

# Anaerobic and Aero Tolerant Bacterial Profile of Halitosis

Qasim Najem Thewaini<sup>1</sup>, Oda Mizil Yasser ALzamey<sup>2</sup>, Ameera Merbee Zarzoor ALFadili<sup>3</sup>

<sup>1</sup>College of Biotechnology, Al-Qasim Green University, Iraq

<sup>2</sup>College of Science, University of Babylon, Iraq

<sup>3</sup>Kut Technology Institute, Middle Technical University, Iraq

## Email address:

Thewaini@yahoo.com (Q. N. Thewaini)

## To cite this article:

Qasim Najem Thewaini, Oda Mizil Yasser ALzamey, Ameera Merbee Zarzoor ALFadili. Anaerobic and Aero Tolerant Bacterial Profile of Halitosis. *American Journal of Biomedical and Life Sciences*. Vol. 3, No. 3, 2015, pp. 33-35. doi: 10.11648/j.ajbls.20150303.11

**Abstract:** Bad breath "halitosis" is a frequent unpleasant odor of breath. Bad breath is infected by gram negative anaerobic bacteria in tongue coating. These bacteria have a tendency of producing foul-smelling sulphur containing gases called volatile sulphur compounds (VSCs). Both anaerobic and aero tolerant bacteria associated with human halitosis condition are being reported. The profile includes (*Prevotella intermedia* (6.66%), *Porphyromonas endontalis* (10%) and *Veillonella* spp. (13.3%). (*Erysipelothrix rhusiopathiae* (13.3%), *Streptococcus salivarius* (13.3%) and *Streptococcus oralis* (10%). This profile consists of common, soft tissue and hard tissue associated pathogen as well as an animal associated pathogens.

**Keywords:** Aerobic, Aerotolerant, Halitosis, Bacterial Profile

## 1. Introduction

Halitosis, oral malodor condition is multifactorial condition of human oral cavity. It may be a result of systemic disease such as gastrointestinal disorders, hepatic disease, diabetes, smoking and periodontal diseases(1). The most common mouth part related to halitosis is the tongue. Tongue associated bacteria produce malodorous compounds and fatty acids(2). Volatile sulfur compounds (VSCs) such as hydrogen sulfide, methyl mercaptan produce by oral bacteria in the stomach(3). The volatile sulfur compound are produced through Bacterial metabolism of sulfur amino acids such as cysteine and methionine(4). In various sites the oral cavity where they have easy access to nutrients in mouth microenvironment(5).

The foul-smelling breath produce in two steps;

- (i) Deglycosylation of glycoprotein by Gram-positive bacteria.
- (ii) proteolysis and amino acid utilization of the protein by Gram-negative bacteria<sup>(6) (7) (8) (9)</sup>.

The objective of the present work is to report on the profile of anaerobic and aerotolerant bacterial profile of halitosis condition.

## 2. Main Body

Thirty halitosis condition were diagnosed by professional

dentist and recommended to be abstain from eating odiferous food for 48 hr. before the assessment and refrain from drinking coffee, tea, or juice and smoking(10). Tongue coating material were swabbed by sterile cotton swab then immersed into tubes containing transport media. On reaching Laboratory swabs. were streaked on to Trypticase Soy Agar and Blood Agar plates in duplicate, one for aerobic and the other for anaerobic culture procedures (11). Growth were identified through manual direct, culture, biochemical, antibiogram sensitivity, Api 20 A, and Vitek 2 system(12) (13) (14) (15).

## 3. Result & Discussion

The bacterial profile studies were shown in table 2,3,4,5 and 6. Anaerobic and aerotolerant bacteria were noted. There were including gram negative & gram positive bacteria from both cocci and rods. Commonsal, soft, and hard tissue associated pathogens were noted. Vitek 2 confirm Api 20 and both Api 20 and Vitek 2 confirmed the manual. identification methods and added species level ranking. *Prevotella intermedia*, *Porphyromonas endontalis*, *Veillonella* spp., *Erysipelothrix rhusiopathiae*, *Streptococcus salivarius*, *Streptococcus orals*. These findings were found in agreement with other workers tackling Halitosis Bacterial profiles (16,17,18). The frequency of isolation of these pathogens were higher in Halitosis than in control.

