

SUPPLEMENTARY ELECTRONIC DATA

Pseudomonas fluorescens* pirates both ferrioxamine and ferri-coelichelin siderophores from *Streptomyces ambofaciens

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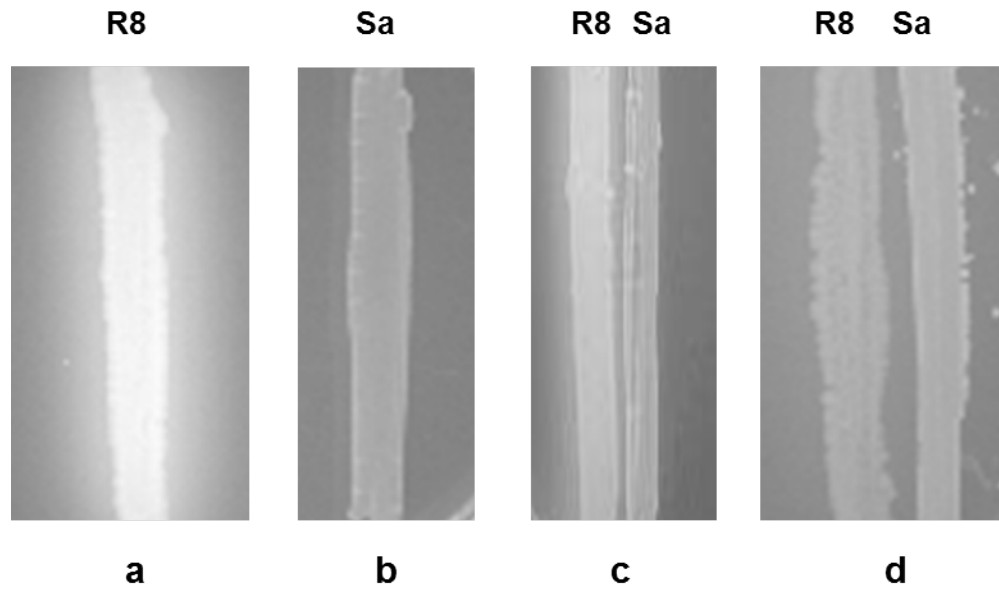


Fig. S1 Effect of *S. ambofaciens* on the pyoverdine production by *P. fluorescens* BBc6R8 grown on 26A agar plate supplemented with 200 μM of 2,2'-bipyridyl. **a** *P. fluorescens* BBc6R8 (R8); **b** *S. ambofaciens* ATCC23877(Sa); **c** *P. fluorescens* BBc6R8 + *S. ambofaciens* ATCC23877; **d** *P. fluorescens* BBc6R8 + *S. ambofaciens* ATCC23877 which has been streaked on plate 30 h before the BBc6R8 strain. Photos were taken under UV from below the plates after a two day incubation at 26.5°C.

