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## Genome sequence and description of *Urinicoccus timonensis* gen. nov., sp. nov., a new bacterium isolated from a human stool sample

M. L. Tall, C. I. Lo, E. Kuete Yimagou, A. Fontanini, J. Delerce, P. -E. Fournier, D. Raoult, F. Fenollar, A. Levasseur

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1       **Genome sequence and description of *Urinicoccus timonensis* gen. nov., sp. nov., a new**  
2                               **bacterium isolated from a human stool sample**

3  
4       Mamadou Lamine TALL<sup>1,2</sup>, Cheikh Ibrahima LO<sup>1,3</sup>, Edmond KUETE YIMAGOU<sup>1,2</sup>,  
5       Anthony FONTANINI<sup>2</sup>, Jeremy DELERCE<sup>1,2</sup>, Pierre-Edouard FOURNIER<sup>1,2</sup>, Didier  
6       RAOULT<sup>1,2</sup>, Florence FENOLLAR<sup>1,3</sup>, Anthony LEVASSEUR<sup>1,2,4,\*</sup>

7  
8       <sup>1</sup> Aix-Marseille Université, UMR MEPHI (Microbes, Evolution, Phylogeny and Infections),  
9       IRD, APHM, Faculté de Médecine, Marseille 13005, France.

10      <sup>2</sup> IHU-Méditerranée Infection, Marseille, France.

11      <sup>3</sup> Aix Marseille Univ, IRD, AP-HM, SSA, VITROME, Marseille, France

12      <sup>4</sup> Institut Universitaire de France (IUF), Paris, France

13  
14      \* Corresponding author : Pr. Anthony Levasseur, AMU, UMR MEPHI (Microbes, Evolution,  
15      Phylogeny and Infection), UM63, IRD, APHM, IHU - Méditerranée Infection, 19-21  
16      Boulevard Jean Moulin, 13385, Marseille cedex 05, France.

17      E-mail: [anthony.levasseur@univ-amu.fr](mailto:anthony.levasseur@univ-amu.fr)

18      **Running title:** *Urinicoccus timonensis* gen. nov., sp. nov.

19  
20      Keywords: *Urinicoccus timonensis* gen. nov., sp. nov., culturomics, gut, taxonogenomics

21

## 1 **Abstract**

2 *Urinicoccus timonensis* gen. nov., sp. nov. strain Marseille-P3926<sup>T</sup> is a new species from the  
3 phylum *Firmicutes* and the family *Peptoniphilaceae* that was isolated from a Human feces  
4 sample. Genome was 1,978,908 bp-long with a 41.1 G+C content. The closest species based  
5 on 16S ribosomal RNA was *Peptoniphilus ivorii* DSM 10022 with 90.8% sequence similarity.  
6 Considering phenotypic features, 16S rRNA sequence and comparative genome studies, we  
7 proposed Marseille- P3926<sup>T</sup> as the strain type of *Urinicoccus timonensis* gen. nov., sp. nov.

## 8 **Introduction**

9 The deciphering of the bacterial diversity linked to normal and pathogenic functions appears  
10 to be fundamental [1]. The culturomic approach, complementary to the metagenomic method,  
11 based on the increase of culture conditions, has considerably broadened the repertoire of the  
12 human gut microbiota [2-4]. The isolation, culture and characterization of microorganisms are  
13 essential to understand the overall physiology of the microbiota of the human gastrointestinal  
14 (GI) tract [5]. In this report, we report the isolation of a novel genus and species, *Urinicoccus*  
15 *timonensis* which was isolated from the Human feces sample.

## 16 **Isolation and growth conditions**

17 In February 2017, we isolated from human feces sample, a bacterial strain that could not be  
18 identified by Matrix Assisted Laser Desorption Ionization –Time of Flight Mass Spectrometry  
19 (MALDI-TOF MS). The screening was performed on a Microflex LT spectrometer (Bruker,  
20 Daltonics, Bremen, Germany) as previously reported [6]. The spectra obtained (Figure 1)  
21 were imported and analyzed using the Biotyper 3.0 software against the Bruker database that  
22 was continually incremented with MEPHI database. The strain was isolated on 5% sheep  
23 blood-enriched Columbia agar (COS) (bioMérieux, Marcy l’Etoile, France) at 37°C and PH  
24 7.5 in anaerobic atmosphere (anaeroGEN; Oxoid, Dardilly, France) after a 15-days pre-

25 incubation in an anaerobic bottle containing a blood. Culture vial (Becton Dickson, Le Pont-  
26 de-Claix, France) was supplemented with 5 ml of 0.2  $\mu\text{m}$  filtered rumen fluid.

