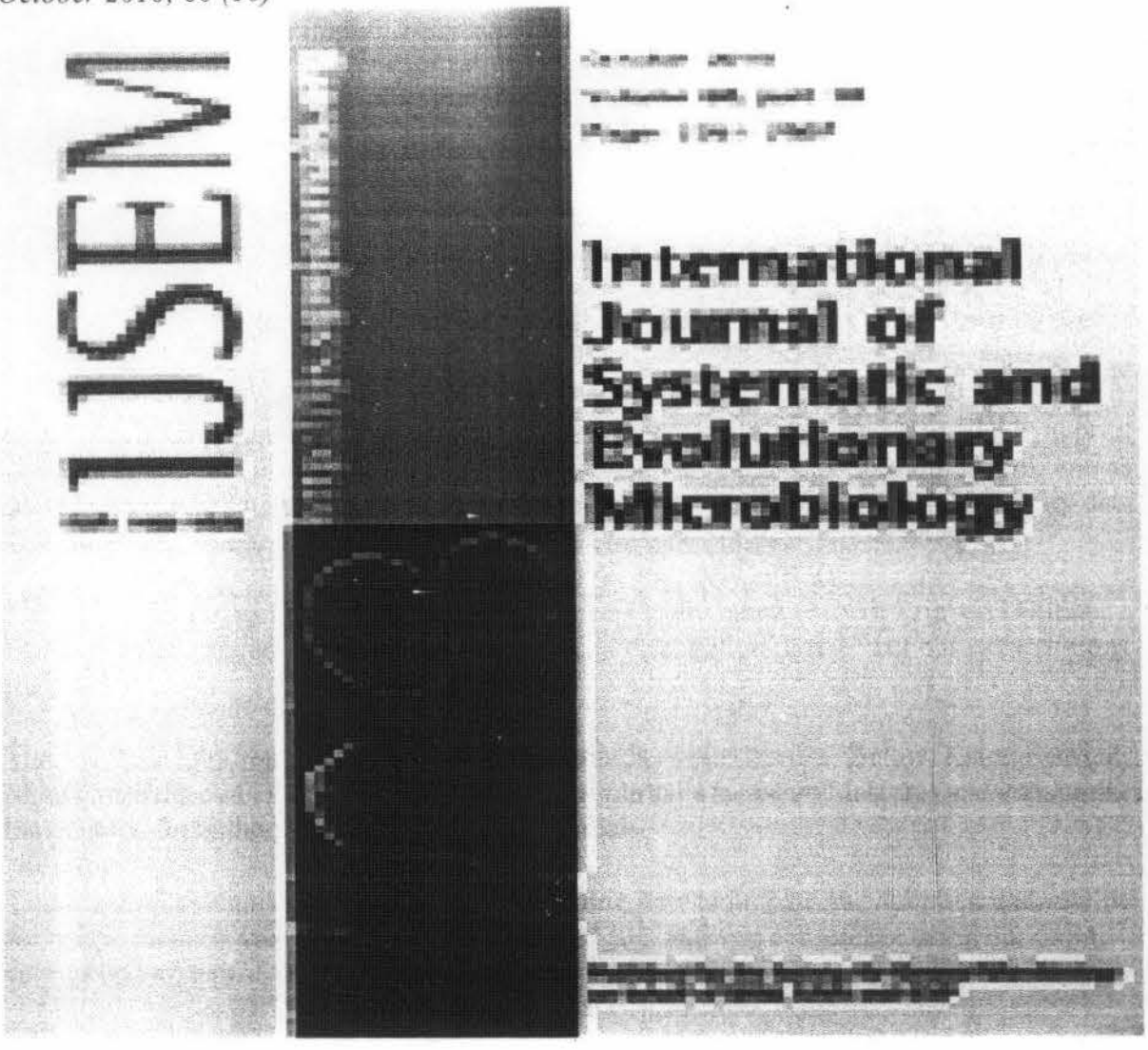
2

October 2010; 60 (10)



SOCIETY FOR GENERAL MICROBIOLOGY

International Journal of Systematic and Evolutionary Microbiology

International Journal of Systematic and Evolutionary Microbiology (IJSEM) is the leading forum for the publication of new taxa of bacteria and yeasts, and it is the official journal of record for bacterial names of the International Committee on Systematics of Prokaryotes (ICSP) of the International Union of Microbiological Societies (IUMS). The current Impact Factor for the journal is 2.112 (2012).

Benefits to authors:

- A distinguished international Editorial Board
- Straightforward online submission
- Official journal of record for bacterial names
- Rigorous, high-quality peer review
- Immediate online publication
- High production standards
- No page charges
- Pubmed Central deposition*
- Free colour reproduction*
- Free supplementary data facility
- 25 free downloads of your published PDF
- Self-archiving
- Paid immediate open access

*Some conditions apply.