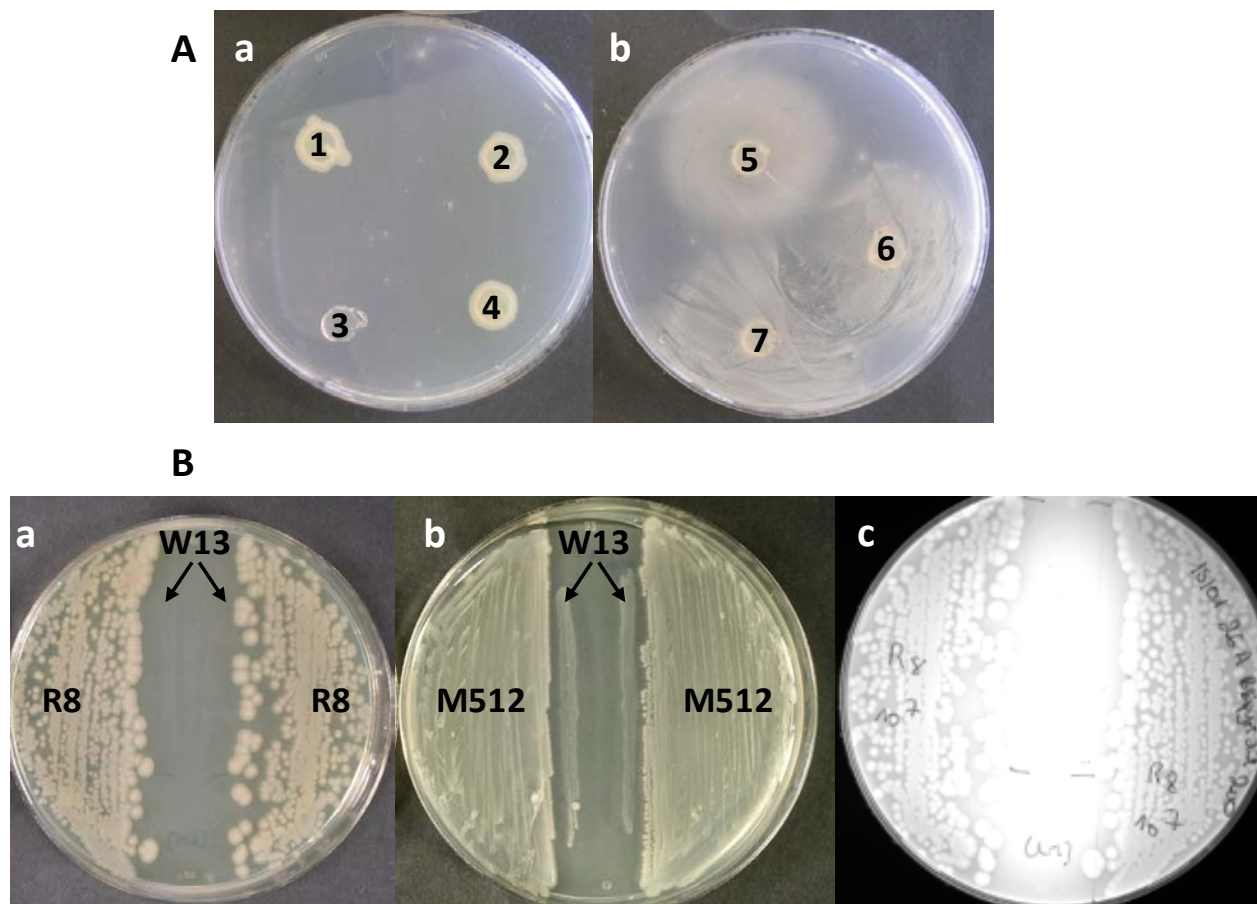


Fig.S2 Extracellular complementation of the *S. coelicolor* $\Delta des\Delta cch$ mutant by exogenous siderophores. **A.** *S. coelicolor* $\Delta des\Delta cch$ (strain W13) was grown for 3 days on 26A agar plate supplemented with 200 μ M of 2,2'-bipyridyl in presence of plugs from a 3 days culture of *P. fluorescens* BBc6R8 (**a**) or *S. coelicolor* M512 (**b**) grown at 26.5°C on 26A plate without iron chelator (1 and 5) or with 2,2'-bipyridyl at 100 μ M (2 and 6) or 200 μ M (4 and 7). The plug 3 in (**a**) correspond to a plug from a non-inoculated 26A agar plate supplemented with 200 μ M of 2,2'-bipyridyl. **B.** *S. coelicolor* $\Delta des\Delta cch$ (strain W13) was streaked on 26A solid medium supplemented with 200 μ M of 2,2'-bipyridyl 3 days after *P. fluorescens* BBc6R8 (**a**) or the *S. coelicolor* M512 (**b**) strain; **c**, the plate shown in **a** was exposed under UV and photo was taken from below the plate. The fluorescence indicates the presence of pyoverdine. **a** to **c**, photos were taken two days after the inoculation with W13. All cultures were carried out at 26.5°C.

