Novel Two-Component Systems Implied in Antibiotic Production in *Streptomyces coelicolor*

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Abstract

The abundance of two-component systems (TCSs) in *Streptomyces coelicolor* A3(2) genome indicates their importance in the physiology of this soil bacteria. Currently, several TCSs have been related to antibiotic regulation, and the purpose in this study was the characterization of five TCSs, selected by sequence homology with the well-known absA1A2 system, that could also be associated with this important process. Null mutants of the five TCSs were obtained and two mutants (SCO1744/1745 and SCO4596/4597/4598) showed significant differences in both antibiotic production and morphological differentiation, and have been renamed as *abr* (anti-biotic regulator). No detectable changes in antibiotic production were found in the mutants in the systems that include the ORFs SCO3638/3639, SCO3640/3641 and SCO2165/2166 in any of the culture conditions assayed. The system SCO1744/1745 (AbrA1/A2) was involved in negative regulation of antibiotic production, and acted also as a negative regulator of the morphological differentiation. By contrast, the system SCO4596/4597/4598 (AbrC1/C2/C3), composed of two histidine kinases and one response regulator, had positive effects on both morphological development and antibiotic production. Microarray analyses of the *AbrC1/C2/C3* and wild-type transcriptomes revealed downregulation of *actII-ORF4* and *cdaR* genes, the actinorhodin and calcium-dependent antibiotic pathway-specific regulators respectively. These results demonstrated the involvement of these new two-component systems in antibiotic production and morphological differentiation by different approaches. One is a pleiotropic negative regulator: *abrA1/A2*. The other one is a positive regulator composed of three elements, two histidine kinases and one response regulator: *abrC1/C2/C3*.

Introduction

Antibiotics are highly valuable secondary metabolites that are broadly produced in different species of the genus *Streptomyces*, a filamentous soil bacterium with a complex life cycle. In fact, this genus produces about half of all known microbial antibiotics [1]. The onset of antibiotic production depends on the growth stage of the microorganism and usually takes place contemporaneous with differentiation of the aerial mycelium into spores. Both differentiation and antibiotic production can be triggered by many environmental changes (physical and chemical), such as nutrient deprivation, pH, temperature, etc. These changes must be sensed and integrated in a cell response to promote rapid adaptation to the new growth conditions. The quickest and most efficient bacterial responses to extracellular stimuli occur via histidine-aspartate (His-Asp) phosphorelay cascades. These systems are made up of inner membrane-spanning protein kinases, which sense the external environment, and their respective (cognate) cytoplasmic response regulator partners, which generally exhibit DNA-binding properties. Most of these signal transduction systems only require a single sensor (HK: histidine kinase) and a cognate response regulator (RR) and are thus referred to as two-component systems (TCSs) [2]. Recently, some atypical systems have been described, such as a kinase phosphorylated by GTP instead of ATP [3] and the phosphorylation independent activation response regulators, named PIARR [4–6].

*S. coelicolor* A3(2) is the best genetically studied *Streptomyces* strain and has become the model organism for these species. The complete sequence of its 8.7 Mbp linear chromosome is available (www.sanger.ac.uk) [7] [8] and contains 84 sensor kinase and 80 response regulator genes, 67 of which lie adjacent on the chromosome and are predicted to form TCSs [9]. The mean HK/RR (TCS) content of *S. coelicolor* (considering the whole 7825 ORFs) is 0.86% as compared with 0.65% for other free-living microorganisms studied or 0.26% for pathogenic bacteria (25% and 70% more in *Streptomyces*, respectively) [10]. This abundance of TCSs could reflect the complexity of the regulatory network of *Streptomyces* that would allow this genus to adapt and survive in multiple and adverse environmental conditions.

*S. coelicolor* A3(2) produces at least four chemically distinct antibiotics: actinorhodin (ACT), undecylprodigiosin (RED), calcium-dependent antibiotic (CDA) and methylenomycin, all of whose
biosynthetic genes are located in clusters. The antibiotic production responds to a hierarchy of different levels of decision, distinguishing global or pathway-specific regulators [11]. Pathway-specific regulators are part of the biosynthetic clusters (i.e., actH-ORF4 for ACT [12]; redD for RED [13] and cdaR for CDA [14]). Global regulators are located elsewhere and have the ability to regulate operons that belong to different metabolic pathways, and as a consequence mutants in these genes usually show pleiotropic phenotypes. Among the global regulators, there are some of which are affecting different processes such as differentiation and antibiotic production (i.e., BldA [15], RelA [16], AbsB [17] and others reported just as global antibiotic regulators (i.e., AbsA1/A2 [18]). TCSs usually act as global regulators that mediate the response from external/internal stimuli to the final target genes.

