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Auteur : p236063

Promoteur(s) : 20814

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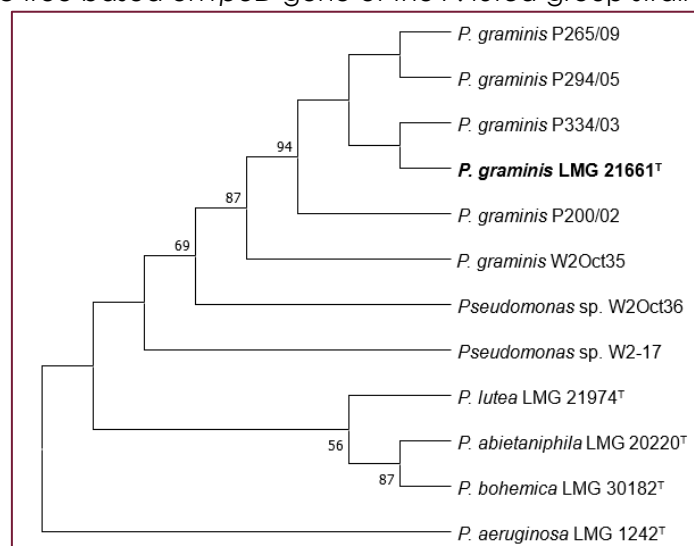
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Annexes

Annex I: Phylogenetic tree based on *rpoD* gene of the *P. lutea* group strains used in this study.



Annex II: List of pyoverdines used in the growth stimulation experiments. The peptide chain and the strain it was purified of are listed. The iron-binding moieties are indicated in blue, red, and orange depending on the residue.

Pyoverdine	Strain pyoverdine purified from	Peptide chain pyoverdine
6 amino acids		
PYO _{B10} = PYO _{W15Aug1}	<i>Pseudomonas</i> sp. W15Aug1	Ser-eLys-OHAsp-Ala-aThr-Ala-cOHOrn
PYO _{GS43}	<i>P. putida</i> GS43	Lys-OHAsp-Ser-Ser-Ser-cOHOrn
PYO _{Ps6-10}	<i>Pseudomonas</i> sp. Ps6-10	Ala-Orn-OHAsp-Dab-AOHOrn-Lys
PYO _{BTP1} = PYO _{90-40A}	<i>P. putida</i> CFML 90-40	Asp-Ala-Asp-AOHOrn-Ser-cOHOrn
7 amino acids		
PYO _{BTP2}	<i>P. fluorescens</i> BTP2	Ser-Val-OHAsp-Gly-Thr-Ser-cOHOrn
PYO ₂₉₀₈	<i>Pseudomonas</i> sp. 2908	Ser-Orn-OHAsp-Ser-Ser-Ser-cOHOrn
PYO _{G176}	<i>Pseudomonas</i> sp. G176	Asp-eLys-OHAsp-Ser-Ala-Ser-cOHOrn
PYO _{G85}	<i>Pseudomonas</i> sp. G85	Ser-Lys-OHAsp-Ser-Orn-Ser-cOHOrn
PYO _{G4R}	<i>P. putida</i> KT2440	Asp-Orn-(OHAsp-Dab)-Gly-Ser-cOHOrn
PYO _{typell} = PYO _{7NSK2}	<i>P. aeruginosa</i> 7NSK2	Ser-FOHOrn-Orn-Gly-aThr-Ser-cOHOrn
