Nonomuraea jiangxiensis sp. nov., isolated from acidic soil

Xiaomin Li,^{1,2} Limin Zhang,¹ Yun Ding,^{1,2} Yongsheng Gao,²
Jisheng Ruan¹ and Ying Huang¹

Correspondence

Ying Huang
huangy@im.ac.cn

¹State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, PR China

²College of Land Resources and Environment, Jiangxi Agricultural University, Nanchang 330045, Jiangxi Province, PR China

An actinomycete, designated FXJ1.102^T, was isolated from acidic soil collected in Jiangxi Province, south-east China. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain FXJ1.102^T belonged to the genus *Nonomuraea* and was most closely related to *Nonomuraea candida* HMC10^T, *Nonomuraea turkmeniaca* DSM 43926^T, *Nonomuraea antimicrobica* YIM 61105^T and '*Nonomuraea aegyptia*' S136 (98.9, 98.3, 97.9 and 97.5 % 16S rRNA gene sequence similarities, respectively). The morphological characteristics were typical of the genus *Nonomuraea*. The chemotaxonomic properties, such as cell-wall chemotype IIIB, phospholipid type IV, MK-9(H₄) as the major menaquinone and iso-C_{16:0} (22.2 %) as the major fatty acid, supported the assignment of the strain to the genus *Nonomuraea*. DNA–DNA relatedness and physiological tests allowed genotypic and phenotypic differentiation of strain FXJ1.102^T from its closest phylogenetic relatives. The isolate therefore represents a novel species, for which the name *Nonomuraea jiangxiensis* sp. nov. is proposed. The type strain is FXJ1.102^T (=CGMCC 4.6533^T=NBRC 106679^T).

The genus *Nonomuraea*, the spelling of which was corrected by Chiba *et al.* (1999), was originally proposed by Zhang *et al.* (1998) as a member of the family *Streptosporangiaceae*, which forms extensively branched substrate and aerial mycelia. The type species is *Nonomuraea pusilla*. At the time of writing, the genus *Nonomuraea* comprised 27 species and two subspecies with validly published names (<http://www.bacterio.cict.fr/index.html>), which were established on the basis of a polyphasic approach (Gyobu & Miyadoh, 2001; Stackebrandt *et al.*, 2001; Quintana *et al.*, 2003; Ara *et al.*, 2007a, b; Le Roes & Meyers, 2008; Kämpfer *et al.*, 2010; Wang *et al.*, 2011; Zhao *et al.*, 2011; Xi *et al.*, 2011).

Strain FXJ1.102^T was isolated from acidic soil (pH 5.0) collected from Jiangxi Agricultural University, Nanchang city, Jiangxi Province, China. The sample was dried at room temperature, ground into powder and then suspended in sterile distilled water and serially diluted. The diluted soil suspension was incubated on humic acid-vitamin agar (pH 5.0; Hayakawa & Nonomura, 1987) supplemented with (mg l⁻¹) cycloheximide (50), nystatin (50) and nalidixic acid (20) at 28 °C for 3 weeks. The strain was maintained on

glucose-yeast extract-malt extract agar [International *Streptomyces* Project medium 2 (ISP 2), pH 5.0; Shirling & Gottlieb, 1966] at 4 °C and as suspensions of mycelial fragments in 20 % (v/v) glycerol at –20 °C.

The morphological properties of the isolate were examined by light microscopy (Zeiss Axioskop) and scanning electron microscopy (model FEI Quanta 200) using cultures grown on ISP 2 at 28 °C for 14 days. For cultural characterization, the isolate was grown at 28 °C for 14–21 days on various agar media as described by Waksman (1961) and Shirling & Gottlieb (1966). Growth at pH 4.0–11.0 (at intervals of one pH unit) was determined on Bennett's medium at 28 °C for 14 days. Growth at 4, 10, 15, 20, 28, 37, 45 and 55 °C and with 0–10 % (w/v) NaCl (at intervals of 1 %) at 28 °C was determined on ISP 2 for 14 days. Decomposition of adenine, guanine, arbutin, hypoxanthine, L-tyrosine, xanthine, casein, aesculin, urea and allantoin was evaluated using the media of Gordon *et al.* (1974). Utilization of various compounds as sole carbon sources was tested using ISP 9 as the basal medium, according to the method of Pridham & Gottlieb (1948).