The function of most of the 67 S. coelicolor TCSs is unknown; only a few have an assigned role. Six of them have been reported to modulate the antibiotic production and the best studied, absA1/A2, is involved in their global regulation [14,18–21]. The aim of this study was to determine the role of other five TCSs of S. coelicolor, whose functions are as yet unknown. Four of them are annotated as homologues to absA1/A2 in the Streptomyces Annotation Server (http://strepdb.streptomyces.org.uk/ [22]). The fifth TCS, although it showed less similarity with absA1/A2, is an interesting system because it is composed of two HKs and one RR and may be considered a three-component system. A sequence comparison of this system with the available databases indicated its conservation in almost all the species of Streptomyces that are being sequenced by the Broad Institute (http://www.broadinstitute.org/annotation genome/streptomyces_group/GenomeDescriptions.html).

In this study, the knockouts of the TCSs encoding genes (sensor and regulator at the same time) were generated and the changes in antibiotic production and morphological differentiation were monitored in several medium cultures. Two of the five TCSs selected (ASCO1744/1745 and ASCO4596/4597/4598) showed significant differences in both antibiotic production and morphological differentiation, and have been renamed as abs (antibiotic regulator). No changes in antibiotic production were detected in the deletion mutants of the other three systems encoded by the ORFs SCO3638/39, SCO2165/66 and SCO3640/41 in any of the conditions tested. The mutant ASCO1744/45 showed a pleiotropic phenotype. The ACT, RED, and CDA productions on some media were triggered, suggesting a negative role of this system in the antibiotic production. In addition, the morphological differentiation was accelerated. An opposite pleiotropic phenotype was revealed for the ASCO4596/97/98 mutant (TCS formed by two HKs and one RR). This mutant showed a decrease in ACT, RED, and CDA antibiotic productions and a delay in differentiation, which indicates that this system is a positive global regulator of the antibiotic production and differentiation. Microarrays analyses of the ASCO4596/97/98 and wild-type transcriptomes were performed.

**Results**

**Construction of null mutant strains**

According to the annotations of the S. coelicolor database genome (http://strepdb.streptomyces.org.uk/ [22]), five TCSs were selected. Four of them, SCO1744/45, SCO2165/66, SCO3638/39, and SCO3640/41, shared about 30% identity between their corresponding HKs and that of the well-known global antibiotic regulator absA1/A2, AbsA1. Additionally 50% identity was found between their RRs and the AbsA2 regulator, which are considered to be homologues (Table S1 and Table S2). The fifth one, composed of two HKs (SCO4597 and SCO4598, which share 57% identity) and one RR (SCO4596), presented less similarity to absA1/A2 (25% HKs-AbsA1 and 33% RR-AbsA2) but both HKs were predicted to be functionally associated to AbsA1 using STRING application (Search Tool for the Retrieval of Interacting Genes/Proteins) (http://string.embl.de/newstring cgi/show_input_page.pl) [23] (AbsA1–SCO4596 association score of 0.726 just below the AbsA1–AbsA2 and Abs1–RedZ scores, 0.949 and 0.923, respectively; AbsA1–SCO4597 association score of 0.691). To determine the relevance of these five TCSs in antibiotic production, null mutant strains of each system were obtained from the S. coelicolor M145 strain by the REDIRECT procedure (see Material and Methods). The correct replacement of the genes by the cassette was confirmed by Southern blot hybridization using appropriate DNA probes (data not shown).

To detect putative alterations in antibiotic production and/or development of cells in the mutant strains compared to the wild type, all of them were grown on several solid media at 30°C. The media were used were a minimal medium (NMMP) and different complex media (NA, YEPD, R2YE, PGA and MSA). Two of the five TCSs selected null mutant strains (ASCO1744/45::accIV and ASCO4596/97/98::accIV) consistently displayed significant differences in antibiotic production and differentiation compared to the wild type (Figure 1). No differences were observed in any conditions for the mutants of the systems SCO3638/39 and SCO3640/41 (data not shown). The absence of the system SCO2165/66 in the mutant seemed to slightly increase production of the three antibiotics (ACT, RED, and CDA) in R2YE, PGA, and NA media respectively but these results were difficult to replicate and need further study (data not shown).