PYO _{PL8}	<i>P. fluorescens</i> PL8	Lys-AOHOrn-Ala-Gly-aThr-Ser-cOHOrn
PYO _{typelll}	<i>P. aeruginosa</i> W15Aug16	(Ser-Dab)-FOHOrn-Gln-Gln-FOHOrn-Gly
PYO _{G173}	<i>P. fluorescens</i> G173	Ser-Ala-AOHOrn-(Orn-Asp-AOHOrn-Ser)
PYO _{LBSA1}	<i>Pseudomonas</i> sp. LBSA1	Asp-Arg-AOHOrn-Lys-Ser-Asp-cOHOrn
PYO _{NCIMB} = PYO ₁₃₅₂₅	10586ΔmchABΔtrbABC, PYO ₁₃₅₂₅ -positive, mupirochelin and triabactine-negative of <i>Pseudomonas</i> sp. NCIMB 10586 (Grosse et al., 2023)	Ser-Lys-Gly-FOHOrn-(Lys-FOHOrn-Ser)
8 amino acids		
PYO _{Pf-5}	<i>P. protegens</i> Pf-5	Asp-FOHOrn-Lys-(Thr-Ala-Ala-FOHOrn-Lys)
PYO _{D-TR133}	<i>P. chlororaphis</i> D-TR133	Asp-FOHOrn-Lys-(Thr-Ala-Ala-FOHOrn-Ala)
PYO _{PL9}	<i>Pseudomonas</i> sp. PL9	Ser-AOHOrn-Ala-Gly-(Ser-Ser-OHAsp-Thr)
PYO _{typel}	<i>P. aeruginosa</i> PAO1	Ser-Arg-Ser-FOHOrn-(Lys-FOHOrn-Thr-Thr)
PYO _{G76}	<i>Pseudomonas</i> sp. G76	Ser-Ser-FOHOrn-Ser-Ser-(Lys-Ser-FOHOrn)
PYO _{solT}	<i>P. salomonii</i> LMG 22120T	Ser-Orn-FOHOrn-Ser-Ser-(Lys-FOHOrn-Ser)
PYO _{GB-1} = PYO ₉₀₋₅₁	<i>P. putida</i> GB-1	Asp-eLys-OHAsp-Ser-Gly-aThr-Lys-cOHOrn
9 amino acids		
PYO _{aspT} = PYO _{G17}	<i>P. asplenii</i> LMG 21749T	2 BOHAsp, 2 Gly, 2 Thr, 1 Dab, 1 Ala, 1 Lys,
PYO _{cost}	<i>P. costantinii</i> LMG 22119T	Ser-AOHOrn-Gly-aThr-Thr-Gln-Gly-Ser-cOHOrn
PYO _{thiT}	<i>P. thivervalensis</i> LMG 21626T ΔhcsEF, histicorrugatin-negative mutant of <i>P.</i>	Ala-AcOHOrn-Gly-Thr-Thr-Gln-Gly-Ser-cOHOrn

