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Molecular genetics of naringenin biosynthesis, a typical plant secondary metabolite produced by *Streptomyces clavuligerus*

Rubén Álvarez-Álvarez^{1,2}, Alma Botas², Silvia M. Albillos², Angel Rumbero³, Juan F. Martín¹ and Paloma Liras^{1*}

Abstract

Background: Some types of flavonoid intermediates seemed to be restricted to plants. Naringenin is a typical plant metabolite, that has never been reported to be produced in prokaryotes. Naringenin is formed by the action of a chalcone synthase using as starter 4-coumaroyl-CoA, which in dicotyledonous plants derives from phenylalanine by the action of a phenylalanine ammonia lyase.

Results: A compound produced by *Streptomyces clavuligerus* has been identified by LC–MS and NMR as naringenin and coelutes in HPLC with a naringenin standard. Genome mining of *S. clavuligerus* revealed the presence of a gene for a chalcone synthase (*ncs*), side by side to a gene encoding a P450 cytochrome (*ncyP*) and separated from a gene encoding a Pal/Tal ammonia lyase (*tal*). Deletion of any of these genes results in naringenin non producer mutants. Complementation with the deleted gene restores naringenin production in the transformants. Furthermore, naringenin production increases in cultures supplemented with phenylalanine or tyrosine.

Conclusion: This is the first time that naringenin is reported to be produced naturally in a prokaryote. Interestingly three non-clustered genes are involved in naringenin production, which is unusual for secondary metabolites. A tentative pathway for naringenin biosynthesis has been proposed.

Keywords: Naringenin, Secondary metabolism, *Streptomyces clavuligerus*, Histidine/phenylalanine ammonium lyase

Background

S. clavuligerus ATCC 27064 is an industrially relevant actinobacteria, used for the production of clavulanic acid (CA) [1]. This strain has a peculiar carbohydrate metabolism [2] and is able to produce in addition to CA other bioactive compounds such as cephalexin C [3], clavams [4] and holomycin [5, 6]. Interestingly, sequencing of the *S. clavuligerus* genome revealed that this organism has potential ability to produce a wealth of additional secondary metabolites [7]. Up to 25 clusters for putative secondary metabolites are located in the 6.8 Mb chromosome

of *S. clavuligerus* and 23 more are present in the 1.8 Mb megaplasmid pSCL4 [7, 8]. They include ten clusters containing genes for nonribosomal peptide synthetases (NRPS), six clusters with genes for polyketide synthases (PKS), as well as NRPS-PKS hybrid clusters and genes for putative terpene synthesizing enzymes.

Gene clusters encoding novel bioactive products are of utmost interest. The homology of some clusters with previously studied orthologous in other *Streptomyces* species suggest that *S. clavuligerus* might produce staurosporine, moenomycin, indigoidine, and enediyne-like compounds, some of which are antitumor agents. Since most of these compounds have never been detected in *S. clavuligerus* cultures they must be silent clusters that are only expressed in response to specific nutritional or physiological signals, or in response to elicitors [9, 10].

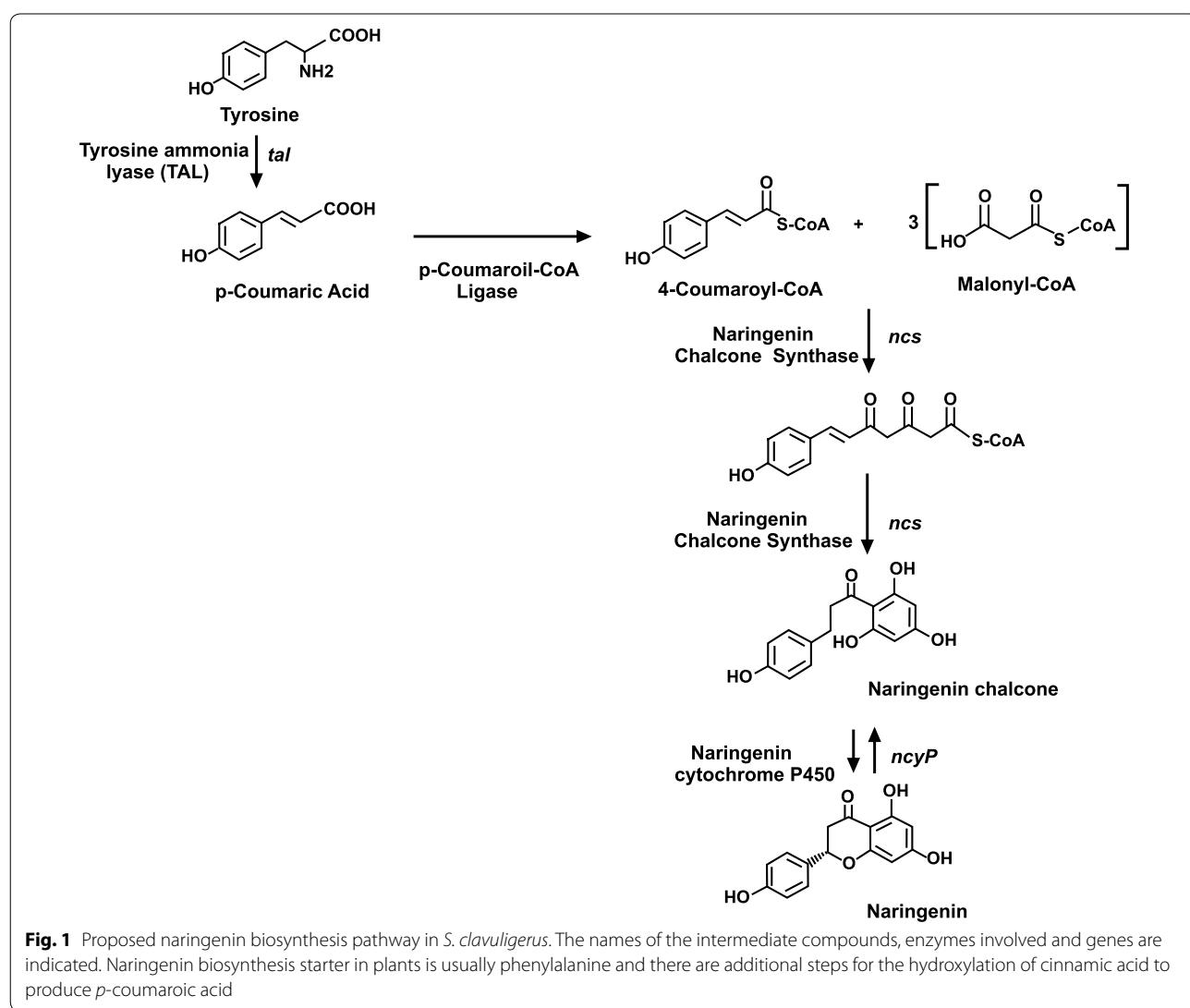
*Correspondence: paloma.liras@unileon.es

¹ Microbiology Section, Department of Molecular Biology, Faculty of Biology and Environmental Sciences, VegaZana Campus, University of León, León 24071, Spain

Full list of author information is available at the end of the article

Chalcone synthases are type III polyketide synthases involved in the condensation of different CoA-activated precursor starter units (i.e. phenylpropenoids) to produce flavonoid-type chalcones. They are very frequent in fungi and in plants, where they serve as precursors of different types of flavonoids [11] but are rare in actinomycetes. Some types of flavonoid intermediates, e.g. naringenin, appeared to be restricted to plants. An interesting question is whether there are chemical structures of secondary metabolites restricted to plants or if many of them can be found in some actinobacteria. In this work we describe that *S. clavuligerus* is able to produce naringenin, a flavanone important as antioxidant [12], described to act as antiinflammatory, chemoprotective and antitumor agent [13, 14].

