

## “*Vaginella massiliensis*” gen. nov., sp. nov., a new genus cultivated from human female genital tract

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### Abstract

We relate the main characteristics of “*Vaginella massiliensis*” strain Marseille P2517 (= DSM 102346 = CSUR P2517), a new member of the *Flavobacteriaceae* family. The strain Marseille P2517 was cultivated from a vaginal swab from a healthy 22-year-old woman.

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**Keywords:** Culturomics, *Flavobacteriaceae*, human microbiota, vaginal flora, “*Vaginella massiliensis*”

**Original Submission:** 4 September 2016; **Revised Submission:** 16 September 2016; **Accepted:** 21 September 2016

**Article published online:** 30 September 2016

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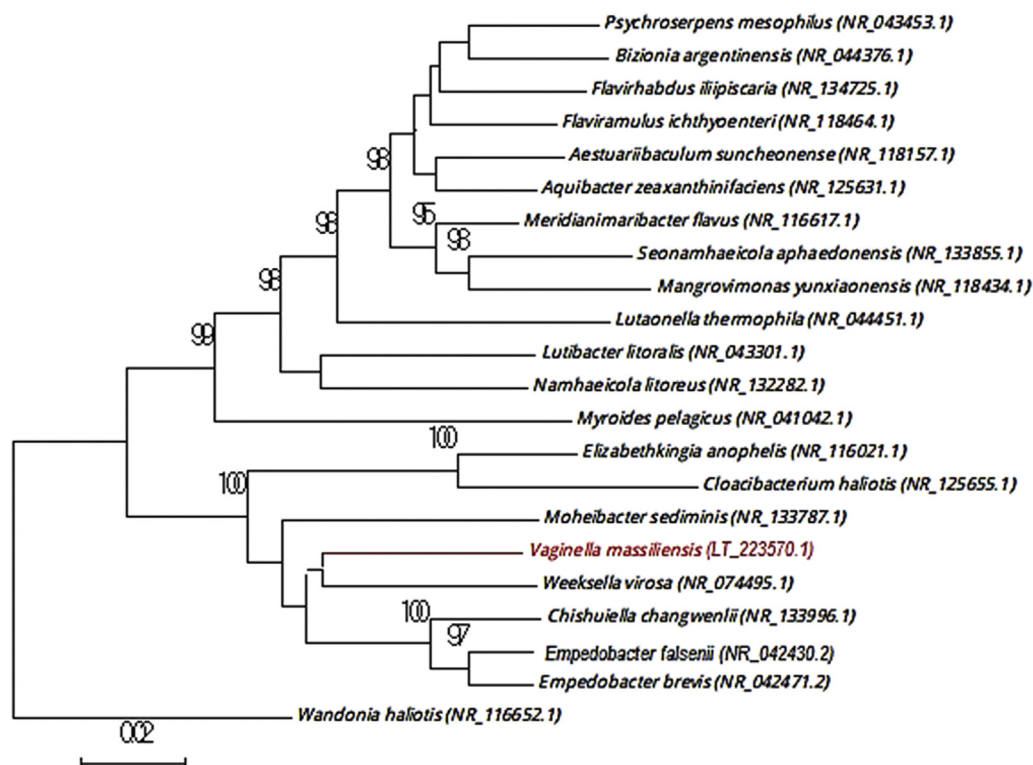
As part of the study of vaginal microbiota by the concept of microbial culturomics [1], in February 2016 we isolated from a vaginal sample from a healthy 22-year-old woman a bacterium that could not be identified using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) performed with a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2]. The study was authorized by the local ethics committee of the IFR48 (Marseille, France) under the agreement 09-022; the patient also provided written consent.

The initial growth of strain Marseille P2517 was obtained at 37°C under aerobic conditions after 2 days of culture on Chocolat PolyViteX agar (BD Diagnostics, Le Pont-de-Claix, France) after 7 days of preincubation in a blood culture bottle (BD Diagnostics) enriched with 4 mL of rumen that was filter sterilized through at 0.2 µm pore filter (Thermo Fisher Scientific, Villebon-sur-Yvette, France) and 3 mL of sheep’s blood (bioMérieux, Marcy l’Etoile, France). Bacterial cells were Gram-negative, rod-shaped bacilli that were nonmotile and

non-spore forming with a diameter ranging from 0.54 to 0.68 µm and a length ranging from 1.2 to 1.5 µm. Strain Marseille P2517 exhibited positive oxydase activity, but catalase was negative. After 2 days of incubation at 37°C under aerobic conditions on blood agar (bioMérieux), colonies were light yellow, opaque, circular and smooth with a diameter of 1.7 to 2 mm. Strain Marseille P2517 is an obligate aerobe.

