



Meta-Analysis on Isolation Frequencies of Selective Pathogenic Bacteria in Complete Denture Patients

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Abstract

Introduction: A number of micro-organisms have been isolated from the oral cavity from dentulous patients. The chances of microorganisms to colonize complete denture surfaces as well as edentulous oral cavity are on the rise. Bacteria namely *Streptococcus spp.*, *Staphylococcus spp.*, *Enterobacter spp.*, *Klebsiella spp.*, *Pseudomonas spp.* and *E.coli* have been implicated in various cardiovascular, respiratory and gastrointestinal infections. All these bacterial spp. have been found to inhabit complete denture surfaces. Hence their isolation frequencies from complete denture have to be studied and compared by means of meta-analysis of similar studies.

Methodology: Pubmed, Google Scholar, Open J Gate, Web of Science data bases were searched for relevant articles.

Result: The isolation frequencies of the selective bacteria from the highest to the lowest is as follows: *Streptococcus spp.*(53.3%), *Staphylococcus spp.*(21.3), *Enterobacter spp.*(16.8%), *Klebisella spp.*(11%), *Pseudomonas spp.*(6.1%), and *E.coli* (5.5%).

Conclusion: Since the isolation frequencies of these bacteria are known, the appropriate disinfection methods of complete dentures targeting the various organisms have to be implemented to prevent systemic disease likely to be caused by their aspiration.

Keywords: pathogenic bacteria, complete dentures, isolation frequencies, meta-analysis.

Introduction

A number of micro-organisms have been isolated from the oral cavity from dentulous patients. The chances of microorganisms to colonize complete denture surfaces as well as edentulous oral cavity are on the rise. This may be due to the fact that the

prostheses act as niches for the growth of the microorganisms mainly due to the rough topographic surface of the complete dentures. Several studies have been done on yeast i.e. candidal spp. harboring on complete denture surfaces.

Comparatively very few studies have been done on bacteria colonizing complete dentures. Bacteria which are of considerable interest are those which are capable of being pathogenic to the systemic health of the patient. For example, Streptococcal spp. are known causative organisms of cardiovascular disease especially endocarditis¹. Other examples include Staphylococcal spp. and Klebsiella spp. which are potential respiratory pathogens^{1,3,4}. Pseudomonas spp. and Staphylococcus spp. are known to cause suppurative infections. Enterobacter spp. and E. coli have a positive role in gastro-intestinal infections^{2,5,6}.

All these bacterial spp. have been found to inhabit complete denture surfaces in both disease and healthy persons. An ecological imbalance of the micro-organisms decides whether the patient might either acquire disease or resistant to disease caused by micro-organisms^{1,2}. These organisms could lead to endocarditis, aspiration pneumonia, pneumonitis as well as gastro-intestinal infections and hence the isolation frequencies of these pathogenic organisms have to be compared and analysed by methodological method namely meta-analysis.

Methodology

The databases searched for the present study are J Gate, Web of science, Pubmed and Google scholar. The time frame for the article search is 26 years starting January 1991 to August 2016. The key words used in searching the data base include “Denture associated bacteria”, “Bacteria in complete dentures” and “Complete denture associated bacteria”.

For the key word “Denture associated bacteria”, the total articles found in Pubmed, J gate and web of science were 54, 36 and 40 respectively.

For the key word “Bacteria in complete dentures”, search results yielded via Pubmed , J gate and web of science were 177, 31 and 6 respectively.

For the keyword “Complete denture associated bacteria”, search results yielded via Pubmed , J

gate and web of science were 19, 8 and 6 respectively.

By Google scholar refined search for the key word “pathogenic denture plaque” 101 articles were obtained which was further refined to keywords “biofilms in edentulous oral cavity” which yielded 96 articles.

The articles were hand searched for getting the isolation frequencies of bacteria which are as follows:

1. Enterobacter spp.
2. Klebsiella spp.
3. Streptococcus spp.
4. Staphylococcus spp.
5. Pseudomonas spp.
6. E.coli

The analysis broadly included the isolation frequencies of bacterial species including the various bacterial genus /serotypes if so mentioned in the study.