Naringenin is naturally produced in several plants, especially in grapefruit, and its biosynthesis has been studied in *Medicago*, parsley and other plants (Fig. 1) but it is unknown if the same pathway occurs in *S. clavuligerus*. The starter unit for naringenin biosynthesis is 4-coumaroyl-CoA, which in dicotyledonous plants derives from phenylalanine by the action of a phenylalanine ammonia lyase (PAL). This compound is hydroxylated at carbon 4 by a cinnamate-4-hydroxylase and activated by a CoA-dependent ligase [15]. Monocotyledonous plants might use, in addition, tyrosine as substrate producing directly *p*-coumaric acid without the need of the cinnamate-4-hydroxylase. A related enzyme, encoded by the *encP* gene has been detected in *Streptomyces maritimus* and found to convert phenylalanine in cinnamic acid, required for enterocin biosynthesis [16],



which lacks the hydroxyl group at the C-4 position, but production of naringenin in prokaryotes has never been reported. It was therefore of interest to study if the naringenin pathway and putative gene cluster(s) in *S. clavuligerus* is similar to that of plants and whether it is expressed under some specific conditions.

Results

Characterization of naringenin as a novel product of *S. clavuligerus* ATCC 27064

In the course of a comparative HPLC study of the compounds produced by *S. clavuligerus* in TSB and SA media a large absorbance peak was found in cultures grown in TSB medium that was not present in the broth of SA grown cultures. TSB is a tryptic hydrolysate of soybean meal rich in plant-derived amino acids whereas SA contains only asparagine as nitrogen source. The peak eluted at a retention time of 6 min under the HPLC conditions used in the assay (Fig. 2) and corresponds to an extracellular compound that is also present in extracts of washed

cells at about 1 % of the concentration found in the broth. No appreciable amount of the compound was found in the unseeded TSB medium indicating that it is formed *de novo* in *S. clavuligerus* cultures.

To purify the compound batch cultures were carried out for 72 h to obtain a total of 2.4 l of culture broth. The centrifuged culture supernatant was concentrated under vacuum and extracted with ethyl acetate as indicated in "Methods". After repeated HPLC injections the compound eluting at 6.0 min was collected and lyophilized to obtain 5 mg of pure material that was used for the chemical characterization of the molecule.

The compound produced by *S. clavuligerus* as identified by LC-MS and NMR is naringenin and coelutes in HPLC with authentic naringenin

A mass $[M+H]^+$ of 273 and a molecular formula of $C_{15}H_{12}O_5$ was obtained from LC-MS and from the ^{13}C -NMR analysis. Examination of NMR data analysis (Fig. 3) suggested that compound 1 was a flavanone. Its 1H -NMR spectrum revealed characteristic resonances of aromatic protons including four proton signals of the B-ring appearing as two doublets at δ 7.37 and 6.87 ppm with $J = 8.6$ Hz due to *ortho*- coupling that were assigned to H-2', 6' and H-3', 5, respectively; the two *meta*-coupled protons at δ 5.95 and 5.94 ppm with $J = 2.0$ Hz were assigned to H-6 and H-8. The presence of the quenched signal of 5-OH with the 4-keto group at δ 12.15 and signals at δ 5.40 (1H, dd, $J = 13.1$ and 3.0 Hz), δ 2.70 (1H, dd, $J = 17.2$ and 3.0 Hz) and δ 3.15 (1H, dd, $J = 17.2$ and 13.1 Hz), in conjunction with the ^{13}C -NMR signals at δ 79.04 and 42.66 ppm, inferred from HMQC spectrum, pointed to the presence of an $-O-CH-CH_2-CO-$ system in the C-ring of the flavanone component. This conclusion was reinforced by the correlation of peak signals at δ 3.15 and 2.70 ppm with the signal at δ 5.40 observed in the 1H - 1H COSY spectrum.

The assignment of the signals of the ^{13}C -NMR spectrum, corresponding at δ 95.00 (C-6), δ 95.8 (C-8), δ 115.22 (C-3' and C-5') and δ 128.10 (C-2' and C-6') was carried out by using the HSQC-HMQC spectrum, which showed a correlation peak via $^1J_{C-H}$. Other heteronuclear correlations deduced from the HMQC spectrum (Fig. 3) via $^2J_{C-H}$ and $^3J_{C-H}$, were used to assign the signals corresponding at δ 196.26 (C-4), δ 157.82 (C-4'), δ 166.59 (C-7), δ 164.11 (C-5), δ 163.50 (C-8a), δ 129.49 (C-1') and δ 102.19 (C-4a).

All these NMR data together with the mass spectrum suggested the structure of naringenin [17] for compound 1. The produced compound was different from genistein, a plant flavonoid intermediate similar to naringenin but carrying an additional double bond; both compounds

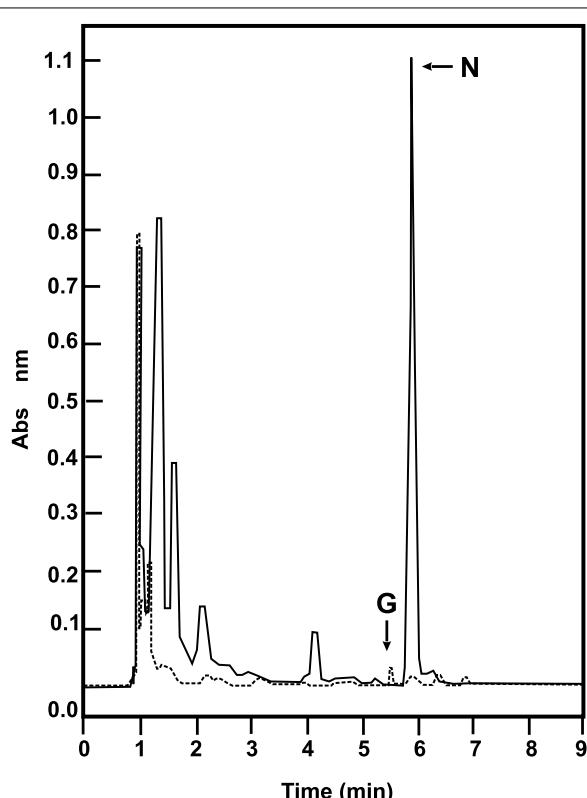
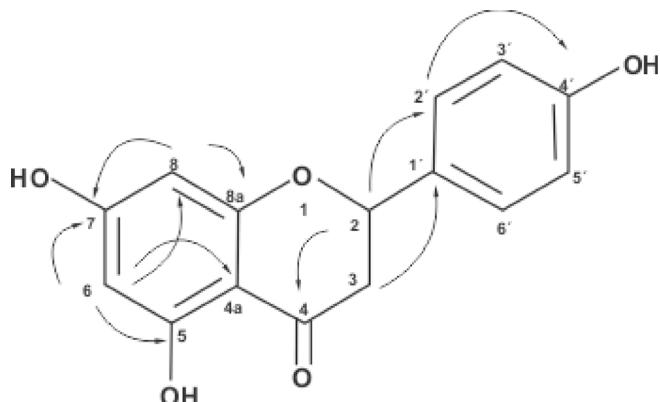


Fig. 2 HPLC analysis of culture broths of *S. clavuligerus*. The broth of cultures grown in SA medium (discontinuous line) and TSB medium (continuous line) were analyzed as indicated in "Methods". The peak with a retention time of 6.0 min coincides with pure commercial naringenin (N). Pure genistein (G) used as standard has a retention time of 5.4 min

a Heteronuclear multiple-bond correlation (HMBC) for compound 1**b** ^1H and ^{13}C -NMR chemical shifts assignments for naringenine (**1**) in acetone-d₆

Nº	^{13}C	^1H
2	79.04	5.40 (dd, $J_{2,3b} = 13.1$; $J_{2,3a} = 3.0$ Hz)
3	42.66	H-3a : 2.70 (dd, $J_{3a,3b} = 17.2$; $J_{3a,2} = 3.0$ Hz) H-3b : 3.15 (dd, $J_{3b,3a} = 17.2$; $J_{3b,2} = 13.1$ Hz)
4	196.26	
4a	102.19	
5	164.11	
6	95.00	5.95 (d, $J_{6,8} = 2.0$ Hz)
7	166.59	
8	95.80	5.94 (d, $J_{8,6} = 2.0$ Hz)
8a	163.50	
1'	129.49	
2', 6'	128.10	7.37 (d, $J_{2',3'} = J_{6',5'} = 8.6$ Hz)
3', 5'	115.22	6.87 (d, $J_{3',2} = J_{5',6} = 8.6$ Hz))
4'	157.82	
5-OH		12.15 s