Strain FXJ1.102^T showed good growth on ISP 2, ISP 3, nutrient agar, tryptic soy agar (TSA; Difco, Becton Dickinson) and glucose-asparagine agar, moderate growth on ISP 4, ISP 6 and ISP 7 and poor growth on ISP 5 and Czapek's agar. The isolate produced an ivory to dark yellow substrate mycelium

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain FXJ1.102^T is FJ418910.

Two supplementary figures are available with the online version of this paper.

on various agar media and a white aerial mycelium that differentiated into spiral spore chains on ISP 2, ISP 3 and ISP 4 (Fig. S1, available in IJSEM Online). No soluble pigments were produced on any of the above media. The physiological and biochemical characteristics that serve to distinguish between strain FXJ1.102^T and closely related strains of species of the genus *Nonomuraea* are shown in Table 1.

Biomass for fatty acid analysis was prepared by scraping colonies from TSA plates that had been incubated for 14 days at 28 °C. For other chemotaxonomic analyses, freeze-dried cells were obtained from cultures grown in ISP 2 broth on a rotary shaker at 180–200 r.p.m. and 28 °C for 7 days. The isomer of the diaminopimelic acid and whole cell sugars were determined using standard procedures (Lechevalier & Lechevalier, 1980; Hasegawa *et al.* 1983). Menaquinones were extracted and purified according to the method of Collins (1985) and analysed by HPLC (Kroppenstedt, 1985). Polar lipids were extracted, examined and identified using the two-dimensional TLC procedure described by Minnikin *et al.* (1984). Fatty acids were analysed using the standard MIDI procedure (Sherlock version 6.0; Microbial Identification; Sasser, 1990) and a gas chromatograph (Agilent GC 6890). The fatty acids were identified using the database library TSBA6 version 6.0.

Strain FXJ1.102^T exhibited chemotaxonomic characteristics that are typical for members of the genus *Nonomuraea*, such as the presence of *meso*-diaminopimelic acid in the peptidoglycan and galactose, glucose, mannose, ribose and madurose as whole-cell sugars (cell-wall chemotype IIIB) (Lechevalier & Lechevalier, 1970). The predominant

menaquinone was MK-9(H₄) (72.9 %) and minor amounts of MK-9(H₆) (12.2 %), MK-9(H₂) (10.7 %) and MK-9 (4.2 %) were also present. The detected phospholipids were diphosphatidylglycerol, phosphatidylmethylethanolamine, phosphatidylethanolamine, hydroxy-phosphatidylmethylethanolamine, two unknown glucosamine-containing phospholipids, phosphatidylinositol, phosphatidylglycerol and an unknown phospholipid (Fig. S2), which corresponds to phospholipid type IV (Lechevalier *et al.*, 1977). The detailed fatty acid composition was iso-C_{16:0} (22.2 %), iso-C_{16:1} G (20.4 %), C_{17:1ω6c} (16.6 %), 10-methyl C_{17:0} (7.8 %), iso-C_{15:0} (7.3 %), anteiso-C_{17:0} (4.0 %), 10-methyl C_{16:0} (3.6 %), 10-methyl C_{19:0} (2.9 %), C_{16:1ω7c} (2.6 %), C_{14:0} (2.0 %), C_{17:1ω8c} (1.9 %), C_{16:0} (1.6 %), iso-C_{14:0} (1.5 %), C_{18:0} (0.9 %), C_{15:0} 2-OH (0.9 %), C_{16:0} 2-OH (0.8 %), C_{17:0} (0.6 %), iso-C_{15:0} G (0.6 %), C_{13:0} (0.5 %), iso-C_{17:0} (0.4 %), 10-methyl C_{18:0} (0.4 %), C_{12:0} (0.2 %), anteiso-C_{15:0} (0.2 %), iso-C_{18:0} (0.1 %), anteiso-C_{17:1ω9c} (0.1 %) and C_{18:1ω9c} (0.1 %).