IJSEM's impact

- Impact Factor: 2.798 (2013)
- Eigenfactor: 0.01856
- Cited Half-life: 6.6

International Journal of Systematic and Evolutionary Microbiology (2010), 60, 2331–2335 DOI 10.1099/ijs.0.013276-0

Actinokineospora baliensis sp. nov., *Actinokineospora cibodasensis* sp. nov. and *Actinokineospora cianjurensis* sp. nov., isolated from soil and plant litter

Puspita Lisdiyanti,[1] Misa Otoguro,[2] Shanti Ratnakomala,[1] Yulin Lestari,[3] Ratih D. Hastuti,[4] Evi Triana,[5] Ando Katsuhiko[2] and Yantyati Widyastuti[1]

Correspondence
Puspita Lisdiyanti
puspita.lisdiyanti@lipi.go.id or p_lisdiyanti@yahoo.com

[1]Research Center for Biotechnology, Indonesian Institute of Sciences, Jl. Raya Bogor Km. 46, Cibinong 16911, Indonesia

[2]Department of Biotechnology, National Institute of Technology and Evaluation, 2-5-8 Kazusa kamatari, Kisarazu, Chiba 292-0818, Japan

[3]Department of Biology, Faculty of Mathematics and Natural Sciences, Bogor Agricultural University, Jalan Raya Pajajaran, Bogor 16144, Indonesia

[4]Soil Research Institute, Jl. Ir. H. Juanda 98, Bogor 16002, Indonesia

[5]Research Center for Biology, Indonesian Institute of Sciences. Jl. Raya Bogor Km. 46, Cibinong 16911, Indonesia

Six actinomycete strains isolated from soil and plant-litter samples in Indonesia were studied for their taxonomic position by using a polyphasic approach. Phylogenetically, all the strains were located in the broad cluster of the genus *Actinokineospora*. Chemotaxonomic data [cell-wall diamino acid, *meso*-diaminopimelic acid; cell-wall peptidoglycan, type III (A1γ); major sugars, galactose and arabinose; major menaquinone, MK-9(H_4); major fatty acid, iso-$C_{16:0}$; major phospholipid, phosphatidylethanolamine] supported the affiliation of all six strains to the genus *Actinokineospora*. The results of DNA–DNA hybridization with DNA from type strains of *Actinokineospora* species with validly published names revealed three DNA–DNA relatedness groups. Group I (ID03-0561^T) showed low relatedness to the other strains studied. The three strains in group II (ID03-0784^T, ID03-0808 and ID03-0809) formed a group with high relatedness (98–100 %) and showed low relatedness to the other strains studied. The two strains in group III (ID03-0810^T and ID03-0813) showed 58–68 % relatedness to *Actinokineospora terrae* NBRC 15668^T and showed low relatedness (2–24 %) to the other strains studied. The description of three novel species is proposed: *Actinokineospora baliensis* sp. nov., for the single strain in group I (type strain ID03-0561^T =BTCC B-554^T =NBRC 104211^T), *Actinokineospora cibodasensis* sp. nov., for the strains in group II (type strain ID03-0784^T =BTCC B-555^T =NBRC 104212^T), and *Actinokineospora cianjurensis* sp. nov., for the strains in group III (type strain ID03-0810^T =BTCC B-558^T =NBRC 105526^T).

The genus *Actinokineospora* was proposed by Hasegawa (1988) for motile, arthrospore-bearing actinomycetes. Recently, Labeda *et al.* (2010) emended the description of the genus to accommodate species that have not been observed to produce motile spores, and transferred *Amycolatopsis fastidiosa* to the genus as *Actinokineospora fastidiosa*. At the time of writing, the genus contains eight species: *Actinokineospora riparia* (the type species), *Actinokineospora inagensis*, *Actinokineospora globicatena*, *Actinokineospora terrae*, *Actinokineospora diospyrosa*, *Actinokineospora auranticolor*, *Actinokineospora enzanensis* and *Actinokineospora fastidiosa* (Hasegawa, 1988; Tamura *et al.*, 1995; Otoguro *et al.*, 2001b; Labeda *et al.*, 2010). These actinomycetes have *meso*-diaminopimelic acid as a cell-wall diamino acid, galactose and arabinose as diagnostic whole-cell sugars, MK-9(H_4) as the predominant menaquinone, phospholipid type II, iso-$C_{16:0}$ fatty acid as

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequence of strains ID03-0561^T, ID03-0784^T and ID03-0810^T are AB447488, AB447489 and AB473945, respectively.

Minimum-evolution and maximum-parsimony 16S rRNA gene sequence-based trees are available as supplementary material with the online version of this paper.