Fig. 3 NMR analysis for the purified compound. **a** Heteronuclear multiple-bond correlation. **b** ^1H and ^{13}C -NMR chemical shifts assignments for naringenin in acetone-d₆

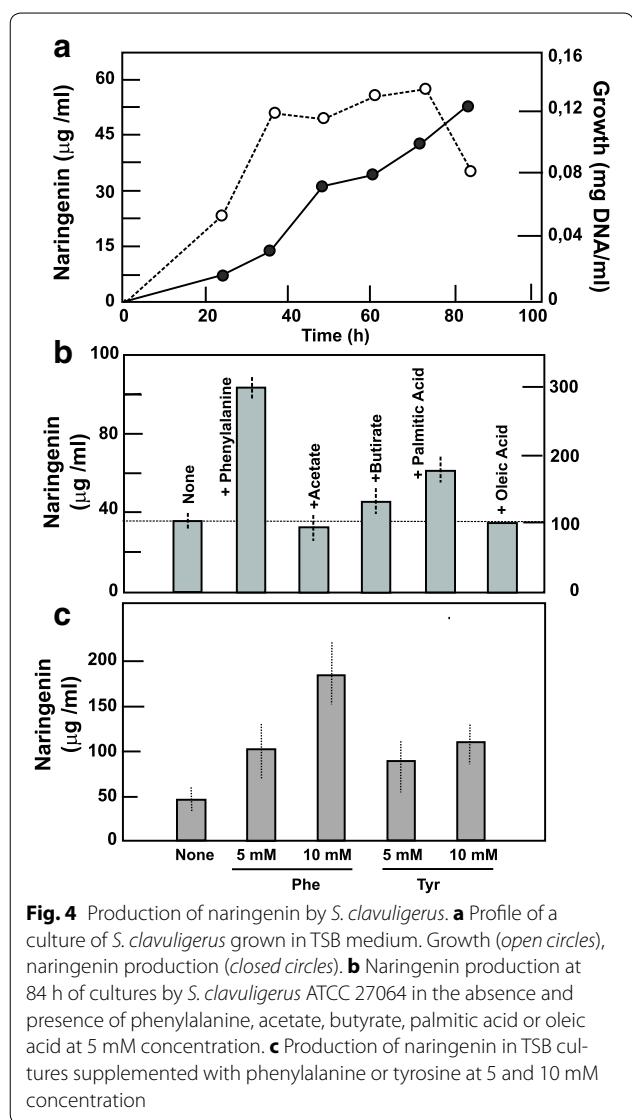
were clearly resolved by HPLC (retention times of 5.4 and 6.0 min for genistein and naringenin, respectively).

Production of naringenin is stimulated by aromatic amino acids

Production of naringenin in TSB medium increases in parallel to the growth of the culture reaching the maximum level at 84 h (Fig. 4). TSB is a complex medium; however, it might not have the adequate precursor requirements for naringenin production. Since this compound is known to be formed from malonate and

tyrosine or phenylalanine in different plants, we supplemented the TSB medium separately with different organic acids (acetic, butyric, palmitic and oleic acid, as sodium salts) at 5 mM concentration and the final production of naringenin was measured in each case. Acetate and oleic acid did not improve naringenin production, but butyrate and palmitic acid improved it 1.15- and 1.63-fold, respectively.

In addition, cultures were supplemented with phenylalanine or tyrosine at 5 and 10 mM concentration (Fig. 4c). Tyrosine improved the naringenin production



by 1.83- and 2.32-fold at 5 and 10 mM concentration, respectively. The best production was observed by addition of phenylalanine, resulting in a naringenin increase of 2.16- and 3.7-fold respectively, at 5 and 10 mM concentration (up to 184 µg/ml). This concentration is much higher than the production obtained by a multistep engineered *E. coli* strain [14] indicating that *S. clavuligerus* ATCC 27064 is a good naringenin producer.

Bioinformatic analysis of genes putatively encoding naringenin biosynthetic enzymes in the *S. clavuligerus* genome

The putative pathway for naringenin biosynthesis (Fig. 1) requires the action of a naringenin chalcone synthase (Ncs) condensing the *p*-coumaroyl-CoA starting unit and three malonyl-CoA molecules. Therefore, using the

sequence of *Glycine max* naringenin chalcone synthase (CAA38456) we searched *S. clavuligerus* genome for homologous genes using the BLAST Program. A single match corresponded to *S. clavuligerus* SCLAV_5492; this gene (named *ncs*) encodes a 351 amino acid protein with characteristics of type III polyketide synthases and a 29 % identity (44 % functionally conserved amino acids) along the entire sequence with *G. max* naringenin chalcone synthase, hereafter named Ncs. Interestingly, this chalcone synthase is closely related to type III PKSs of the RppA family occurring in many *Streptomyces* species (see “Discussion”).

Immediately upstream of *ncs* we found a gene, SCLAV_5491, encoding a 454 amino acid cytochrome P₄₅₀ oxygenase that will be named hereafter *ncyP*. Genes encoding P₄₅₀ oxygenases are frequently present in secondary metabolites gene clusters and we postulated that *ncyP* might encode the enzyme required for the chalcone cyclization (see deletion and complementation experiments). This cytochrome P₄₅₀ gene is more closely related to *rppA*-linked P₄₅₀'s in several *Streptomyces* species than to other P₄₅₀'s genes present in *S. clavuligerus* genome (see “Discussion”).

Genes encoding proteins analogous to Ncs and NcyP are present with the same organization in *S. coelicolor* (SCO1206 and 1207), *S. lividans* (Sli_1485 and 1486) or *S. griseus* (SGR_6619 and 6620) while in *S. venezuelae* (SVEN_5366 and 5367) are located tail to tail, and in *S. avermitelis* (SAV_1171 and SAV_7131) are separated in the genome. The linkage of the *ncs* and *ncyP* genes may be relevant for efficient formation of naringenin (see “Discussion”). A tyrosine, at position 224, conserved in the *S. clavuligerus* Ncs protein, might be involved in the recognition of the first (starter) unit of *p*-coumaroyl-CoA, or malonyl-CoA, as proposed in the RppA synthase of *S. coelicolor* [18, 19].

Location of genes putatively involved in the formation of the 4-coumaroyl-CoA precursor

Naringenin is formed from a 4-coumaric acid starting unit. In order to find genes encoding the enzyme required for 4-coumaroyl biosynthesis, the *encP* gene of *Streptomyces maritimus*, encoding a phenylalanine/tyrosine ammonia lyase [16], was used to search *S. clavuligerus* genome. One single matching gene, SCLAV_5457, was found. This gene, located 47.3 kb upstream of the *ncs-ncyP* cluster encodes a 559 amino acid protein with 37 % amino acids identity (51 % conserved residues) to EncP along the whole sequence. This protein is related to TAL or PAL phenylalanine/tyrosine ammonia lyases and the gene will be named *tal* hereafter [20]. These enzymes are able to deaminate phenylalanine to form cinnamic acid and tyrosine to produce coumaric acid. A short chain

dehydrogenase/reductase encoded by SCLAV_5458, located downstream of the former gene may act on the double bond of the propenoyl side chain of 4-coumaric acid to reduce the double bond.

Activation of coumaric acid is likely to be mediated by the action of the aryl-CoA ligase encoded by SCLAV_3408. This last enzyme contains an ATP binding site (TGDIL, amino acids 386–390) for activation of the aromatic acid as an acyl-adenylate and is similar to coumaroyl-CoA ligases of plants and *Penicillium chrysogenum* [20–22] and to the benzoyl-CoA ligase of *S. maritimus* involved in the biosynthesis of enterocin [16].

