Novel Isolation and Identification Methods for Veillonella Species Involved in Halitosis

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Abstract

Purpose: The purpose of the present study was to develop a novel selective medium (OVSM) and useful identification method for oral Veillonella species, to assess the prevalence of this species using the selective medium, and to investigate whether the monitoring of oral Veillonella species levels is useful as a clinical indicator for the diagnosis of halitosis.

Methods: To examine bacterial populations in the oral cavity, a novel selective medium (OVSM) and multiplex PCR method were developed for isolating and identifying oral Veillonella species. OVSM consists of tryptic soy agar, sheep blood, sodium lactate, vancomycin, and oxacillin.

Results: Oral Veillonella species grew well on OVSM. Oral Veillonella species accounted for 5.4% and 27.2%, respectively, of all bacteria in the tongue biofilm samples of healthy and halitosis subjects. Oral Veillonella species produced larger amounts of volatile sulfur compounds than other representative oral bacteria.

Conclusion: These results indicate that monitoring the levels of these organisms is useful as a clinical indicator for the diagnosis of halitosis.

Keywords

Veillonella Species, Selective Medium, Multiplex PCR

1. Introduction

The genus Veillonella belongs to the family Veillonellaceae in the phylum Firmicutes [1]. The genus Veillonella currently comprises 15 species (https://lpsn.dsmz.de/search?word=Veillonella). These species are members of the oral, genito-urinary, respiratory, and intestinal microbiota of humans and other mammals. The genus Veillonella is anaerobic Gram-negative cocci, with
cells typically forming pairs or short chains and lacking a flagellum, spore, or capsule [2]. Members of the genus *Veillonella* utilize short-chain organic acids, particularly lactic acid, as an energy source instead of carbohydrates or amino acids, subsequently producing acetic acid and propionic acid [3] [4].

Of the 15 species belonging to the genus *Veillonella*, *V. atypica*, *V. denticariosi*, *V. dispar*, *V. infantium*, *V. parvula*, *V. rogosae*, and *V. tobetsuensis* are representative species isolated from the human oral cavity, such as human saliva or tongue or dental biofilms, and are generally called oral *Veillonella* species. Oral *Veillonella* species are one of the main members of the human oral microbiome [5] [6]. Previous studies identified oral *Veillonella* species as rare causative organisms of meningitis, endocarditis, bacteremia, discitis, vertebral osteomyelitis, and prosthetic joint infection [7]. In addition, *V. tobetsuensis* was also isolated from the intraoperative bronchial fluids of elderly individuals with pulmonary carcinoma [8].

Periasamy and Kolenbrander demonstrated that oral *Veillonella* species were early colonizers during the formation of oral biofilms, along with *Streptococcus* species, which were identified as the initial colonizers in multispecies communities developing on oral biofilms [9]. Oral *Veillonella* species are associated with severe early childhood caries [10] and intraradicular infections, including abscesses [11], apical root canals [12], and dental tubules [13]. Oral *Veillonella* species were also predominant in the subgingival biofilm samples of patients with chronic periodontitis [14]. Previous findings showed that their distribution and frequency at the species level varied depending on the oral site and oral hygiene status [15] [16] [17] [18] [19]. Therefore, it is important to elucidate the role of oral *Veillonella* species in the formation of oral biofilms in order to improve the prevention and treatment of oral infectious diseases.

Halitosis is caused due by the metabolic products of bacteria in the oral cavity, particularly those on the dorsum of the tongue [20]. Some cases of halitosis have been associated with periodontitis [21] [22], and, thus, various periodontitis-related bacteria species have been detected in tongue coatings. These findings also suggest that the tongue coating plays a role as a reservoir of these bacteria [23]. Most of these bacteria have the ability to produce hydrogen sulfide (H$_2$S), one of the major components of halitosis [24]. Washio et al. focused on halitosis in patients without oral diseases, such as periodontitis and caries, and found that the predominant H$_2$S-producing bacteria were not periodontitis-related bacteria, but were mainly indigenous bacteria of the oral cavity, such as *Veillonella* and *Actinomyces* [25]. Moreover, *Veillonella* species, including *V. atypica*, *V. dispar*, and *V. parvula*, were predominant among these microorganisms.

Previous studies [5] [6] [26] [27] [28] that examined the prevalence of oral *Veillonella* species used the well-known selective medium for *Veillonella* species, *Veillonella* agar (VA) [29]. In a pilot study, we attempted to detect oral *Veillonella* species in oral samples using VA. However, it was impossible to detect some bacterial species among these organisms because VA inhibited their growth. There-
fore, previous findings may not have precisely reflected the prevalence of oral Veillonella species. A novel suitable selective medium is needed to accurately assess the prevalence of oral Veillonella species involved in dental caries, intraradicular infections, and halitosis in the oral cavity.

Veillonella strains are relatively easy to identify at the genus level, but remain difficult to identify at the species level because there are no useful phenotypic or biochemical examinations to distinguish them [30]. A sequence analysis of several target genes is the most reliable method for identifying bacterial species; however, it is expensive, laborious, and time-consuming. Therefore, a simple and more reliable assay for identifying oral Veillonella species at the species level, such as a polymerase chain reaction (PCR) amplification method, is needed.

The purpose of the present study was to develop a novel selective medium for the isolation of oral Veillonella species, to assess the prevalence of these species in the oral cavity, and to investigate whether the monitoring of Veillonella species levels is useful as a clinical indicator for the diagnosis of halitosis. Furthermore, the ability of each oral Veillonella species to produce volatile sulfur compounds (VSCs) was investigated in vitro and quantitatively compared to other representative oral bacteria using sensor gas chromatography.

2. Materials and Methods

2.1. Bacterial Strains and Culture Conditions

All bacterial strains used in the present study are listed in Tables 1-4. Strains of anaerobic bacteria except for Veillonella species were maintained by cultivating them on Anaerobic Blood Agar (CDC) that consists of a Tryptic soy agar (Becton, Dickinson and Co., Sparks, MD, USA) supplemented with vitamin K₁, hemin, L-cysteine, yeast extract, and sheep blood. Veillonella strains were maintained by cultivating them on tryptic soy agar blood (TS-LAC-Blood) composed of tryptic soy agar (TS) (Becton, Dickinson and Co., Sparks, MD, USA) supplemented with 2.1% sodium lactate and 5% sheep blood. These organisms were cultured at 37°C for 48 h in an anaerobic jar with a gas pack system (Anaeropack®, Mitsubishi Gas Chemical Co., Inc., Tokyo, Japan).

