# Halotolerant *Bacillus* spp. strains isolated from the Great Sebkha of Oran (Algeria): a source of antimicrobial secondary metabolites

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## Abstract

*Bacillus* species are Gram-positive bacteria found in abundance in nature, they could colonize different habitats even under extreme conditions and their secondary metabolites were found to possess various potential activities, notably antimicrobial. In this study, three-halotolerant *Bacillus* sp. LMB3051, LMB3073 and LMB3093 were isolated from water of the Great Sebkha of Oran, they exhibited interesting antimicrobial activities against a broad spectrum of reference bacterial and fungal strains. Their metabolites were extracted with chloroform and ethyl acetate solvents. Structural elucidation of actives compounds was carried out using gas chromatography–mass spectrometry (GC-MS). Fifty-six compounds were identified; they include tert-butyl phenol compounds, fatty acid methyl esters due to the methylation procedure, hydrocarbons, aldehydes, benzoquinones, pyrrols, and terpenes. Literature reports such compounds to have wide biological and pharmaceutical applications. Partial 16S rRNA gene sequencing of the three isolates showed very high similarity with many species of *Bacillus*. The comparison with 16S rRNA EzBioCloud database revealed that the isolates LMB3051 (529 bp) and LMB3073 (429 bp) showed a similarity of 99.81% and 98.60%, respectively, with *Bacillus licheniformis* ATCC 14,580, *B. aureus* 24 K, *B. paralicheniformis* KJ-16, *B. glicinifermentans* GO-13, *B. haynesii* NRRL B-41327, and *B. piscis*16MFT21. The isolate LMB3093 (400 bp) showed 98.75% of similarity with Bacillus paralicheniformis KJ-16 and *B. haynesii* NRRL B-41327. The findings suggest that the Great Sebkha of Oran is a valuable source of strains exhibiting variety of beneficial attributes that can be utilized in the development of biological antibiotics.

## Materials and Methods

**Phenotypical characterization** 

Molecular

identification

morphological, cultural, biochemical, and physiological characterization was realized as described by **Logan** *et al.* (2009)

- Genomic DNA was extracted using the standard phenol/chloroform method (Ettoumi *et al.* 2013).
- The amplification of the 16S rRNA gene was carried out using, the universal Primers 5'-S-D-Bact-0008-a-S-20–3' and 5'-S-D-Bact-1495-a-S-20–3' (Daffonchio *et al.* 2000).

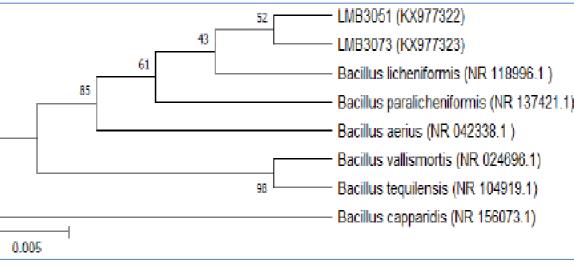
The amplified 16S rRNA fragments were sequenced and identified using EzBioCloud databases (Yoon *et al.* 2017).

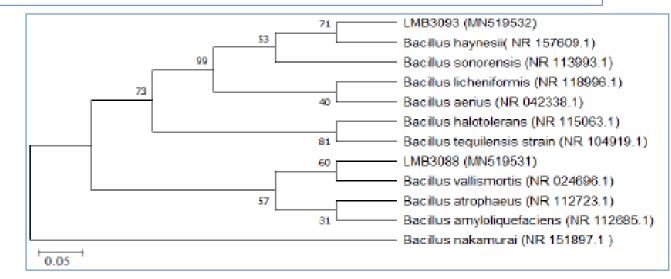
The antagonistic properties of the isolates were screened by the agar plug method (Balouiri et al. 2016) against Gram positive bacteria (Bacillus cereus ATCC11778 and Staphylococcus aureus ATCC