Deletion of *S. clavuligerus* ncs and ncyP genes blocks naringenin biosynthesis

In order to elucidate if the *ncs* or *ncyP* genes are involved in naringenin biosynthesis we deleted, separately, each of these genes using the Red/shift procedure. Seven clones of *S. clavuligerus* Δ n_{cs}::aac were obtained. The deleted strains showed the same pigmentation, aerial mycelium and spores formation as the parental strain. However, when tested for naringenin biosynthesis in TSB liquid cultures, production of naringenin was drastically reduced to about 9 % of that in the parental strain, in the seven clones at 84 h cultures (Fig. 5).

Deletion of *ncyP* produced two exconjugants designated as *S. clavuligerus* Δ n_{cyP}::aac. Both mutants produced only traces of naringenin, about 4 % of the level

of the parental strain indicating that *ncyP* (but not other P₄₅₀ oxygenases present in the cell) is strictly required for naringenin biosynthesis. Therefore, for the first time it is demonstrated that both genes, *ncs* and *ncyP*, are involved in naringenin formation.

Complementation of the ncs and ncyP genes in the deleted mutants restores naringenin production

Streptomyces clavuligerus mutants Δ n_{cs}::aac and Δ n_{cyP}::aac were complemented with each of the deleted genes subcloned in the integrative plasmid pAV11 downstream of the anhydrotetracycline-inducible *tcp80* promoter. The complemented strains were grown in TSB medium in the presence of anhydrotetracycline (10 µg/ml) to induce the *tcp80* promoter [23]. Production of naringenin was measured after 96 h of culture in all strains. *S. clavuligerus* ATCC 27064 produced 58 µg/ml. The control transformant with the integrated empty plasmid, *S. clavuligerus* [pAV11], produced a slightly lower naringenin level (48 µg/ml). The production in the deleted mutants and their controls transformed with the empty plasmid dropped to 2–7 µg/ml in the different strains. However, complementation of the *ncs*-deleted mutant resulted in restoration of naringenin production (to 55 µg/ml) and complementation of the *ncyP*-deleted mutant resulted in naringenin concentrations of 42 µg/ml (Fig. 5b). These results confirmed the involvement of *ncs* and *ncyP* in naringenin biosynthesis.

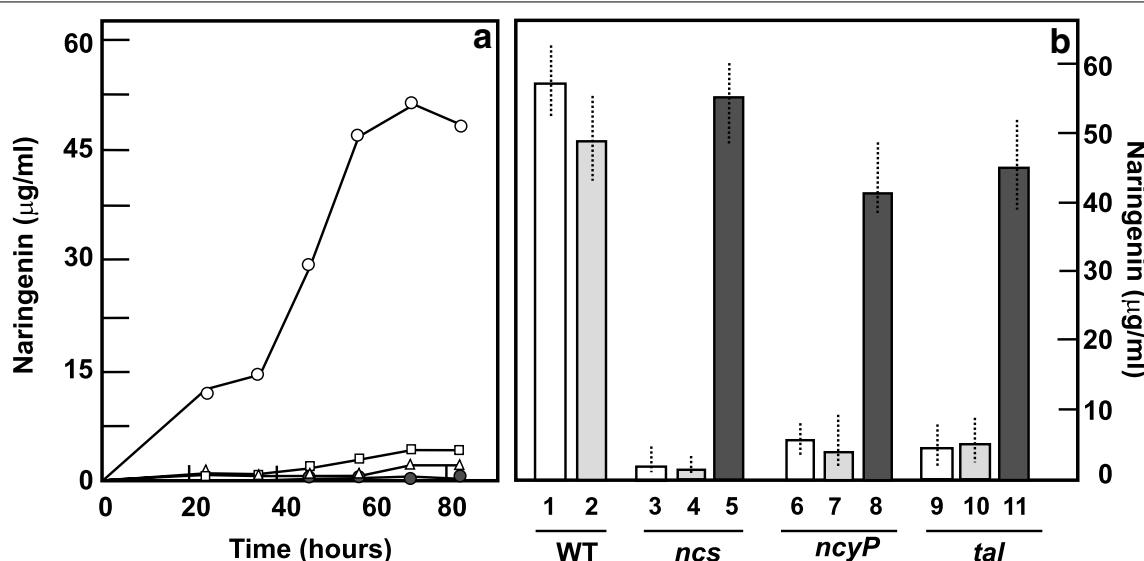


Fig. 5 Production of naringenin by *S. clavuligerus* deleted mutants and complemented strains. **a** Production of naringenin by *S. clavuligerus* 27064 (open circles), *S. clavuligerus* Δ n_{cs}::aac (closed circles), *S. clavuligerus* Δ n_{cyP}::aac (open triangles), *S. clavuligerus* Δ tal::aac (open squares). **b** Production of naringenin by *S. clavuligerus* deleted and complemented strains at 96 h of growth. (1) *S. clavuligerus* ATCC27064, (2) *S. clavuligerus* [pAV11], (3) *S. clavuligerus* Δ n_{cs}::aac (4) *S. clavuligerus* Δ n_{cs}::aac [pAV11], (5) *S. clavuligerus* Δ n_{cs}::aac [pAV11-ncs], (6) *S. clavuligerus* Δ n_{cyP}::aac (7) *S. clavuligerus* Δ n_{cyP}::aac [pAV11], (8) *S. clavuligerus* Δ n_{cyP}::aac [pAV11-ncyP], (9) *S. clavuligerus* Δ tal::aac, (10) *S. clavuligerus* Δ tal::aac [pAV11], and (11) *S. clavuligerus* Δ tal::aac [pAV11-tal]

***S. clavuligerus* Δtal::aac, deleted in the tal gene, does not produce naringenin but production is restored by complementation**

The *tal* gene, encoding a TAL/PAL enzyme was cloned from *S. clavuligerus* genomic DNA. Using oligonucleotides *tal_F* and *tal_R* a 1929 bp DNA fragment was amplified, sequenced and used to locate a cosmid containing the *tal* gene. Two cosmids D6-6 and D9-10 gave positive hybridization with the 1.9 kb DNA fragment. The sequencing of the insert of both cosmids showed that the *tal* gene was in a central position in cosmid D9-10 which was used for further studies. Seven apramycin resistant kanamycin sensitive clones, deleted in *tal*, were obtained by the Redirect technique. The seven clones were identical by restriction mapping, PCR amplification and sequencing confirming that the *tal* gene was substituted by the *aac* gene; the deleted strain was named *S. clavuligerus* Δtal::aac. The *tal* mutants showed a normal behavior in sporulation and aerial mycelium formation in TSB and ME media. When they were grown in TSB liquid cultures the naringenin production at 96 h was lower than 6 % in comparison to the wild type strain. Complementation of one of these mutants with the *tal* gene results in a transformant producing 46 µg/ml, which is 95 % of the production of the control strain *S. clavuligerus* [pAV11] (Fig. 5b). This confirms that the ammonia lyase encoded by *tal* is involved in naringenin formation, probably by using tyrosine or phenylalanine as substrate(s) to form the 4-coumaric acid precursor unit. In this respect, *S. clavuligerus* is similar to monocotyledonous plants that are able to use a TAL to form directly *p*-coumaric acid and differs from dicotyledonous plant cells which form coumaric acid through a hydroxylation of trans-cinnamic acid by the enzyme cinnamate-4-hydroxylase. Our study showed that *S. clavuligerus* genome does not contain a cinnamate-4-hydroxylase.