### 27 **Phenotypic characteristics**

28 Colonies were white and smooth with a mean diameter of 1 to 4 mm. Bacterial cells were  
29 Gram-positive cocci with a mean diameter of 0.67  $\mu\text{m}$  (Figure 2). Strain Marseille-P3926<sup>T</sup>  
30 exhibited neither catalase nor oxidase activities. API 50 CH and API ZYM test were  
31 performed at 37°C under anaerobic condition and the results are summarized in table 1.

### 32 **Strain identification**

33 In order to classify this bacterium, the 16S rRNA gene was amplified using the primer pair  
34 fD1 and rP2 (Eurogentec, Angers, France) and sequenced using the Big Dye® Terminator  
35 v1.1 Cycle Sequencing Kit and 3500xLGenetic Analyzer capillary sequencer (ThermoFisher,  
36 Saint-Aubin, France) as previously described [7]. The 16S rRNA nucleotide sequence was  
37 assembled and corrected using CodonCode Aligner software (<http://www.codoncode.com>).  
38 Strain Marseille-P3926<sup>T</sup> exhibited a 90.80 % 16S rRNA similarity with *Peptoniphilus ivorii*  
39 DSM 10022 (Genbank accession number: NR\_026359). We consequently proposed to  
40 classify Strain Marseille-P3926<sup>T</sup> as a new species within the genus *Urinicoccus* in the phylum  
41 *Firmicutes* (Figure 3).

### 42 **Genome sequencing**

43 Genomic DNA was extracted using the EZ1 biorobot with the EZ1 DNA tissue kit (Qiagen,  
44 Hilden, Germany) and then sequenced on a MiSeq sequencer (Illumina Inc, San Diego,  
45 CA, USA) with the Nextera Mate Pair sample prep kit and Nextera XT Paired End (Illumina),  
46 as previously described [8]. The assembly was performed using a pipeline containing several  
47 software (Velvet [9], Spades [10] and Soap Denovo [11]), on trimmed (MiSeq and  
48 Trimmomatic [12] software) or untrimmed data (only MiSeq software). GapCloser was used  
49 to reduce assembly gaps. Scaffolds < 800 base pairs (bp) and scaffolds with a depth value

50 lower than 25% of the mean depth were removed. The best assembly was selected using  
51 different criteria (number of scaffolds, N50, number of N). The genome of strain Marseille-  
52 P3926<sup>T</sup> was 1,978,908 bp-long with a 41.1 mol% G+C content (Figure 4; Table 2). The  
53 values dDDH obtained from *U. timonensis* strain Marseille-P3926 by comparison with other  
54 close strains were detailed in Table 3. These dDDH values were below 70% of the  
55 recommended threshold for species demarcation [13], confirming that the strain studied is  
56 representative of a new species. Of the 1,931 predicted genes, 1,871 were protein-coding  
57 genes and 60 were RNAs. A total of 1,619 genes were assigned as putative function and 427  
58 genes were annotated as hypothetical proteins (Figure 5; Table 4). The degree of genomic  
59 similarity of strain Marseille-P3926<sup>T</sup> with closely related species was estimated using the  
60 OAT software [14]. OrthoANI values among closely related species (Figure 5) ranged from  
61 62.22% between *Tissierella creatinini* and *Peptoniphilus ivorii* to 82.9 % between  
62 *Peptoniphilus asaccharolyticus* and *Peptoniphilus indolicus*. When *Urinicoccus timonensis*  
63 was compared to that of these closely species, values ranged from 63.78 % with *T. creatinini*  
64 to 70.75 % with *Peptoniphilus grossensis*.

## 65 **Conclusion**

66 On the basis of phenotypic features, including MALDI-TOF spectrum, a 16S rRNA sequence  
67 divergence greater than > 1.3 % and, an OrthoANI value lower than 95% with the  
68 phylogenetically closest species with standing in nomenclature, we formally proposed the  
69 creation of *Urinicoccus timonensis* gen. nov., sp. nov., whose type strain is strain Marseille-  
70 P3926.

## 71 **Description of *Urinicoccus* gen. nov.**

72 U.ri.ni.coc.cus N.L. fem. n. *Urinicoccus*, refers to *urina*, which is the latino name of urine  
73 and *coccus* which is the name of bacteria with around shape. Colonies were white and smooth  
74 with a mean diameter of 1 to 4 mm. Bacterial cells were Gram-positive cocci with a mean

75 diameter of 0.67  $\mu\text{m}$  (Figure 2). Strain Marseille-P3926<sup>T</sup> exhibited neither catalase nor  
76 oxidase activities. The type species of the genus is *Urinicoccus timonensis*.