V. atypica isolate (NUM 9110), V. tobetsuensis isolate (NUM 9122), V. rogosae isolate (NUM 9135), V. parvula isolate (NUM 9142), V. dispar isolate (NUM 9145) and V. denticariosi isolate (NUM 9163) were obtained from the human oral cavity in the present study using a non-selective medium, i.e., TS-LAC-Blood.

2.2. Development of the New Selective Medium

2.2.1. Evaluation of the Base Medium

TS, TS with 2.1% sodium lactate (TS-LAC), TS with 5% sheep blood (TS-blood), and TS-LAC-Blood were examined as the base medium in the selective medium. Ten-fold dilutions of cultures were made in 0.9 ml of Tris-HCl buffer (0.05 M, pH 7.2) and aliquots of 0.1 ml were spread onto the test media. The plates were cultured at 37°C for 4 days under anaerobic conditions. After cultivation, the number of colony-forming units (CFU)/ml was counted.
2.2.2. Susceptibility Tests
Preliminary studies on antibiotic selection were performed using disk susceptibility tests (Sensi-Disk, Becton Dickinson Co., MD, USA). The microbroth dilution method was employed for susceptibility testing [31].

2.3. Recovery of Oral Veillonella Species
The recoveries of the Veillonella reference strains and Veillonella isolates were calculated as CFU/ml on selective medium and compared with those on TS-LAC-Blood for total cultivable bacteria and on conventional selective medium (VA) for Veillonella species. All Veillonella strains used in the present study are listed in Table 1. VA contained 5 g of tryptone, 5 g of yeast extract, 0.75 g of sodium thioglycolate, 0.002 g of basic fuchsin, 2.1% sodium lactate, and 15 g of agar.

All bacterial strains were pre-incubated in TS (Becton, Dickinson and Co., Sparks, MD, USA) supplemented with 2.1% sodium lactate at 37˚C overnight under anaerobic conditions. Ten-fold dilutions of cultures were made in 0.9 ml of Tris-HCl buffer (0.05 M, pH 7.2) and aliquots of 0.1 ml were spread onto the test media. The plates were cultured at 37˚C for 4 days under anaerobic conditions. After cultivation, the number of CFU/ml was counted.

2.4. Clinical Samples
One hundred volunteers (43 men, 57 women; mean age 34 years, range 19 - 61 years) participated in the present study. They had no systemic disease and

Table 1. Recovery of oral Veillonella species on VA and OVSM.

| Strain               | Base medium tryptic soy agar sheep blood sodium lactate CFU/ml, x10⁹ | VA Conventional selective medium Recovery, % | OVSM Selective medium in this study Recovery, % |
|----------------------|---------------------------------------------------------------------|---------------------------------------------|-----------------------------------------------|
| Veillonella atypica   | DSM 20739 1.8                                                        | 27.8                                        | 99.9                                          |
| NUM 9110             | 2.1                                                                | 19.3                                        | 99.3                                          |
| Veillonella tobetsuensis | JCM 17876 1.1                                                               | 0                                           | 93.3                                          |
| NUM 9122             | 0.6                                                                | 0                                           | 94.4                                          |
| Veillonella rogosae   | JCM 15642 0.9                                                         | 25.5                                        | 99.3                                          |
| NUM 9135             | 0.8                                                                | 23.1                                        | 98.5                                          |
| Veillonella parvula   | JCM 12972 0.7                                                         | 23.1                                        | 99.1                                          |
| NUM 9142             | 0.6                                                                | 29.7                                        | 99.6                                          |
| Veillonella dispar    | DSM 20735 1.8                                                         | 11.1                                        | 99.8                                          |
| NUM 9155             | 1.6                                                                | 8.5                                         | 99.7                                          |
| Veillonella denticariosi | JCM 15641 0.7                                                               | 3.1                                         | 99.1                                          |
| NUM 9163             | 0.9                                                                | 2.9                                         | 98.7                                          |
received no antibiotic therapy for at least 3 months. A sensor gas chromatograph (ODSA-P3-A, Yamato Scientific Co., Ltd., Tokyo, Japan) was used to measure the concentrations of VSCs. All participants were asked not to brush, rinse, or smoke immediately prior to the assessment and not to eat or drink for at least 2 h beforehand. A gas chromatography analysis was performed in duplicate. After closing the lips for 1 min, 1 ml of mouth air was obtained with a gastight syringe (Termosyringe® SS-02SZ, Termo Co., Tokyo, Japan) and immediately injected into the sensor gas chromatograph. In the present study, the threshold level for genuine halitosis was defined as >200 ppb total VSCs than in mouth air, according to which participants were divided into two subject groups: healthy subjects without halitosis (n = 50) and halitosis subjects (n = 50).

To collect tongue biofilms, the rear dorsal whole surface of the tongue was firmly scraped 10 times with sterilized cotton swabs. All samples were suspended in a sterile microcentrifuge tube containing 1 ml of Tris-HCl buffer (0.05 M, pH 7.2). Samples were dispersed by sonication for 30 s in an ice bath (50 W, 20 kHz, Astrason® System model XL 2020, NY, USA). Portions (100 μl) of appropriate dilutions of these samples were plated in triplicate on several types of selective medium plates and CDC plates for total cultivable bacteria. Selective medium plates and CDC plates were cultured at 37°C for 4 days under anaerobic conditions. CDC plates were also cultured at 37°C for 4 days in an atmosphere of 5% CO₂ in a CO₂ incubator (NAPCO® Model 5400; Precision Scientific, Chicago, IL, USA). The selective media used in the present study were a novel selective medium for oral Veillonella species, Mitis-salivarius agar for Streptococcus species, Fusobacterium selective agar for Fusobacterium species, and Bacteroides selective agar for Porphyromonas and Prevotella species. After cultivation, CFU/ml was calculated. The number of anaerobic bacteria was calculated by subtracting CFU on CDC in an atmosphere of 5% CO₂ from that under anaerobic conditions. The present study was approved by the Ethics Committee of Nihon University School of Dentistry at Matsudo, Japan (EC 18-032).

2.5. Identification of Oral Veillonella Species Isolated from Clinical Samples

Twenty-four out of the approximately 50 colonies that grew on a novel selective medium for oral Veillonella species per subject were randomly isolated and subcultured, and their identity was then confirmed by a PCR analysis.