RT-PCR transcription analysis of the genes involved in naringenin biosynthesis

Expression of *ncs* and *ncyP* in two different media (SA and TSB) was tested by RT-PCR at 24 and 48 h of culture. As shown in Fig. 6 a very weak amplification band of these two genes is observed in cultures grown in SA medium while a strong amplification signal was found in TSB medium what corroborates our initial results on production of naringenin in each of these media. Expression of these genes might be induced by soja-derived compounds in the triptic soja broth as reported for other P₄₅₀ genes [24]. Using the oligonucleotides indicated in the Additional files 1, 2 an RT-PCR analysis was done for the intergenic *ncs-ncyP* region. No amplification of the intergenic fragment was detectable (not shown) in RNA samples in which both *ncs* and *ncyP* were clearly amplified,

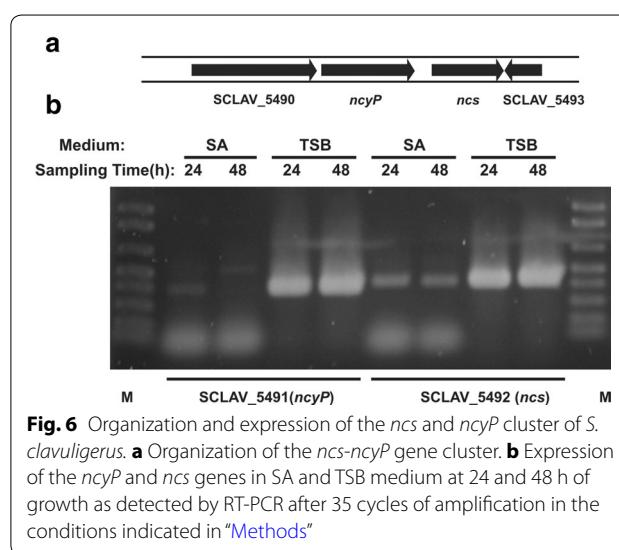


Fig. 6 Organization and expression of the *ncs* and *ncyP* cluster of *S. clavuligerus*. **a** Organization of the *ncs-ncyP* gene cluster. **b** Expression of the *ncyP* and *ncs* genes in SA and TSB medium at 24 and 48 h of growth as detected by RT-PCR after 35 cycles of amplification in the conditions indicated in "Methods"

indicating that each of these genes was expressed as a monocistronic unit.

To determine whether the stimulatory effect observed by phenylalanine and tyrosine addition to the cultures was a precursor availability effect, or if it was due to an induction effect, quantification by qRT-PCR of the *ncs*, *ncyP* and *tal* transcripts in control cultures and cultures supplemented with phenylalanine or tyrosine (each at 5 and 10 mM concentration) was made. No significant differences in the transcription of the three genes was observed following phenylalanine or tyrosine addition, and only a very weak stimulation of the *ncs* transcription was observed in the presence of phenylalanine. Therefore the stimulatory effect of these two aromatic amino acids on naringenin production is likely due to a precursor effect and not to induction of the naringenin biosynthetic genes.

RppA versus Ncs: *Streptomyces coelicolor* forms tetrahydroxynaphthalene but does not produce naringenin

Bacterial type III polyketide synthases are a group of PKSs that contain two KS domains and catalyze repeated condensations of malonyl/CoA units. They are similar to plant chalcone synthases [25] in amino acid sequence, although the plant chalcone synthases are usually larger enzymes. Some type III PKSs have been described in soil dwelling *Streptomyces* species and some related actinobacteria [26]. Several of these PKSs are involved in the production of red-brown pigments and consequently the encoding gene was named *rppA* [27–29]. The best known of these PKSs are the 1,3,6,8 tetrahydroxynaphthalene (THN) synthases of *S. griseus* and *S. coelicolor* encoded

by *rppA* genes. In the formation of THN the RppA PKS uses malonyl-CoA as starter unit and three additional malonyl-CoA as elongation units [30]. In some *Streptomyces* species the THN is further oxidized to flaviolin [26]. Although *S. clavuligerus* Ncs and *S. coelicolor* RppA are related enzymes our study showed that *S. clavuligerus* does not produce red brown THN pigment and, additionally, the Δncs mutant culture broth remains of the same colour as the wild type cultures. Moreover, *S. coelicolor* A3(2), that is well known to synthesize THN does not produce naringenin when cultured in TSB medium under conditions in which *S. clavuligerus* produces this compound.

It was therefore of interest to know if *S. coelicolor* is able to produce naringenin when supplied, exogenously or endogenously, with *p*-coumaric acid. To test if the *S. coelicolor* RppA might be able to produce naringenin, two different experimental approaches were followed. First, *S. coelicolor* M145 cultures were supplemented with coumaric acid (5 mM). Second, *S. coelicolor* M145 was transformed with the *S. clavuligerus tal* gene (SCLAV_5457) expressed from the anhydrotetracyclin inducible *tcp830* promoter in plasmid pAV11 to provide endogenous coumaric acid. Cultures of *S. coelicolor* [pAV11-tal] were supplemented with phenylalanine, tyrosine or coumaric acid (5 mM) and compared with cultures of *S. coelicolor* [pAV11] transformed with the empty plasmid, grown in the same conditions. None of this strategies resulted in detectable levels of naringenin production by *S. coelicolor* suggesting that the RppA chalcone synthase is unable to use *in vivo* efficiently *p*-coumaroyl-CoA instead of malonyl-CoA as starter unit.

Discussion

In plants and in *S. clavuligerus*, as shown in this article, the initial product of the Ncs is the naringenin chalcone, that plants usually converted later to flavonoids. Naringenin is synthesized by cyclization of a tetraketide formed by condensation of a *p*-coumaroyl-CoA starter and three malonyl-CoA elongation units (Fig. 1). The cyclization mechanism catalyzed by Ncs that leads to the formation of the pyrone ring of naringenin (Fig. 1) is different from the aromatization mechanism that results in the formation of THN, which involves a C–C condensation with the free carboxyl group of the starter malonyl-CoA.

The *ncs-ncyP* gene cluster and the *tal* gene, although located in two separate positions (47.3 kb apart) in the genome cooperate in the formation of the *p*-coumaric acid precursor unit and in the assembly of the naringenin molecule, an usual feature of genes for secondary metabolites that normally are clustered in *Streptomyces*.

The crystal structure of some CHSs [31, 32] revealed an important role of the size of the cavity of the active center

in the selection of the starter unit, and therefore, of the product of the pathway. This may explain the different products of NCS versus other related type III PKSs.

Streptomyces RppA's were hypothesized to have a small active center cavity that allowed only the entry of small acyl-CoA derivatives such as malonyl-CoA [33] different from plant chalcone synthases that use bulky starter units such as *p*-coumaroyl-, caffeyl- or *trans*-cinnamoyl-CoA.

The amino acid sequence of *S. clavuligerus* Ncs and the RppAs of *S. avermitilis* and *S. coelicolor* are very similar (76 and 74 % identity, respectively). All these proteins posseses the four amino acid residues characteristics of chalcone synthases active center (Cys¹³⁸, Phe¹⁸⁸, His²⁷⁰ and Asn³⁰³ in Ncs enzyme) [31]. The sequence of amino acids around the active center is different in *Streptomyces* and plant chalcone synthetases (Additional file 1: Figure S1), but 50 % of these amino acids are conserved. Therefore, *S. clavuligerus* Ncs is a member of the RppA family and is phylogenetically closer to *Streptomyces* than to plant chalcone synthases in spite of giving a final plant typical product. However, *S. clavuligerus* does not produce significant amounts of THN or THN-derived pigments indicating that *p*-coumaroyl-derived naringenin is the major product of this enzyme. Furthermore, the *S. clavuligerus* Δncs mutant is not albino at difference of the *S. griseus* $\Delta rppA$ mutant and does not change in colour with respect to its parental strain.

The Tyr²²⁴ in the entry channel of RppA's was proposed as the amino acid determining the selective use of malonyl-CoA as starter unit, although this hypothesis was later disputed by new evidence provided by a set of mutants in the Tyr²²⁴ amino acid [18]. Interestingly, the *S. clavuligerus* Ncs has a conserved Tyr at position 224 thus indicating that this amino acid is not strictly required for the entry of *p*-coumaroyl-CoA as starter unit of the polypeptide, which is in agreement with the finding of Li et al. [18].

