A New Acyl-homoserine Lactone Molecule Generated by *Nitrobacter* winogradskyi

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Pharmacokinetic parameters	Control group	C10:1-HSL group
First-order kinetic equation	<i>y</i> =-0.1336 <i>x</i> +5.1022	<i>y</i> =-0.1442 <i>x</i> +5.1077
R^2	0.95705	0.97785
k	0.1336	0.1442
t _{1/2}	5.19	4.81

Supplementary Table S1. Pharmacokinetic parameters of the decrease in the nitrite concentration decrease in the control and C10:1-HSL groups

Strain or plasmid	Description	Reference
Strains		
Nitrobacter winogradskyi	Type strain	ATCC
ATCC 25391		
Escherichia coli BL21(DE3)	$F ompT hsdS_B(r_B m_B)$	Promega
	dcm gal λ (DE3) Cm ^r	
Agrobacterium tumefaciens	AHL biosensor strain, Tc ^r ,	1
KYC55(pJZ372) (pJZ384) (pJZ410)	Spe ^r , Gm ^r	
Plasmids		
pGEX-4T-1	<i>E. coli</i> cloning and	GE
	expression vector	
pGEX-nwiI	nwiI of N. winogradskyi	This study
	expressed from	
	pGEX-4T-1 tac promoter	

Supplementary Table S2. Bacterial strains and plasmids used in this study

Locus tag	Gene name/description	Primers
nwi0773	cyt. C class 1	5' TAAGGGTGATGCTGAGAACG (F)
		5' CTTCATGGTCGGAGTGGG (R)
nwi0774	nxrA	5' CACTCCGCACTTTAATCGTA (F)
		5' GCGCCAGATGAACCACAT (R)
nwi0775	nxrX	5' TCAACTACGACGTACCCG (F)
		5' TTACCGCCCGAAGATGCT (R)
nwi0776	nxrB	5' CGGTTCGCAGGTTTACGC (F)
		5' CCGTCCTCACCACGCTTGTA (R)
nwi0777	narJ	5' CGTGATCTGCGAAAGCAA (F)
		5' CGTAAAGCATCTAGCACCTGA (R)
nwi0778	nxrC	5' GACTCCCACGGCACTTTA (F)
		5' CCTGTAAGCCAGCGAAAC (R)
nwi0779	nark	5' CAGCATTCCACTCGGTATTT (F)
		5' CCCTGCTTAGACTTCGGATA (R)
nwi0780	C4 dicarboxylic	5' CACGTCGTGGCGACTTAT (F)
	acids/malic acid or	5' CATGATCGTCAGGTTAGCG (R)
	tellurium transporter	

