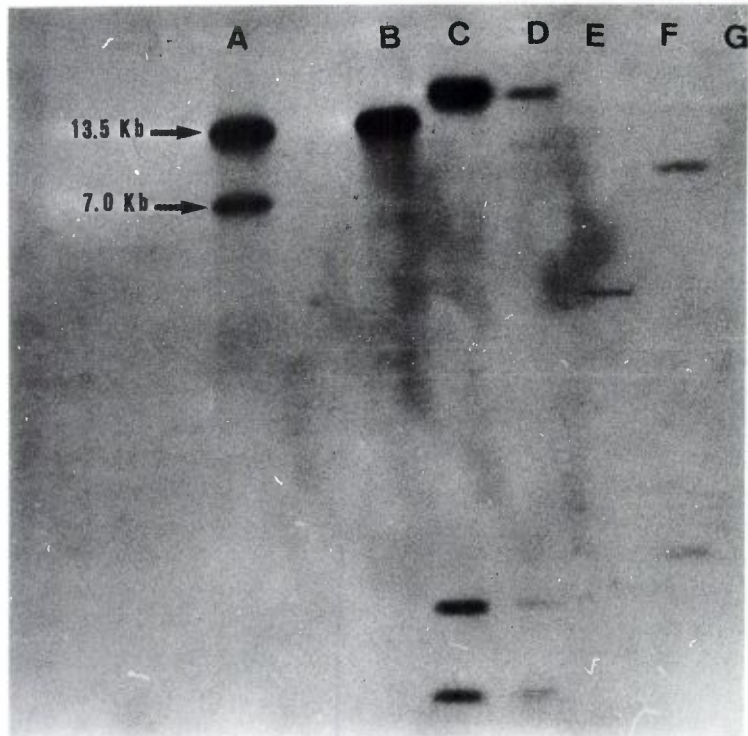


Figure 1. Hybridization of blotted total DNA from several *Azospirillum* strains digested with *Sal* I. The probe was the Tn5-containing 13.5 Kb *Sal* I 32 P-labelled fragment cloned in pUC19 from the mutant SpM7918.

- (a) *A. brasilense* Sp6 Tn5 insertional mutant SpM7918
- (b) *A. brasilense* Sp7
- (c) *A. brasilense* Sp245
- (d) *A. lipoferum* Sp59
- (e) *A. lipoferum* Brl7
- (f) *A. halopraeferens* Au4
- (g) *A. irakense* KBC1

From previous papers, it is clear that IAA biosynthesis in *A. brasilense* appears to be quite complex. Nevertheless our results clearly demonstrate that *A. brasilense* contains a functional gene that encodes conversion of IAM to IAA. Further experiments to elucidate the structure of this gene and its regulation in *A. brasilense* will help to understand the IAA biosynthetic pathways in *A. brasilense*.

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