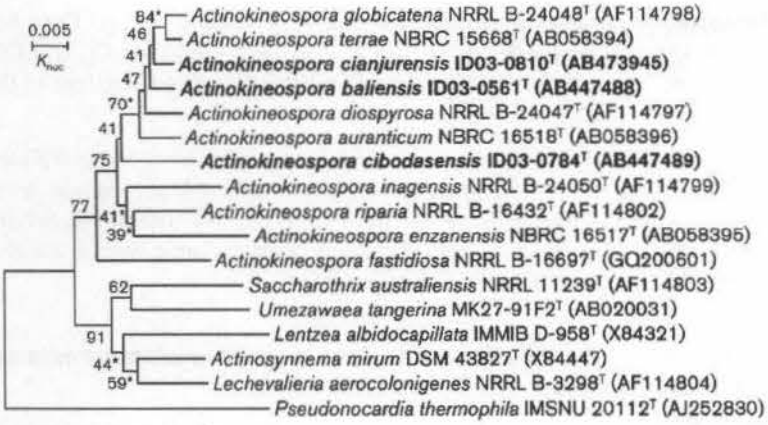


Fig. 1. 16S rRNA gene sequence dendrogram reconstructed by the neighbour-joining method using the software MEGA version 4 (Tamura *et al.*, 2007) displaying the relatedness of the novel strains and other members of the genus *Actinokineospora*. The sequence of *Pseudonocardia thermophila* IMSNU 20112^T was used as the outgroup. Bar, 0.005 substitutions per nucleotide position. Asterisks indicate branches of the tree that were also recovered using the minimum-evolution and maximum-parsimony methods (these trees are available as Supplementary Figs S1 and S2 in IJSEM Online).

Table 2. The range of G+C content of the isolates was 70.2–71.9 mol%. DNA–DNA hybridization revealed that the six Indonesian isolates were divided into three DNA–DNA relatedness groups. Group I contained a single isolate (ID03-0561^T), group II contained three isolates (ID03-0784^T, ID03-0808 and ID03-0809) and group III contained two isolates (ID03-0810^T and ID03-0813). Group I showed low relatedness to the other Indonesian strains and the reference strains used. Strains of group II showed high relatedness to each other (98–100 %) and low relatedness to the other tested strains. The strains of group III showed 58–68 % relatedness to *Actinokineospora terrae* NBRC 15668^T and low relatedness (2–24 %) to the other reference strains.

The results of phenotypic characterization, performed as described previously (Seino *et al.*, 1985; Shirling & Gottlieb, 1966; Otoguro *et al.*, 2001b), are given in the species descriptions. The isolates used for phenotypic tests were grown in yeast extract/glucose broth medium as described for chemotaxonomic analysis and resuspended in distilled water. DNA–DNA relatedness groups I–III could be distinguished from the type strains of other species of the genus *Actinokineospora* by using a combination of phenotypic properties. Strain ID03-561^T in group I was positive for utilization of mannose and sucrose and negative for utilization of arabinose, galactose, fructose and rhamnose. The isolates in group II were positive for utilization of galactose, mannose, fructose, sucrose and maltose and negative for utilization of arabinose and rhamnose as sole carbon sources. The two isolates in group III were distinguished from *Actinokineospora terrae* by being positive for utilization of galactose and negative for utilization of arabinose and rhamnose.

It is clear from the genotypic, chemotaxonomic and phenotypic data that the six Indonesian strains represent three novel species in the genus *Actinokineospora*. The

Table 2. DNA base composition and DNA–DNA hybridization of *Actinokineospora* strains

Strain	G+C content (mol%)	DNA–DNA hybridization (%) with labelled DNA from strain:									
		1	2	3	4	5	6	7	8	9	10
1. ID03-0561^T	71.4	(100)	12	13	16	27	10	24	37	17	2
2. ID03-0784^T	71.3	12	(100)	ND	14	ND	6	15	17	17	14
ID03-0808	71.9	15	93	ND	17	ND	11	23	35	32	9
3. ID03-0809	71.5	13	94	(100)	15	ND	ND	52	ND	2	ND
4. ID03-0810^T	70.2	25	23	12	(100)	ND	3	26	25	58	16
ID03-0813	70.3	31	10	13	91	ND	9	ND	ND	65	25
5. *A. riparia* NBRC 14541^T	ND	7	7	7	8	(100)	19	25	2	7	38
6. *A. inagensis* NBRC 15663^T	ND	ND	20	ND	ND	ND	(100)	27	30	25	30
7. *A. globicatena* NBRC 15664^T	ND	26	24	ND	ND	28	1	(100)	13	26	32
8. *A. diospyrosa* NBRC 15665^T	ND	20	7	9	12	16	9	20	(100)	24	39
9. *A. terrae* NBRC 15668^T	ND	29	15	19	68	20	4	30	10	(100)	20
10. *A. enzaensis* NBRC 16517^T	ND	13	13	ND	ND	27	17	33	4	24	(100)
A. auranticolor NBRC 16518^T	ND	6	5	8	8	17	12	16	5	10	2

ND, Not determined.

which radioisotopes are used to determine genetic relatedness among bacterial strains. *Int J Syst Bacteriol* **39**, 224–229.

Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* **39**, 783–791.