**Table (1).** The characteristics of human study groups.

Entity	Halitosis	Control
Age range	21- 60	21- 60
Age average	42.5 ± 10.9	36.73 ± 12.6
Sex		
- Male	17:30 (56.6%)	15:30 (50%)
-Female	13:30 (43.3%)	15:30 (50%)
Malodor	30:30(100%)	5:30(16.6%)
	Chronic Persistent	Transient

**Table (2).** Direct and Culture studies for patients and controls.

Procedures	Halitosis	Control
Direct		
Gram Positive-	13:30 (28.3%)	4:30 (13.3%)
- Gram Negative	9:30 (30%)	4:30 (13.3%)
Culture:		
-Gram Positive	11:30 (36.6)	4:30 (13.3%)
Gram Negative-	9:30 (30%)	4:30 (13.3%)
Total	20:30 (66.6%)	8:30 (26.6%)

**Table (3).** Profile of Culturable bacteria associated with Halitosis.

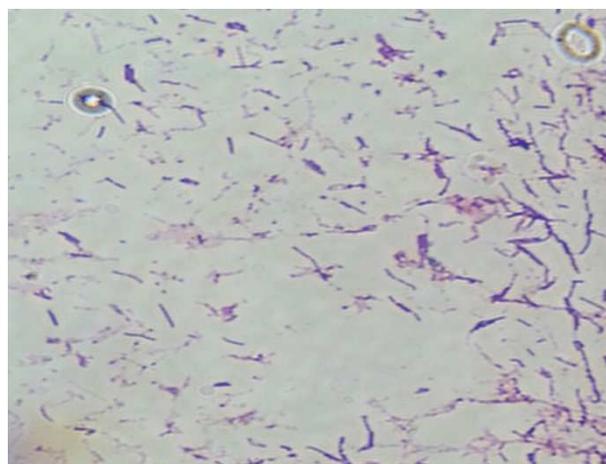
A-
1- Commensal
2- Associated soft tissue pathogen
3- Associated dental tissue pathogen
4- Animal associated pathogen
B-
1- Aerobic
2- Aerotolerant anaerobic
3- Strict anaerobic
C-
1- Gram positive rods
2- Gram positive cocci
3- Gram Negative rods
4- Gram Negative cocci

**Table (4).** Special Potency Antimicrobial Disks for presumptive & Main Distinguishing Biochemical Characters Identification of Anaerobic and Aerotolerant Bacteria.

Criteria	Microbes				
	<i>Veillonella spp</i>	<i>Prophyromonas spp</i>	<i>Prevotella spp</i>	<i>Erysipelothrix spp</i>	<i>Streptococcus spp</i>
Kanamycin (1000 mg)	S	R	S	V	S
Vanamycin (5 mg)	R	S	R	R	S
Collistin (10 mg)	S	R	V	R	R
Hemolysis	alpha	Beta	ND	Alpha	ND
Catalase	-	-	ND	-	-
Oxidase	-	-	-	-	-
Urease	-	-	-	-	-
H <sub>2</sub> S (TSI)	+	+	+	+	+

**Table (5).** Bacterial profile of Halitosis patients & Control.

Bacterial groups		
A-Gram Negative:	Control	Halitosis
1 <i>Prevotella intermedia</i>	1:30 (3.33%)	2:30 (6.66%)
2 <i>Porphyromonas endontalis</i>	1:30 (3.33%)	3:30 (10%)
3 <i>Veillonella spp</i>	2:30 (6.66%)	4:30 (13.3%)
B- Gram positive		
1 <i>Erysipelothrix rhusiopathiae</i>	0:30 (0.0%)	4:30(13.3%)
2 <i>Streptococcus salivarius</i>	2:30(6.66%)	4:30(13.3%)
3 <i>Streptococcus oralis</i>	2:30(6.66%)	3:30 (10%)

**Fig. 1.** Colonies of *Erysipelothrix rhusiopathiae* isolate on blood agar plate (48 hour incubation).**Fig. 2.** Gram- stained smear of *Erysipelothrix rhusiopathiae*.

## 4. Conclusion

1. It affix that a part of multifactorial halitosis condition is bacterial associated.
2. The profile covers commensal, soft tissue associated pathogen, hard tissue associated pathogen as well as Un-successful animal associated pathogens.
3. Both gram positive & negative anaerobic and aerotolerant cocci and rods.