Extraction of genomic DNA and amplification and sequencing of the 16S rRNA gene were carried out using the method of Ara & Kudo (2006). An almost full-length 16S rRNA gene sequence (1486 bp) was aligned with related sequences obtained from public databases using CLUSTAL X version 1.8 (Thompson *et al.*, 1997) and the calculation of pairwise 16S rRNA gene sequence similarities was achieved using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). Neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) trees were constructed using MEGA version 4.0 (Tamura *et al.*, 2007). The reliability

Table 1. Comparison of the phenotypic properties of strain FXJ1.102^T and its closest phylogenetic neighbours

Strains: 1, *Nonomuraea jiangxiensis* sp. nov. FXJ1.102^T; 2, *N. candida* HMC10^T; 3, *N. antimicrobica* YIM 61105^T; 4, '*N. aegyptia*' S136; 5, *N. turkmeniaca* DSM 43926^T; 6, *N. rubra* JCM 3389^T. All data were taken from this study. +, Positive; w, weakly positive; –, negative.

Characteristic	1	2	3	4	5	6
Nitrate reductase	+	–	–	–	+	+
Degradation of:						
Gelatin	–	w	–	–	+	+
Aesculin	+	+	–	–	–	+
Casein	+	+	+	–	+	–
L-Tyrosine	w	–	–	–	–	+
Adenine	–	+	–	–	+	+
Guanine	w	w	–	–	w	–
Hypoxanthine	–	–	–	–	+	+
Utilization as sole carbon source:						
L-Arabinose	+	w	–	+	+	+
<i>meso</i> -Erythritol	–	–	+	w	–	–
<i>myo</i> -Inositol	–	+	–	+	+	+
Cellobiose	+	w	–	+	+	+
Sucrose	–	+	+	+	+	+
Xylose	–	+	–	+	+	+
Ribose	–	+	+	–	–	–
Maximum NaCl concentration for growth (% w/v)	6	5	5	6	7	6
Temperature for growth (°C)	20–45	15–45	15–37	15–37	10–37	10–45

Fig. 1. Neighbour-joining tree based on nearly complete 16S rRNA gene sequences (>1376 bp, without gaps) showing the relationships between strain FXJ1.102^T and the type strains of recognized species of the genus *Nonomuraea*. Bootstrap values (>50 %) based on 1000 resampled datasets are given at branch nodes. Asterisks indicated that the corresponding nodes were also recovered using the maximum-parsimony method. Bar, 0.005 substitutions per nucleotide position.

of the tree topology was evaluated by bootstrap analysis (Felsenstein, 1985).

Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain FXJ1.102^T belonged to the genus *Nonomuraea*. The isolate formed a subcluster with *Nonomuraea antimicrobica* YIM 61105^T and '*Nonomuraea aegyptia*' S136, recovered by both the neighbour-joining and the maximum-parsimony algorithms (Fig. 1), with which it shared 97.9 and 97.5 % 16S rRNA gene sequence similarity, respectively. The isolate also shared high 16S rRNA gene sequence similarity with other members of the cluster to which the subcluster belonged (*Nonomuraea candida* HMC10^T, 98.9 %; *Nonomuraea turkmeniaca* DSM 43926^T, 98.3 %; *Nonomuraea rubra* DSM 43768^T, 98.0 %) and a relatively distant cluster (*Nonomuraea kuesteri* GW 14-1925^T, 98.5 %; *Nonomuraea maheshkhaliensis* 16-5-14^T, 98.1 %).