Linked to *ncs* in *S. clavuligerus* genome is a *ncyP* gene encoding a P₄₅₀ oxygenase that is strictly required for naringenin biosynthesis. Similarly the P₄₅₀ gene associated with *rppA* in *S. griseus* (known as *rppB*) is also required for THN formation [32, 34]. Our studies show that those two genes separately transcribed whereas in *S. griseus* they appear to be co-transcribed and translationally coupled, suggesting that both proteins are likely to form a functional complex. Cortés et al. [27] suggested that the RppA associated P₄₅₀ has a role in cross-linking of THN molecules and this hypothesis was later supported by the study of strains overexpressing *rppB* that form dimers and trimmers of flaviolin, the quinone derived from THN. Moreover, this P₄₅₀ oxygenase has probably a role as a helper in the first cyclization of the tetraketides, both in THN and naringenin biosynthesis, what explains the

essential role of these P₄₅₀ oxygenases in the formation of THN and naringenin, that later proceed by different final cyclization processes.

Tyrosine ammonia lyase and formation of *p*-coumaroyl-CoA

Phenylalanine and tyrosine ammonia lyases belong to a family of aromatic amino acid ammonia lyases that are closely related to bacterial histidine ammonia lyases and aminomutases [35]. These enzymes catalyze the non-oxidative deamination of aromatic amino acids resulting in the formation of trans-*p*-coumaric acid when the substrate is L-tyrosine or trans-cinnamic acid when the substrate is phenylalanine. The biosynthesis of trans-cinnamic acid in dicotyledonous plants is catalyzed by a large PAL that works as a tetramer. A separate enzyme cinnamate 4-hydroxylase introduces the hydroxyl group at position 4 of the aromatic ring. In monocotyledonous plants both reactions are catalyzed by a single enzyme with TAL/PAL enzyme that uses both tyrosine and phenylalanine as substrates [36]. The bacterial aryl ammonia lyases are smaller (about 400 amino acids) tetrameric ammonia lyases [35]. Based on the crystal structure of the *Rhodobacter* histidine ammonia lyase and on the kinetics data of some mutant enzymes Louie and coworkers [36] proposed that His⁸⁹ has an important role in this enzyme recognition of histidine or aromatic amino acids as substrates, since His⁸⁹ forms hydrogen bridges with the substrates of the enzyme.

S. clavuligerus TAL, as the homologous enzyme of *Saccharothrix spanaensis* involved in the biosynthesis of saccharomicin [37], has a rather different amino terminal region when compared with the *Rhodobacter* enzyme, although six motifs described in the *Rhodobacter* enzyme

to interact with the substrate are conserved to some degree (Fig. 7). The H⁸⁹ present in one of these motifs in the *Rhodobacter* ammonia lyase corresponds to Y¹⁰⁵ in *S. clavuligerus* TAL; this Y¹⁰⁵ is conserved (or substituted by Phe) in a small group of actinobacteria which have ammonia lyases with 50–60 % identity to *S. clavuligerus* TAL, while the bulk of *Streptomyces* ammonia lyases have about 40 % identity with the *S. clavuligerus* enzyme, and differ in that they have an IVRSH sequence with serine at the corresponding 105 position. Using in vitro reactions with the *Saccharothrix* enzyme, that has a LIKYH domain carrying tyrosine [37] it has been clearly demonstrated that the product of this ammonia lyase is *p*-coumaric acid and not trans-cinnamic acid and the substrate used is L-tyrosine. Similar observations have been made for tyrosine amino mutase of *Streptomyces globisporus* that forms *p*-coumaric acid as an intermediate in the α- to β- tyrosine isomerization and has 37 % identity to the *S. clavuligerus* TAL.

Aromatic amino acid ammonia lyases were thought to contain a dehydroalanine prosthetic group derived from serine (in the *Rhodobacter sphaeroides* HAL protein) but later molecular genetics and spectrophotometric studies [38, 39] established that the prosthetic group is methylidene-imidazol-5-one (MIO). This molecule is formed by autocatalytic dehydration and cyclization of the internal tripeptide ala-ser-gly that in *S. clavuligerus* TAL corresponds to amino acids A¹⁶⁴-S¹⁶⁵-G¹⁶⁶ (Fig. 7). This tripeptide precursor of the prosthetic MIO group is present in all putative aromatic amino acid ammonia lyases and amino acid mutases in several *Streptomyces* species. The prosthetic group MIO of aromatic amino acid ammonia lyases is also present in the *S. clavuligerus* TAL protein as deduced from spectrophotometric studies [Álvarez-Álvarez, unpublished results].

75	102	161	316	365	452		
YGVTTGFG...	LITYH...	SVGASGDLV...	QDPYSIR...	GGNFYGG...	EAHNQDKV...	<i>Streptomyces clavuligerus</i>	
YGVTTGFG...	LITYH...	SVGASGDLV...	QDRYSIR...	GGNFYGG...	EAHNQDKV...	<i>Saccharopolyspora spinosa</i> 67%	
YGVTTGFG...	LIKYH...	SVGASGDLV...	QDRYSVR...	GGNFYGG...	SAMQEDHV...	<i>Saccharothrix espanaensis</i> 67%	
YGVTTGFG...	LIRYH...	SLGASGDLV...	QDRYSVR...	GGNFYGG...	EAHNQDKV...	<i>Amycolatopsis decaplanina</i> 56%	
YGVTSFGF...	LIRFL...	SVGASGDLV...	QDRYSVR...	GGNFYGG...	EAHNQDKV...	<i>Streptomyces rimosus</i> 56%	
YGVTTGFG...	MLRFL...	SCGASGDLI...	QDKYSIR...	GGNFYGS...	EAHNQDKV...	<i>Solirubrobacter soli</i> 52%	
YGVSTGFG...	IVRSH...	SLGCSGDLA...	QDAYSVR...	NGNFHGA...	SAMQEDHV...	<i>Streptomyces coelicolor</i> 39%	
YGVSTGFG...	IVRSH...	SLGCSGDLA...	QDAYSVR...	NGNFHGA...	SAMQEDHV...	<i>Streptomyces avermitilis</i> 39%	
YGVSTGFG...	IVRSH...	SLGCSGDLA...	QDAYSVR...	NGNFHGA...	SAMQEDHV...	<i>Streptomyces globisporus</i> 41%	
YGVNTSMG...	LINAV...	SLGTSGDLG...	EDAYSIR...	NGHFHQ...	TADFQDIV...	<i>Streptomyces maritimus</i> 37%	
YGLTTGFG...	LVHHL...	TVGASGDLT...	QDAYSLR...	GGNFMQ...	NAANQDVV...	<i>Rhodobacter sphaeroides</i> 40%	
** * . * * . * * . * * . * * . * . .		

Fig. 7 Partial amino acid sequence alignment of regions known to form the active site of TAL proteins. Above are indicated the amino acid positions in *S. clavuligerus* SCLAV_5457 sequence. At the right side is shown the % of amino acids identity of the whole protein. The sequences used in this figure are ammonia lyases from *Saccharopolyspora spinosa* (WP_029535616.1), *Saccharothrix espanaensis* (WP_015102494), *Amycolatopsis decaplanina* (WP_007032994), *Streptomyces globisporus* (WP_029182093.1), *Streptomyces rimosus* subsp. *rimosus* ATCC 10970 (ELQ83456.1), *Streptomyces maritimus* EncP (gb|AAF81735.1), *Solirubrobacter soli* (WP_028063475.1), *Streptomyces coelicolor* (WP_629085.1), *Streptomyces avermitilis* (WP_010984755.1) and *Rhodobacter sphaeroides* (WP_011339422.1)

In summary, three enzymes Ncs, NcyP and Tal are involved in naringenin formation in *S. clavuligerus*, a strain that does not produce the THN pigment in spite of the similarity of Ncs to the *S. coelicolor* RppA protein.

Methods

Strains and culture conditions

The wild type strain, *Streptomyces clavuligerus* ATCC 27064 was used to purify naringenin. Strains *S. clavuligerus Δncs::aac*, *S. clavuligerus Δnyp::aac* and *S. clavuligerus Δtal::aac* were obtained from the wild type strain by the REDIRECT Technique. *Streptomyces coelicolor* [pAV11-tal] and *S. coelicolor* [pAV11] derive from *S. coelicolor* M145 and were used to study possible naringenin production.