Clearly, the effect of mutations ASCO1744/45::accIV and ASCO4596/97/98::accIV was medium-dependent, especially in the production of ACT. Although differences could also be seen on R2YE and YEPD media (data not shown), the strongest effects in ACT production were on NMMP and on NA (Figure 1A, 1B). Both mutants showed different phenotypes on both solid media: the mutant ASCO1744/45::accIV displayed an ACT overproduction after three days’ growth, while ASCO4596/97/98::accIV strain produced significantly less of this antibiotic molecule compared to the wild type (Figure 1A, 1B). To quantify these observations, liquid cultures were performed determining the rate growth and ACT production of each strain in both media at different times. As shown in Figure 1A (lower panel), the ACT production in the mutant ASCO1744/45::accIV in liquid NMMP was increased more than sixfold compared to the wild type at 96 h and the production in the mutant ASCO4596/97/98::accIV was about the half of the wild type. On the other hand, ACT production of ASCO4596/97/98::accIV strain in PB was about 40% of that of the wild type but less production of ACT in the mutant ASCO1744/45::accIV in PB was also observed showing a more complex nutritional behaviour of this mutant. The growth rates of the strains were similar in both liquid media (Figure S1).

Differences in undecylprodigiosin production were also observed on R2YE but mainly on PGA solid media (Figure 1C). Quantification of RED production in PG liquid medium showed that ASCO1744/45::accIV produces 67% more and ASCO4596/97/98::accIV approximately 50% less compared to the wild-type strain. As mentioned, this is not due to a growth defect because the growth curves of the three strains were almost identical in the culture conditions used (Figure S1).

CDA production, measured as the inhibition halo against Bacillus subtilis, was evaluated on NA plates in the presence or absence of calcium (see Materials and Methods) (Figure 1D). Once again, ASCO1744/45::accIV had higher CDA production than the
The wild-type strain (8.5%, the average of seven independent assays) and $D\text{SCO4596/97/98::accIV}$ presented a decrease of 32% of the inhibition halo.

Finally, YEPD was the medium used to document the morphological development. $D\text{SCO1744/45::accIV}$ mutant presented an accelerated formation of aerial mycelium, while $D\text{SCO4596/97/98::accIV}$ showed a clear delay in the differentiation in these culture conditions (Figure 1E).

In summary, mutant $ASCO4596/97/98::accIV$ overproduced the three antibiotics and also showed a positive role in differentiation (the aerial mycelia and spores appeared sooner than in the wild-type strain). In contrast, strain $ASCO4596/97/98::accIV$ showed a decreased production of the antibiotics ACT, CDA, and RED, and the differentiation was delayed.

From these results we can conclude that the two-component systems composed by the ORFs: SCO1744/45 and SCO4596/97/98, acted as anti-biotic production regulators, and thus they were called $abrA1/A2$, and $abrC1/C2/C3$, respectively.

**Genetic complementation of TCSs null mutants**

To make sure that the null mutant phenotypes observed were due to the absence of TCSs genes and not to mutagenesis polar
effects, the genetic apramycin cassette of the each null mutant strain (ΔabrA1/A2::accIV and ΔabrC1/C2/C3::accIV) was eliminated to avoid possible polar effects (see Materials and Methods). The resulting strains harboured a small scar (83 bp) in place of the former antibiotic resistance sequence (ΔabrA1/A2 and ΔabrC1/C2/C3) and displayed the same phenotypes as the original mutants (data not shown).

The reversioning strains were obtained by ectopic integration of plasmids derived from pKC796Hyg in the ΦC31 attachment site: pHabrA (whole system), pHabrC1/2/3 (whole system), pHabrC1/3 (with a deletion in the gene encoding kinase AbrC2), and pHabrC2/3 (with a deletion in the gene encoding kinase AbrC1) (see Materials and Methods). Wild type and mutant strains with the integrated pKC796Hyg plasmid were used as controls. It is worth mentioning that integration of any plasmid in the ΦC31 site provokes a decrease in the antibiotic production [24], especially on NMMP medium. As shown in Figure 2, both ΔabrA1/A2 (pHabrA) and ΔabrC1/C2/C3 (pHabrC1/2/3) restored the phenotypes of ACT production and differentiation of wt (pKC796Hyg), although partially in the case of ACT production in ΔabrC1/C2/C3 (pHabrC1/2/3) strain (Figure 2B). The ΔabrC1/C2/C3 mutant phenotype could also be reverted by complementation with pHabrC2/3 but not with pHabrC1/3 (Figure 2C) suggesting a more important role of HK AbrC2 (SCO4597) in the signalling network in this medium.

