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Mesorhizobium waimense sp. nov. isolated from *Sophora longicarinata* root nodules and *Mesorhizobium cantuariense* sp. nov. isolated from *Sophora microphylla* root nodules in New Zealand

Sofie E. De Meyer[a,b*], Heng Wee Tan[c], Peter B. Heenan[d], Mitchell Andrews[c] and Anne Willems[b]

[a] Centre for *Rhizobium* Studies, Murdoch University, Western Australia 6150, Australia

[b] Laboratory of Microbiology, Dept. Biochemistry and Microbiology, Ghent University, K.L. Ledeganckstraat 35, B-9000 Ghent, Belgium

[c] Faculty of Agriculture and Life Sciences, Lincoln University, Lincoln 7647, New Zealand

[d] Allan Herbarium, Landcare Research, Lincoln 7640, New Zealand

*Corresponding author: Sofie De Meyer, Centre for *Rhizobium* Studies, Murdoch University, Western Australia 6150, Australia. Tel: +61893602439, Fax: +61893107084, E-mail: Sofdemey@outlook.com

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA, *glnII*, *recA* and *rpoB* gene sequences reported in this paper are respectively for *Mesorhizobium waimense* sp. nov. ICMP 19557^T: KC237387, KC237613, KC237667 and KJ450929, and for *Mesorhizobium cantuariense* sp. nov. ICMP 19515^T: KC237397, KC237624, KC237677 and KJ450941. Accession numbers for the remaining strains can be found in Table S1.

Abstract

In total 14 strains of gram-negative, rod-shaped bacteria were isolated from *Sophora longicarinata* and *Sophora microphylla* root nodules and authenticated as rhizobia on these hosts. Based on the 16S rRNA gene phylogeny, they were shown to belong to the genus *Mesorhizobium*, and the *S. longicarinata* strains were most closely related to *Mesorhizobium amorphae* ACCC 19665^{T} (99.8 – 99.9%), *Mesorhizobium huakuii* IAM 14158^{T} (99.8 – 99.9%), *Mesorhizobium loti* USDA 3471^{T} (99.5 – 99.9%) and *Mesorhizobium septentrionale* SDW 014^{T} (99.6 – 99.8%), whilst the *S. microphylla* strains were most closely related to *Mesorhizobium ciceri* UPM-Ca7^{T} (99.8 – 99.9%), *Mesorhizobium qingshengii* CCBAU 33460^{T} (99.7%) and *Mesorhizobium shangrilense* CCBAU 65327^{T} (99.6%). Additionally, these strains formed two distinct groups in phylogenetic trees of the housekeeping genes *glnII*, *recA* and *rpoB*. Chemotaxonomic data, including fatty acid profiles supported the assignment of our strains to the genus *Mesorhizobium* and allowed differentiation from the closest neighbours. Results of DNA-DNA hybridisations, MALDI-TOF MS analysis, ERIC-PCR, physiological and biochemical tests allowed genotypic and phenotypic differentiation of our strains from their nearest neighbouring species. Therefore, the *S. longicarinata* and *S. microphylla* strains represent two novel species for which the names *Mesorhizobium waimense* sp. nov. (ICMP 19557^{T} = LMG 28228^{T} = HAMBI 3608^{T}) and *Mesorhizobium cantuariense* sp. nov. (ICMP 19515^{T} = LMG 28225^{T} = HAMBI 3604^{T}), are proposed respectively.

New Zealand (NZ) *Sophora* species (tribe *Sophoreae* in the *Fabaceae* plant family) are woody trees and shrubs that occur in a variety of habitats (Heenan *et al.*, 2001; Heenan *et al.*, 2004). The most recent taxonomic revision of New Zealand *Sophora* recognized eight endemic species: *S. chathamica, S. fulvida, S. godleyi, S. longicarinata, S. microphylla, S. molloyi, S. prostrata* and *S. tetraptera* (Heenan *et al*., 2001). *S. longicarinata* is an upright small tree with multiple trunks and main branches or densely branched shrub, characterized by numerous and small leaflets that are distant from each other, uniform in size, dark green, glabrous or with a few appressed hairs, and with distinct petiolules (Heenan *et al.*, 2001). This species is geographically restricted to the northern South Island (Nelson and Marlborough) and is a basicole, predominantly occurring on eroding and unstable bluffs, rock outcrops, and hill slopes derived from marble and limestone (Heenan *et al.*, 2001). *Sophora microphylla,* also known as small-leaved kowhai (tribe *Sophoreae*), contains trees up to 25 m high with distant leaflets, a moderate number of appressed leaf hairs, and a distinct divaricating and/or strongly flexuose juvenile phase (Heenan *et al.*, 2001; Heenan *et al.*, 2004). *S. microphylla* occurs throughout the North and South Island, and is predominantly an inland species. It most commonly grows on alluvial river terraces, flood plains, lake margins, and on hill slopes among loose and rubbly rock (Heenan *et al.*, 2001).