4. Prevotellaintermedia, Porphyromonas endontalis, Veillonellaspp, Erysipelothrix rhusiopathiae, Streptococcus salivarius and Streptococcus oralis.

## References

- [1] Greenman, J.(1999).Microbial aetology of halitosis .In Dental Plaque Revisited. Oral Biofilms in Health and Disease, PP.419-442.Edited by H. N. Newman&M. Wilson. Cardiff. Biolin.
- [2] Nachnani, S (2011). "Oral malodor: Causes, assessment, and treatment". *Compendium of continuing education in dentistry (Jamesburg, N.J.:1995)*32 (1): 22–4, 26–8, 30–1; quiz 32, 34.
- [3] Ayers, K. M. & Colquhoun, A. N. (1998). Halitosis: causes, diagnosis, and treatment. *N Z Dent J* 94,156– 160.
- [4] Persson, S., Edlund, M. B., Claesson, R. & Carlsson, J. (1990). The formation of hydrogen sulfide and methyl mercaptan by oral bacteria. *Oral Microbiol Immunol* 5, 195–201.
- [5] Roldan, S., Herrera, D. & Sanz, M. (2003). Biofilms and the tongue: therapeutical approaches for the control of halitosis. *Clin Oral Investig* 7,189–197.
- [6] Sterer N, Shaharabany M, Rosenberg M. beta-Galactosidase activity and H<sub>2</sub>S production in Experimental oral biofilm. *J Breath Res* 2009; 3(1):016006.
- [7] Aas JA, Paster BJ, Strokes LN, Olsen I, Dewhirst FE, Defining the normal bacteria flora of the oral cavity. *J Clin Microbiol* 2005; 43(11):5721-32.
- [8] Ryan CS, Kleinberg IA comparative study of glucose and galactose uptake in pure cultures of human oral bacteria, salivary sediment and dental plaque.*Arch Oral Biol* 1995;40(8)742-52.
- [9] Washio J, Sato T, Koseki Takahashi T. Hydrogen Sulfide – producing bacteria in tongue biofilmand their relationship with oral malodor. *J Med Microbiol* 2005; 54(pt 9):889-95.
- [10] Q. Wang, B.J.chang, Th. V. Riley(2010)."Erysipelothrix rhusiopathiae ".*Journal of VeterinaryMicrobiology*140: 405 – 417.
- [11] Woodbine M: *Erysipelothrix rhusiopathiae* bacteriology and chemotherapy .*Bacterial Rev.*14:161-178, 1960.
- [12] Reboli AC, Farrar WE. The genus *Erysipelothrix*. In: Balows A, Truper HG, Dworkin M, Harder W, Schleifer K (eds) *The prokaryotes. A handbook on the biology of bacteria: ecophysiology, isolation, identification, applications*. New York, Springer-Verlag. 1992: 1629- 1642.
- [13] NCCLS: Performance standards for antimicrobial disk susceptibility tests .3d,National Committee For Clinical Laboratory Standards ,Villanova,1984.
- [14] Gresser, M.E., Shanholtzer ,C. J., Gerding , D.N., Garrett, C.R. and Deterson ,L.N.(1984) Evaluation of the 24h API 20A anaerobe system for identification of clostridium difficile .*J. clin. Microbiol.*19, 915-916.
- [15] Livermor DM, Struelens M, Amorim J, et al (2002)Multicentre evaluation of the VITEK2 Advanced Expert System for interpretive reading of antimicrobial resistance tests. *J Antimicrobchemother* 49:289-300.
- [16] Azechi, H., H. Nakamura, S. Yonezawa, I. Takahashi, and K. Suzuki. 1971. Sensitivity of freshly Isolated strains of *Erysipelothrix insidiosa* to antibiotics.*J.Jpn.Vet.Med.Assoc.*24:92-97.
- [17] Gorby, G. L., and J.E.Peacock.1988.*Erysipelothrix rhusiopathiae* endocarditis: microbiologic, Epidemiologic, and clinical features of an occupational disease .*Rev.Infect.Dis.*10:317-325.
- [18] Morita M, Wang HL. Association between oral malodor and adult periodontitis: a review. *J. Clin. Periodontol* 2001; 28:813–9.