77 **Description of *Urinicoccus timonensis* sp. nov.**

78 *Urinicoccus timonensis* sp. nov. (ti.mo.nen'sis. L. gen. masc. timonensis, of Timone, the  
79 name of the hospital where strain Marseille-P3926<sup>T</sup> was cultivated) is classified as a member  
80 of the family *Peptoniphilaceae* in the phylum *Firmicutes*. Strain Marseille-P3926<sup>T</sup> is the type  
81 strain of the new species '*Urinicoccus timonensis*' gen. nov., sp. nov. It is a strictly anaerobic,  
82 Gram-positive cocci. Colonies of Strain Marseille-P3926<sup>T</sup> were white and smooth with a  
83 mean diameter of 1 to 4 mm. This bacterial strain does not present any catalase and oxidase  
84 activities. The genome size of *Urinicoccus timonensis* strain Marseille-P3926<sup>T</sup> is 1,978,908  
85 bp with 41.1 mol% G+C content. The Genbank Accession number for the 16S rRNA gene  
86 sequence of strain Marseille-P3926<sup>T</sup> is LT908436 and for the whole genome shotgun project  
87 is NZ\_OCTU00000000.1. It was isolated from human feces sample.

88 **Nucleotide sequence accession number.** The 16S rRNA gene and genome sequences were  
89 deposited in Genbank under accession number LT908436 and NZ\_OCTU00000000.1,  
90 respectively.

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94 team of Japan (Hitachi High-Technologies Corporation, Science & Medical Systems Business  
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96 Méditerranée Infection.

97 **Conflicts of interest:**

98 None to declare

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103 Paris, France) to Professor Anthony Levasseur.

104 **Ethics and consent**

105 The study was approved by the ethics committee of the Institut Hospitalo-Universitaire  
106 Méditerranée Infection (IHU-MI) under reference 2016-010.

107 **References**

- 108 [1] The Human Microbiome Project | Nature n.d.  
109 <https://www.nature.com/articles/nature06244> (accessed May 4, 2018).
- 110 [2] Lagier J-C, Armougom F, Million M, Hugon P, Pagnier I, Robert C, et al. Microbial  
111 culturomics: paradigm shift in the human gut microbiome study. *Clin Microbiol Infect*  
112 2012;18:1185–93. doi:10.1111/1469-0691.12023.
- 113 [3] Lagier J-C, Hugon P, Khelaifia S, Fournier P-E, La Scola B, Raoult D. The rebirth of  
114 culture in microbiology through the example of culturomics to study human gut microbiota.  
115 *Clin Microbiol Rev* 2015;28:237–64. doi:10.1128/CMR.00014-14.
- 116 [4] Lagier J-C, Khelaifia S, Alou MT, Ndongo S, Dione N, Hugon P, et al. Culture of  
117 previously uncultured members of the human gut microbiota by culturomics. *Nat Microbiol*  
118 2016;1:16203. doi:10.1038/nmicrobiol.2016.203.
- 119 [5] Ramasamy D, Mishra AK, Lagier J-C, Padhmanabhan R, Rossi M, Sentausa E, et al.  
120 A polyphasic strategy incorporating genomic data for the taxonomic description of novel  
121 bacterial species. *Int J Syst Evol Microbiol* 2014;64:384–91. doi:10.1099/ijs.0.057091-0.
- 122 [6] Seng P, Drancourt M, Gouriet F, La Scola B, Fournier P-E, Rolain JM, et al. Ongoing  
123 revolution in bacteriology: routine identification of bacteria by matrix-assisted laser  
124 desorption ionization time-of-flight mass spectrometry. *Clin Infect Dis* 2009;49:543–51.  
125 doi:10.1086/600885.
- 126 [7] Morel A-S, Dubourg G, Prudent E, Edouard S, Gouriet F, Casalta J-P, et al.  
127 Complementarity between targeted real-time specific PCR and conventional broad-range 16S  
128 rDNA PCR in the syndrome-driven diagnosis of infectious diseases. *Eur J Clin Microbiol*  
129 *Infect Dis* 2015;34:561–70. doi:10.1007/s10096-014-2263-z.
- 130 [8] Diop A, Khelaifia S, Armstrong N, Labas N, Fournier P-E, Raoult D, et al. Microbial  
131 culturomics unravels the halophilic microbiota repertoire of table salt: description of



132 *Gracilibacillus massiliensis* sp. nov. *Microb Ecol Health Dis* 2016;27.  
133 doi:10.3402/mehd.v27.32049.

134 [9] Zerbino DR, Birney E. Velvet: Algorithms for de novo short read assembly using de  
135 Bruijn graphs. *Genome Res* 2008;18:821–9. doi:10.1101/gr.074492.107.

136 [10] Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, et al.  
137 SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J*  
138 *Comput Biol* 2012;19:455–77. doi:10.1089/cmb.2012.0021.

139 [11] Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, et al. SOAPdenovo2: an empirically  
140 improved memory-efficient short-read de novo assembler. *Gigascience* 2012;1:18.  
141 doi:10.1186/2047-217X-1-18.

142 [12] Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for Illumina  
143 sequence data. *Bioinformatics* 2014;30:2114–20. doi:10.1093/bioinformatics/btu170.