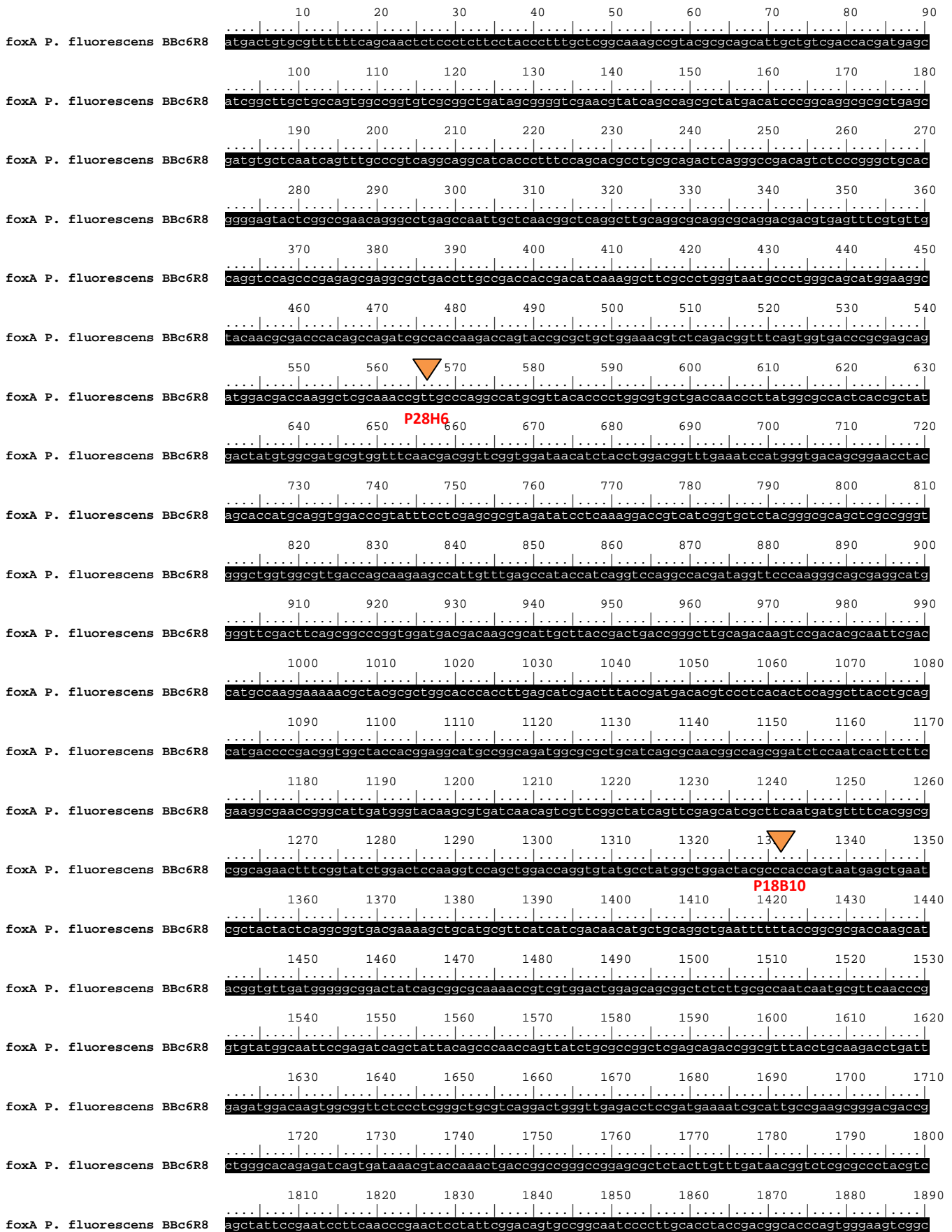




Fig. S3 Sequence of the *P. fluorescens* BBc6R8 *foxA* gene and location of the insertion site of the Tn5 transposon in the P28H6 and P18B10 mutants.