The reversioning of the mutant phenotypes was also analysed using multicopy plasmids derived from pN702GEM3 (high copy number: 40–100 copies/genome) harbouring either abrA1/A2 (plasmid pNXabrA) or abrC1/C2/C3 genes (plasmid pNabrC) (see Materials and Methods). When abrA1/A2 genes were expressed in the multicopy plasmid the mutant phenotype was not only reverted (Figure S2), but also antibiotic production (ACT, RED, and CDA) was even lower than in the wt (pN702GEM3). Additionally, the strain ΔabrA1/A2 (pN702GEM3) had an accelerated aerial mycelium formation, as opposed to ΔabrA1/A2 (pNXabrA) and wt (pN702GEM3) strains.

Unexpectedly, the ΔabrC1/C2/C3 (pNabrC) strain had even less antibiotic production (ACT, RED, and CDA) than the mutant ΔabrC1/C2/C3 (pN702GEM3) strain (Figure S3). However, when the genes were expressed from a low copy number plasmid pAbrC (derived from pHJL401 5–10 copies/genome see Materials and Methods), both phenotypes, antibiotics production and morphological differentiation, were reverted (Figure S3).

Our results confirm that both systems have different roles in regulation; while both affect antibiotic production and morphological differentiation pathways, the AbrA1/A2 is a negative pleiotropic regulator and AbrC1/C2/C3 is a positive pleiotropic regulator.

**Microarray analysis of the ΔabrC1/C2/C3 strain**

In order to determine the genes whose expression could be affected by the lack of the three-component system, microarrays assays comparing gene expression levels between ΔabrC1/C2/C3 and wild-type strains were performed. Total RNA preparations were obtained from cultures (four replicates) grown for 50 h on NA solid medium (see Materials and Methods). Statistical analysis of the microarray results using limma provided a differential expression value and an associated p-value for each gene. After correction of these p-values for multiple testing (FDR or pdf, see Materials and Methods), only a few genes were statistically significant (p<0.05) (see Table 1). Most of them, however, encoded either hypothetical proteins or proteins of putative functions, which were not easily correlated with the phenotype observed. If uncorrected p-values were considered (p<0.05), 201 genes appeared to be upregulated and 202 genes downregulated in the mutant strain. This set of genes should be taken with caution since it might contain false positives. Nevertheless, certain genes showed expression changes that could be correlated with phenotypic observations or with a shared function. Thus, the lower antibiotic production of the mutant ΔabrC1/C2/C3 was reflected in the expression changes of structural and regulatory genes. Particularly, the ACT and CDA pathway-specific regulators actIIORF4 and cdaR were slightly downregulated (see Table 1). Semiqualitative RT-PCR (see Materials and Methods) confirmed this (see Materials and Methods). When compared to the wild-type strain M145 the transcript levels of these genes in the mutant strain decreased to 60% and 16%, respectively (Figure 3).

Therefore, the downregulation of the mentioned SARPs encoding genes causes, at least partially, a decrease in ACT and CDA production in ΔabrC1/C2/C3 as indeed the phenotypic assays showed.

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**Figure 2. Mutant complementation.** A: Complementation of ΔabrA1/A2 phenotypes by the integrative plasmid pHabrA derived from pKC796Hyg on NMMP. Top: morphological differentiation. Bottom: ACT production. B: Complementation of ΔabrC1/C2/C3 phenotypes by the integrative plasmid pHabrC1/2/3 derived from pKC796Hyg on NA (2 days). Top: morphological differentiation. Bottom: ACT production. C: Complementation of ΔabrC1/C2/C3 phenotypes by the integrative plasmid pHabrA1/2 (pKC796Hyg) and pHabrA1/2 (pHabrC1/2/3) strain (Figure 2B). The ΔabrC1/C2/C3 mutant phenotype could also be reverted by complementation with pHabrC2/3 but not with pHabrC1/3 (Figure 2C) suggesting a more important role of HK AbrC2 (SCO4597) in the signalling network in this medium.
Expression differences in translation-related genes were also found (Table 1). Some genes encoding ribosomal proteins and amino acid transporters proteins were downregulated in the mutant strain, while the ribosomal recycling factor encoding gene (\textit{frr}, \textit{SCO5627}) was upregulated.