144 [13] Meier-Kolthoff, J. P., Auch, A. F., Klenk, H.-P., & Göker, M. (2013). Genome  
145 sequence-based species delimitation with confidence intervals and improved distance  
146 functions. *BMC Bioinformatics*, **14**, 60. doi:10.1186/1471-2105-14-60

147 [14] Lee I, Ouk Kim Y, Park S-C, Chun J. OrthoANI: An improved algorithm and software  
148 for calculating average nucleotide identity. *Int J Syst Evol Microbiol* 2016;66:1100–3.  
149 doi:10.1099/ijsem.0.000760.

150 [15] Grant JR, Stothard P. The CGView Server: a comparative genomics tool for circular  
151 genomes. *Nucleic Acids Res.* 2008;36(Web Server issue):W181–W184.  
152 doi:10.1093/nar/gkn179

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158 **Table 1:** Phenotypic characterization of *Urinicoccus timonensis* based on the biochemical  
 159 tests.

160 Profile Index: (A) API 50 CH, (B) API ZYM.

161 (A)

<b>Bacteria : <i>Urinicoccus timonensis</i></b>			
<b>API 50 CH</b>			
<b>Test</b>	<b>Results (+/-)</b>	<b>Test</b>	<b>Results (+/-)</b>
Control	-	Esculine	-
Glycerol	-	Salicine	-
Erythrol	-	D-cellobiose	-
D-arabinose	-	D-maltose	-
L-arabinose	-	D-lactose	-
D-ribose	-	D-melibiose	-
D-xylose	-	D-saccharose	-
L-xylose	-	D-trehalose	-
D-adonitol	-	Inuline	-
Methyl-βD-xylopyranoside	-	D-melezitose	-
D-galactose	+	D-raffinose	-
D-glucose	+	Amidon	-
D-fructose	-	Glycogene	-
D-mannose	-	Xylitol	-
L-sorbose	-	Gentibiose	-
L-rhamnose	-	D-turanose	-
Dulcitol	-	D-lyxose	-
Inositol	-	D-tagatose	-
D-mannitol	-	D-fucose	-
D-sorbitol	-	L-fucose	-
Methyl-αD-mannopyranoside	-	D-arabitol	-
Methyl-αD-glucopyranoside	-	L-arabitol	-
N-acetylglucosamine	-	Potassium gluconate	-
Amygdaline	-	Potassium 2-cetogluconate	-
Arbutine	-	Potassium 5-cetogluconate	+

162

163 (B)

<b>Bacteria: <i>Urinicoccus timonensis</i></b>	
<b>API ZYM</b>	

<b>Test</b>	<b>Results (+/-)</b>
Control	-
Alkaline phosphatase	-
Esterase (C 4)	-
Esterase Lipase (C 8)	-
Lipase (C 14)	-
Leucine arylamidase	-
Valine arylamidase	-
Cystine arylamidase	-
Trypsine	-
$\alpha$ -chymotrypsine	-
Acid phosphatase	-
Naphtalo-AS-BI-phosphohydrolase	-
$\alpha$ -galactosidase	-
$\beta$ -galactosidase	-
$\beta$ -glucuronidase	-
$\alpha$ -glucosidase	-
$\beta$ -glucosidase	-
N-acetyl- $\beta$ -glucosaminidase	-
$\alpha$ -mannosidase	-
$\alpha$ -fucosidase	-

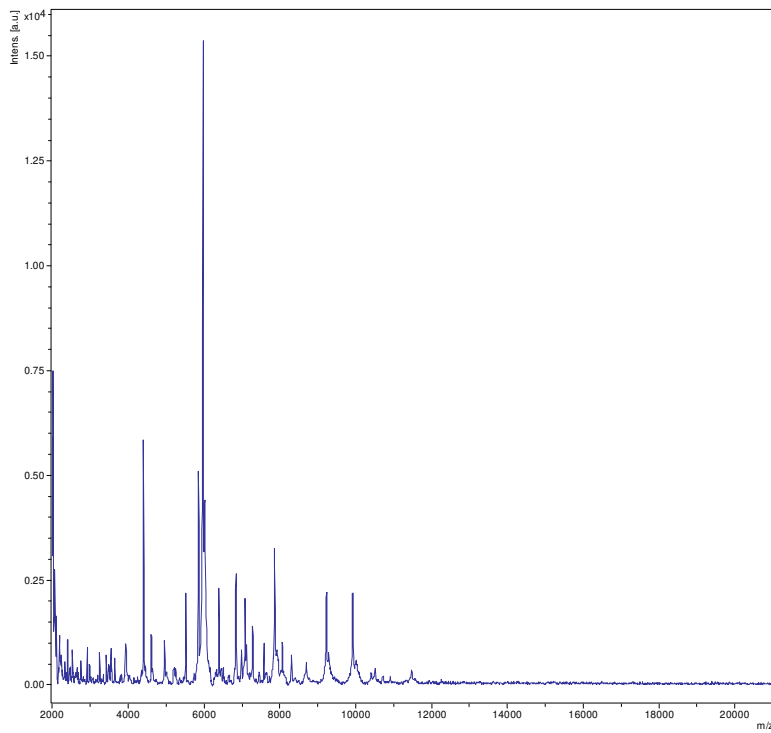
Table2 : Genomic comparison of *Urinicoccus timonensis* gen. nov., sp. nov., and other closely related species with standing in nomenclature.