Previous studies investigating the nitrogen fixing symbionts of *Sophora* species have revealed the presence of *Mesorhizobium* root nodule endosymbionts (Weir *et al.*, 2004). However, only a limited number of bacterial isolates were investigated. As part of a continuing study on native New Zealand legumes, and their associated rhizobia, forty-eight strains were isolated from surface sterilized root nodules of *Sophora* species sampled in natural ecosystems. Sequence analysis showed that all isolates belonged to the genus *Mesorhizobium* and that they grouped in seven different clusters (Tan *et al.*, 2015). In the present study eight strains originating from *S. longicarinata* root nodules collected from plants growing on limestone alluvium at Waima River, Marlborough and six strains originating from *S. microphylla* root nodules collected in Canterbury (Tan *et al.*, 2015), were selected for further investigation using a polyphasic approach. Strain ICMP 19557^{T} and ICMP 19515^{T} have been deposited in the BCCM/LMG bacteria collection (http://www.belspo.be/bccm) and the HAMBI Culture Collection, University of Helsinki, Finland (http://www.helsinki.fi/hambi/). All strains were subcultured on Yeast Manitol Agar (YMA) medium (Vincent, 1970) at 28 °C unless

otherwise indicated. For PCR, genomic DNA of all isolates was prepared using the standard Qiagen-Gentra PUREGENE DNA Purification Kit as described previously (Tan *et al.*, 2015).

The ERIC-PCR fingerprints were obtained as described previously (Versalovic *et al.*, 1994) and analysed using the Phoretix 1D Pro v12.2 software package (Phoretix Ltd, UK). The similarity among the digitised profiles was calculated using the Dice coefficient (Dice, 1945) and an unweighted pair group using arithmetic averages (UPGMA) dendrogram was derived from the similarity matrix. The Dice coefficient is used as a general measure of similarity (if two lanes are identical, Distance (D) = 0 and if two lanes are totally different, Distance (D) =1) but gives more weight to matching bands. Figure S1a and b show the ERIC-PCR fingerprints of the *S. longicarinata* and *S. microphylla Mesorhizobium* isolates, respectively. The DNA fingerprints suggest that all *S. longicarinata* and *S. microphylla* strains representing two novel species form two separate cluster that could be distinguished from their closest neighbours (Fig. S1a and b). Matrix-Assisted Laser Desorption/Ionization Time-of-Flight mass spectrometry (MALDI-TOF MS) was performed as described previously (Wieme *et al.*, 2012). All conditions were exactly as previously described except that YMA growth medium was used to culture the strains prior to protein extraction (Wieme *et al.*, 2012). The MALDI-TOF MS profiles indicate that the isolates represent different strains that can be distinguished from the closest neighbours (Fig. S2a and b).

Nearly full-length amplicons for the 16S rRNA gene were obtained for all strains using the primers and conditions described previously by Tan *et al*. (2015). The resulting 16S rRNA gene sequences were aligned using the MEGA 5 software package and phylogenetic trees were constructed with the Maximum Likelihood (ML) method and Neighbor Joining (NJ) method / Kimura 2 parameter model with G substitutions (Tamura *et al.*, 2011). Bootstrap analysis with 500 replicate data sets was performed to assess the support of the clusters. The overall topologies of the phylogenetic trees obtained with the ML and NJ methods were similar (data not shown). Our strains formed two novel branches within the *Mesorhizobium* genus (Fig. 1), and group 1 containing strain ICMP 19557^{T} shared sequence similarities of 99.8 – 99.9% with *Mesorhizobium amorphae* ACCC 19665^{T}, 99.8 – 99.9% with *Mesorhizobium huakuii* IAM 14158^{T}, 99.5 – 99.9% with *Mesorhizobium loti* USDA 3471^{T} and 99.6 – 99.8% with *Mesorhizobium septentrionale* SDW 014^{T}, and group 2 containing strain ICMP 19515^{T} shared sequence similarities of 99.8 – 99.9% with *Mesorhizobium ciceri*