## Results

#### Table 1. Morphological, physiological, and biochemical characteristics of LMB3051, LMB3073, and LMB3093 strains

Characteristics	LMB3051	LMB3073	LMB3093		
Gram staining	+	+	+		
Motility	Motile	Motile	Motile		
Cell morphology	Long and straight rods	Short rods	Long big rods		
Arrangement	Singly or in chains	Singly and in irregular clumps	Singly		
Spore	Ellipsoidal subterminal	Ellipsoidal subterminal	Ellipsoidal subterminal		
Colonies (24 h on nutrient agar at 15% of NaCl)	3 to 4 mm in diameter, cream, opaque, circular, smooth, shiny, slimy, convex, and odorous	3 to 4 mm in diameter, whitish, opaque, circular, smooth, shiny, slimy, convex, no smell	2 to 4 mm of diameter, cream, opaque, circular, smooth, slimy, shiny, flat, and odorous		
NaCl tolerance	0 to 20% (w/v)	0 to 20% (w/v)	0 to 20% (w/v)		
NaCl optimum (%)	0%	0%	0%		
Range of temperature for growth	15 to 60 °C	15 to 60 °C	15 to 60 °C		
Temperature optimum °C	30–40 °C	30–37 °C	30–37 °C		
Range of pH for growth	5 to 11	5 to 11	5 to 11		
pH optimum	6–7	6–7	6–7		
Catalase	+	+	+		
Oxydase	+	+	+		
Respiratory test	Aero-anaerobic facultative	Aero-anaerobic facultative	Aero-anaerobic facultative		





**Fig 1.** Phylogenetic tree constructed by performing bootstrap analysis of 1000 data sets using the MEGA 6 program, based on the analysis of 16S rRNA partial sequences showing the relationships between isolates LMB3051 and LMB3073 and related species. *Bacillus capparidis* was used as an outgroup The bar indicates 0.005 substitution per nucleotide position. Accession numbers are given in parentheses

**Fig 2.** Phylogenetic analyses of the isolate LMB3093 basing on 16S rRNA partial sequences. Phylogenetic dendrogram was evaluated by performing bootstrap analysis of 1000 data sets using MEGA 6. 16S rRNA sequence. *Bacillus nakamurai* was used as an outgroup. The bar indicates 5 substitution per 100 nucleotide. Accession numbers of the reference strains were indicated in parentheses

Benzoic acid, pentadecyl ester

Z, 5 Methyl-6-Heneicosen-11-one None 1.254

None 1.805

Screening of antimicrobial activities ATCC 11778 and Staphylococcus dureus ATCC 25,923), Gram-negative bacteria (*Escherichia coli* ATCC 25,922 and *Acinetobacter baumannii* ATCC 19,606), and fungi (*Candida albicans* ATCC 444, *Candida albicans* ATCC 10,231, and *Aspergillus flavus* MNHN994294

Extraction of secondary metabolites Was performed from solid substrate fermentation (agar culture) with two organic solvents, ethyl acetate, and chloroform, using the method of **Kim** *et al.* (2016)

#### GC-MS analysis of bioactive crude extract

 The analysis was carried out using Agilent 7890B gas chromatography instrument coupled with an Agilent MS 240 Ion Trap with capillary column HP-5MS (5% phenyl methyl polysiloxane, 30 m, 250 µM, 0.25 µM)

### References

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**Table 2**. Inhibitory effects of the chloroform and ethyl acetate extracts of the isolates using disc diffusion method