2.6. Identification of Bacteria Species Isolated from Clinical Samples

Bacterial species, i.e., Streptococcus, Fusobacterium, oral Veillonella, Porphyromonas, and Prevotella species, except for oral Veillonella species on each selective medium, were identified by colony morphology and Gram staining.

2.7. Design of Species-Specific Primers for Oral Veillonella Species

Species-specific primers for six oral Veillonella species were designed as pre-
Previously reported [31]. Briefly, the RNA polymerase B (rpoB) gene sequences of *V. atypica* (accession no. EF185159), *V. denticariosi* (EF185162), *V. parvula* (EF185158), *V. dispar* (EF185161), *V. rogosae* (EF211831), and *V. tobetsuensis* (AB698649), the citrate synthase (gltA) gene sequences of *V. atypica* (accession no. KJ580470), *V. denticariosi* (KJ580471), *V. parvula* (KJ580466), *V. dispar* (KJ580469), *V. rogosae* (KJ580467), and *V. tobetsuensis* (KJ580468), and the dnaK gene sequences of *V. atypica* (accession no. AF440436), *V. denticariosi* (AF219278), *V. parvula* (AB678219), *V. dispar* (AF440435), *V. rogosae* (AB678220), and *V. tobetsuensis* (AB698650) were obtained from the DNA Data Bank of Japan (DDBJ; https://www.ddbj.nig.ac.jp/services.html, Mishima, Japan), and a multiple sequence alignment analysis was performed with the CLUSTAL W program; i.e., the rpoB, gltA, and dnaK gene sequences of six oral *Veillonella* species were aligned and analyzed, respectively. Homology among the primers selected for each oral *Veillonella* species and their respective rpoB, gltA, and dnaK gene sequences were confirmed by a BLAST search.

2.8. Development of a Multiplex PCR Method for Identifying Oral *Veillonella* Species Using Designed Primers

Bacterial cells were cultured in TS supplemented with 2.1% sodium lactate for 24 h, and 1 ml of samples was then collected in microcentrifuge tubes and resuspended at a density of 1.0 McFarland standard (approximately 10⁷ CFU/ml) in 1 ml of sterile distilled water. A total of 3.6 μl of the suspension was then used as the PCR template. The detection limit of PCR was assessed by serially diluting known numbers of bacterial cells in sterile distilled water and then subjecting each suspension to PCR. The multiplex PCR mixture contained 0.2 μM of each primer, 10 μl of 2 × MightyAmp Buffer Ver.3 (Takara Bio Inc., Shiga, Japan), 0.4 μl of MightyAmp DNA Polymerase (Takara), and 5 μl of the template in a final volume of 20 μl. PCR reactions were performed in a DNA thermal cycler (Applied Biosystems 2720 Thermal Cycler; Applied Biosystems, CA, USA). PCR conditions included an initial denaturation step at 98°C for 2 min, followed by 30 cycles consisting of 98°C for 30 s, 63°C for 30 s, and 72°C for 30 s. PCR products were analyzed by 2.0% agarose gel electrophoresis before being visualized by electrophoresis in 1 × Tris-borate-EDTA on a 2% agarose gel stained with ethidium bromide. A 100-bp DNA ladder (Takara Biomed, Shiga, Japan) was used as a molecular size marker. All experiments were performed in triplicate.

2.9. Assessment of VSC-Producing Abilities

The VSC-producing abilities of oral *Veillonella* species and other representative oral bacteria *in vitro* were assessed as previously reported [32]. In the present study, VSC levels were measured using a sensor gas chromatograph (ODSA-P3-A, Yamato Scientific Co., Ltd., Tokyo, Japan). All bacterial strains were pre-incubated as described above. Each bacteria culture solution was inoculated into 19 × 55-mm sample vials (1880 SV10; AGC Techno Glass Co., Ltd., Shizuoka, Japan) containing TS supplemented with vitamin K₁ (10 μg/ml), hemin (5 μg/ml), 0.5%
yeast extract, L-cysteine (25 mM), and L-methionine (25 mM). All chemicals were purchased from Sigma Chemical Co. (St. Louis, MO, USA). After the inoculation, sample vials were loosely sealed with silicon caps and cultured at 37˚C under anaerobic conditions until a density of 3.0 McFarland Standard. After the incubation, sample vials were immediately sealed tightly with silicon caps. One milliliter of each sample vial headspace air was aspirated by puncturing a silicon cap with the needle of the gastight syringe (Termosyringe® SS-02SZ2232), and immediately injected into the sensor gas chromatograph. The VSC levels of the sample vial headspace were measured using the sensor gas chromatograph (ODSA-P3-A).

2.10. Statistical Analysis

The number of total bacteria and oral Veillonella species and the proportions of the anaerobes, Streptococcus species, Fusobacterium species, oral Veillonella species, and Porphyromonas and Prevotella species in samples of tongue biofilms from healthy subjects without halitosis and halitosis subjects were compared using the Mann-Whitney U test. P values < 0.05 were considered to be significant.

3. Results

3.1. Development of Selective Media

3.1.1. Selection of the Base Medium

A base medium was selected for the growth of oral Veillonella species. All of the oral Veillonella species grew well on TS-LAC-Blood. The growth of V. atypica, V. denticariosi, V. parvula, and V. dispar was enhanced by supplementing with 2.1% sodium lactate, whereas that of V. tobetsuensis and V. rogosae was markedly inhibited on TS and TS-LAC free from sheep blood (data not shown). Therefore, TS-LAC-Blood was ultimately selected as the base medium.

3.1.2. Susceptibility to Antibiotics

Oral Veillonella species were more resistant to vancomycin than oral Gram-positive bacteria, such as Streptococcus, Actinomyces, and Corynebacterium species. The minimal inhibitory concentration (MIC) of vancomycin for oral Veillonella species was 60 μg/ml. Oral Gram-positive bacteria were sensitive to 16 μg/ml of vancomycin. Oral Veillonella species were more resistant to oxacillin than oral Gram-negative rods, such as Fusobacterium, Porphyromonas, and Prevotella species. The MIC of oxacillin for oral Veillonella species was 8 μg/ml. Oral Gram-negative bacteria were sensitive to 1 μg/ml of oxacillin. Neisseria species, which are Gram-negative cocci similar to Veillonella species, were also resistant to vancomycin and oxacillin, but were inhibited in an aerobic culture.