Annexes

	<i>thiervalensis</i> LMG 21626 ^T (Matthijs et al., 2016)	
PYO _{PkiIT}	<i>P. kilonensis</i> LMG 21624 ^T	Lys-AOHOrn-Gly-aThr-Thr-Gln-Gly-Ser-cOHOrn
PYO _{A6}	<i>Pseudomonas</i> sp. A6	Lys-AOHOrn-Gly-aThr-Thr-Gln-Gly-Ser-cOHOrn
PYO _{Pf0-1}	<i>P. fluorescens</i> Pf0-1	Ala-AcOHOrn-Orn-Ser-Ser-Ser-Arg-OHAsp-Thr
PYO _{PutC}	<i>P. putida</i> PutC	Asp-OHbutOHOrn-Dab-Thr-Gly-Ser-Ser-OHAsp-Thr
PYO _{fulT}	<i>P. fulva</i> LMG	Asp-eLys-OHAsp-Ser-Ser-Thr-Thr-Thr-cOHOrn
PYO _{putT}	<i>P. putida</i> LMG 2257 ^T	Asp-eLys-OHAsp-Ser-Thr-Ala-Glu-Ser-cOHOrn
PYO _{L1}	<i>P. putida</i> WCS 358	Asp-eLys-OHAsp-Ser-aThr-Ala-Thr-Lys-cOHOrn
PYO _{lurT}	<i>P. lurida</i> LMG 21995 ^T	Ser-Ser-FOHOrn-Ser-Ser-(Lys-FOHOrn-Lys-Ser)
PYO _{Lille1}	<i>P. monteilii</i> Lille 1	Asp-Lys-AcOHOrn-Ala-Ser-Ser-Gly-Ser-cOHOrn
10 amino acids		
PYO _{L48T}	<i>P. entomophila</i> L48 ^T	Ala-Asn-Dab-OHHis-Gly-Gly-Ala-Thr-Ser-cOHOrn
PYO _{PbreT}	<i>P. brenneri</i> LMG 23068 ^T	Ser-Dab-Gly-Ser-OHAsp-Ala-Gly-Ala-Gly-cOHOrn
PYO _{Gwose}	<i>P. fluorescens</i> Gwose	Ser-Thr-Ser-Orn-OHAsp-(Gln-Dab)-Ser-aThr-cOHOrn
PYO _{Pf11.3}	<i>P. fluorescens</i> 1.3	Ala-Lys-Gly-Gly-OHAsp-(Gln-Dab)-Gly-Ser-cOHOrn
PYO _{Pf118.1}	<i>Pseudomonas</i> sp. Pf118.1	Ser-Lys-Gly-FOHOrn-Ser-Ser-Gly-(Lys-FOHOrn-Ser)
PYO _{rho} = PYO _{Lille25}	Prho ^T ΔtrbABC, triabactin-negative mutant of <i>P. rhodesiae</i> LMG 17764 ^T , unpublished	Ser-Lys-FOHOrn-Ser-Ser-Gly-(Lys-FOHOrn-Ser-Ser)
PYO _{TolT}	<i>P. tolaasii</i> LMG 2342 ^T	Ser-Lys-Ser-Ser-Thr-Ser-AcOHOrn-Thr-Ser-cOHOrn
PYO ₉₀₋₁₃₆	<i>Pseudomonas</i> sp. CFML 90-136	Ser-Lys-Ser-Ser-Thr-Thr-AcOHOrn-Ser-Ser-cOHOrn
PYO ₉₀₋₄₄	<i>Pseudomonas</i> sp. CFML 90-44	Asp-Lys-AOHOrn-Thr-Ser-Ser-Gly-Ser-Ser-cOHOrn
11 amino acids		
PYO _{51W}	<i>P. fluorescens</i> 51W	Ala-Lys-Gly-Gly-OHAsp-Gln-Ser-Ala-Gly-aThr-cOHOrn
PYO _{Pf112}	<i>P. fluorescens</i> Pf112	Ser-Lys-Gly-FOHOrn-Ser-Ser-Gly-(Lys-FOHOrn-Glu-Ser)
12 amino acids		
PYO _{Pflii}	<i>P. fluorescens</i> Pflii	Ala-Lys-Gly-Gly-OHAsp-Gln-Ser-Ala-Ala-Ala-Ala-cOHOrn
PYO _{G24} = PYO ₁₅₄₇	<i>P. fluorescens</i> G24	Ser-Lys-Ala-AOHOrn-Thr-Ala-Gly-Gln-Ala-Ser-Ser-cOHOrn
PYO _{W15Oct28}	<i>P. putida</i> W15Oct28	Asp-Ala-AOHOrn-Thr-Gly-c(Thr-(O)-Hse-Hya-Ser-Orn-Hse-Ser-O)
Novel, uncharacterized pyoverdines		
PYO _{G400}	<i>Pseudomonas</i> sp. G400	novel pyoverdine, structure unknown, molecular mass = 1509
PYO _{GS37}	<i>P. putida</i> GS37	novel pyoverdine, structure unknown, molecular mass = 1651
PYO _{W15Oct11}	<i>Pseudomonas</i> sp. W15Oct11	novel pyoverdine, structure unknown
PYO _{cedT}	<i>P. cedrina</i> subsp. <i>cedrina</i> LMG 23661 ^T	novel pyoverdine, structure unknown
PYO _{W15Apr2}	<i>Pseudomonas</i> sp. W15Apr2	novel pyoverdine, structure unknown
PYO _{citT}	<i>P. citronellolis</i> LMG 18378 ^T	novel pyoverdine, structure unknown
PYO _{agaT}	<i>P. agarici</i> LMG 2112 ^T	novel pyoverdine, structure unknown
PYO _{azoT}	<i>P. azotoformans</i> LMG 21611 ^T	novel pyoverdine, structure unknown
PYO _{W2Jun44A}	<i>Pseudomonas</i> sp. W2Jun44A	novel pyoverdine, structure unknown

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Annexes

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Matthijs S, Brandt N, Ongena M, Achouak W, Meyer JM, Budzikiewicz H. Pyoverdine and histocorrugatin-mediated iron acquisition in *Pseudomonas thivervalensis*. *Biometals.* 2016 Jun;29(3):467-85.