Test microorganisms	Zone's diameter (mm)						
		LMB3051		LMB3073		LMB3093	
		Chloroform	Ethyl acetate	Chloroform	Ethyl acetate	Chloroform	Ethyl acetate
Bacillus cereus ATCC 11,778	$15.33 \pm 0.57^{a}$		$14.33 \pm 0.57^{a}$	$17.33 \pm 0.57^{a}$	$22.33 \pm 0.57^{a}$	$13.33 \pm 0.57^{a}$	$12.66 \pm 0.57^{a}$
Staphylococcus aureus ATCC 25,923	$19.66 \pm 0.57^{a}$		$17.66 \pm 0.57^{a}$	$16 \pm 1^{a}$	$19.33 \pm 0.57^{a}$	$15.33 \pm 1.52^{\rm a}$	$14 \pm 1^{a}$
Escherichia coli ATCC 25,922	$13.33 \pm 0.57^{a}$		$12.33 \pm 0.57^{a}$	$12.33 \pm 0.57^{a}$	$14 \pm 1^{a}$	$11.33 \pm 1.15^{a}$	$10 \pm 0^{a}$
Acinetobacter baumannii ATCC 19,606	$10\pm0^{a}$		$9.66 \pm 1.52^{a}$	$12.66 \pm 1.15^{a}$	$15.66 \pm 0.57^{a}$	$09.66 \pm 1.52^{a}$	$09 \pm 1^{a}$
Candida albicans IP 444	$13 \pm 0^{a}$		$12 \pm 1^{a}$	$11.66 \pm 0.57^{a}$	$16\pm0^{a}$	$10.33 \pm 1.52^{a}$	$10 \pm 1^{a}$
Candida albicans ATCC 10,231	$12.66 \pm 0.57^{a}$		$11.66 \pm 0.57^{a}$	$11.33 \pm 0.57^{a}$	$13.66 \pm 1.15^{a}$	$11 \pm 1^{a}$	$10 \pm 0^{a}$
Aspergillus flavus MNHN994294	$33.33 \pm 0.57^{\rm a}$		$31.66 \pm 0.57^{a}$	$34.66 \pm 1.52^{a}$	$37.66 \pm 0.57^{a}$	$30.33 \pm 0.57^{a}$	$29 \pm 1^{a}$

Values were expressed as mean  $\pm$  standard deviation (n=3). Values in same columns with superscript (a) were strongly significant different (p<0.001)