The DNA G + C content of strain FXJ1.102^T was determined by HPLC and found to be 72.6 mol% (Tamaoka & Komagata, 1984). Using the method described by Rong & Huang (2010), DNA–DNA hybridization was carried out between the isolate and the type strains that were most closely related in terms of both 16S rRNA gene sequence similarity or phylogenetic position, i.e. *N. candida* DSM 45086^T, *N. turkmeniaca* DSM 43926^T, *N. antimicrobica* YIM 61105^T and '*N. aegyptia*' S136. Strain FXJ1.102^T showed low DNA–DNA relatedness with the reference strains (22.4 ± 4.2, 21.0 ± 4.0, 19.4 ± 2.2 and 16.0 ± 2.6 %, respectively).

These values are well below the 70 % cut-off point for assigning strains to the same species (Stackebrandt & Goebel, 1994). Previous studies have shown that members of the genus *Nonomuraea* that exhibit high 16S rRNA gene sequence similarity (ranging from 97.6 to 99.4 %) can exhibit low DNA–DNA relatedness (Fischer *et al.*, 1983; Poschner *et al.*, 1985; Stackebrandt *et al.* 2001; Kämpfer *et al.*, 2005); therefore, DNA–DNA hybridizations were not carried out between strain FXJ1.102^T and other members of the genus *Nonomuraea*.

The morphological, chemotaxonomic and phylogenetic data clearly support the assignment of strain FXJ1.102^T to the genus *Nonomuraea*, but the physiological characters and DNA–DNA relatedness demonstrate that the strain can be differentiated from its closest relatives in the genus *Nonomuraea*. Therefore, on the basis of genotypic and phenotypic evidence, strain FXJ1.102^T represents a novel species of the genus *Nonomuraea*, for which the name *Nonomuraea jiangxiensis* sp. nov. is proposed.

Description of *Nonomuraea jiangxiensis* sp. nov.

Nonomuraea jiangxiensis (ji.ang.xi.en'sis. N.L. fem. adj. *jiangxiensis* of or belonging to Jiangxi Province, south-east China, the source of the type strain).

Substrate mycelium is ivory on ISP 3 and Czapek's agar, dark yellow on ISP 2 and yellow on ISP 4, ISP 5, ISP 6, ISP

7, TSA, nutrient agar and glucose-asparagine agar. White aerial mycelium is produced on ISP 2, ISP 3 and ISP 4. No soluble pigments are produced on any of the above media. The micromorphological characteristics are typical for the genus *Nonomuraea*. Casein, aesculin, allantoin and arbutin are hydrolysed and L-tyrosine and guanine are weakly hydrolysed, but adenine, hypoxanthine, gelatin, starch, xanthine and urea are not hydrolysed. Catalase-positive. Nitrate is reduced. H₂S is not produced. Utilizes L-arabinose, cellobiose, dextrin, D-galactose, D-glucose, glycerol, lactose, maltose, mannitol, D-mannose, melibiose, raffinose, rhamnose, salicin, adonitol and methyl α -D-glucoside as sole carbon sources, but not *myo*-inositol, sucrose, xylose, ribose, D-fructose, trehalose, D-sorbitol or *meso*-erythritol. Grows with up to 6% (w/v) NaCl (optimum 0% NaCl), at pH 5.0–9.0 (optimum pH 6.0) and at 20–45 °C (optimum 25–35 °C). The diagnostic diamino acid of the peptidoglycan is *meso*-diaminopimelic acid. Cell hydrolysates contain madurose, glucose, mannose, ribose and galactose. The polar lipids include diphosphatidylglycerol, phosphatidylmethylethanolamine, phosphatidylethanolamine, hydroxy-phosphatidylmethylethanolamine, two unknown glucosamine-containing phospholipids, phosphatidylinositol, phosphatidylglycerol and an unknown phospholipid. The predominant menaquinone of the type strain is MK-9(H₄). The major fatty acids (>10%) are iso-C_{16:0}, iso-C_{16:1} G and C_{17:1}ω6c.