All the strains were grown at 28 °C in an orbital shaker incubator at 220 rpm for 24 h in 500 ml baffled flasks containing 100 ml of TSB medium. A 5 % (v/v) of this seed culture was used to inoculate TSB (trypticaseine broth) or SA (starch-asparagine) cultures grown in the same conditions [40]. All the cultures were made in triplicate flasks. The TSB was supplemented with tyrosine, phenylalanine or with organic acids (acetate, butirate, oleic acid, palmitic acid) as sodium salts, when required. Cultures of transformants strains were supplemented with kanamycin (50 µg/ml), anhydrotetracycline (10 µg/ml), hygromycin (50 µg/ml), apramycin (50 µg/ml) or nalidixic acid (25 µg/ml) when required. Complex ME medium [41] was used for sporulation purposes.

Naringenin purification by HPLC

Naringenin was purified by HPLC using an Alliance 2695 HPLC with a refrigerated autosampler, a column furnace and a photodiode array detector (PDA) 2998 (Waters Corp.). Naringenin was quantified at its maximum absorption peak (290 nm). The system was equipped with a 3.5 µm particle size XBridge™ C18 (2.1 × 150 µm, Waters Corp.) column.

The culture samples were centrifuged at 13,000 rpm for 5 min and the supernatants filtered through sterile 0.2 µm polyethersulphone (PES) syringe filters (VWR, Intl.). The whole sample (100 ml) was loaded in multiple injections. HPLC conditions were as follows: column temperature 40 °C; the flow was kept at 0.32 ml/min from 0 to 2 min and then increased gradually to reach 0.40 ml/min at 10 min. A mixture of Milli Q water with 0.01 % trifluoroacetic acid (A) and acetonitrile (B) were used as solvent with the following program: 0–2 min increase from 20 to 30 % B and kept at 30 % B thereafter. The peak eluting at 6 min from repeated injections was collected and pooled and the solvent from the pooled preparation was evaporated under low pressure (SpeedVac Savant Sc110, Thermo Sci.). The concentrated solution was

lyophilized and kept at –20 °C until NMR analysis and identification. Pure naringenin and genistein (Sigma Ch. Co.) were used as standards.

NMR analysis

NMR spectra were recorded in methanol-d₄ at room temperature using a Bruker WM 500 spectrometer [500 MHz (¹H NMR) and 125 MHz (¹³C NMR)]. Chemical shifts are given on the δ-scale and were referenced to the solvent (δc = 49.0 ppm) and to the TMS as internal standard. The pulse programs of the following 2D experiments were taken from the Bruker software library and the parameters were as follows: 500/125 MHz gradient-selected HMQC spectra [1]: relaxation delay D₁ = 1.5 s; 500/125 MHz gradient-selected HMBC spectra [1]: relaxation delay D₁ = 1.5 s; evolution delay D₂ = 3.33 ms; delay for evolution of long range coupling D₆ = 60 ms. 500 MHz gradient-selected ¹H, ¹H COSY spectra [2]: relaxation delay D₁ = 1.5 s; 90° pulse for ¹H.

Mass spectrometry

The mass spectra were determined by HPLC–MS (Agilent Technologies). Using a HP-1100 Series HPLC and MS: 6120 Quadrupole LC/MS.

Extraction and purification of RNA

RNA was extracted from 1.5 ml samples taken at 24 and 48 h of growth in TSB and SA media. Two volumes of RNA-protect (Qiagen) were added to the samples. The commercial system Qiagen, RNAeasy was used following the manufacturer instructions as described previously [40].

RT-PCR

For RT-PCR amplification the final 20 µl reaction contained RNA (200–300 ng), reaction mixture 1×, 0.5 mM each oligonucleotide (see Additional file 2: Table S1); 5 % DMSO; *SuperScriptTM II* Reverse Transcriptase and *Platinum® Taq* (Invitrogen) 1–2 units. Control reactions were done with the same procedure but only with *Platinum® Taq*. Amplification conditions: cDNA was formed in a 50 °C 30 min cycle. Then, an initial 94 °C 2 min denaturation cycle was followed by 25–35 30-s cycles at 95 °C. A final extension cycle of 10 min at 72 °C reaction was allowed.

Construction of the complemented strains

In order to complement the *ncs*, *nyp* and *tal*-deleted strains, each of those genes was obtained by PCR amplification, sequenced to confirm their integrity and subcloned downstream of the anhydrotetracycline-inducible *tcp-830* promoter in the EcoRV site of the conjugative-integrative vector pAV11 [23]. The constructions were

introduced in *E.coli* ET12567/pUZ8002, and then were transferred to the adequate *Streptomyces* strain by conjugation. Hygromycin resistant exconjugants were tested by PCR to confirm the presence of the complementing genes.

Additional files

Additional file 1: Figure S1. A) Conserved sequences around the key amino acids located in chalcone synthases active center. The numbers given in the sequence correspond to *S. clavuligerus* Ncs, where the key amino acids are Cys¹³⁸, Phe¹⁸⁸, His²⁷⁰ and Asn³⁰³. B) Phylogenetic tree of plant and *Streptomyces* chalcone synthases. The origin of the sequences used is indicated at the right side. Numbers at the far right side correspond to the genetic distance index.

Additional file 2: Table S1. Oligonucleotides used in this work.

Authors' contributions

RA fermented the supplemented strains, analyzed the transcription of the genes and cloned, deleted and complemented the *ncs* and *tal* genes. AB cloned, deleted and complemented the *ncyP* gene. AR identified naringenin by LC and NMR. SA purified the naringenin and performed the HPLC analysis. JFM and PL directed the experimental work and write the manuscript. All authors read and approved the final manuscript.

Author details

¹ Microbiology Section, Department of Molecular Biology, Faculty of Biology and Environmental Sciences, Vegaazana Campus, University of León, León 24071, Spain. ² Institute of Biotechnology, INBIOTEC, Av. Real 1, León 24006, Spain. ³ Organic Chemistry Department, University Autónoma of Madrid, Cantoblanco, 28049 Madrid, Spain.

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Competing interests

The authors declares that they have no any competing interests in the manuscript.