**Discussion**

In this paper, we reported the study of five new TCSs from \textit{S. coelicolor} M145 and the involvement of two of them, named \textit{AbrA1/A2} and \textit{AbrC1/C2/C3}, in antibiotic production. Notoriously, the phenotype of both knockout strains was conditional. This fact is not surprising since the TCSs are frequently aimed to respond to specific environmental signals (i.e. \textit{AfsQ1-Q2-sigQ} [25]), which can be easily missed in some culture media or conditions.

Additionally, our data show how both TCS systems studied played pleiotropic roles in bacteria since not only affected different antibiotic pathways but also different biological processes such as morphological differentiation. Up to date most of the characterized TCSs in \textit{S. coelicolor} have been reported to have an effect on antibiotic production (i.e. \textit{CutR/S} [26], \textit{EcrA1/A2} [27], \textit{PhoR/P} [28], \textit{AbsA1/A2} [18], \textit{RapA1/A2} [29]). However, just one among them, (\textit{AlsQ1-Q2-sigQ}) has been described to be involved in both secondary metabolism and morphological development [25].
As detailed in the results section, the null mutant strain *AabrA1/A2* (SCO1744/A5) overproduced the three antibiotics tested in a medium dependent manner. This fact makes this system extremely interesting since it could be used to overproduce clinical useful antibiotics by expressing *AabrA1/A2* alleles in heterologous streptomycetes as has been recently reported for the system *AbyrA1/A2* [30]. Interestingly, this system only has an orthologue in *Streptomyces* being absent in all the other *Streptomyces* species sequenced to date. However, the *S. lividans* knockout does affect neither antibiotic production nor morphological differentiation (data not shown). Therefore, this system seems to represent a *S. coelicolor* specific antibiotic regulator.

The system, *AbrC1/C2/C3*, must be considered special because it has two kinases and one regulator. Besides, each gene is separated from the upstream ORF by a DNA sequence long enough to have its own promoter (286, 112, and 171 nt, respectively). Therefore, each gene might be expressed independently in order to suit its own needs. This system is conserved in all the *Streptomyces* species sequenced so far as well as in the ones that are in the process of being sequenced. Furthermore, the response regulator protein SCO4596 shares about 80% identity at the amino acid level in all the species. This consistently indicates an important role for this special system.

Our data demonstrate that the deletion of the three genes originates a strain with reduced capacity to produce the three antibiotics studied, ACT, RED, and CDA. Similar phenotypes were obtained with the expression of these three genes in a high copy number plasmid but not in a low copy number where the phenotypes were reverted to the wild type ones (Figure S3), showing that this effect was dose dependent. On the contrary, the mutant phenotype with respect to morphological differentiation was reverted even in multicopy number plasmid (Figures 2 and S3). This suggests that separate mechanisms underlie the effects of *AbrC1/C2/C3* on antibiotic production and differentiation, as was found with AbsB protein [31].

Microarray analysis and RT-PCR studies demonstrated the role of *AbrC1/C2/C3* over antibiotic production was at least partly through transcription of pathway-specific regulator genes *ac-thiorf4* and *cdaR*. However, with the data obtained to date, we cannot determine whether this is a direct regulation due to the binding of *AbrC3* to the specific promoters of the pathway regulators or an indirect effect through a complex regulatory network. Therefore, deeper studies will be performed to understand the role of this TCS in the regulation of antibiotic production in the pigmented streptomycete *S. coelicolor*. Expression differences between *AabrC1/C2/C3* mutant and wild-type strains have also been found in genes associated with translation machinery. We hypothesized that a lower expression of some ribosomal protein genes (9 out of 62) in the mutant may affect the synthesis of proteins needed for the production of antibiotics, and in response cells try to compensate this by increasing the ribosomal recycling factor. The relation between enhanced protein synthesis during the stationary phase and the expression of regulatory proteins governing antibiotic production has been suggested previously [32,33]. In addition, previous work has correlated the ribosomal proteins and the fr overexpression with ACT production [34] and more recently with avermectin overproduction [35].

It is widespread known that antibiotic production in *S. coelicolor* is a complex process that is regulated by a broad network of genes. In this paper two new two-component global regulators in this network have been identified. It is noteworthy that, they are among the very few TCSs identified on *S. coelicolor* that are affecting two different but related processes: the antibiotic production and developmental differentiation. One, *AabrA1/A2*, is a negative regulator; the other, *AbrC1/C2/C3*, a three-component system composed by two HKs and one RR, is a positive regulator.