The type strain, FXJ1.102^T (=CGMCC 4.6533^T=NBRC 106679^T), was isolated from acidic soil in Nanchang city, Jiangxi Province, China. The DNA G+C content of the type strain is 72.6 mol%.

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References

- Ara, I. & Kudo, T. (2006). Three novel species of the genus *Catellatospora*, *Catellatospora chokoriensis* sp. nov., *Catellatospora coxensis* sp. nov. and *Catellatospora bangladeshensis* sp. nov., and transfer of *Catellatospora citrea* subsp. *methionotrophica* Asano and Kawamoto 1988 to *Catellatospora methionotrophica* sp. nov., comb. nov. *Int J Syst Evol Microbiol* **56**, 393–400.
- Ara, I., Kudo, T., Matsumoto, A., Takahashi, Y. & Omura, S. (2007a). *Nonomuraea maheshkhaliensis* sp. nov., a novel actinomycete isolated from mangrove rhizosphere mud. *J Gen Appl Microbiol* **53**, 159–166.
- Ara, I., Kudo, T., Matsumoto, A., Takahashi, Y. & Omura, S. (2007b). *Nonomuraea bangladeshensis* sp. nov. and *Nonomuraea coxensis* sp. nov. *Int J Syst Evol Microbiol* **57**, 1504–1509.
- Chiba, S., Suzuki, M. & Ando, K. (1999). Taxonomic re-evaluation of '*Nocardiopsis*' sp. K-252^T (=NRRL 15532^T): a proposal to transfer this strain to the genus *Nonomuraea* as *Nonomuraea longicatena* sp. nov. *Int J Syst Bacteriol* **49**, 1623–1630.
- Chun, J., Lee, J.-H., Jung, Y., Kim, M., Kim, S., Kim, B. K. & Lim, Y.-W. (2007). EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. *Int J Syst Evol Microbiol* **57**, 2259–2261.
- Collins, M. D. (1985). Isoprenoid quinone analysis in classification and identification. In *Chemical Methods in Bacterial Systematics*, pp. 267–287. Edited by M. Goodfellow & D. E. Minnikin. London: Academic Press.
- Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* **39**, 783–789.
- Fischer, A., Kroppenstedt, R. M. & Stackebrandt, E. (1983). Molecular-genetic and chemotaxonomic studies on *Actinomadura* and *Nocardiopsis*. *J Gen Microbiol* **129**, 3433–3446.
- Fitch, W. M. (1971). Toward defining the course of evolution: minimum change for a specific tree topology. *Syst Zool* **20**, 406–416.
- Gordon, R. E., Barnett, D. A., Handerhan, J. E. & Pang, C. H.-N. (1974). *Nocardia coeliaca*, *Nocardia autotrophica*, and the nocardin strain. *Int J Syst Bacteriol* **24**, 54–63.
- Gyobu, Y. & Miyadoh, S. (2001). Proposal to transfer *Actinomadura carminata* to a new subspecies of the genus *Nonomuraea* as *Nonomuraea roseoviolacea* subsp. *carminata* comb. nov. *Int J Syst Evol Microbiol* **51**, 881–889.
- Hasegawa, T., Takizawa, M. & Tanida, S. (1983). A rapid analysis for chemical grouping of aerobic actinomycetes. *J Gen Microbiol* **29**, 319–322.
- Hayakawa, M. & Nonomura, H. (1987). Humic acid-vitamin agar, a new medium for selective isolation of soil actinomycetes. *J Ferment Technol* **65**, 501–509.
- Kämpfer, P., Kroppenstedt, R. M. & Grün-Wollny, I. (2005). *Nonomuraea kuesteri* sp. nov. *Int J Syst Evol Microbiol* **55**, 847–851.
- Kämpfer, P., Busse, H. J., Tindall, B. J., Nimtz, M. & Grün-Wollny, I. (2010). *Nonomuraea rosea* sp. nov. *Int J Syst Evol Microbiol* **60**, 1118–1124.
- Kroppenstedt, R. M. (1985). Fatty acid and menaquinone analysis of actinomycetes and related organisms. In *Chemical Methods in Bacterial Systematics* (Society for Applied Bacteriology Technical Series vol. 20), pp. 173–199. Edited by M. Goodfellow & D. E. Minnikin. New York: Academic Press.
- Le Roes, M. & Meyers, P. R. (2008). *Nonomuraea candida* sp. nov., a new species from South African soil. *Antonie van Leeuwenhoek* **93**, 133–139.
- 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. & Lechevalier, H. A. (1980). The chemotaxonomy of actinomycetes. In *Actinomycete Taxonomy* (Special Publication no. 6), pp. 227–291. Edited by A. Dietz & J. Thayer. Arlington, VA: Society for Industrial Microbiology.
- Lechevalier, M. P., De Bièvre, C. & Lechevalier, H. A. (1977). Chemotaxonomy of aerobic actinomycetes: phospholipid composition. *Biochem Syst Ecol* **5**, 249–260.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, K. & Parlett, J. H. (1984). An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Poschner, J., Kroppenstedt, R. M., Fischer, A. & Stackebrandt, E. (1985). DNA–DNA reassociation and chemotaxonomic studies on *Actinomadura*, *Microbispora*, *Microtetraspora*, *Micropolyspora* and *Nocardiopsis*. *Syst Appl Microbiol* **6**, 264–270.
- Pridham, T. G. & Gottlieb, D. (1948). The utilization of carbon compounds by some *Actinomycetales* as an aid for species determination. *J Bacteriol* **56**, 107–114.