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References

- Bagaley KH, Brown AG, Schofield CJ. Chemistry and biosynthesis of clavulanic acid and other clavams. *Nat Prod Rep.* 1997;14:309–33.
- Pérez-Redondo R, Santamaría I, Bovenberg R, Martín JF, Liras P. The enigmatic lack of glucose utilization in *Streptomyces clavuligerus* is due to inefficient expression of the glucose permease gene. *Microbiology.* 2010;156:1527–37.
- Liras P, Demain AL. Enzymology of β-lactam compounds with cepham structure produced by actinomycete. In: Hopwood D, editor. *Methods in enzymology*, vol. 458. Burlington: Academic Press; 2009. p. 401–29.
- Jensen SE. Biosynthesis of clavam metabolites. *J Ind Microbiol Biotechnol.* 2012;39:1407–19.
- Li B, Walsh CT. Identification of the gene cluster for the dithiopyrrolone antibiotic holomycin in *Streptomyces clavuligerus*. *Proc Natl Acad Sci USA.* 2010;107:19731–5.
- Robles-Reglero V, Santamaría I, Álvarez-Álvarez R, Martín JF, Liras P. Transcriptional analysis and proteomics of the holomycin gene cluster in overproducer mutants of *Streptomyces clavuligerus*. *J Biotechnol.* 2013;163:69–76.
- Medema MH, Trefzer A, Kovalchuk A, vandenBerg M, Müller U, Heijne W, Wu L, Alam MT, Ronning CM, Nierman WC, Bovenberg RA, Breitling R, Takano E. The sequence of a 1.8-Mb bacterial linear plasmid reveals a rich evolutionary reservoir of secondary metabolic pathways. *Genome Biol Evol.* 2010;2:212–24.
- Song JY, Jeong H, Yu DS, Fischbach MA, Park HS, Kim JJ, Seo JS, Jensen SE, Oh TK, Lee KJ, Kim JF. Draft genome sequence of *Streptomyces clavuligerus* NRRL 3585, a producer of diverse secondary metabolites. *J Bacteriol.* 2010;192:6317–8.
- Ochi K, Hosaka T. New strategies for drug discovery: activation of silent or weakly expressed microbial gene clusters. *Appl Microbiol Biotechnol.* 2013;97:87–98.
- Martín JF, Liras P. Novel antimicrobial and other bioactive metabolites obtained from silent gene clusters. In: Sanchez S, Demain AL, editors. *Antibiotics current innovations and future trends*. Nordfolk: Caister Academic Press; 2014. p. 275–92.
- Schröder J. Probing plant polyketide biosynthesis. *J Nat Struct Biol.* 1999;6:714–6.
- Cavia-Saiz M, Bustos MD, Pilar-Izquierdo MC, Ortega N, Pérez-Mateos M, Muñiz P. Antioxidant properties, radical scavenging activity and biomolecule protection capacity of flavonoid naringenin and its glycoside naringenin: a comparative study. *J Sci Food Agric.* 2010;90:1238–44.
- Jagetia A, Jagetia GC, Jha S. Naringin, a grapefruit flavanone, protects V79 cells against the bleomycin-induced genotoxicity and decline in survival. *J Appl Toxicol.* 2007;27:122–32.
- Wu J, Zhou T, Du G, Zhou J, Chen J. Modular optimization of heterologous pathways for de novo synthesis of (2S)-naringenin in *Escherichia coli*. *Plos One.* 2014;9:e101492.
- Kyndt JA, Meyer TE, Cusanovich MA, Van Beeumen JJ. Characterization of a bacterial tyrosine ammonia lyase, a biosynthetic enzyme for the photoactive yellow protein. *FEBS Lett.* 2002;512:240–4.
- Xiang L, Moore BS. Inactivation, complementation, and heterologous expression of *encP*, a novel bacterial phenylalanine ammonia-lyase gene. *J Biol Chem.* 2002;277:32505–9.
- Zhang XF, Hung TM, Phuong PT, Ngoc TM, Min B-S, Song K-S, Seong YH, Bae KH. Anti-inflammatory activity of flavonoids from *Populus davidiana*. *Arch Pharm Res.* 2006;29(12):1102–8.
- Li S, Gruscow S, Dordik J, Sherman DH. Molecular analysis of the role of tyrosine 224 in the active site of *Streptomyces coelicolor* RppA, a bacterial Type III polyketide synthase. *J Biol Chem.* 2007;282:12765–72.
- Appert C, Logemann E, Hahlbrock K, Schmid J, Amrhein N. Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsley. *Eur J Biochem.* 1994;225:491–9.
- Schneider K, Hövel K, Witzel K, Hamberger B, Schomburg D, Kombrink E, Stuible HP. The substrate specificity-determining amino acid code of 4-coumarate:CoA ligase. *Proc Natl Acad Sci USA.* 2003;100:8601–6.
- Lamas-Maceiras M, Vaca I, Rodríguez E, Casqueiro J, Martín JF. Amplification and disruption of the phenylacetyl-CoA ligase gene of *Penicillium chrysogenum* encoding an aryl-capping enzyme that supplies phenylacetic acid to the isopenicillin N-acyltransferase. *Biochem J.* 2006;395:147–55.
- Martín JF, Ullán RV, García-Estrada C. Role of peroxisomes in the biosynthesis and secretion of β-lactams and other secondary metabolites. *J Ind Microbiol Biotechnol.* 2012;39:367–82.
- Rodríguez-García A, Combes P, Pérez-Redondo R, Smith MC, Smith MC. Natural and synthetic tetracycline-inducible promoters for use in the antibiotic-producing bacteria *Streptomyces*. *Nucleic Acids Res.* 2005;33:e87.
- Sariaslani FS, Kunz DA. Induction of cytochrome P-450 in *Streptomyces griseus* by soybean flour. *Biochem Biophys Res Commun.* 1986;141:405–10.
- Austin MB, Noel JP. The chalcone synthase superfamily of type III polyketide synthases. *Nat Prod Rep.* 2003;20:79–110.
- Zeng J, Decker R, Zhan J. Biochemical characterization of a type III polyketide biosynthetic gene cluster from *Streptomyces toxytricini*. *Appl Biochem Biotechnol.* 2012;166:1020–33.
- Cortés J, Velasco J, Foster G, Blaackby AP, Rudd BAM, Wilkinson B. Identification and cloning of a type III polyketide synthase required for diffusible pigment biosynthesis in *Saccharopolyspora erythraea*. *Mol Microbiol.* 2002;44:1213–24.
- Ikeda K, Masujima T, Suzuki K, Sugiyama M. Cloning and sequence analysis of the highly expressed melanin-synthesising gene operon

- from *Streptomyces castaneoglobisporus*. *Appl Microbiol Biotechnol*. 1996;4:80–5.
29. Funo N, Funabashi M, Ohnishi Y, Horinouchi S. Biosynthesis of hexahydroxyperylenequinone melanin via oxidative aryl coupling by cytochrome P-450 in *Streptomyces griseus*. *J Bacteriol*. 2005;187:8149–55.
 30. Funo N, Ohnishi Y, Fujii I, Shibuya M, Ebizuka Y, Horinouchi S. A new pathway for polyketide synthesis in microorganisms. *Nature*. 1999;400:897–9.
 31. Ferrer JL, Jez JM, Bowman ME, Dixon RA, Noel JP. Structure of chalcone synthase and the molecular basis of plant polyketide biosynthesis. *Nat Struct Biol*. 1999;6:775–84.
 32. Jez JM, Noel JP. Mechanism of chalcone synthase. pKa of the catalytic cysteine and the role of the conserved histidine in a plant polyketide synthase. *J Biol Chem*. 2000;275:39640–6.
 33. Funo N, Ohnishi Y, Ebizuka Y, Horinouchi S. Properties and substrate specificity of RppA, a chalcone synthase-related polyketide synthase in *Streptomyces griseus*. *J Biol Chem*. 2002;277:4628–35.
 34. Ueda K, Kim KM, Beppu T, Horinouchi S. Overexpression of a gene cluster encoding a chalcone synthase-like protein confers redbrown pigment production in *Streptomyces griseus*. *J Antibiot*. 1995;48:638–46.
 35. Louie GV, Bowman ME, Moffitt MC, Baiga TJ, Moore BS, Noel JP. Structural determinants and modulation of substrate specificity in phenylalanine-tyrosine ammonia-lyases. *Chem Biol*. 2006;13:1327–38.
 36. Rosler J, Krekel F, Amrhein N, Schmid J. Maize phenylalanine ammonia-lyase has tyrosine ammonia-lyase activity. *Plant Physiol*. 1997;113:175–9.
 37. Berner M, Krug D, Bihlmaier C, Vente A, Müller R, Bechthold A. Genes and enzymes involved in caffeic acid biosynthesis in the actinomycete *Saccharothrix espanaensis*. *J Bacteriol*. 2006;188:2666–73.
 38. Schwede TF, Rétey J, Schulz GE. Crystal structure of histidine ammonia-lyase revealing a novel polypeptide modification as the catalytic electrophile. *Biochemistry*. 1999;38:5355–61.
 39. Röther D, Merkel D, Rétey J. Spectroscopic evidence for a 4-methylidene imidazol-5-one in histidine and phenylalanine ammonia-lyases. *Angew Chem Int Ed Engl*. 2000;39:2462–4.
 40. Santamaría I, López-García MT, Kurt A, Nárdiz N, Álvarez-Álvarez R, Pérez-Redondo R, Martín JF, Liras P. Characterization of DNA-binding sequences for CcaR in the cephamycin-clavulanic acid supercluster of *Streptomyces clavuligerus*. *Mol Microbiol*. 2011;81:968–81.
 41. Sánchez L, Braña A. Cell density influences antibiotic biosynthesis in *Streptomyces clavuligerus*. *Microbiology*. 1996;142:1209–20.

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