3.1.3. Composition of the New Selective Medium

The new selective medium, designated Oral Veillonella selective medium (OVSM), comprised the following (per liter): 40 g of tryptic soy agar, 21 ml of
sodium lactate, 50 ml of sheep blood, 16 mg of vancomycin, and 1 mg of oxacillin. Sheep blood and antibiotics, i.e., vancomycin and oxacillin, were added after the base medium had been sterilized and cooled to 50˚C.

3.2. Multiplex PCR

3.2.1. Primer Design

Twelve specific primers covering the upstream region of the rpoB, gltA, and dnaK gene sequences of six oral *Veillonella* species were designed in the present study (Figures 1-3). Specific forward primers were designated as VaF2 for *V. atypica*, VtF2 for *V. tobetsuensis*, VrF2 for *V. rogosae*, VpF2 for *V. parvula*, VdisF2 for *V. dispar*, and VdenF2 for *V. denticariosi*, whereas specific reverse primers were designated as VaR2 for *V. atypica*, VtR2 for *V. tobetsuensis*, VrR2 for *V. rogosae*, VpR2 for *V. parvula*, VdisR2 for *V. dispar*, and VdenR2 for *V. denticariosi*. The amplicon sizes of *V. atypica*, *V. tobetsuensis*, *V. rogosae*, *V. parvula*, *V. dispar*, and *V. denticariosi* were 93, 186, 325, 397, 516, and 607 bp, respectively.

3.2.2. Detection Limit

Our multiplex PCR method for identifying and detecting six oral *Veillonella* species, i.e., *V. atypica*, *V. tobetsuensis*, *V. rogosae*, *V. parvula*, *V. dispar*, and *V. denticariosi* successfully amplified DNA fragments of the expected size for each species (Figure 4). The detection limit was assessed in the presence of titrated bacterial cells, and the sensitivity of the PCR assay was between 5 × 1 and 5 × 10

![Figure 1. Locations and sequences of species-specific primers for the dnaK gene of *V. dispar*. The nucleotide sequence of each primer has been underline.](image-url)
Figure 2. Locations and sequences of species-specific primers for the gltA gene of V. denticariosi and V. parvula. The nucleotide sequence of each primer has been underlined.

Figure 3. Locations and sequences of species-specific primers for the rpoB gene of V. atypica, V. rogosae, and V. tobetsuensis. The nucleotide sequence of each primer has been underlined.
The primer mixture contained VaYF, VaYR, VdenYF, VdenYR, VpYF, VpYR, VdisYF, VdisYR, VrTF, VrTR, VtYF, and VtYR. Lanes: 1, Veillonella atypica DSM 20739; 2, Veillonella tobetsuensis JCM 17876; 3, Veillonella rogosae JCM 15642; 4, Veillonella parvula JCM 12972; 5, Veillonella dispar DSM 20735; 6, Veillonella denticariosi JCM 15641; 7, Mixture of V. atypica, V. tobetsuensis, V. rogosae, V. parvula, V. dispar, and V. denticariosi; 9, S. goldonii ATCC 10558; 10, S. oralis ATCC 10557; 11, S. sanguinis ATCC 10556; 12, S. salivarius JCM 5707; 13, S. anginosus ATCC 33397; 14, S. mutans NCTC 10449; 15, Actinomyces naeslundii ATCC 12104; 16, A. oris ATCC 27044; 17, A. odontolyticus ATCC 17929; 18, A. israelii ATCC 12102; 19, Corynebacterium matruchotii ATCC 14266; 20, C. durum ATCC 33449; 21, Neisseria sicca ATCC 29256; M, molecular size marker (100-bp DNA ladder).

**Figure 4.** Multiplex PCR assay for identifying Veillonella species.

CFU per PCR template (5.0 μl) for the V. atypica-specific primer set with strain DSM 20739, the V. tobetsuensis-specific primer set with strain JCM 17876, the V. tobetsuensis-specific primer set with strain JCM 17876, the V. rogosae-specific primer set with strain JCM 15642, the V. parvula-specific primer set with strain JCM 12972, the V. dispar-specific primer set with strain DSM 20735, and the V. denticariosi-specific primer set with strain JCM 15641 (data not shown).

### 3.2.3. Assay of Representative Oral Bacteria

Some Streptococci, Actinomyces, Neisseria, and Corynebacterium species were used as representative oral bacteria in PCR using the designed primer set. No amplicons were produced from any of the representative oral bacteria (**Figure 4**).

### 3.3. Recovery of Oral Veillonella Species and Inhibition of Other Representative Oral Bacteria on Selective Medium

**Table 1** shows the recovery of oral *Veillonella* species on VA and OVSM relative to TS-LAC-Blood. The average growth recoveries of the oral *Veillonella* species reference strains and isolates on VA and OVSM were 14.5 (range: 0 - 29.7) and 98.4% (range: 93.3 - 99.9), respectively. The growths of *V. tobetsuensis* and *V. denticariosi* were markedly inhibited on VA.

### 3.4. Clinical Examination

The detection frequencies of oral *Veillonella* species in tongue biofilm samples from healthy subjects without halitosis (n = 50) and halitosis subjects (n = 50) are shown in **Table 2**. The total VSC levels of healthy and halitosis subjects were 78.2 and 812.6 ppb, respectively. The mean numbers of total bacteria in healthy
and halitosis subjects were $1.43 \times 10^7$ CFU/ml and $5.21 \times 10^7$ CFU/ml, respectively. Oral *Veillonella* species were detected in all samples from healthy and halitosis subjects. The mean numbers of oral *Veillonella* species in healthy and halitosis subjects were $3.97 \times 10^7$ CFU/ml (range: $7.0 \times 10^6$ - $1.3 \times 10^7$) and $2.58 \times 10^7$ CFU/ml (range: $4.7 \times 10^6$ - $5.4 \times 10^7$), respectively. The mean numbers of total bacteria and oral *Veillonella* species in tongue biofilm samples were significantly higher in halitosis subjects than in healthy subjects ($P < 0.01$).