UPM-Ca7^T, 99.7% with *Mesorhizobium qingshengii* CCBAU 33460^T, 99.6% with *Mesorhizobium shangrilense* CCBAU 65327^T, as determined with the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net/, Kim *et al.*, 2012). G*lnII* [336 bp], *recA* [381 bp] and *rpoB* [840 bp] gene sequence analysis was based on the method described by Tan *et al.* (2015) and the sequences are deposited in NCBI (Accession numbers in Table S1). The gene sequences were aligned using the MEGA 5 software package (Tamura *et al.*, 2011) and phylogenetic trees were constructed using the ML method, with the Tamura-3-parameter model and G substitutions. Bootstrap analysis with 500 replicates was performed to assess the support of the clusters. Congruence between the different gene sequences was investigated using the partition homogeneity tests (Farris *et al.*, 1994) performed with PAUP software v. 4.0b10 (Swofford, 1991). Congruence ($p > 0.01$) was found between all investigated genes and subsequent concatenation using the software SeaView v. 4.4.3 was performed (Gouy *et al.*, 2010). The phylogenetic tree based on the concatenated *glnII*, *recA* and *rpoB* gene sequences of our strains (Fig. 2) revealed two monophyletic clusters supported by high bootstrap values (99.9% – 100%). Levels of gene sequence similarity between group 1 containing strain ICMP 19557^T and the closest neighbour *M. septentrionale* SDW 014^T was 94.7% for *glnII,* 94.5 – 96.8% for *recA* and 97.6% for *rpoB;* and with *M. amorphae* ACCC 19665^T, 94.8% for *glnII,* 95.4 – 95.7% for *recA* and 97.3 - 97.4% for *rpoB.* Levels of gene sequence similarity between group 2 containing strain ICMP 19515^T and the closest neighbour *M. ciceri* UPM-Ca7^T was 95.9 – 96.0% for *glnII,* 96.6 – 96.8% for *recA* and 97.2% for *rpoB;* and with *M. loti* LMG 6125^T, 89.8 – 89.9% for *glnII,* 96.6 – 96.7% for *recA* and 96.5% for *rpoB.*

Phenotypic analysis was performed with cells grown on YMA medium at 28 °C unless otherwise indicated. Cells were Gram stained (Vincent, 1970). Cell morphology and motility were observed by phase contrast microscopy. Oxidase activity was detected by immersion of cells in 1% N,N,N′,N′-tetramethyl-p-phenylenediamine solution and catalase activity was determined by flooding a colony with 10% H_2O_2 and checking for the presence of bubbles. Biochemical tests were performed by inoculating API 20NE and API 20E strips (BioMérieux) and Biolog GENIII MicroPlates™ (Biolog Inc, CA, USA), according to the manufacturer's instructions. GENIII MicroPlates™ were read using the MicroStation™ ID System reader (Biolog Inc, CA, USA). Growth was tested at 28 °C in Yeast Mannitol broth with 1% to 8% NaCl and with pH4 - pH9, buffered with acetic acid/sodium acetate (pH4 - 5), citric acid/Na_2HPO_4 (pH6 - 7), NaH_2PO_4/Na_2HPO_4 (pH8) or Tris/HCl (pH9). Growth on YMA

medium was tested at 4, 7, 15, 20, 25, 28, 30 and 37 °C. Colonies were visible after 48 h growth at 15 – 30 °C on YMA medium. The results of the phenotypic and biochemical tests are given in Table 1 and supplementary Table S2a and b. Most notably for group 1 containing strain ICMP 19557^{T}, Biolog GENIII MicroPlates™ carbon source utilisation positive reactions were recorded for N-Acetyl-Beta-D-Mannosamine, 3-Methyl glucose, citric acid and methyl pyruvate; negative reactions for L-serine and weak positive reactions for pectine. For group 2 containing strain ICMP 19515^{T} positive reactions were recorded for D-saccharic acid and propionic acid; weak positive reactions for citric acid, D-lactic acid methyl ester, methyl pyruvate, alpha-D-lactose, glucuronamide and pectine; and negative reactions for stachyose, N-acetyl neuronimic acid and formic acid. Additional antibiotic susceptibility tests were performed on YMA medium using the antibiotic Sensi-disc dispenser system (Oxoid) with bio-discs (Oxoid) containing ampicillin (10 µg), chloramphenicol (30 µg), erythromycin (15 µg), gentamycin (10 µg), kanamycin (30 µg), and streptomycin (25 µg). All strains were grown on YMA for 72 h prior to testing. The plates were incubated at 28°C and read between two and seven days. All strains from group 1 were resistant to erythromycin, and sensitive to ampicillin, chloramphenicol, gentamycin and streptomycin; all strains from group 2 were resistant to chloramphenicol, erythromycin and kanamycin, and sensitive to gentamycin and streptomycin.