**Materials and Methods**

**Strains, media and culture conditions**

*Escherichia coli* strains growth was accomplished as described previously [36], BW25113 [pJ790] (containing the λRed system) is an *E. coli* K12 (AaraBAD, AphaBAD) derivative [37]; non-methylyating ET12567 (pUZH002) is *dam*, *dcm*, *hsdS*, *cat*, *tet* containing the *ata* genes [38] and *E. coli* DH5α (pBT30) is *recA*, *cat*, *bla* containing *flp* gene [37]. For CDA bioassays a wild-type strain of *Bacillus subtilis* (CECT 4522) was grown as an overlay on NA medium. *S. coelicolor* M145 (prototroph, SCP1, SCP2, methylenomycin−) and its mutant strain derivatives were grown on R2YE, NA, MSA, PGA, YEPD, and NMMP [39]. Liquid cultures were performed in 100 ml baffled flasks with 15 ml medium each. When necessary, the medium was supplemented with antibiotics (*E. coli* media: 100 μg ml−1 for ampicillin, 50 μg ml−1 for apramycin, 50 μg ml−1 for kanamycin, 34 μg ml−1 for chloramphenicol, and 25 μg ml−1 for nalidixic acid. *S. coelicolor* media: 20 μg ml−1 for neomycin and 20 μg ml−1 for hygromycin).

**Isolation and manipulation of DNA**

Plasmid isolation, restriction enzyme digestion, ligation, and transformation of *E. coli* and *S. coelicolor* were carried out by methods of Sambrook et al [40] and Kieser et al [39], respectively. The plasmids and cosmids used are listed in Table 2. Total genomic DNA from *S. coelicolor* (gDNA) was isolated from a 24–36 h cultures in TS4 medium following the procedure described in Hopwood et al [41], but scaled to 1–2 g of mycelium.

**Deletion of the TCSs selected**

REDIRECT PCR-targeting technology [42] was used to replace the genes of the entire coding region of each TCS (comprising histidine kinase and response regulator) to an apramycin (aac(3)IV gene) resistance cassette. Mutagenic cassettes were flanked by the recognition sequence of *E. coli* Flippase (FRT) and contained the conjugation transfer origin onT (FRT-aac(3)IV-orT-FRT) and were amplified using the High-Fidelity Expand PCR system (Roche Co.) with the primers listed in Table S3 using plasmid pJ773 as template. The generated cassettes were introduced into *E. coli* BW25113 [pJ790] harbouring the appropriate cosmid for each studied system (Table 2: SCI1, SCI5, SCI10 and SCI20) [22] and preinduced for λRed functions, by the addition of arabinose, to obtain a target gene-disrupted version of the mutant cosmid. The disrupted cosmids, confirmed by restriction analysis, were isolated and transferred from *E. coli* ET12567 (pUZH002) to *S. coelicolor* M145 by conjugation. Exconjugants were selected on MSA medium containing apramycin (50 μg ml−1), and the double crossover products identified by screening their sensitivity to kanamycin (30 μg ml−1). The disruptions were confirmed by Southern hybridization and the DIG DNA labelling and detection kit (Roche Co.) was used for probe preparation (obtained with primers of Table S3).

To avoid putative polar effects of the mutagenesis cassette gene replacement in *S. coelicolor* M145, the antibiotic resistant marker and the onT region were eliminated in two steps. In a first step, the corresponding disrupting cosmids were introduced in *E. coli* DH5α (pBT30) strain (harbouring the Flippase gene, FLP) in which, the recombination between both FRT mutagenesis cassette-flanking
regions, in the second step, the SCAR cosmids were transferred to the Streptomyces plasmid, yielding pHabrA plasmid. A fragment of 260 nt containing the promoter and the 5′ end of the gene, yielding pHabrA plasmid.

pNXabrA plasmid was obtained by cloning the fragment NdeI/HindIII from pAY002 plasmid in the sites of the pNX24 plasmid (pN702GEM3 derivative [45]). In this shuttle (E. coli-Streptomyces) multicopy plasmid the xylanase promoter xyxA controls abrA1/A2 gene expression.