Figure 5 shows a comparison of the bacteria flora in tongue biofilms between the 2 groups. The proportions of anaerobe and *Veillonella* species were significantly higher in halitosis subjects than in healthy subjects ($P < 0.05$). Increases in anaerobe species in the tongue biofilm samples of halitosis subjects were attributed to elevations in oral *Veillonella* species, which are anaerobic Gram-negative cocci. No significant differences were observed in the proportions of *Fusobacterium*, *Porphyromonas*, and *Prevotella* species between the 2 groups. Comparisons of oral *Veillonella* species in tongue biofilms between the 2 groups are shown in Table 3. The average CFU of each oral *Veillonella* species was higher in halitosis subjects than in healthy subjects. *V. rogosae* was predominant and detected in all subjects, followed by *V. tobtuensis*, *V. atypica*, and *V. dispar*. *V. denticariosi* and *V. parvula* were rarely detected in both groups.

| VSCs (ppb)          | No. of total bacteria (CFU) | No. of oral *Veillonella*-positive subjects (% frequency) | No. of oral *Veillonella* species (CFU) |
|---------------------|-----------------------------|----------------------------------------------------------|------------------------------------------|
| Healthy subjects without halitosis (n = 50) | 78.2 65.8 8.2 4.2 | $1.43 \times 10^7*$ | 50 (100) | $3.97 \times 10^7*$ |
| Halitosis subjects (n = 50) | 812.6 772.3 24.6 15.7 | $5.21 \times 10^7*$ | 50 (100) | $2.58 \times 10^7*$ |

The threshold level for genuine halitosis was defined as >200 ppb total VSCs in mouth air. *Mann-Whitney U test; $p < 0.01$.

Figure 5. Comparison of the bacteria flora in tongue biofilm samples between 2 groups.
Table 3. Comparison of oral Veillonella species in tongue biofilms between 2 groups.

|                                | Healthy subjects without halitosis (n = 50) | Halitosis subjects (n = 50) |
|--------------------------------|---------------------------------------------|-----------------------------|
|                                | No. of positive subjects (%) | Average CFU | No. of positive subjects (%) | Average CFU |
| Veillonella atypica             | 42 (84) | $7.56 \times 10^5$ | 44 (88) | $1.30 \times 10^6$ |
| Veillonella denticariosi        | 0 (0)   | 0                  | 2 (4)   | $1.07 \times 10^5$ |
| Veillonella dispar              | 18 (36) | $4.20 \times 10^5$ | 23 (46) | $1.13 \times 10^6$ |
| Veillonella parvula             | 1 (2)   | $1.10 \times 10^6$ | 7 (14)  | $6.20 \times 10^5$ |
| Veillonella rogosae             | 50 (100)| $1.93 \times 10^5$ | 50 (100)| $1.35 \times 10^5$ |
| Veillonella tobetsuensis        | 47 (94) | $1.18 \times 10^5$ | 50 (100)| $9.11 \times 10^6$ |

Figure 6. Stereomicroscope images of each oral Veillonella species colony on OVSM.

In the first isolation, colonies of oral Veillonella species on OVSM commonly had a smooth and circular appearance. The colony color and average colony size of oral Veillonella species on OVSM were translucent light white and 1.0 mm in diameter, respectively (Figure 6).

3.5. VSC-Producing Abilities of Oral Veillonella Species and Other Representative Oral Bacteria in Vitro

Comparisons of VSC-producing abilities among six oral Veillonella species and other representative oral bacteria are shown in Table 4. F. nucleatum produced the highest VSC level, followed by F. nucleatum, P. gingivalis, P. nigrescens, P. intermedia, and six oral Veillonella species.

4. Discussion

Halitosis is a relatively common condition in which an individual either has bad breath or perceives oneself to have an offensive mouth odor. Although it has
Table 4. VSC-producing ability of Veillonella species and other representative oral bacteria in vitro.

| Ranking | Bacteria species          | VSCs (ppb) |  |  |  |
|---------|---------------------------|------------|---|---|---|
|         |                           | Total | H$_2$S | CH$_3$SH | (CH$_3$)$_2$S |
| 1       | Fusobacterium nucleatum   | 32085.2 | 17174.7 | 14910.5 | 0 |
| 2       | Porphyromonas gingivalis  | 31708.8 | 15030.2 | 16678.6 | 0 |
| 3       | Prevotella nigrescens     | 18523.2 | 17537.1 | 986.1 | 0 |
| 4       | Prevotella intermedia     | 16357.6 | 14301.2 | 2056.4 | 0 |
| 5       | Veillonella atypica       | 14484.5 | 12041.7 | 2442.8 | 0 |
| 6       | Veillonella dentocariosi  | 11829.6 | 11829.6 | 0 | 0 |
| 7       | Veillonella rogosae       | 11860.3 | 11860.3 | 0 | 0 |
| 8       | Veillonella dispar        | 11679.1 | 11679.1 | 0 | 0 |
| 9       | Veillonella parvula       | 11594.7 | 10186.7 | 1408.0 | 0 |
| 10      | Veillonella tobetsuensis  | 10954.1 | 10133.0 | 821.1 | 0 |
| 11      | Neisseria sicca          | 9673.5 | 8835.1 | 838.4 | 0 |
| 12      | A. actinomycetemcomitans | 9588.5 | 9588.5 | 0 | 0 |
| 13      | Tannerella forsythia     | 6246.5 | 6246.5 | 0 | 0 |
| 14      | Streptococcus sanguinis   | 4909.3 | 2792.1 | 2117.2 | 0 |
| 15      | Actinomyces israelii     | 4977.5 | 4977.5 | 0 | 0 |
| 16      | Streptococcus salivarius | 3758.7 | 3206.5 | 0 | 0 |
| 17      | Rothia aeria             | 3303.6 | 3262.8 | 40.8 | 0 |
| 18      | Actinomyces oris         | 2727.4 | 440.5 | 2286.9 | 0 |
| 19      | Streptococcus oralis     | 2577.7 | 2577.7 | 0 | 0 |
| 20      | Leptotrichia buccalis    | 2048.2 | 1683.7 | 364.5 | 0 |
| 21      | Corynebacterium durum    | 1753.6 | 541.5 | 1148.0 | 64.1 |
| 22      | Rothia dentocariosa      | 1735.5 | 729.8 | 938.5 | 67.2 |
| 23      | C. matruchotii           | 1165.5 | 361.3 | 804.2 | 0 |
| 24      | Rothia mucilaginosa      | 1149.6 | 39.1 | 1110.5 | 0 |
| 25      | Actinomyces odontolyticus| 1118.5 | 988.4 | 120.1 | 0 |
| 26      | Actinomyces naeslundii   | 891.7 | 196.2 | 679.6 | 15.9 |

multifactorial origins, bad breath originates from the oral cavity in most cases [33]. The causes of bad breath, except for an oral origin, include nasal and pharyngeal infections, respiratory conditions, gastrointestinal issues, metabolic conditions, such as diabetes, and liver diseases [33]. Halitosis originating from the oral cavity is caused by products generated through bacterial metabolic degradation. In individuals with a healthy oral cavity, an important site for the accumulation of bacteria associated with halitosis is the dorsum of the tongue, particul-
larly its posterior portion, which provides a suitable environment for the growth of anaerobes because a low oxygen concentration is present in the deep crypts of the tongue [33]. Poor oral hygiene that results in the accumulation of bacterial biofilms in subgingival areas and that may lead to periodontal disease has also been associated with halitosis [34].