The whole-cell fatty acid composition was analysed and the fatty acid methyl esters were extracted from cells grown on YMA medium according to the MIDI protocol (http://www.microbialid.com/PDF/TechNote_101.pdf). All characteristics such as temperature and physiological age (overlap area of the second and third quadrant from a quadrant streak) were as in the MIDI protocol. The profiles were generated using an Agilent Technologies 6890N gas chromatograph (Santa Clara, CA USA), identified and clustered using the Microbial Identification System software and MIDI TSBA database version 5.0. Fatty acid profiles are listed in Table 2. The most abundant fatty acids for our strains were $C_{18:1}$ ω7c (58.9 – 51.4%), $C_{16:0}$ (26.8 – 15.7%) and $C_{19:0}$ CYCLO ω8c (15.3 – 4.4%) for group 1 and $C_{18:1}$ ω7c (37.1 – 44.2%), $C_{16:0}$ (16.6 – 21.4%) and $C_{19:0}$ CYCLO ω8c (14.2 – 18.9%) for group 2. All strains lacked $C_{20:3}$ ω6,9,12cis which is characteristic for *Mesorhizobium* species (Tighe *et al.*, 2000). Additionally, there were noticeable differences between the fatty acid profiles of our strains and most closely related *Mesorhizobium* type strains (Table 2).

For DNA-DNA hybridization and for the determination of the DNA G+C content, high-molecular weight DNA was prepared as described by Pitcher *et al*. (1989). DNA-DNA hybridizations were performed using a microplate method and biotinylated probe DNA (Ezaki *et al.*, 1989). As described previously, the DNA hybridisation values of ICMP 19557^T and ICMP 19515^T were 28.8% and 32.3%, respectively with *M. septentrionale* LMG 23930^T, and 29.2% and 28.9% with *M. ciceri* LMG 14989^T (Tan *et al.*, 2015). The G+C content of the DNA was determined by HPLC according to the method of Mesbah *et al.* (1989) using a Waters Breeze HPLC system and XBridge Shield RP18 column thermostabilised at 37°C. The solvent was 0.02 M $NH_4H_2PO_4$ (pH 4.0) with 1.5% (v/v) acetonitrile. Non-methylated lambda phage (Sigma) and *E. coli* DNA were used as calibration reference and control, respectively. The DNA G+C content of ICMP 19557^T and ICMP 19515^T was 62.6 mol% and 62.5 mol% (Table 1), respectively, which is within the range reported for *Mesorhizobium* (59 - 64 mol%) (Jarvis *et al.*, 1997).

The nodulation and nitrogen fixation capacity of all strains was previously studied on their original host (*S. longicarinata* or *S. microphylla*) and a selection of strains was also tested on additional *Sophora* species, *Carmichaelia australis* and *Clianthus puniceus*, using the sterile jar system described by Tan *et al.*(2015). These results confirmed that all strains could form effective N_2-fixing symbioses with their original host (Tan *et al.*, 2015). Strains ICMP 19557^T, ICMP 19558, ICMP 19568, ICMP 19569, ICMP 19515^T and ICMP 19514 were also able to effectively nodulate *S. microphylla*, *S. prostrata* and *Cl. puniceus*. Strain ICMP 19567 however was able to effectively nodulate *S. microphylla* and *S. prostrata*, and ineffectively with *Cl. puniceus* and *C. australis* (Tan *et al.*, 2015).

The genotypic and phenotypic data presented in this study demonstrate that the eight strains isolated from New Zealand native *Sophora longicarinata* root nodules form a novel species and the six strains isolated from New Zealand native *Sophora microphylla* root nodules form a second novel species in the genus *Mesorhizobium*. Therefore we propose to classify the strains as *Mesorhizobium waimense* sp. nov. (ICMP 19557^T = LMG 28228^T = HAMBI 3608^T) and *Mesorhizobium cantuariense* sp. nov. (ICMP 19515^T = LMG 28225^T = HAMBI 3604^T), respectively.

Description of *Mesorhizobium waimense* sp. nov.