	<b>GenBank accession numbers</b>	<b>Size</b>	<b>Number of RNAs</b>	<b>Number of protein-coding genes</b>	<b>Number of genes</b>	<b>G + C content (%)</b>
<i>Urinicoccus timonensis</i>	OCTU01000001.1	1,978,908	60	1871	1,931	41.1
<i>Tissierella creatinini</i>	SUSSS01000001.1	2,611,442	58	2471	2,533	37.7
<i>Peptoniphilus indolicus</i>	NZ_JH165061.1	2,237,864	33	2133	2166	29.7
<i>Peptoniphilus grossensis</i>	NZ_HE978566.1	2,101,866	29	1983	2012	32.7
<i>Peptoniphilus coxii</i>	NZ_KQ960154.1	1,837,050	39	1713	1752	44.5
<i>Peptoniphilus asaccharolyticus</i>	NZ_FWWR0100017.1	2,232,586	32	2283	2315	32.2
<i>Keratinibaculum paraultunense</i>	SWAE01000001.1	2,248,613	55	2156	2211	29.4
<i>Peptoniphilus ivorii</i>	NZ_LR134523.1	1,587,771	64	1488	1574	53.2



168 Table 4 : Number of genes associated with the 25 general clusters of orthologous group (COG) functional categories.

	<i>Urinicoccus_timonensis</i>	<i>Peptoniphilus_ivorii</i>	<i>Tissierella_creatinini</i>	<i>Peptoniphilus_indolicus</i>	<i>Peptoniphilus_grossensis</i>	<i>Peptoniphilus_coxii</i>	<i>Peptoniphilus_asaccharolyticus</i>	<i>Keratinibaculum_paraaltunense</i>	<i>Description</i>
[J]	178	178	209	186	179	182	188	196	Translation, ribosomal structure and biogenesis
[A]	0	0	0	0	0	0	0	0	RNA processing and modification
[K]	115	79	141	130	126	111	116	140	Transcription
[L]	90	74	110	99	104	88	133	99	Replication, recombination and repair
[B]	1	1	1	1	1	1	1	2	Chromatin structure and dynamics
[D]	27	22	43	24	30	23	32	44	Cell cycle control, cell division, chromosome partitioning
[Y]	0	0	0	0	0	0	0	0	Nuclear structure
[V]	59	48	66	85	89	68	73	100	Defense mechanisms
[T]	79	63	104	69	74	73	70	120	Signal transduction mechanisms
[M]	63	69	132	74	71	67	73	100	Cell wall/membrane/envelope biogenesis
[N]	7	9	14	6	8	8	10	60	Cell motility
[Z]	0	0	2	0	0	0	0	1	Cytoskeleton
[W]	3	3	13	1	2	3	2	15	Extracellular structures
[U]	15	13	20	21	18	16	29	31	Intracellular trafficking, secretion, and vesicular transport
[O]	71	62	99	86	69	62	77	97	Posttranslational modification, protein turnover, chaperones
[X]	83	13	38	30	30	13	205	27	Mobilome: prophages, transposons
[C]	93	82	130	105	106	89	86	88	Energy production and conversion
[G]	48	49	67	66	52	40	43	80	Carbohydrate transport and metabolism
[E]	132	123	245	177	127	118	159	162	Amino acid transport and metabolism
[F]	68	59	80	83	67	61	78	62	Nucleotide transport and metabolism
[H]	90	79	144	98	77	93	81	107	Coenzyme transport and metabolism
[I]	57	47	62	62	55	57	58	57	Lipid transport and metabolism
[P]	104	92	121	97	82	82	94	78	Inorganic ion transport and metabolism
[Q]	15	12	34	30	19	11	24	24	Secondary metabolites biosynthesis, transport and catabolism
[R]	135	125	219	175	145	125	145	171	General function prediction only
[S]	86	65	138	96	84	85	98	103	Function unknown
-	427	290	523	536	546	407	614	450	Not in cog