The three genes abrC1/C2/C3, and their intergenic regions were cloned in a pN702GEM3 plasmid yielding a multicopy plasmid in several steps. An intermediate E. coli monofunctional plasmid called pSCD20 was constructed by cloning a BspEI/PmlI fragment from a subclone of SCD20 cosmid in the BspEI/Eco136II sites of pHJL401 [46]. Afterwards, the fragment EcoRV/HindIII from pSCD20 was introduced in pN702GEM3 to get pNabrC. The low copy number pAbC plasmid derived from pHJL401 [46] was obtained by cloning the BglII/HindIII fragment from pNabrC in the BamH1/HindIII sites of pHJL401.

To obtain the integrative plasmid for mutant ΔabrC1/C2/C3 complementation, pNXCD20 was digested with HindIII, filled with Klenow polymerase, and BglII digested. This fragment was inserted into the BglII/EcoRV sites of pKC796Hyg to get pHabrC1/2/3. Plasmid with abrC1 gene disrupted was got by digesting pHabrC1/2/3 with Xhol and religated (eliminating a fragment of 260 nt containing the promoter and the 5′ end of the gene), yielding pHabrC2/3. To disrupt abrC2 gene an inner

Table 2. Plasmids and cosmids used in this work.

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<th>Vector</th>
<th>Characteristics</th>
<th>Reference</th>
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<td>ASCD20-1 SCAR</td>
<td>SCD20 , SCD4596/97/98</td>
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<tr>
<td>pXHis1</td>
<td>E. coli plasmid Amp resistance</td>
<td>[45]</td>
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<tr>
<td>pAY001</td>
<td>pXHis1 derivative containing promoter region of SCD744/45</td>
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<td>pAY002</td>
<td>pAY001 derivative containing SCD744/45</td>
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<tr>
<td>pN702GEM3</td>
<td>E. coli–Streptomyces shuttle vector; Neo/Kan resistance</td>
<td>[45]</td>
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<td>pNabrA</td>
<td>pN702GEM3 derivative containing SCD744/45</td>
<td>This work</td>
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<tr>
<td>pNabrC</td>
<td>pN702GEM3 derivative containing SCD4596/97/98</td>
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<td>pHLJ401</td>
<td>E. coli–Streptomyces shuttle vector; Amp/Tsr resistance</td>
<td>[46]</td>
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<tr>
<td>pKC796Hyg</td>
<td>Integrative plasmid with hygromycin resistance</td>
<td>[43]</td>
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<td>pHabrA</td>
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doi:10.1371/journal.pone.0019980.t002
fragment of 1180 nt was eliminated from pHabrC1/2/3 using SmI/AgCl sites and by treatment with T4 DNA polymerase before ligation, the plasmid got was named pHabrC1/3.

The new plasmids were introduced into the corresponding strains by protoplast transformation as previously described [39].

Antibiotic determination

Antibiotic production was assayed on solid media as described below. Plates were inoculated with 10^7 spores streaked or added to a 5 μl drop. For CDA production the strains were grown on NA medium at 30°C for 2 days. Afterwards, the plates were overlaid with 5 ml of soft agar plus 60 mM Ca(NO₃)₂ inoculated with B. subtilis as the test microorganism (0.2 ml, 0.25 DO) and incubated at 30°C for 20 h. A replica plate without calcium was used as a negative control. For ACT production on solid media, the strains were grown on different media (YEPD, R2YE, NMMP, NA) at 30°C for at least 3 days to observe the blue halo around the colonies. RED production was detected on PGA medium after 2 days as the red colour of colonies.

The ACT and RED antibiotic productions were quantified in liquid cultures using the standard spectrophotometric method [39] with minor modifications. 15 ml of medium were inoculated with 4×10⁶ spores/ml. Culture samples were mixed with 1N KOH overnight at 4°C, centrifuged (15000 g, 10 min), and A₆₄₀ of supernatants were determined to quantify ACT (ε₆₄₀ = 25320). To quantify RED, pellets were washed twice in 0.5 M HCl and extracted in 0.5 M HCl-methanol for 2 h. After centrifugation (15000 g, 5 min), supernatant absorbance was measured (ε₆₃₀ = 100500). Dry weight of samples at different times was measured to monitor culture growth.