- Quintana, E., Maldonado, L. & Goodfellow, M. (2003). *Nonomuraea terrinata* sp. nov., a novel soil actinomycete. *Antonie van Leeuwenhoek* **84**, 1–6.
- Rong, X. & Huang, Y. (2010). Taxonomic evaluation of the *Streptomyces griseus* clade using multilocus sequence analysis and DNA–DNA hybridization, with proposal to combine 29 species and three subspecies as 11 genomic species. *Int J Syst Evol Microbiol* **60**, 696–703.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Sasser, M. (1990). *Identification of bacteria by gas chromatography of cellular fatty acids*, MIDI Technical Note 101. Newark, DE: MIDI Inc.
- Shirling, E. B. & Gottlieb, D. (1966). Methods for characterization of *Streptomyces* species. *Int J Syst Bacteriol* **16**, 313–340.
- Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA–DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.
- Stackebrandt, E., Wink, J., Steiner, U. & Kroppenstedt, R. M. (2001). *Nonomuraea dietzii* sp. nov. *Int J Syst Evol Microbiol* **51**, 1437–1441.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reversed-phase high-performance liquid chromatography. *FEMS Microbiol Lett* **25**, 125–128.
- 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.
- Waksman, S. A. (1961). *The Actinomycetes*, vol. 2. Baltimore: Williams & Wilkins.
- Wang, F., Xu, X.-X., Qu, Z., Wang, C., Lin, H.-P., Xie, Q.-Y., Ruan, J.-S., Sun, M. & Hong, K. (2011). *Nonomuraea wenchangensis* sp. nov., isolated from mangrove rhizosphere soil. *Int J Syst Evol Microbiol* **61**, 1304–1308.
- Xi, L., Zhang, L., Ruan, J. & Huang, Y. (2011). *Nonomuraea maritima* sp. nov., isolated from coastal sediment. *Int J Syst Evol Microbiol* **61**, 2740–2744.
- Zhang, Z., Wang, Y. & Ruan, J. (1998). Reclassification of *Thermomonospora* and *Microtetraspora*. *Int J Syst Bacteriol* **48**, 411–422.
- Zhao, G.-Z., Li, J., Huang, H.-Y., Zhu, W.-Y., Xu, L.-H. & Li, W.-J. (2011). *Nonomuraea rhizophila* sp. nov., an actinomycete isolated from rhizosphere soil. *Int J Syst Evol Microbiol* **61**, 2141–2145.