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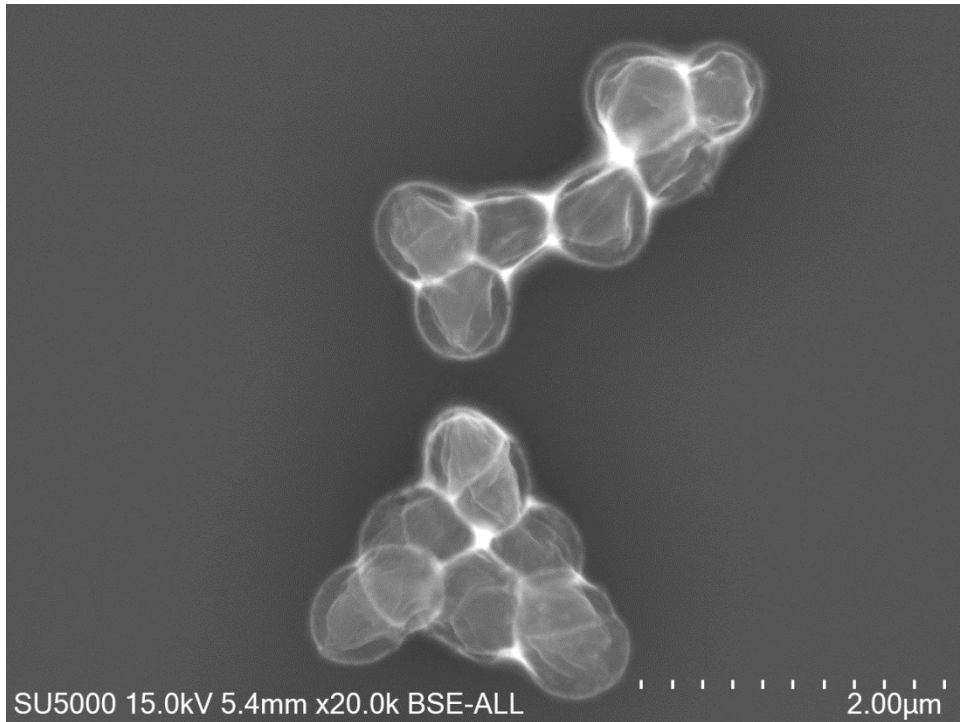
171 **Figure 1:** MALDI-TOF MS reference spectrum of *Urinicoccus timonensis* gen. nov., sp. nov.

172 The reference spectrum was generated by comparison of spectra from 12 individual colonies.

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177 **Figure 2:** Scanning electron microscopy of stained *Urinicoccus timonensis* gen. nov., sp. nov.

178 A colony was collected from agar and immersed into a 2.5 % glutaraldehyde fixative solution.

179 Then, a drop of the suspension was directly deposited on a poly-L-lysine coated microscope

180 slide for 5 minutes and treated with 1 % phosphotungstic acid (PTA) aqueous solution (pH

181 2.0) for 2 minutes to increase SEM image contrast. The slide was gently washed in water; air

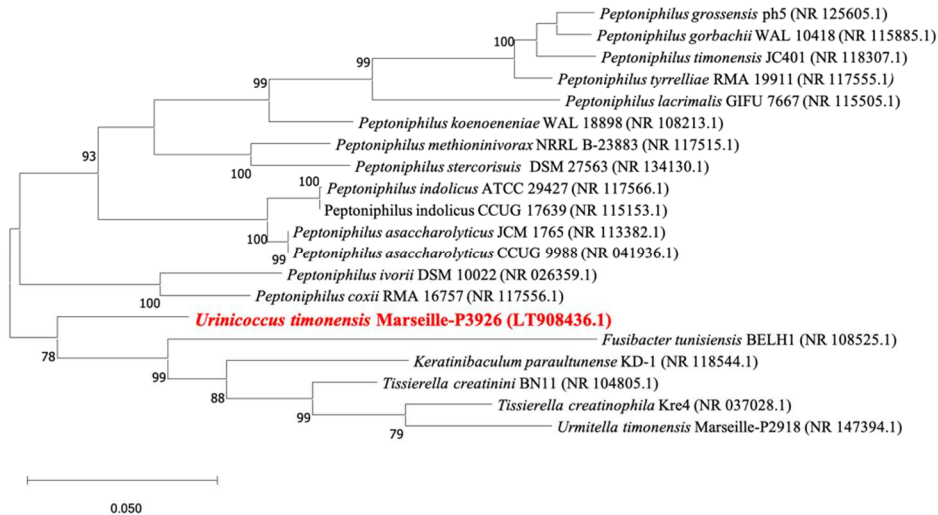
182 dried and examined in a tabletop SEM (Hitachi SU5000) with approximately 60 centimeters

183 in height and 33 cm in width to evaluate bacteria structure. Scales and acquisition settings are

184 shown in figure.