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      10      20      30      40      50      60      70      80
FoxA P. fluorescensBBc6R8  -----MTVRFFFSNSP--SSYPLLGKAVRAALLSTTMSIGLLEVAGVAADSGVERISQRYDTPAGALSDVLNQFARQAGIT
FoxA P. fluorescens pf0-1  -----MLPGLSMAAN-ASEVSSHRYNTAAGPLGEALNQFARQAGIT
FoxA P. protegens pf-5    -----MTLRDTRPSS--PCARPLCOAIRAALLCSSIGLGTVAPQVLAAASAVDAPRHSYSVAPGNLGDALNQFARQAGIT
FoxA P. aeruginosa PAO1  MTATAVVLRNAPSSLDFPRASRLSRSVRAALLSLAMAACAALLCASAAEAAAEQARP-YATPAGQLGDVLNRFARBAGIT

      90      100     110     120     130     140     150     160
FoxA P. fluorescensBBc6R8  LSSTPAQTQGRQSPGLHGEYSAEQGLSQLLNSGSLQAAQDDVSVFLVQVQESEALILPTTDIKGFALGNALGSMBGYNA
FoxA P. fluorescens pf0-1  LSMTPQOTQGRQSPGVQGEYSTDASHLLCGSGLEAVSQDGSSVYLRSVAETEALALPTDIKGFALGNALGSMBGYNA
FoxA P. protegens pf-5    LSTTPALTQGRQSPGLQGDYSIPQGLNQLLRCGSLEAVSQDGGSVYLRPLEQSALILPPATEVKGFALGNALGSMBGYNA
FoxA P. aeruginosa PAO1  LSATPAQTQGVYSQGLRGSFTVQGLARLLADTPLEAEDQDGGSFVLREAPAKDGDVLNMQAVEVFALGNILGSTDCYLA

      170     180     190     200     210     220     230     240
FoxA P. fluorescensBBc6R8  THSQIATKTSTALLETSQITVSVVTREQMDDQSQTVAQAMRYTPGVLTNPYGATHRYDYVAMRGFNDGSVDNIYLDGLKS
FoxA P. fluorescens pf0-1  THSQIATKTSTALLETSQSSVSVVTREQMDDQSQTVAQAMRYTPGVLTNPYGATHRYDYVAMRGFNDGSVDNIYLDGLKS
FoxA P. protegens pf-5    THSQIATKTSTALLETSQSSVSVVTREQMDDQGAQTVAQTMRYTPGVLTNPYGATHRYDYVAMRGFNDGSVDNIYLDGLKS
FoxA P. aeruginosa PAO1  THSQIATKTSKPLLETSQITVSVITREQIDDTASKTVQAMRYTPGLETGQVCASNRYDVYVMRGFLNSVDNIYLDGLKFA

      250     260     270     280     290     300     310     320
FoxA P. fluorescensBBc6R8  MGDSGTYSTMQVDPYFLERVDILKGPSSVLYGRSSPGGLVALTSSKPLYEPHQVQATIGSQQQRCMGFDFSGPVDDDKR
FoxA P. fluorescens pf0-1  MGDSGTYSTMQVDPYFLERVDILKGPSSVLYGRSSPGGLVALTSSKPLYEPHQVQATIGSQQQRCMGFDFSGPVDDDKR
FoxA P. protegens pf-5    MGDSGTYSSMQVDPYFLERVDILKGPSSVLYGRSSPGGLVALTSSKPLYEPHQVQATIGSQQQRCMGFDFSGPVDDDKH
FoxA P. aeruginosa PAO1  MGDSGTFSSMQVDPYFLERDILKGPSSVLYGRSLPGGLVALTSSKPLYEDYRQITGSICNMGQKEMGFDSGPVDDEKR

      330     340     350     360     370     380     390     400
FoxA P. fluorescensBBc6R8  IAYRLIGLADKSDTQFDHAKEKRYALAPTLSIDFTDTSLTLQAYLQHDPDGGYHGGMPADGALHQRNGORISNHFFEGE
FoxA P. fluorescens pf0-1  IAYRLIGLTDQSDTQFDHNKEKRFALAPTVSIDFNBDTSLTLQAYLQHDPDGGYHGGVPADGTLHQRNGNRISPHFFEGE
FoxA P. protegens pf-5    IAYRLIGLTDKSDTQFDHAKEKRFALSPTLSIDFSEDTSLTLQAYLQNDPDGGYHGGMPANGTLNORNGORISEHFFEGE
FoxA P. aeruginosa PAO1  IAYRLIGLGKSDTQFDHVKERYALAPTLAIDFSDDTLTLQGYLQHDPDGGYHGGVPADGTLSHHNGRISREFFDGE