Annex III: Predicted functions of the proteins encoded by the different *mrB* genes based on the presence of motifs similarities (InterPro, <https://www.ebi.ac.uk/interpro>).

Protein (length)	Domain localization	InterPro family (F), domain (D), or superfamily entry (SF)	Domain prediction	Description
MrbA (189 aa)	26-186	IPR039425	RNA polymerase sigma-70 like	ECF σ^{70} factor
MrbB (564 aa)	16-291	IPR011527	ABC transporter type 1, transmembrane domain	ABC transporter
	325-555	IPR003439	ABC transporter-like, ATP-binding domain	
MrbC (448 aa)	4-431	IPR025700	L-lysine 6-monooxygenase/L-ornithine 5-monooxygenase	L-lysine 6-monooxygenase/L-ornithine 5-monooxygenase
MrbD (3244 aa)	19-567	IPR040097	Fatty acyl-AMP ligase /fatty acyl-CoA ligase	Non-ribosomal peptide synthetase
	19-462	IPR000873	AMP-dependent synthetase/ligase domain	
	591-666	IPR009081	Phosphopantetheine binding ACP domain	
	691-1121	IPR001242	Condensation domain	
	1147-1538	IPR000873	AMP-dependent synthetase/ligase domain	
	1551-1617	IPR025110	AMP-binding enzyme, C-terminal domain	
	1635-1709	IPR009081	Phosphopantetheine binding ACP domain	
	1725-2156	IPR001242	Condensation domain	
	2179-2621	IPR001242	Condensation domain	
	2642-3046	IPR000873	AMP-dependent synthetase/ligase domain	
	3054-3128	IPR025110	AMP-binding enzyme, C-terminal domain	
	2146-3221	IPR009081	Phosphopantetheine binding ACP domain	
MrbE (5412 aa)	56-495	IPR001242	Condensation domain	Non-ribosomal peptide synthetase
	516-912	IPR000873	AMP-dependent synthetase/ligase domain	
	1009-1083	IPR009081	Phosphopantetheine binding ACP domain	
	1097-1527	IPR001242	Condensation domain	
	1560-2002	IPR001242	Condensation domain	
	2029-2425	IPR000873	AMP-dependent synthetase/ligase domain	
	2433-2504	IPR000873	AMP-dependent synthetase/ligase domain	
	2617-3057	IPR001242	Condensation domain	
	3078-3474	IPR000873	AMP-dependent synthetase/ligase domain	
	3482-3553	IPR025110	AMP-binding enzyme, C-terminal domain	
	35-71-3646	IPR009081	Phosphopantetheine binding ACP domain	
	3661-4113	IPR001242	Condensation domain	
	4144-4535	IPR000873	AMP-dependent synthetase/ligase domain	
	4543-4614	IPR025110	AMP-binding enzyme, C-terminal domain	
	4632-4706	IPR009081	Phosphopantetheine binding ACP domain	
MrbF (476 aa)	4719-5143	IPR001242	Condensation domain	Thioesterase
	5179-5285	IPR001031	Thioesterase	
MrbG (732 aa)	2-472	IPR005814	Aminotransferase class-III	Aminotransferase
MrbH (66 aa)	36-732	IPR012910	TonB-dependent receptor, plug domain	TonB-dependent siderophore receptor
	258-731	IPR000531	TonB-dependent receptor-like, beta-barrel	
MrbI (330 aa)	1-51	IPR005153	MbtH-like protein	MbtH-like protein
MrbJ (277 aa)	22-316	IPR003819	TauD/TfdA-like domain	Taurine dioxygenase
MrbK (237 aa)	113-270	SIPR036477	Formyl transferase, N-terminal domain	Formyl transferase
	57-236	IPR008090	Ferric iron reductase	Ferric iron reductase