VSCs, which include $H_2S$, $CH_3SH$, and $(CH_3)_2S$, are considered to be the primary compounds responsible for halitosis originating from the oral cavity, although amines (cadaverine, putrescine, and indole) and short-chain fatty acids (isobutyric and isovaleric acids) also contribute to oral malodor. VSCs are generated through enzymatic modifications to sulfur-containing amino acids (cysteine and methionine), which are made available following the proteolytic degradation of proteins or glycoproteins [33]. Bacteria that have been classically associated with halitosis include oral Veillonella species, *F. nucleatum*, *P. intermedia*, *P. gingivalis*, and *Treponema denticola* [25] [33]. Most of these bacteria have the ability to produce $H_2S$, one of the major components of halitosis. Washio et al. [25] focused on oral malodor in patients without oral diseases, such as periodontitis and dental caries, and reported that the predominant $H_2S$-producing bacteria were not periodontitis-related bacteria, but were mainly indigenous bacteria of the oral cavity, such as the genus *Veillonella*.

VA is used worldwide as the selective medium for *Veillonella* species. In our pilot study, VA inhibited the growth of some *Veillonella* species. The findings obtained also indicated that VA was not appropriate for investigating the prevalence of oral *Veillonella* species. Therefore, a novel suitable selective medium is needed to accurately assess the prevalence of oral *Veillonella* species involved in severe early childhood caries and intraradicular infections as well as halitosis in the oral cavity. In the present study, oral *Veillonella* species grew better on TS-LAC-Blood than on media that did not contain lactic acid and sheep blood. *Veillonella* species utilize lactic acid as carbon and energy sources instead of carbohydrates [3] [4]. Lactic acid and animal blood have been identified as growth factors that promote the growth of these organisms.

Oral *Veillonella* species were more resistant to vancomycin and oxacillin than other representative oral bacteria. The growth of the representative oral bacterial strains used in the present study was inhibited by the addition of 16 mg/L vancomycin and 1 mg/L oxacillin to TS-LAC-Blood. All of the oral *Veillonella* reference strains and isolates tested grew well on the new selective medium, designated as OVSM, while the growth of other bacteria was markedly inhibited (data not shown). Moreover, OVSM allowed the identification of oral *Veillonella* species based on their characteristic colony morphologies.

Moreover, characteristic colony morphologies on OVSM allowed oral *Veillonella* species to be easily distinguished.

*Veillonella* strains are relatively easy to identify at the genus level, but remain difficult to identify at the species level because there are currently no useful phenotypic or biochemical examinations to distinguish them [19]. To overcome this issue, Mashima *et al.* established a novel one-step PCR method with spe-
cies-specific primer sets based on the variable region of the *rpoB* gene sequences of oral *Veillonella* species [27]. However, the findings of our pilot study showed that the size of each PCR fragment by this method was similar; therefore, it was difficult to accurately identify each oral *Veillonella* species. Moreover, including DNA extraction, it took more than 5 hours to finish the identification. Therefore, a reliable identification method is needed to accurately assess the prevalence of oral *Veillonella* species.

In the present study, we designed species-specific primers with the already mentioned methods for the identification and detection of six *Veillonella* species using a PCR-based method. These primers were able to distinguish each *Veillonella* species and did not display cross-reactivity with representative oral bacteria. Moreover, we developed a one-step multiplex PCR method with the ability to identify and differentiate oral *Veillonella* species (*i.e.*, *V. atypica*, *V. dentiariosi*, *V. dispar*, *V. infantium*, *V. parvula*, *V. rogosae*, and *V. tobetsuensis*) using only one PCR tube per sample. Our multiplex PCR method is easy because the use of MightyAmp DNA Polymerase Ver.3 (Takara) means that DNA extraction is not necessary, and species identification and detection using this method only takes approximately 2 hours. Therefore, the method described herein will allow the prevalence of oral *Veillonella* species and their involvement in various infections to be fully clarified in future studies.

Previous studies [5] [6] [26] [27] [28] investigated the prevalence of oral *Veillonella* species using VA. In the present study using OVSM, oral *Veillonella* species were detected in all samples from healthy and halitosis subjects. This result demonstrated that oral *Veillonella* species are one of the main members of the human oral microbiome, which is consistent with previous findings [5] [6]. In the present study, *V. rogosae* was predominant and was detected in the samples of all subjects, followed by *V. tobetsuensis*, *V. atypica*, and *V. dispar*. Beighton et al. [26], Mashima et al. [27], and Djais et al. [28] also reported that *V. rogosae*, *V. atypica*, and *V. dispar* were the predominant *Veillonella* species in the human oral cavity, which is consistent with the present results. However, previous studies using VA reported that *V. tobetsuensis* was rarely detected in the human oral cavity [27] [28]. On the other hand, *V. tobetsuensis* was the second predominant *Veillonella* species in the present study using the novel selective medium, OVSM. Since VA inhibits the growth of *V. tobetsuensis*, previous findings may not have accurately reflected the prevalence of oral *Veillonella* species. In the present study, *V. denticariosi* and *V. parvula* were rarely detected in both groups, as previously reported [26] [27] [28]. Therefore, *V. denticariosi* and *V. parvula* do not appear to be a part of the normal microbiome in human tongue biofilms.