      410     420     430     440     450     460     470     480
FoxA P. fluorescensBBc6R8  PGIDGYKRDQSFGYQEHRFNDVFTARQNFRYLDSKVQLDQVYAYGWTTPSTSNELNRYYSGGDEKLHAFIDNMLQAEF
FoxA P. fluorescens pf0-1  PGIDGYSRDQSFGYQEHRFNDVFTARQNFRYLDSKVNMDQVYAYGWTSPTSNELNRYTGGDERLHAFIVDNMLQAEF
FoxA P. protegens pf-5    PGVDGYKRDQSFGYQEHRFNDTFTARQNFRYLDSKVKLDQVYAYGWTNATSNDLNRYYSGGGEKLHSFIVDNMLQAEF
FoxA P. aeruginosa PAO1  PSKDDFDRTQRMFGYQEHRTDDVSARQNFRYLDSDVDLSOVYAYGWSASEPNKLNRYFSGAREHLQAIVDNMLQAEF

      490     500     510     520     530     540     550     560
FoxA P. fluorescensBBc6R8  FTGATKHTVLMGADYQRRKTVVDWSSGSLAPINAFNPVYGNSEISYYSPTSYLRRLEQTGVYLQDLIEMDKWRFSLGLRQ
FoxA P. fluorescens pf0-1  FTGATKHTVLMGADYQRRKTVVDWTSGGLAPINAFNPESGNSAITPYGETSYLRRLEQTGVYLQDLIEMNKWRFSLGLRQ
FoxA P. protegens pf-5    LTGDVKHTLLMGADYQRRKTVVDWDQGTLQPINAFNPVYGNSTINYSHTSYLRRLEQTGVYLQDLIELDKWRFSLGLRQ
FoxA P. aeruginosa PAO1  ATGAARHTLLLGLDYQRRRTVVDWSSGSASALDAFNPVYGDDAISYFPDDNHTRRLEQTGVYLQDLIDIDQWRFSLGLRQ

      570     580     590     600     610     620     630     640
FoxA P. fluorescensBBc6R8  DWVETSDENRLAEAGRPLGTEISDKRTKLTGRAGALYLFDNGLAPVVSYSESFNPNSYSDSAGNPLAPTDGTQWEVGLKY
FoxA P. fluorescens pf0-1  DWVETSDENRLAEAGRPVGTEINDRRTKLTGRAGALYLFDNGLAPVVSYSESFNPNSYADSAGNPLAPTDGTQWEMGLKY
FoxA P. protegens pf-5    DWVETSDENRLAEAQRPLGTEISDKRTKLTGRAGALYLFDNGLAPVVSYSESFNPNSYADSAGNPLPTDGTQWEVGLKY
FoxA P. aeruginosa PAO1  DWVSVTDKN-----RSTGSKADDWEKFTGRIGALYLFDNGLAPVVSYSESFNPNAYSASGTPLAPTECKQWEVGLKF

      650     660     670     680     690     700     710     720
FoxA P. fluorescensBBc6R8  QPPGTDNLFTASLFRIDQENLATKLQENFYRAVGAVRSQGLEAHMQLTDHLKLGSYTFTDIBYSKSMVSTLSTADN
FoxA P. fluorescens pf0-1  QPPGTDNLFTASLFRIDQENLATKLQENFYRAVGAVRSQGLEAHMQLTDNLKVLGSYTFTDIBYSKSMVSTLSTPTN
FoxA P. protegens pf-5    QPPGTDNLFTASLFRIDQENLASKLQENFYRAVGAVRSQGLEAHMQLTDNLKLSYTFTDIQSKSMVSTLSATN
FoxA P. aeruginosa PAO1  QAPGSNSFYTASLFHLIQENVASKEPQDNFYTSVGEVRSQGLEAHTQLSDNLKLGSYTYTDIYTKSLDG-----