Mesorhizobium waimense (wai.men.se. N.L. gen. n. *waima*, of Waima river, referring to the vicinity of the river where the nodules were collected and this species was first isolated from.)

Cells are rod shaped (approx. 0.4 – 0.6 x 1.0 – 2.0 µm), gram-negative, catalase positive and oxidase negative. Colonies are white, smooth, round, diameter 0.1 – 0.5 mm and convex with entire margins on YMA medium after 72 h. Growth occurs on YMA medium between 15 °C and 30 °C but not at 4, 7 and 37 °C. Growth was visible in YMB medium with 1 – 8% NaCl and pH 5 – 8 at 28 °C. Detailed phenotypic and biochemical information can be found in Table 1 and Table S2. This species is sensitive to ampicillin, chloramphenicol, gentamycin and streptomycin, and resistant to erythromycin. The whole-cell fatty acids profile is given in Table 2. The DNA G+C content of the type strain is 62.6 mol%. The type strain ICMP 19557^{T} (= LMG 28228^{T} = HAMBI 3608^{T}) was isolated from root nodules of *Sophora longicarinata* from alluvial limestone river terrace, Waima/Ure River, Marlborough, New Zealand.

Description of *Mesorhizobium cantuariense* sp. nov.

Mesorhizobium cantuariense (can.tu. ar'i.ense. N.L. neut. adj. *cantuariense*, of Canterbury, referring to the place this species was first isolated from.)

Cells are rod shaped (approx. 0.5 – 0.8 x 1 – 2 µm), gram-negative, catalase positive and oxidase negative. Colonies are light cream/white, smooth, round, diameter 0.2 – 0.8 mm and convex with entire margins on YMA medium after 72 h. Growth occurs on YMA medium between 15 °C and 30 °C but not at 4, 7 and 37 °C. Growth was visible in YMB medium with 1 – 8% NaCl and pH 4 – 9 at 28 °C. Detailed phenotypic and biochemical information can be found in table 1 and table S2. This species is sensitive to gentamycin and streptomycin, and resistant to chloramphenicol, erythromycin and kanamycin. The whole-cell fatty acids profile is given in table 2. The DNA G+C content of the type strain is 62.5 mol%. The type strain ICMP 19515^{T} (= LMG 28225^{T} = HAMBI 3604^{T}) was isolated from root nodules of *Sophora microphylla* from alluvial Greywacke river terrace, upper Rakaia River, Canterbury, New Zealand.

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Legends to figures

Fig. 1: Maximum likelihood tree based on almost complete 16S rRNA gene sequences (approx. 1265bp) of the novel *Mesorhizobium* strains and phylogenetically related species. Bootstrap values after 500 replicates are expressed as percentages, values less than 50% are not shown. *Bradyrhizobium elkanii* USDA 76^T is included as outgroup. The scale bar indicates the fraction of substitutions per site.

Fig. 2: Maximum likelihood tree based on the concatenated *glnII, recA* and *rpoB* gene sequences (approx. 1557bp) of the novel *Mesorhizobium* strains and phylogenetically related species. Bootstrap values after 500 replicates are expressed as percentages, values less than 50% are not shown. *Bradyrhizobium elkanii* USDA 76^T is included as outgroup. The scale bar indicates the fraction of substitutions per site. Gene accession numbers are shown in table S1.

Table 1. Phenotypic characteristics distinguishing our novel *Mesorhizobium* species from other *Mesorhizobium* species. Strains: 1, *M. waimense* (n = 3); 2, *M. cantuariense* (n = 2); 3, *M. ciceri* LMG 14989^{T}; 4, *M. septentrionale* LMG 23930^{T}. +, Positive reaction; +^{W}, weak reaction; -, negative reaction, R, Resistant; I, Intermediate; S, Sensitive. Data taken from $^{\$}$Nour *et al.* (1994) and §Gao *et al.* (2004).