Hasegawa, T. (1988). *Actinokineospora*: a new genus of the Actinomycetales. *Actinomycetologica* **2**, 31–45.

Hayakawa, M. & Nonomura, H. (1987). Humic acid-vitamin agar, a new medium for selective isolation of soil actinomycetes. *J Ferment Technol* **65**, 501–509.

Hayakawa, M. & Nonomura, H. (1989). A new method for the intensive isolation of actinomycetes from soil. *Actinomycetologica* **3**, 95–104.

Hayakawa, M., Otoguro, M., Takeuchi, T., Yamazaki, T. & Iimura, Y. (2000). Application of a method incorporating differential centrifugation for selective isolation of motile actinomycetes in soil and plant litter. *Antonie van Leeuwenhoek* **78**, 171–185.

Kluge, A. G. & Farris, J. S. (1969). Quantitative phyletics and the evolution of anurans. *Syst Zool* **18**, 1–32.

Labeda, D. P. & Kroppenstedt, R. M. (2000). Phylogenetic analysis of *Saccharothrix* and related taxa: proposal for *Actinosynnemataceae* fam. nov. *Int J Syst Evol Microbiol* **50**, 331–336.

Labeda, D. P., Price, N. P., Tan, G. Y. A., Goodfellow, M. & Klenk, H.-P. (2010). Emended description of the genus *Actinokineospora* Hasegawa 1988 and transfer of *Amycolatopsis fastidiosa* Henssen *et al.* 1987 as *Actinokineospora fastidiosa* comb. nov. *Int J Syst Evol Microbiol* **60**, 1444–1449.

Lechevalier, M. P. & Lechevalier, H. A. (1970). Chemical composition as a criterion in the classification of aerobic actinomycetes. *Int J Syst Bacteriol* **20**, 435–443.

Lechevalier, M. P., Stern, A. E. & Lechevalier, H. A. (1981). Phospholipids in the taxonomy of actinomycetes. In *Actinomycetes. Proceedings of the Fourth International Symposium on Actinomycete Biology*, pp. 111–116. Edited by K. P. Schaal & G. Pulverer. New York: Gustav Fischer.

Otoguro, M., Hayakawa, M., Yamazaki, T. & Iimura, Y. (2001a). An integrated method for the enrichment and selective isolation of *Actinokineospora* spp. in soil and plant litter. *J Appl Microbiol* **91**, 118–130.

Otoguro, M., Hayakawa, M., Yamazaki, T., Tamura, T., Hatano, K. & Iimura, Y. (2001b). Numerical phenetic and phylogenetic analysis of *Actinokineospora* isolates, with a description of *Actinokineospora auranticolor* sp. nov. and *Actinokineospora enzaensis* sp. nov. *Actinomycetologica* **15**, 30–39.

Rzhetsky, A. & Nei, M. (1993). Theoretical foundation of the minimum-evolution method of phylogenetic inference. *Mol Biol Evol* **10**, 1073–1095.

Saito, H. & Miura, K. (1963). Preparation of transforming deoxyribonucleic acid by phenol treatment. *Biochim Biophys Acta* **72**, 612–629.

Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.

Seino, A., Arai, M., Enokida, R., Okazaki, T. & Furuichi, A. (1985). *Identification Manual of Actinomycetes.* Tokyo: The Society for Actinomycetes.

Shirling, E. B. & Gottlieb, D. (1966). Methods for characterization of *Streptomyces* species. *Int J Syst Bacteriol* **16**, 313–340.

Tamura, T. & Hatano, K. (2001). Phylogenetic analysis of the genus *Actinoplanes* and transfer of *Actinoplanes minutisporangius* Ruan *et al.* 1986 and '*Actinoplanes aurantiacus*' to *Cryptosporangium minutisporangium* comb. nov. and *Cryptosporangium aurantiacum* sp. nov. *Int J Syst Evol Microbiol* **51**, 2119–2125.

Tamura, T., Nakagaito, Y., Nishii, T., Hasegawa, T., Stackebrandt, E. & Yokota, A. (1994). A new genus of the order *Actinomycetales*, *Couchioplanes* gen. nov., with descriptions of *Couchioplanes caeruleus* (Horan and Brodsky 1986) comb. nov. and *Couchioplanes caeruleus* subsp. *azureus* subsp. nov. *Int J Syst Bacteriol* **44**, 193–203.