      730     740     750     760     770     780     790     800
FoxA P. fluorescensBBc6R8  VLENKGNSPTQAPRHMASVWADYKFDSALDGLRLGGGVRVGYSWADAENTMKVPAYTLFDASMGYDLGKVGLKGVDVR
FoxA P. fluorescens pf0-1  VLENKGNSPTQAPRHMASLWADYKFDSAALDGLRLGGGVRVGYSWADAENTMKVPSYTLFDASIGYDLGKVGLKGVDVR
FoxA P. protegens pf-5    LLENKGNSPTQAPRQMASLWADYKFDSATLDGLRLGGGVRVGYSWADAENTMKVPAYTLFDASIGYDLGKLGLKGVDVR
FoxA P. aeruginosa PAO1  ---NQCHTPNQAPKHMASLWADYAFDAGLLSGLSIGGGARYVGETWADKENTLRVDYTLDARIGYDLGKLGLKGVDVS

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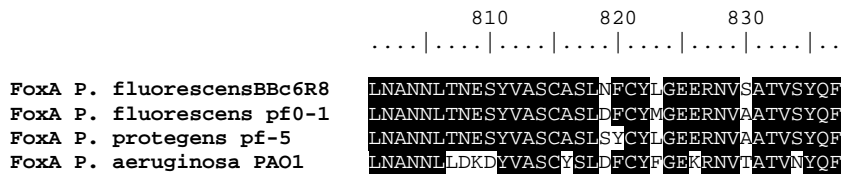


Fig.S4 Sequence alignment of the *P. fluorescens* BBc6R8 TonB-dependent receptor FoxA with the FoxA proteins of *P. fluorescens* Pf0-1, *P. protegens* Pf-5 and *P. aeruginosa* PAO1.

The aa residues conserved in at least 3/4 of the proteins are shaded in black.