185

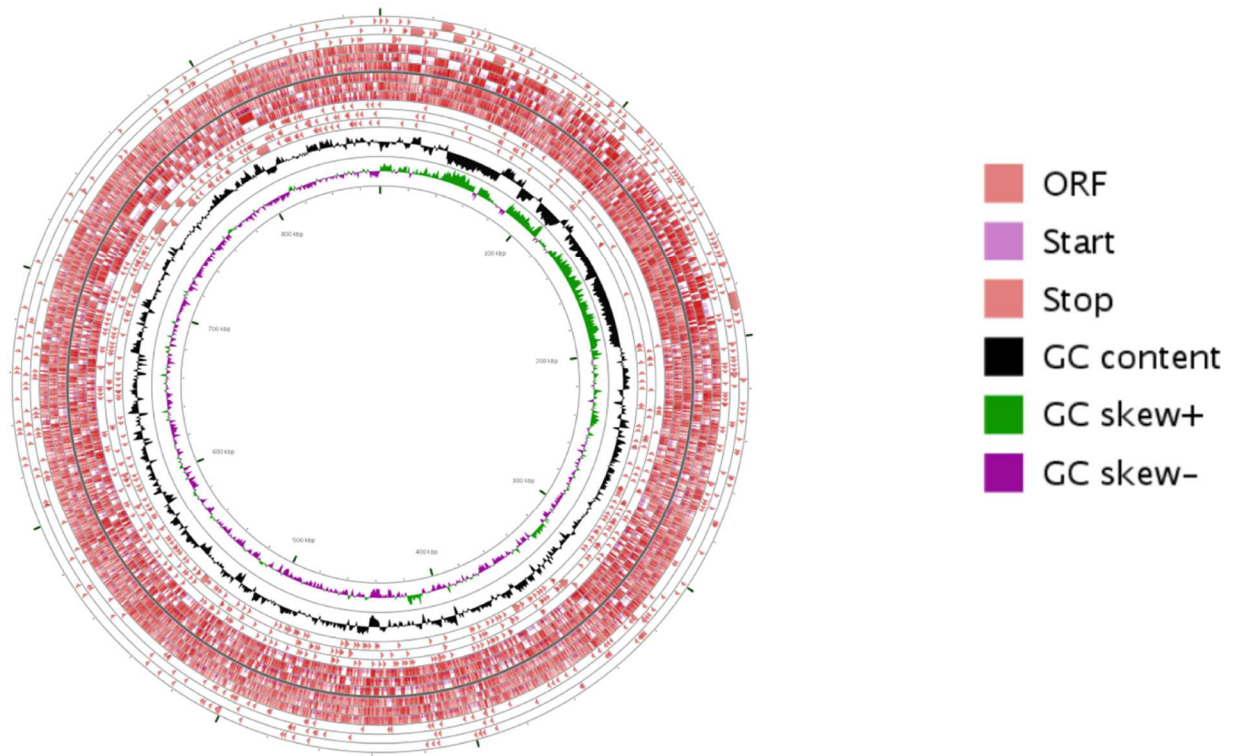




186  
 187 **Figure 3:** Phylogenetic tree highlighting the position of *Urinicoccus timonensis* gen. nov., sp.  
 188 nov. with regard to other closely related species. Genbank accession numbers of 16S rRNA  
 189 are indicated in parentheses. Sequences were aligned using MUSCLE with default  
 190 parameters. Phylogenetic inferences were obtained using the Maximum Likelihood method  
 191 and the MEGA 7 software. Bootstrap values obtained by repeating the analysis 1,000 times to  
 192 generate a majority consensus tree are indicated at the nodes. The scale bar indicates a 5 %  
 193 nucleotide sequence divergence.

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198 **Figure 4:** A circular map generated using the CGView [15] Server showing a complete view

199 of the genome of *Urinicoccus timonensis* gen. nov., sp. nov.