Supplementary Table S3. Primers used in the quantitative PCR

A	NwiI BjaI LasI	MIHIVTAENIGSYQYEMEQAYRIRHNYFYDEMGWDDLRKPDGREIDQFDDGRALHMLYIE MIHAISAVNRHLYEDVLEQHFRIRHDIFVEERHWETLRRPDGREMDSYDDEDTVYLLALE -MIVQIGRREEFDKKLLGEMHKLRAQVFKERKGWDVS-VIDEMEIDGYDALSPYYMLIQE : : : : : :** :: *: *: * * *: *: *: *: *:
	NwiI BjaI LasI	EDRVLGYQRMLPSMRPHLLTEVLPHLCEG-DFPVGPHIWEWTRYCVTRQHRDRGRIL GRRVVGGHRLYPTTKPSMMSEVFPHLAAVRGCPSDPLIWEWSRYFVVRDRRD DTPEAQVFGCWRILDTTGPYMLKNTFPELLHGKEAPCSPHIWELSRFAINSGQKGSLG-F :*.* *: : *:::::*.* *.* *.*
	NwiI BjaI LasI	SPVGNLLLSAIVEWGLASGVQKIIIEMNPLWLLRLVQLNFRVTPLGLPQQIGKDSIIAVT GALNLQLMAAVQEFCLDQGIAQVSAIMETWWLPRFHEAGFVVTPLGLPALVENAWTMAAT SDCTLEAMRALARYSLQNDIQTLVTVTIVGVEKMMIRAGLDVSRFGPHLKIGIERAVALR . : *: .: *: : : : : : : : : : : : :
	NwiI BjaI LasI	AAFDRRILKKLQEVRGNIVPAIVAQPEADQRLRA VDIRRQILDVLHDRIGMPSIVQQDGPRLDAVARANLCGLAAAQRKSA IELNAKIQIALYGGVLVEQRLAVS : :* *
В	LasR NwiR BjaR1	MALVDGFLELERSSGKLEWSAILQKMASDLGFSKILFGLLPKDSQDYENA -MSRRTLDDTLTFIARVDKASTPAEIADAVVDVARPLGFSHVLAGIIPIPGMTAEQQISN MSAVDYGREALDFIEGLGVYRKVPDAMNALEAAFGRFGFETIIVTGLPNPDQRFAQM : : : : : : : : : : : : : : : : : : :
	LasR NwiR BjaR1	FIVGNYPA4WREHYDRAGYARYDPTVSHCTQSVLPIFWEPSIYQTRKQHEFFEEASA VVLHRWPK4WSERYFTKGYLFDDPTIQRVNTSTEPFLWSELEPTYRNTPAPTRVMGEARE VLAKRWPAGWFNLYTQNNYDRFDPVVRLCRQSVNPFEWSEAPYDAELEPSAAEVMNRAGD .: .:*.*:* .* .* .* .* .* .*. *. *: *
	LasR NwiR BjaR1	AGLVYGLTMPLHGARGELGALSLSVEAENRAEANRFIESVLPTLWMLKDYALQSGAGLAF FNLGGGFTVPMITLNGQTAGFSLASERAEVPSILRGQLQLIAMYAFARALG FRMSRGFIVPIHGLTGYEAAVSLGGVHLDLNPRSKPALHLMAMYGFDHIRRLL : *: :*: ***. : : *
	LasR NwiR BjaR1	EHPVSKPVVLTSREKEVLQWCAJGKTSWEISVICNCSEANVNFHMGNIRRKFGVTSRRVA QKYKPAPVNLTPREMDILQWMAEGKSDWEISVILKVSEHLVDKIARQLRAKLNATNRTQT EPTPYPSTRLTPREREVISWASGGKSAWEIGEILHITQRTAEEHLATAARKLGAVNRTHA :**.** :::.* : **: ***. * ::: .: *:*
	LasR NwiR BjaR1	AIMAVNLGLIIL VAVALRINLIR- VALAIRHKIINP . :*:. :*

Supplementary Figure S1. Sequence alignment of NwiI and NwiR. The amino acid sequences of NwiI/R were compared to BjaI/R and LsaI/R, respectively. Identical and similar amino acid residues in the three proteins are indicated by asterisks and colons, respectively, and nine conserved residues in the LuxI/R family are highlighted in black boxes.



0.2

Supplementary Figure S2. Phylogenetic tree of LuxI and HdtS family members.

The scale bar indicates the number of substitutions per residue. Bootstrap values as the percentage of 500 samplings are shown for nodes with values of 50% or greater. The subfamily tree of AHL synthases containing BraI, RapI, BjaI and NwiI is highlighted in red.



Supplementary Figure S3. LC-MS chromatograms of LB and 756 medium. (A)

LB medium. (B) 756 medium.



Supplementary Figure S4. ¹H NMR purified from the extracts of recombinant *E. coli* strain contain *nwil* gene. ¹H-NMR (CDCl₃, 400 MHz) sprctrum: $\delta_{\rm H} 0.88(3\text{H}, \text{t}, \text{a})$, 1.29(8H, m, b), 2.01(2H, m, c), 2.11(1H, m, β), 2.86(1H, m, β), 3.08(2H, d, e), 4.28(1H, m, γ), 4.47(1H, t, α), 4.53(1H, m, γ), 5.54(1H, m, d), 5.73(1H, m, d), 6.17(1H, m, f).



Supplementary Figure S5. ¹³C NMR purified from the extracts of recombinant *E. coli* strain contain *nwiI* gene. ¹³C NMR (100MHz, CDCl₃): δ 14.07, 27.37, 28.94, 29.19, 29.69, 30.64, 31.67, 34.73, 49.30, 66.02, 120.64, 136.15, 171.63, 175.18.



Supplementary Figure S6. LC-MS chromatograms of putative AHLs molecules

in *E. coli* containing pGEX-nwil. (A) C8:1-HSL, (B) C9:1-HSL, (C) C11:1-HSL.



Supplementary Figure S7. LC-MS chromatograms of C10:1-HSL obtained by preparative HPLC. (A) Chromatogram of the lactone moiety at m/z 102. (B) The mass spectra reveal molecular ion [M+H] of m/z 254. The major fragmentation products with their respective m/z are labeled.

Reference

 Zhu, J., Chai, Y., Zhong, Z., Li, S. & Winans, S. C. Agrobacterium bioassay strain for ultrasensitive detection of N-acylhomoserine lactone-type quorum-sensing molecules: detection of autoinducers in Mesorhizobium huakuii. Appl. Environ. Microbiol. 69, 6949-6953 (2003).