Microarrays assays

For RNA extraction from S. coelicolor wild-type and ΔabrC1/C2/C3 mutant strains, NA plates covered with a cellophane sheet were inoculated with 7.5×10^6 spores and incubated at 30°C for 50 h. Prior to RNA isolation using a RNeasy Midi Kit (Qiagen) the mycelia was harvested and suspended in RNA-protect Bacteria Reagent (Qiagen). An additional step with RNase free DNase (Qiagen) was incorporated to remove any contaminating DNA. The quality and concentration of RNA were assayed using gel electrophoresis and spectrophotometer assays (Q-bit and Agilent bioanalyzer). Four biological replicates were used.

cDNA versus gDNA microarrays experiments were chosen due to the advantages described elsewhere [47,48]. The S. coelicolor SCo40 microarrays used were obtained from the Functional Genomics Laboratory of Surrey University (UK) [49]. The Pronto! Universal Microarray Hybridization kit (Corning, #40026) was used for pretreatment and prehybridization. Cy3-cDNA and Cy5-gDNA labelling reactions were performed according to the recommendations described by http://www.surrey.ac.uk/SBMS/Fgenomics [49]. Hybridization assays were done as in Rodriguez-Garcia et al. [28] and TIFF images were generated by Genepix DNA Microarray Scanner 4000B and processed with GenePix Pro 4.0 software. Bioconductor software package limma (linear models for microarray analysis) and rank products were used to analyse and assess the statistical significance of the data [28,50]. Background correction was applied using the normexp function. Then, the log of Cy3/Cy5 intensities were normalized using block-weighted medians and global loess. The different p-values of the contrast between both strains were corrected for multiple testing FDR (false discovery rate) or by the rank products pp method (proportion of false positives). To consider a gene differentially expressed, it should have passed at least one of these criteria: limma FDR-corrected p-value<0.05 or rank products pp value<0.05. All data is MIAME compliant and the raw data has been deposited in a MIAME compliant database (ArrayExpress, accession number E-MEXP-2841).

Semiquantitative RT-PCRs

RT-PCR assays were performed with 200 ng RNA in a final volume of 20 μl with the Superscript™ One-Step RT-PCR with Platinum® Taq System Kit (Invitrogen). The primers used are specified in Table S3. Reactions were made as follows: 30 min at 55°C (cDNA synthesis); 2 min at 95°C; 20–40 cycles: 45 sec at 94°C, 30 sec at 65°C and 40 sec at 65°C; 10 min at 72°C. To check the DNA absence in the RNA samples, similar reactions avoiding the cDNA synthesis step were done in parallel. 2 μl of each reaction were run in 1.6% agarose gel buffered with TAE 1X. Each set of reactions was repeated varying the number of cycles to ensure that the PCR had not reached the plateau phase. As a positive internal control RT-PCR of 16S RNA was used. RT-PCR band images were quantified using Quantity One Analysis software 4.6.6 (Bio-Rad).

Supporting Information

Table S1 Identity percentages among the sensor kinases by a local alignment (Emboss).

Table S2 Identity percentages among the response regulators by a local alignment (Emboss).

Table S3 Primers used in this work.

Figure S1 Growth curves of the different strains in NMMP (A), NB (B) and PGA (C) S. coelicolor M145 (triangles), S. coelicolor ΔabrA1/A2 (circles) and S. coelicolor ΔabrC1/C2/C3 (squares). Error bars correspond to standard deviation of two independent experiments measured by duplicate.

Figure S2 Phenotypes of strains expressing abrA1/A2 in multicopy plasmid. A: Effect of the expression of abrA1/A2 genes by the high copy number plasmid pNXabxA derived from pN702GEM3 on NMMP medium. Top: morphological differentiation. Bottom: ACT production. B: CDA bioassays on NA medium, RED production on PGA medium, and morphological differentiation on YEPD medium (2 days), in the different strains.

Figure S3 Phenotypes of strains expressing abrC1/C2/C3 in multicopy plasmids. A: Effect of expression of abrC1/C2/C3 genes by the high copy number plasmid pNXabrA derived from pN702GEM3: ACT production on NA medium, CDA bioassays on NA medium, RED production on PGA medium, and MD morphological differentiation on YEPD medium (2 days), by the different strains. B: Effect of expression of abrC1/C2/C3 genes by the low copy number pAbrC plasmid derived from pHJL401: ACT production on NA medium, CDA bioassays on NA medium, RED production on PGA medium, and MD morphological differentiation on YEPD medium (3 days), by the different strains.
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Author Contributions

Conceived and designed the experiments: MD RIS AY. Performed the experiments: AY SR. Analyzed the data: AY AR-G MD. Contributed reagents/materials/analyses tools: AR-G. Wrote the paper: MD RIS AR-G.

References