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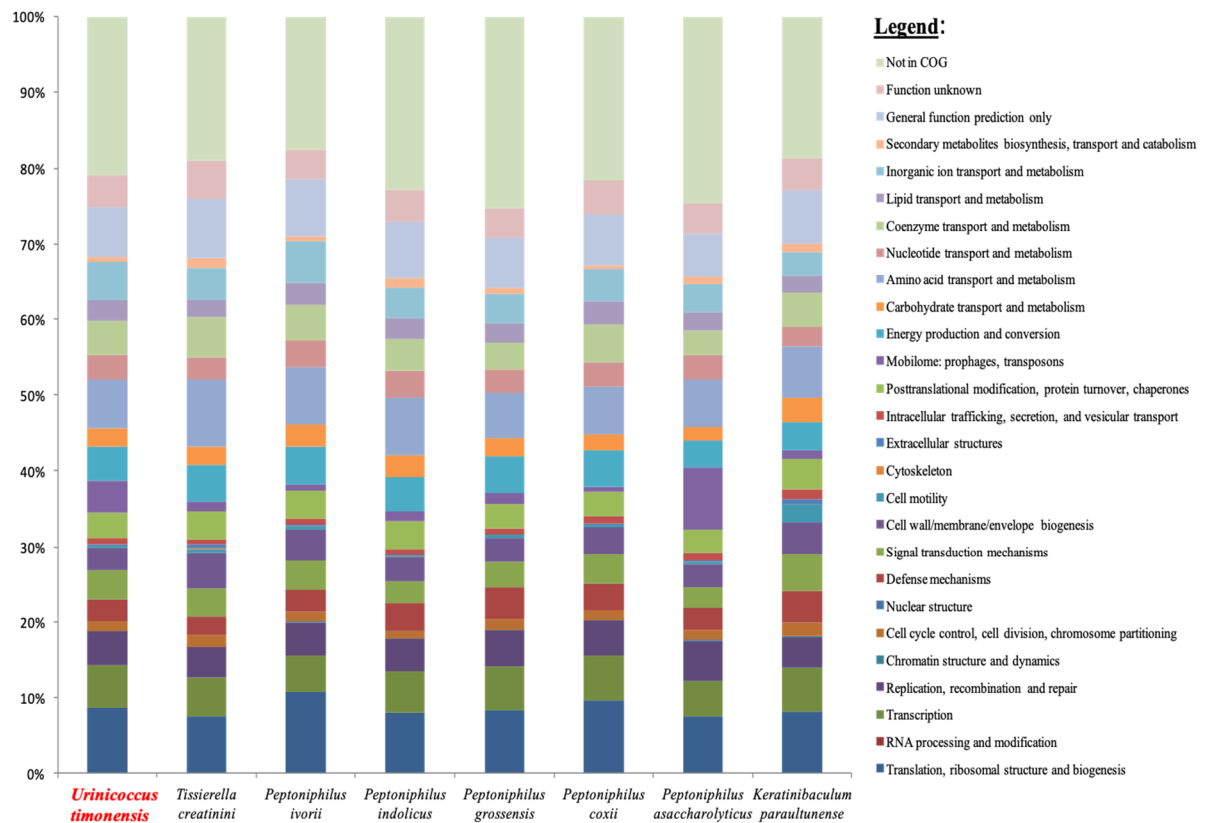
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**Figure 5:** Distribution of functional classes of predicted genes according to the clusters of

208 orthologous groups of proteins of *Urinicoccus timonensis* gen. nov., sp. nov., among other

209 closely related species.

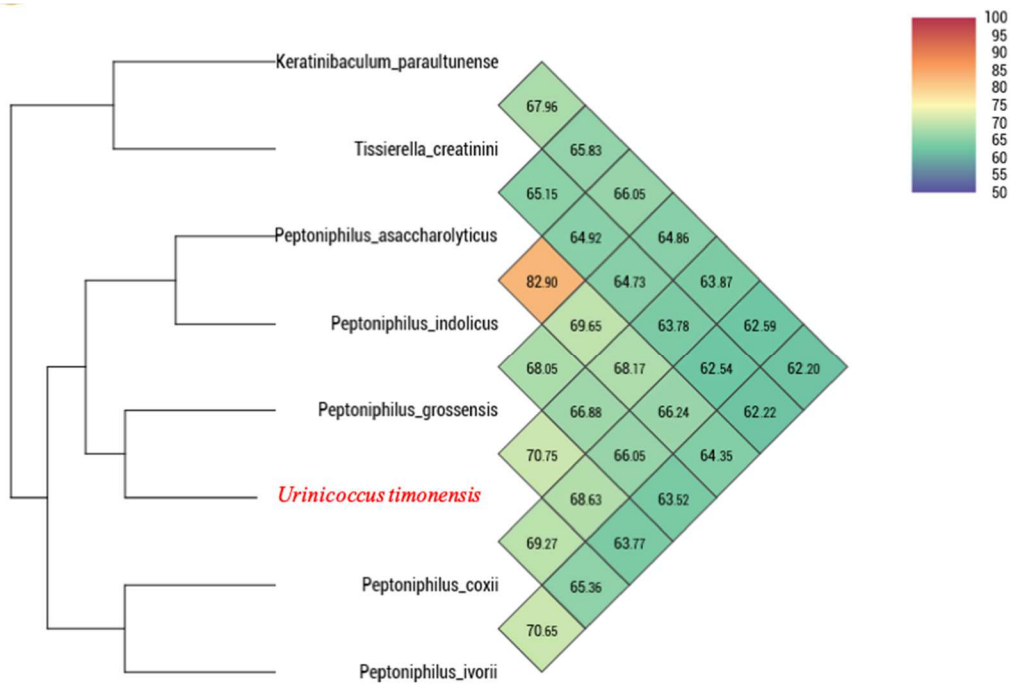
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216 **Figure 6:** Heatmap generated with OrthoANI values calculated using the OAT software

217 between *Urinicoccus timonensis* gen. nov., sp. nov. and other closely related species with

218 standing in nomenclature.