<b>Table 2.</b> Chemical composition of the chloroformic and ethyl acetate extracts of the isolate LMB3051				<b>Table 2.</b> Chemical composition of the chloroformic and ethyl acetate extracts of the isolate LMB3073				<b>Table 2.</b> Chemical composition of the chloroformicAnd ethyl acetate extracts of the isolate LMB3093				
Solvent	Compounds identified	CAS n	%	Solvent	Compounds identified	CAS n	%	Solvent	Compounds identified	CAS n	(%)	
Chloroform	Hexadecanoic acid bis (2ethylhexyl) ester	103-23-1	100		<ol> <li>3- Di-tert-butyl benzene</li> <li>Fluorododecane</li> <li>Nonyl cycloheptane</li> <li>6-Di-tert-butyl-1,4-</li> <li>benzoquinone</li> </ol>	1014-60-4 334-68-9 None 719-22-2	1.548 5.125 0.767 0.597	1, 3- Di-tert-butyl benzene1- Fluorododecane1-Nonyl cycloheptane2,6-Di-tert-butyl-1,4-benzoquinone		1014-60-4 334-68-9 None 719-22-2	1.955 8.089 1.459 0.735	
	3-n-hexylthiolane, S, S, dioxid	71053-07-1	6,059		2,6-di-tert-butyl-4- (dimethylaminomethyl) phenol	88-27-7	24.741		2,6-di-tert-Butyl-4- (dimethylaminomethyl) phenol	88-27-7	19.297	
	1, 3- Di-tert-butyl benzene	1014-60-4	1.360		<ul><li>2, 4- di- tert- butyl phenol</li><li>3, 5- di- tert- butyl -4-</li><li>hydroxyacetophenone</li></ul>	96-76-4 14035-33- 7	4.649 1.075		<ul> <li>2, 4- di- tert- Butyl phenol</li> <li>3, 5- di- tert- butyl -4-</li> <li>hydroxyacetophenone</li> </ul>	96-76-4 14035-33- 7	5.059 1.433	
ite	2, 5- Di- tert- butyl- 1, 4- benzoquinone	2460-77-7	0.512	Chloroform	2, 4, 6- Tri -tert- butylphenol, 3,5-Di-tert-butyl-4- hydroxybenzaldehyde	phenol, 732-26-3 0.874 1620-98-0 13.340	a	2, 4, 6- Tri -tert- butylphenol 3,5-Di-tert-butyl-4-	732-26-3 1620-98-0	1.188 11.839		
Ethyl aceta	2,6-Di-tert-butyl- 1,4-benzoquinone	719-22-2	27.646	734 963	4,4'-Ethylenebis(2,6-di-tert- butylphenol)	1516-94-5	2.756	Chloroform	hydroxybenzaldehyde <u>Propanohydrazide, N2-(3,5-di-tert-butyl-4-hydroxybenzyl)</u> -N2-	304870- 86-8	2.687	
	2, 4- Di- tert- butyl phenol	96-76-4	8.310		Pyrrolo [1,2-a] pyrazine-1,4- dione, hexahydro-3- <u>2-Propenoic acid, 3-(4-</u>	5654-86-4 830-09-1	6.928 2.969		phenyl Pyrrolo [1,2-a] pyrazine-1,4-dione,	5654-86-4	10.012	
	1-Nonyl cycloheptane 3,5-Di-tert-butyl-4-	None 1620-98-0	13,734 5.963		<u>methoxyphenyl)</u> Tetracontane, 3, 5, 24, trimethyl				hexahydro-3-(2-methylpropyl)- Tritetracontane 4,4'-Ethylenebis (2,6-di-tert-	7098-21-7 1516-94-5	1.818 1.270	
	hydroxybenzaldehyde Hexadecanoic acid bis	ecanoic acid bis 103-23-1 35.957	35.957		Carbonic acid eicosyl vinyl ester	None	5.74		butylphenol) 2-Propenoic acid, 3-(4-	830-09-1	2.185	
	(2ethylhexyl) ester				9- Octadeoenamide, (z)-301-02-03.7281-Nonyl cycloheptaneNone11.205			<u>methoxyphenyl</u> ) Z -8-methyl -9- tetradecenoic acid	None	1.018		
				1, 3- Di-tert-butyl benzene	1014-60-4	1.449		9- Octadecenamide, (z)-	301-02-0	0.509		
		fe	2 (3H)- Naphtalenone,4, 4a, 5, 6, 7,8-hexahydro-4a-5- dimethyl-3-(1-	19598-45- 9	10.539		Hexadecanoic acid bis (2ethylhexyl) ester	103-23-1	1.579			
			methylethyldiene)-4ar-cis				13-Docosenamide, (Z)	112-84-5	5.160			
			2, 4- di- tert- butyl phenol Cyclo pentane acetic acid, 3- oxo-2 pentyl-methyl ester	96-76-4 24851-98- 7	4.667 4.066		1-Undecyne <u>3-n-hexylthiolane</u> , S, S, dioxide	2243-98-3 71053-07- 1	0.840 5.467			
				l acetate	Tridecanoic acid, 12-methyl-, methyl ester	5129-58-8	0.788		1-Tetradecyne 2, 5- di- tert- butyl- 1, 4-	765-10-6 2460-77-7	1.189 0.464	
				Ethyl	3,5-Di-tert-butyl-4- hydroxybenzaldehyde	1620-98-0	3.382	ate	benzoquinone 2,6-Di-tert-butyl-1,4-benzoquinone	719-22-2	4.103	
					7-Acetyl-6-ethyl-1,1,4,4- tetramethyl-1,2,3,4- tetrahydronaphthalene	88-29-9	3.103	rl acetate	2, 4- di- tert- butyl phenol 1-Nonyl cycloheptane	96-76-4 None	6.031 10.564	
					Hexadecanoic acid methyl ester Heptadecanoic acid, 16 methyl,	112-39-0 5129-61-3	5.807 4.806	Ethyl	2-Propenoicacid,3-(4-methoxyphenyl)Oleyl alcohol, trifluoro acetate	830-09-1 None	4.75 1.004	
					methyl ester <u>Hexadecanoic acid bis (2 ethyl-</u>	103-23-1	36.781		Benzoic acid, tridecyl ester	None	2,966	
					<u>hexyl) ester</u>				Hexadecanoic acid bis (2ethylhexyl) ester	103-23-1	3.609	
									Danzoia agid nantadagul astan	Nona	1 005	

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