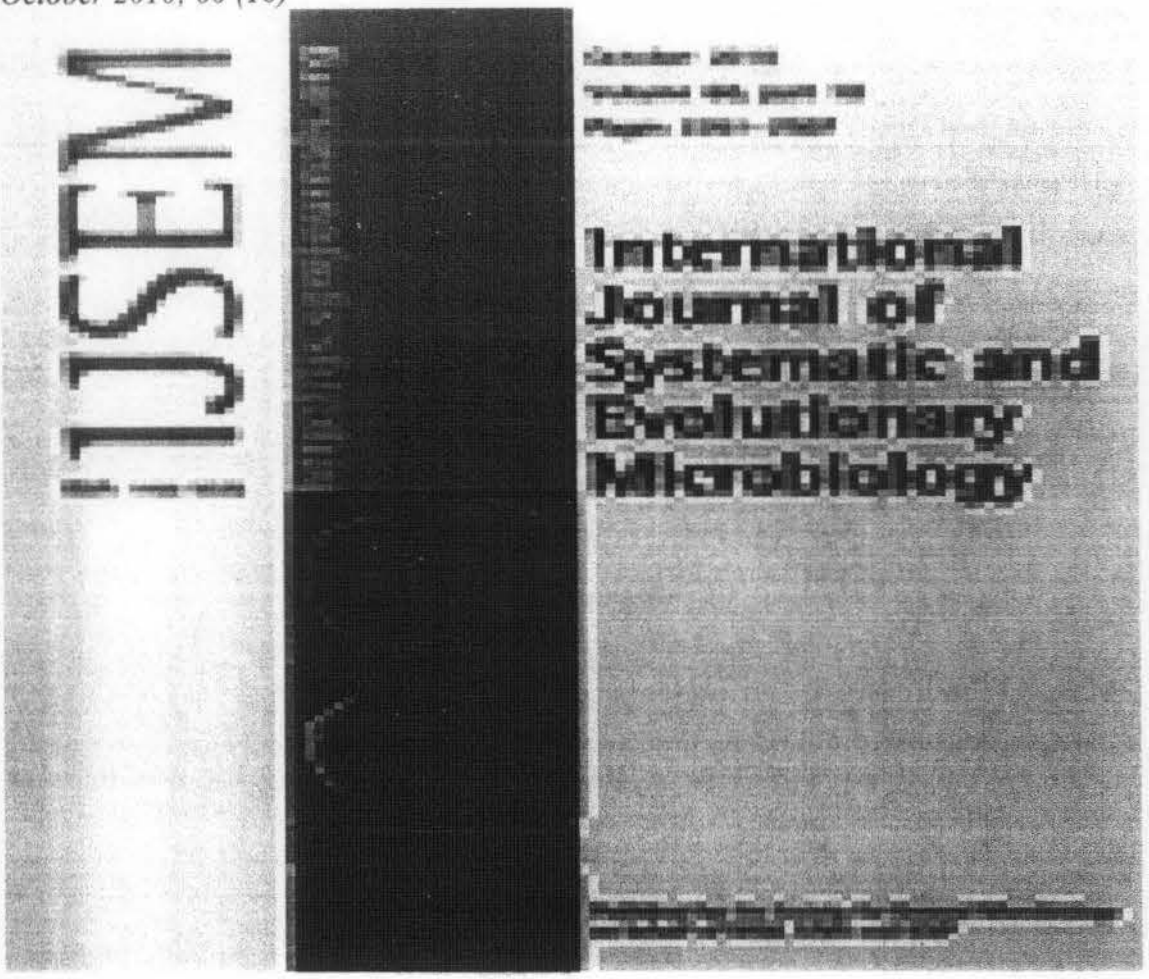
Tamura, T., Hayakawa, M., Nonomura, H., Yokota, A. & Hatano, K. (1995). Four new species of the genus *Actinokineospora*: *Actinokineospora inagensis* sp. nov., *Actinokineospora globicatena* sp. nov., *Actinokineospora terrae* sp. nov. and *Actinokineospora diospyrosa* sp. nov. *Int J Syst Bacteriol* **45**, 371–378.

Tamura, K., Dudley, J., Nei, M. & Kumar, S. (2007). MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0. *Mol Biol Evol* **24**, 1596–1599.

Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. & Higgins, D. G. (1997). The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* **25**, 4876–4882.

This Issue

October 2010; 60 (10)



International Journal of Systematic and Evolutionary Microbiology

Table of Contents

October 2010; 60 (10)

NOTIFICATION LIST

NEW TAXA: Archaea

- Xia Gao,
- Xin-Yi Li,
- Xue-Wei Xu,
- Yu-Guang Zhou,
- Hong-Can Liu,
- and Pei-Jin Zhou

Halosarcina limi* sp. nov., a halophilic archaeon from a marine solar saltern, and emended description of the genus *Halosarcina

Int J Syst Evol Microbiol October 2010 60:2462-3466; published ahead of print November 27, 2009, doi:10.1099/ijs.0.018697-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Figures

NEW TAXA: Actinobacteria

- ☐ Select this article
  - Pavan Kumar Pindi,
  - Ruth Manorama,
  - Zareena Begum,
  - and S. Shivaji

***Arthrobacter antarcticus* sp. nov., isolated from an Antarctic marine sediment**

Int J Syst Evol Microbiol October 2010 60:2263-2266; published ahead of print September 25, 2009, doi:10.1099/ijs.0.012989-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Figure