The mean numbers of oral *Veillonella* species in tongue biofilm samples were significantly higher in halitosis subjects than in healthy subjects (*P* < 0.01). The proportions of *Veillonella* species were significantly higher in halitosis subjects than in healthy subjects (*P* < 0.05), compared with those of *Fusobacterium*, *Porphyromonas*, and *Prevotella* species. In addition, six oral *Veillonella* species
produced high VSC levels, particularly H₂S, \textit{in vitro}. Higher production levels of VSCs were observed in the presence of cysteine, which is transformed into H₂S, ammonia, and pyruvate by cysteine desulphhydrase [35]. Accordingly, the monitoring of oral \textit{Veillonella} species levels may be useful as a clinical indicator for the diagnosis of genuine halitosis.

5. Conclusion

We developed a selective medium, designated OVSM, to isolate oral \textit{Veillonella} species in the oral cavity of humans. Since OVSM is highly selective for oral \textit{Veillonella} species, it will be useful for assessing the distribution and role of these organisms at various locations in humans. A novel selective medium (OVSM) and our multiplex PCR method as isolation and identification methods, respectively, for oral \textit{Veillonella} species may contribute to the diagnosis of halitosis as well as severe early childhood caries and intraradicular infections.

Authors’ Contribution

Ono Y., Fukatsu A. and Tsuzukibashi O. corrected the data. Ono Y. and Tsuzukibashi O. drafted and wrote the manuscript. The concept of this manuscript was devised by Ono Y. All authors read and approved the final manuscript.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] Marchandin, H., Teyssier, C., Campos, J., Jean-Pierre, H., Roger, F., Gay, B., Carlier, J.P. and Jumas-Bilak, E. (2010) \textit{Negativicoccus succinicivorans} Gen. Nov., Sp. Nov., Isolated from Human Clinical Samples, Emended Description of the Family \textit{Veillonellaceae} and Description of \textit{Negativicutes} Classis Nov., \textit{Selenomonadales} Ord. Nov. and \textit{Acidaminococcaceae} Fam. Nov. in the Bacterial Phylum \textit{Firmicutes}. \textit{International Journal of Systematic and Evolutionary Microbiology}, 60, 1271-1279. \url{https://doi.org/10.1099/ijs.0.013102-0}

[2] Mays, T.D., Holdeman, L.V., Moore, W.E.C., Rogosa, M. and Johnson, J.L. (1982) Taxonomy of the Genus \textit{Veillonella} Prévot. \textit{International Journal of Systematic and Evolutionary Microbiology}, 32, 28-36. \url{https://doi.org/10.1099/00207713-32-1-28}

[3] Foubert, E.L. and Douglas, H.C. (1948) Studies on the Anaerobic Micrococci. II. The Fermentation of Lactate by \textit{Micrococcus lactilyticus}. \textit{Journal of Bacteriology}, 56, 35-36. \url{https://doi.org/10.1128/jb.56.1.35-36.1948}

[4] Ng, S.K. and Hamilton, I.R. (1971) Lactate Metabolism by \textit{Veillonella parvula}. \textit{Journal of Bacteriology}, 105, 999-1005. \url{https://doi.org/10.1128/jb.105.3.999-1005.1971}

[5] Mashima, I., Theodorea, C.F., Thaweboon, B., Thaweboon, S., Scannapieco, F.A. and Nakazawa, F. (2017) Exploring the Salivary Microbiome of Children Stratified by the Oral Hygiene Index. \textit{PLOS ONE}, 12, e01852. \url{https://doi.org/10.1371/journal.pone.0185274}
[6] Mashima, I., Theodorea, C.F., Thaweboon, B., Thaweboon, S., Vichayanrat, T., Scannapieco, F.A. and Nakazawa, F. (2019) Characterization of Salivary Microbiome in Healthy Thai Children. *Asian Pacific Journal of Tropical Medicine*, 12, 163-169. https://doi.org/10.4103/1995-7645.257116

[7] Marriott, D., Stark, D. and Harkness, J. (2007) *Veillonella parvula* Discitis and Secondary Bacteremia: A Rare Infection Complicating Endoscopy and Colonoscopy? *Journal of Clinical Microbiology*, 45, 672-674. https://doi.org/10.1128/JCM.01633-06

[8] Mashima, I., Miyoshi-Akiyama, T., Tomida, J., Kutsuna, R., Washio, J., Takahashi, N., Nakazawa, F., Sato, T. and Kawamura, Y. (2019) Draft Genome Sequences of Two *Veillonella tobetsuensis* Clinical Isolates from Intraoperative Bronchial Fluids of Elderly Patients with Pulmonary Carcinoma. *Microbiology Resource Announcements*, 8, e00397-19. https://doi.org/10.1128/MRA.00397-19

[9] Periasamy, S. and Kolenbrander, P.E. (2010) Central Role of the Early Colonizer *Veillonella* Sp. in Establishing Multispecies Biofilm Communities with Initial, Middle, and Late Colonizers of Enamel. *Journal of Bacteriology*, 192, 2965-2972. https://doi.org/10.1128/JB.01631-09

[10] Kanasi, E., Dewhirst, F.E., Chalmers, N.I., Kent, R., Moore, A., Hughes, C.V., Pradhan, N., Loo, C.Y. and Tanner, C.R. (2010) Clonal Analysis of the Microbiota of Severe Early Childhood Caries. *Caries Research*, 44, 485-497. https://doi.org/10.1159/000320158

[11] Khemaleelakul, S., Baumgartner, J.C. and Pruksakorn, S. (2009) Identification of Bacteria in Acute Endodontic Infections and Their Antimicrobial Susceptibility. *Oral Surgery, Oral Medicine, Oral Pathology, Oral Radiology and Endodontology*, 94, 746-755. https://doi.org/10.1067/moe.2002.129535

[12] Peters, L.B., Wesselink, P.R., Buijs, J.F. and van Winkelhoff, A.J. (2001) Viable Bacteria in Root Dentinal Tubules of Teeth with Apical Periodontitis. *Journal of Endodontics*, 27, 76-81. https://doi.org/10.1097/00004770-200102000-00002

[13] Rogosa, M. (1965) The Genus *Veillonella* IV. Serological Groupings, and Genus and Species Emendations. *Journal of Bacteriology*, 90, 704-709. https://doi.org/10.1128/jb.90.3.704-709.1965