Characteristic	**1**	**2**	**3**	**4**
Carbohydrate utilisation				
N-Acetyl-Beta-D-Mannosamine	+	+	+	+^{W}
N-Acetyl-Beta-D-Galactosamine	+^{W}	+	+	+^{W}
3-Methyl Glucose	+	+	+	-
Pectine	+^{W}	+^{W}	+	+
D-Salicin	+^{W}	+^{W}	+	+^{W}
Stachyose	-	-	+^{W}	-
Carboxylic acid utilisation				
N-Acetyl Neuraminic acid	-	-	+^{W}	-
Citric acid	+	+^{W}	+	+^{W}
Formic acid	-	-	+	-
Propionic acid	+	+	-	+
Amide utilisation				
Glucuronamide	+^{W}	+^{W}	+	+^{W}
Amino acid utilisation				
Alpha-Hydroxy-Butyric acid	-	-	+	-
Alpha-Keto-Butyric acid	-	+^{W}	+^{W}	-
L-Serine	-	-	-	+^{W}
Chemical sensitivity				
Troleandomycin	R	R	R	I
Vancomycin	I	I	R	S
Sodium Lactate (1%)	R	R	R	S
Potassium Tellurite	S	I	R	S
Ester utilisation				
Methyl Pyruvate	+	+^{W}	+	+^{W}
D-Lactic Acid Methyl Ester	+^{W}	+^{W}	+	+^{W}
%GC	62.6	62.5	63.0$^{\$}$	59.4§

Table 2. Fatty acid composition of the *Mesorhizobium* strains investigated in this study. All values are given as a percentage of the total composition. SF3 = 16:1 ω7c/15 iso 2OH, N.D. = Not Detected, TR: Trace amounts (= values lower than 1%). All strains were grown on YMA medium prior to extraction.

Strain	11 methyl 18:1 w7c	12:0 3OH	13:0 ISO 3OH	14:00	15:0 ISO	16:00	17:00	17:0 CYCLO	17:0 ISO	17:1 w8c	18:00	18:1 w7c	19:0 10 methyl	19:0 CYCLO w8c	20:1 w7c	SF 3
M. waimense																
ICMP 19557^{T}	2.7	1.9	2.6	N.D.	1.3	16.2	N.D.	1.1	1.2	N.D.	2.0	55.3	5.2	5.6	N.D.	3.8
ICMP 19558	2.5	2.1	1.9	N.D.	TR	16.5	N.D.	N.D.	1	N.D.	TR	58.9	5.9	4.4	N.D.	3.8
ICMP 19564	3.3	1.7	1.5	N.D.	1.3	17.3	N.D.	1.5	1.4	N.D.	2.0	51.4	4.5	9.7	N.D.	4.5
ICMP 19565	2.8	1.3	1.6	N.D.	1.2	16.5	N.D.	N.D.	1.8	N.D.	1.3	56.9	2.6	11.0	N.D.	3.0
ICMP 19566	2.6	2.5	3.6	N.D.	2.0	19.5	N.D.	N.D.	N.D.	N.D.	N.D.	52.0	3.9	9.7	N.D.	4.4
ICMP 19567	N.D.	N.D.	N.D.	N.D.	N.D.	26.8	N.D.	N.D.	N.D.	N.D.	N.D.	57.9	N.D.	15.3	N.D.	N.D.
ICMP 19568	3.0	1.3	2.0	N.D.	TR	16.2	N.D.	1.3	1.4	N.D.	2.0	51.7	3.2	13.4	N.D.	2.6
ICMP 19569	3.1	1.5	1.7	N.D.	1.1	15.7	N.D.	1.1	1.4	N.D.	1.3	55.7	4.3	10.4	N.D.	2.7
M. cantuariense																
ICMP 19514	9.7	TR	TR	TR	TR	17.2	TR	2.3	2.0	TR	1.1	44.2	1.3	14.2	TR	3.6
ICMP 19515^{T}	10.8	TR	TR	TR	1.1	18.0	TR	2.6	2.2	TR	1.3	37.1	1.1	17.5	TR	4.6
ICMP 19516	11.4	N.D.	N.D.	N.D.	1.2	17.7	N.D.	2.7	2.4	TR	1.2	39.2	1.0	17.7	N.D.	4.8
ICMP 19518	12.1	TR	TR	TR	TR	16.6	TR	2.3	2.2	TR	1.2	39.3	1.3	18.6	TR	2.9
ICMP 19551	9.9	N.D.	N.D.	N.D.	N.D.	21.4	N.D.	N.D.	N.D.	N.D.	N.D.	42.7	N.D.	18.9	N.D.	7.1
M. ciceri																
LMG 14989^{T}	9.3	N.D.	N.D.		N.D.	15.9		N.D.	N.D.		N.D.	74.8	N.D.	N.D.		N.D.
M. septentrionale																
LMG 23930^{T}	4.7	N.D.	N.D.		N.D.	14.6		N.D.	5.3		N.D.	38.6	N.D.	36.8		N.D.