- ☐ Select this article
  - Deanna Jannat-Khah,
  - Reiner M. Kroppenstedt,
  - Hans-Peter Klenk,
  - Cathrin Spröer,
  - Peter Schumann,
  - Brent A. Lasker,
  - Arnold G. Steigerwalt,
  - Hans P. Hinrikson,
  - and June M. Brown

***Nocardia mikamii* sp. nov., isolated from human pulmonary infections in the USA**

Int J Syst Evol Microbiol October 2010 60:2272-2276; published ahead of print November 13, 2009, doi:10.1099/ijs.0.015594-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Figures and Tables

- ☐ Select this article
  - Syed G. Dastager,
  - Jae-Chan Lee,
  - Ashok Pandey,
  - and Chang-Jin Kim

***Nocardioides mesophilus* sp. nov., isolated from soil**

Int J Syst Evol Microbiol October 2010 60:2288-2292; published ahead of print November 13, 2009, doi:10.1099/ijs.0.019059-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Fig. S1

- ☐ Select this article
  - Nadege Toney,
  - Toidi Adekambi,
  - Sean Toney,
  - Mitchell Yakrus,
  - and W. Ray Butler

Revival and emended description of '*Mycobacterium paraffinicum*' Davis, Chase and Raymond 1956 as *Mycobacterium paraffinicum* sp. nov., nom. rev.

Int J Syst Evol Microbiol October 2010 60:2307-2313; published ahead of print November 13, 2009, doi:10.1099/ijs.0.016972-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Figures

- ☐ Select this article
  - Midori Kurahashi,
  - Yukiyo Fukunaga,
  - Yayoi Sakiyama,
  - Shigeaki Harayama,
  - and Akira Yokota

***Euzebya tangerina* gen. nov., sp. nov., a deeply branching marine actinobacterium isolated from the sea cucumber *Holothuria edulis*, and proposal**

of *Euzebyaceae* fam. nov., *Euzebyales* ord. nov. and *Nitriliruptoridae* subclassis nov.

Int J Syst Evol Microbiol October 2010 60:2314-2319; published ahead of print November 13, 2009, doi:10.1099/ijs.0.016543-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Figure

- ☐ Select this article
  - Puspita Lisdiyanti,
  - Misa Otoguro,
  - Shanti Ratnakomala,
  - Yulin Lestari,
  - Ratih D. Hastuti,
  - Evi Triana,
  - Ando Katsuhiko,
  - and Yantyati Widyastuti

***Actinokineospora baliensis* sp. nov., *Actinokineospora cibodasensis* sp. nov. and *Actinokineospora cianjurensis* sp. nov., isolated from soil and plant litter**

Int J Syst Evol Microbiol October 2010 60:2331-2335; published ahead of print November 20, 2009, doi:10.1099/ijs.0.013276-0

- Abstract
- Full Text
- Full Text (PDF)
- Supplementary Figures

SJR SCImago Journal & Country Rank

EST MODUS IN REBUS

Home
Journal Rankings
Journal Search
Country Rankings
Country Search
Compare
Map Generator
Help
About Us

Show this information in your own website

International Journal of Systematic and Evolutionary Microbiology

Indicator	2006-2013	Value
SJR		0.99
Cites per doc		2.71
Total		4131

Journal Search

Search query

in Journal Title Search

Exact phrase

International Journal of Systematic and Evolutionary Microbiology

Country: United Kingdom

Subject Area: Agricultural and Biological Sciences | Immunology and Microbiology

Subject Category:

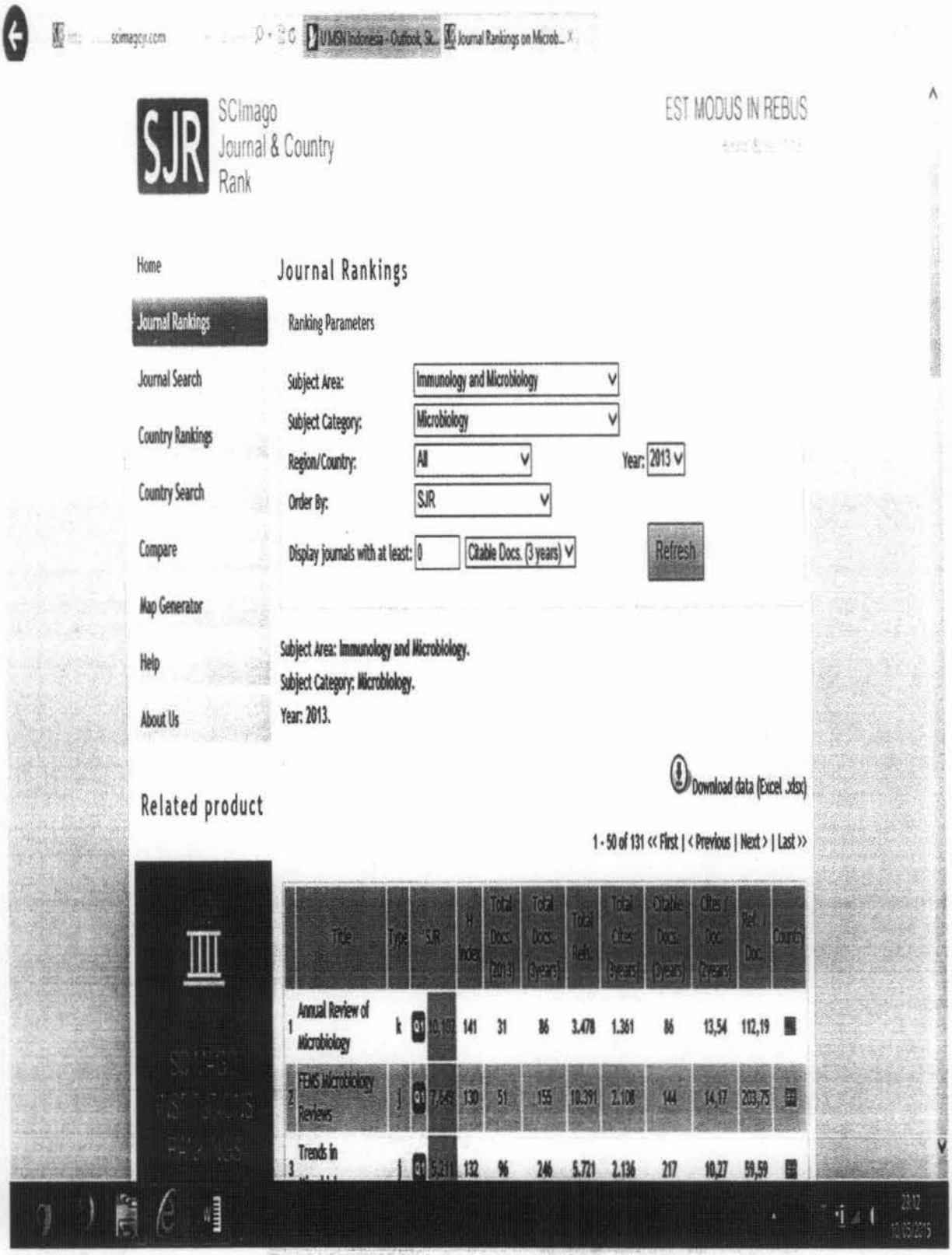
Category	Quartile (Q1 means highest values and Q4 lowest values)														
	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013
Ecology, Evolution, Behavior and Systematics	Q1	Q1	Q1	Q1	Q1	Q1	Q1	Q1	Q2	Q2	Q2	Q2	Q2	Q2	Q2
Microbiology	Q1	Q1	Q1	Q1	Q1	Q1	Q1	Q2	Q2	Q2	Q2	Q2	Q2	Q2	Q2

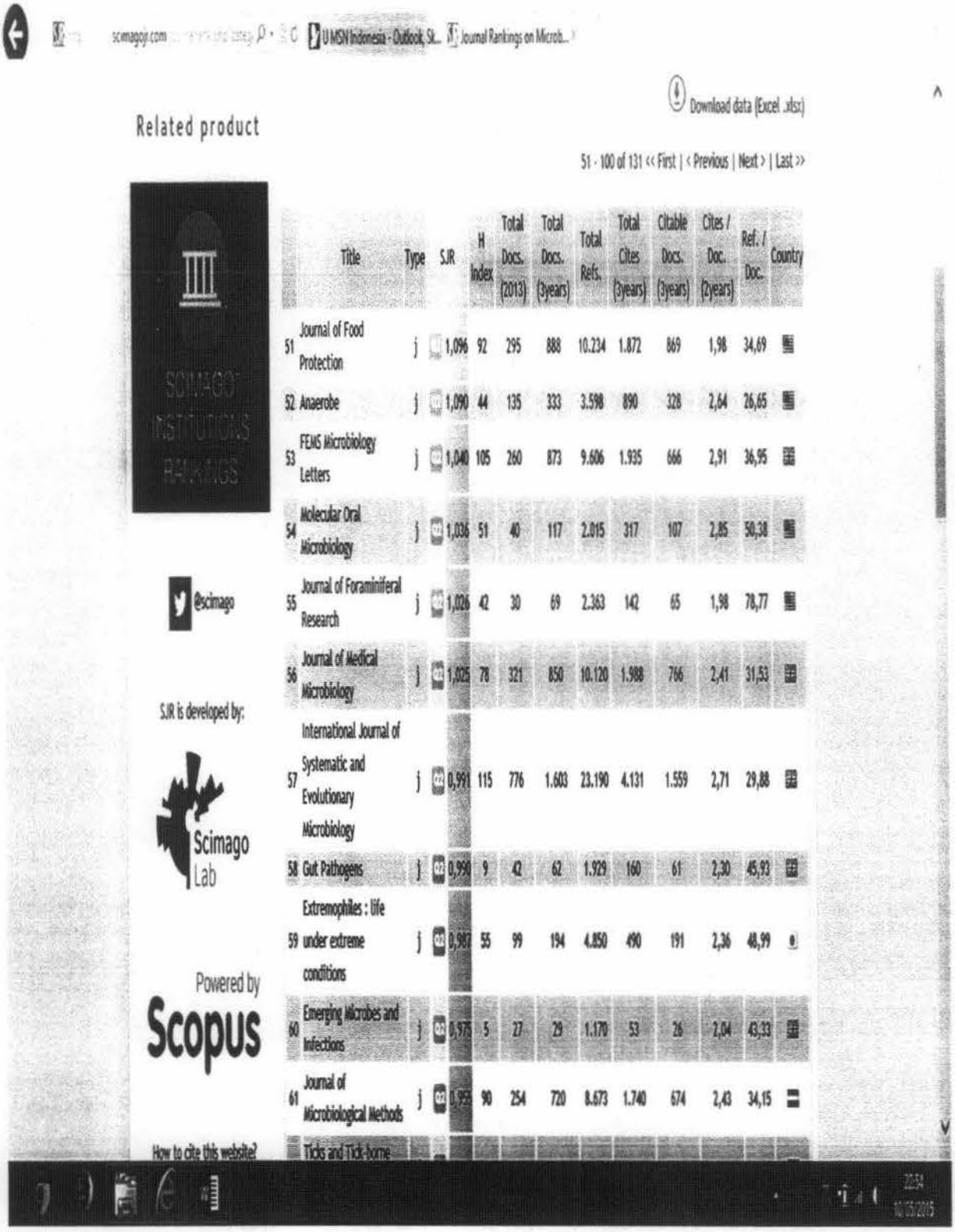
Publisher: Society for General Microbiology. Publication type: Journals. ISSN: 14665026, 14665034