[14] Beighton, D., Silva-Boghossian, C.M., do Souto, R.M. and Colombo, A.P. (2012) Subgingival Microbial Profiles of Generalized Aggressive and Chronic Periodontal Diseases. *Archives of Oral Biology*, 57, 973-980. https://doi.org/10.1016/j.archoralbio.2012.02.003
ogy, 63, 1443-1449. https://doi.org/10.1099/jis.0.042515-0
[19] Mashima, I., Liao, Y.C., Miyakawa, H., Theodorea, C.F., Thawboon, B., Thawboon, S., Scannapieco, F.A. and Nakazawa, F. (2018) *Veillonella infantium* Sp. Nov., an Anaerobic, Gram-Stain-Negative Coccus Isolated from Tongue Biofilm of a Thai Child. *International Journal of Systematic and Evolutionary Microbiology*, 68, 1101-1106. https://doi.org/10.1099/ijsem.0.02632
[20] Kazor, C.E., Mitchell, P.M., Lee, A.M., Stokes, L.N., Loesche, W.J., Dewhirst, F.E. and Paster, B.J. (2003) Diversity of Bacterial Populations on the Tongue Dorsa of Patients with Halitosis and Healthy Patients. *Journal of Clinical Microbiology*, 41, 558-563. https://doi.org/10.1128/JCM.41.2.558-563.2003
[21] Persson, S., Edlund, M.B., Claesson, R. and Carlsson, J. (1990) The Formation of Hydrogen Sulfide and Methyl Mercaptan by Oral Bacteria. *Oral Microbiology and Immunology*, 5, 195-201. https://doi.org/10.1111/j.1399-302X.1990.tb00645.x
[22] Yaegaki, K. and Sanada, K. (1992) Biochemical and Clinical Factors Influencing Oral Malodor in Periodontal Patients. *Journal of Periodontology*, 63, 783-789. https://doi.org/10.1902/jop.1992.63.9.783
[23] Faveri, M., Feres, M., Shibli, J.A., Hayacibara, R.F., Hayacibara, M.M. and de Figueiredo, L.C. (2006) Microbiota of the Dorsum of the Tongue after Plaque Accumulation; an Experimental Study in Humans. *Journal of Periodontology*, 77, 1539-1546. https://doi.org/10.1902/jop.2006.050566
[24] Fukamachi, H., Nakano, Y., Okano, S., Shibata, Y., Abiko, Y. and Yamashita, Y. (2005) High Production of Methyl Mercaptan by L-Methionine-Deamino-Mercaptomethane Lyase from *Treponema denticola*. *Biochemical and Biophysical Research Communications*, 331, 127-131. https://doi.org/10.1016/j.bbrc.2005.03.139
[25] Washio, J., Sato, T., Koseki, T. and Takahashi, N. (2005) Hydrogen Sulfide-Producing Bacteria in Tongue Biofilm and Their Relationship with Oral Malodor. *Journal of Medical Microbiology*, 54, 889-895. https://doi.org/10.1099/jmm.0.46118-0
[26] Beighton, D., Clark, D., Hanakuka, B., Gilbert, S. and Do, T. (2008) The Predominant Cultivable *Veillonella* Spp. of the Tongue of Healthy Adults Identified Using *rpoB* Sequencing. *Oral Microbiology Immunology*, 23, 344-347. https://doi.org/10.1111/j.1399-302X.2007.00424.x
[27] Mashima, I., Theodorea, C.F., Thawboon, B., Thawboon, S. and Nakazawa, F. (2016) Identification of *Veillonella* Species in the Tongue Biofilm by Using a Novel One-Step Polymerase Chain Reaction Method. *PLOS ONE*, 11, e0157516. https://doi.org/10.1371/journal.pone.0157516
[28] Djas, A.A., Theodorea, C.F., Mashima, I., Otomo, M., Saitoh, M. and Nakazawa, F. (2019) Identification and Phylogenetic Analysis of Oral *Veillonella* Species Isolated from the Saliva of Japanese Children. *F1000Research*, 8, 616. https://doi.org/10.12688/f1000research.18506.5
[29] Rogosa, M., Fitzgerald, R.J., Mackintosh, M.E. and Beaman, J. (1958) Improved Medium for Selective Isolation of *Veillonella*. *Journal of Bacteriology*, 76, 455-456. https://doi.org/10.1128/jb.76.4.455-456.1958
[30] Marchandin, H., Teyssier, C., Siméon, D.B., Jean, P.H., Carriere, C. and Jumas, B.E. (2003) Intrachromosomal Heterogeneity between the Four 16S rRNA Gene Copies in the Genus *Veillonella*: Implications for Phylogeny and Taxonomy. *Microbiology*, 149, 1493-1501. https://doi.org/10.1099/mic.0.26132-0
[31] Tsuzukibashi, O., Uchibori, S., Kobayashi, T., Umezawa, K., Mashimo, C., Nambu, T., Saito, M., Hashizume-Takizawa, T. and Ochiai, T. (2017) Isolation and Identifi-
cation Methods of Rothia Species in Oral Cavities. *Journal of Microbiological Methods*, **134**, 21-26. [https://doi.org/10.1016/j.mimet.2017.01.005](https://doi.org/10.1016/j.mimet.2017.01.005)

[32] Krespi, Y.P., Shrime, M.G. and Kacker, A. (2006) The Relationship between Oral Malodor and Volatile Sulfur Compound-Producing Bacteria. *Otolaryngology*, **135**, 671-676. [https://doi.org/10.1016/j.otohns.2005.09.036](https://doi.org/10.1016/j.otohns.2005.09.036)

[33] Hughes, F.J. and McNab, R. (2010) Oral Malodour—A Review. *Archives of Oral Biology*, **53**, S1-S7. [https://doi.org/10.1016/S0003-9969(08)70002-5](https://doi.org/10.1016/S0003-9969(08)70002-5)

[34] Morita, M. and Wang, H.L. (2001) Association between Oral Malodor and Adult Periodontitis: A Review. *Journal of Clinical Periodontology*, **28**, 813-819. [https://doi.org/10.1034/j.1600-051x.2001.028009813.x](https://doi.org/10.1034/j.1600-051x.2001.028009813.x)

[35] Hiranmayi, K.V., Sirisha, K., Ramoji, R.M.V. and Sudhakar, P. (2017) Novel Pathogens in Periodontal Microbiology. *Journal of Pharmacy and Bioallied Sciences*, **9**, 155-163. [https://doi.org/10.4103/jpbs.JPBS_288_16](https://doi.org/10.4103/jpbs.JPBS_288_16)