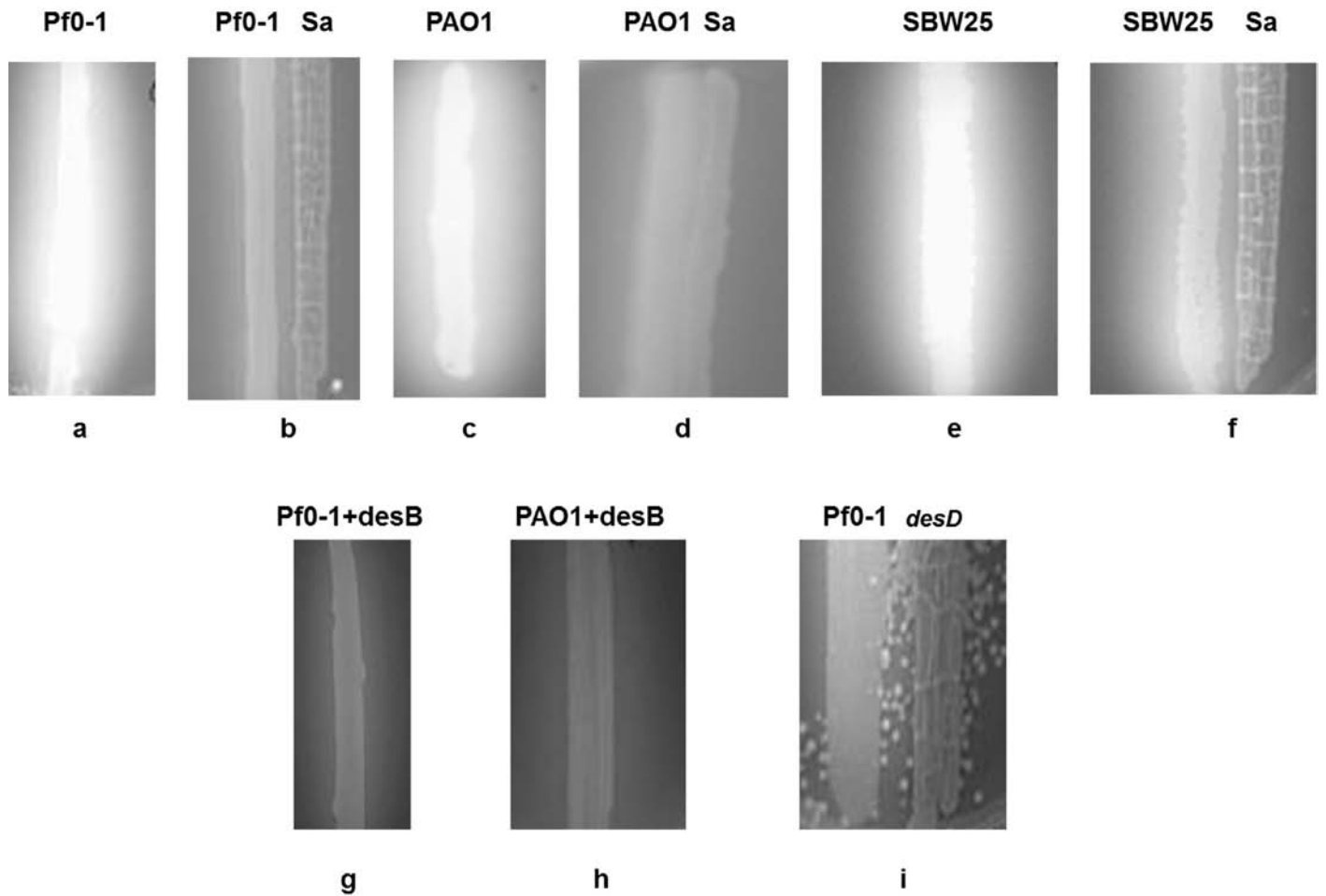


Fig.S5 Effect of *S. ambofaciens* ATCC23877 on the pyoverdine production by *P. fluorescens* Pf0-1, *P. fluorescens* SBW25 and *P. aeruginosa* PAO1 grown on 26A agar medium. **a** *P. fluorescens* Pf0-1; **b** *P. fluorescens* Pf0-1 + *S. ambofaciens* ATCC23877 (Sa); **c** *P. aeruginosa* PAO1; **d** *P. aeruginosa* PAO1 + *S. ambofaciens* ATCC23877; **e** *P. fluorescens* SBW25; **f** *P. fluorescens* SBW25 + *S. ambofaciens* ATCC23877; **g** and **h** *P. fluorescens* Pf0-1 and *P. aeruginosa* PAO1 cultivated in presence of 200 μ M of desferrioxamine B mesylate; **i** *P. fluorescens* Pf0-1 + *S. coelicolor* M512 *desD*. The *Streptomyces* strains were streaked on plate 30 h before the *Pseudomonas* strains. Photos were taken under UV from below the plates after a two day (co-)culture at 26.5°C.

Table S1 Potential function encoded by the genes analyzed by RT-qPCR based on their conservation with their homologues in *P. aeruginosa* PAO1

Gene names	<i>P. fluorescens</i> BBC6R8 genome locus	Potential function	% of identity with <i>P. aeruginosa</i> PAO1 homologues at the amino acid level
<i>pvdD</i>	MHB_002071	NRPS pyoverdine biosynthesis	49.6%
<i>pvdE</i>	MHB_002068	ABC export system fused ATPase and permease components	73.2%
<i>pvdO</i>	MHB_002067	pyoverdine responsive serine/threonine kinase	73.4%
<i>pvdQ</i>	MHB_000555	acyl-homoserine lactone acylase	55.2%
<i>pvdS</i>	MHB_005722	sigma factor controlling pyoverdine synthesis	90.7 %
<i>phcF</i>	MHB_01018	NRPS adenylation domain, enantio-pyochelein biosynthesis	40.6 %
<i>foxA</i>	MHB_05767	TonB-dependent receptor of ferrioxamines	66.6 %
<i>foxR</i>	MHB_05768	anti-sigma factor	57.3 %
<i>foxI</i>	MHB_05769	sigma factor	75.3 %
<i>pepSY</i>	MHB_001025	PepSY- associated TM helix protein	35 %
<i>fur</i>	MHB_006398	Transcriptionnal repressor	82,4%