The 16S rRNA sequence was obtained after amplification using the universal primer pair (fD1 and rp2) and a 3130-XL sequencer (Applied Biosciences, Saint-Aubin, France), as previously reported [3]. 16S rRNA gene sequence-based identification of strain Marseille P2517 showed 93% identity with *Weeksella virosa* DSM 16922 (GenBank accession no. NR\_074495), the phylogenetically closest bacterium with a validly published name (Fig. 1). Because this sequence was below the 95% threshold set by Stackebrandt and Ebers [4] to define a new genus without carrying out DNA-DNA hybridization, strain Marseille P2517 was classified as the representative strain of a new genus belonging to the family *Flavobacteriaceae* in the phylum *Bacteroidetes* (<http://www.bacterio.net/classificationsz.html#Weeksella>).

*Weeksella virosa* was first described in 1987 by Holmes et al. [5]. This bacterium is rod shaped, aerobic, Gram-negative, nonmotile and nonsaccharolytic, exhibiting a positive activity for catalase and oxidase [5]. *Weeksella virosa* is mostly isolated from the human urogenital tract.



**FIG. 1.** Phylogenetic tree highlighting phylogenetic position of "*Vaginella massiliensis*" strain Marseille P2517<sup>T</sup> relative to other species close members of *Flavobacteriaceae*. GenBank accession numbers are indicated in brackets after name. Sequences were aligned using CLUSTALW and phylogenetic inferences obtained using approximately maximum-likelihood method within MEGA6 software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstrap scores of  $\geq 95\%$  were retained. Scale bar indicates 2% nucleotide sequence divergence.

Because strain Marseille P2517 presents a 16S rRNA divergence of approximately 7% with its phylogenetically closest species [6], we propose that it may be the representative strain of a novel genus, preliminarily named here "*Vaginella*" (va.gi.nel'la, L. fem. n. *vagina*, "vagina," a part of the female genital tract; L. dim. suff. *-ella*; N.L. dim. fem. n. *Vaginella*, "small vagina," referring to the source of the isolation of the type strain). Strain Marseille P2517 is the type strain of the new species "*Vaginella massiliensis*" (mas.si.li.en'sis, L. gen. adj. *massiliensis*, from Massilia, the Latin name from Marseille, France, where the organism was first grown, identified and characterized).

### MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of "*Vaginella massiliensis*" is available at <http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database>.

### Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in European Molecular Biology Laboratory–European Bioinformatics Institute under accession number LT223570.

### Deposit in culture collection

Strain Marseille P2517 was deposited in the collection Deutsche Sammlung von Mikroorganismen (DSM) and in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under numbers I02346 and P2517, respectively.

### Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

## Conflict of Interest

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None declared.

## References

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- [1] Lagier JC, Hugon P, Khelaifia S, Fournier PE, La Scola B, Raoult D. The rebirth of culture in microbiology through the example of culturomics to study human gut microbiota. *Clin Microbiol Rev* 2015;28:237–64.
- [2] Seng P, Abat C, Rolain JM, Colson P, Lagier JC, Gouriet F, et al. Identification of rare pathogenic bacteria in a clinical microbiology laboratory: impact of matrix-assisted laser desorption ionization–time of flight mass spectrometry. *J Clin Microbiol* 2013;51:2182–94.
- [3] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral JP, Raoult D. 16S ribosomal DNA sequence analysis of a large collection of environmental and clinical unidentifiable bacterial isolates. *J Clin Microbiol* 2000;38:3623–30.
- [4] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;33:152–5.
- [5] Holmes B, Steigerwalt AG, Weaver RE, Brenner DJ. *Weeksella virosa* gen. nov., sp. nov. (formerly group If), found in human clinical specimens. *Syst Appl Microbiol* 1986;8:185–90.
- [6] Yarza P, Richter M, Peplies J, Euzéby J, Amann R, Schleifer KH, et al. The All-Species Living Tree project: a 16S rRNA-based phylogenetic tree of all sequenced type strains. *Syst Appl Microbiol* 2008;31:241–50.