Coverage: 2000-2014

H Index: 115

Scope:


scimagojr.com
U MSN Indonesia - Outlook, Si...
Journal Rankings on Microb...
SJR
SCImago
Journal & Country
Rank
EST MODUS IN REBUS
Home
Journal Rankings
Journal Search
Country Rankings
Country Search
Compare
Map Generator
Help
About Us
Journal Rankings
Ranking Parameters
Subject Area: Immunology and Microbiology
Subject Category: Microbiology
Region/Country: All
Year: 2013
Order By: SJR
Display journals with at least: 0
Citable Docs. (3 years)
Refresh
Subject Area: Immunology and Microbiology.
Subject Category: Microbiology.
Year: 2013.
Download data (Excel .xlsx)
Related product
1 - 50 of 131 « First | ‹ Previous | Next › | Last »
Title
Type
SJR
H Index
Total Docs. (2013)
Total Docs. (3years)
Total Refs.
Total Cites (3years)
Citable Docs. (3years)
Cites / Doc. (2years)
Ref. / Doc.
Country
1 Annual Review of Microbiology
2 FEMS Microbiology Reviews
3 Trends in



scimagojr.com ... MSN Indonesia - Outlook, St... Journal Rankings on Microb...

Download data (Excel .xlsx)

Related product

51 - 100 of 131 << First | < Previous | Next > | Last >>

	Title	Type	SJR	H index	Total Docs. (2013)	Total Docs. (3years)	Total Refs.	Total Cites (3years)	Citable Docs. (3years)	Cites / Doc. (2years)	Ref. / Doc.	Country
51	Journal of Food Protection	j	Q2 1,096	92	295	888	10.234	1.872	869	1,98	34,69	
52	Anaerobe	j	Q2 1,090	44	135	333	3.598	890	328	2,64	26,65	
53	FEMS Microbiology Letters	j	Q2 1,040	105	260	873	9.606	1.935	666	2,91	36,95	
54	Molecular Oral Microbiology	j	Q2 1,036	51	40	117	2.015	317	107	2,85	50,38	
55	Journal of Foraminiferal Research	j	Q2 1,026	42	30	69	2.363	142	65	1,98	78,77	
56	Journal of Medical Microbiology	j	Q2 1,025	78	321	850	10.120	1.988	766	2,41	31,53	
57	International Journal of Systematic and Evolutionary Microbiology	j	Q2 0,991	115	776	1.603	23.190	4.131	1.559	2,71	29,88	
58	Gut Pathogens	j	Q2 0,990	9	42	62	1.929	160	61	2,30	45,93	
59	Extremophiles : life under extreme conditions	j	Q3 0,987	55	99	194	4.850	490	191	2,36	48,99	
60	Emerging Microbes and Infections	j	Q2 0,975	5	27	29	1.170	53	26	2,04	43,33	
61	Journal of Microbiological Methods	j	Q3 0,955	90	254	720	8.673	1.740	674	2,43	34,15	
	Ticks and Tick-borne											

SCIMAGO INSTITUTIONS RANKINGS

@scimago

SJR is developed by:

Scimago Lab

Powered by Scopus

How to cite this website?