Initially abstracts of 177 articles were read through to sort out the relevance of the articles to the topic. From the initial screening (*Level-1*) only 90 articles were related to the topic. Those articles which are based on isolation of yeast i.e. candidal spp. were not included in the analysis. Review articles were not included as much of data could not be collected from them. However, references from review articles were utilized to search for articles of interest.

The next level of screening (*Level-2*) included distinction of articles based on prostheses type. Only articles in which complete dentures were the sources of the samples were included in the analysis. Articles wherein samples were obtained from dentate individuals, RPDs, FPDs and Implants were not included. 55 articles were sorted out with this screening.

Level-3 screening included distinguishing articles based on whether the study was done in vitro or in vivo. This screening yielded 32 articles.

All the 32 articles were thoroughly examined for obtaining details of isolation frequencies (*Level-4*) screening. Among the 32 articles only 14 articles yielded isolation frequencies. Other articles

mentioned colony forming units' values, probability values as well as isolation frequencies of other bacteria not relevant to the topic. The screening method is illustrated in the following Flowchart:1.

Results and Discussion

The spreadsheet showing the isolation frequencies of the selective bacteria according to various studies is tabulated in Table 1. This data was subject to Meta analysis by comprehensive meta-analysis software version 2. The analyzed data and the respective forest plot for individual bacteria are illustrated in Tables: 2, 3,4,5,6, 7 and 8.

From the Tables: 2, 3 and 4 the isolation frequencies of *Enterobacter spp.* and *Klebsiella spp.* were 16.8 and 11 percent respectively. As seen from the Table:3, the study done by Goldberg et al⁸, the isolation frequency of *Enterobacter spp.* was 48 percent which was

statistically insignificant ($p > 0.05$). But careful analysis of the journal article showed that the combined isolation frequencies of *Enterobacter spp.* and *Klebsiella spp.* was found to 48 percent. Hence a higher isolation frequency was found.

From Table 2 and 5 the isolation frequency of *Staphylococcus spp.* was found to be 21.3 percent which is statistically significant ($p < 0.001$). But, the isolation frequency of *Streptococcus spp.* was found to be highest which was 53.3 percent that was statistically significant ($p < 0.001$) (Table 2 and 6). On the contrary Jaffari et al (2013)²⁰ have indicated that the isolation frequencies of *Streptococcus* and *Staphylococcus spp.* to be 100 percent.

With regard *Pseudomonas spp.* and *E.coli*, the isolation frequencies were 6.1 and 5.5 percent respectively which has statistical high significance ($p < 0.001$) (Table 2, 7 and 8).

TABLE:1 Representing The Spreadsheet Which Tabulates The Study Details, Selective Bacteria And Their Isolation Frequencies

NAME OF STUDY	(N)	YE AR	IN VIVO	SOUR CE	ENTEROBAC TER spp.	KLEBSIELL A spp.	STAPHYLOC OCUS spp.	STREPTOCOC OUS spp.	PSEUDOMON AS spp.	E.COLI
GOLDBERG ET AL	62	1997	IN VIVO	C.D	48					
DANILUK ET AL	57	2006	IN VIVO	C.D	17.5	8.80%	21.1	93.1	8.8	3.5
RITSUKO ET AL	5	1999	IN VIVO	C.D				31		
MARCELLE ET AL	41	2009	IN VIVO	C.D	9	1.5		4.5	7.5	
DOROTA ET AL	53	2014	IN VIVO	C.D	17.9	10.4	22.4		6	1.5
SEDGLEY ET AL	100	1995	IN VIVO	C.D	16	14			7	6
DANIELA ET AL	90	2012	IN VIVO	C.D			34.4	53.3		
KAKLAMANOS ET AL	148	2005	IN VIVO	C.D	7.4		21.6			
SUMI ET AL	50	2002	IN VIVO	C.D	18	16	10	0	2	8
HARDING ET AL	20	1991	IN VIVO	C.D			15	31		
LEWIS ET AL	100	2015	IN VIVO	C.D			30			
NISHI ET AL	96	2012	IN VIVO	C.D	3.5	0.7	13.4	93.7	2.8	
OCAMPO GRACIA ET AL	160	2015	IN VIVO	C.D	2		5	5		
KANONEN ET AL	51	1991	IN VIVO	C.D				84		

Table: 2 Representing The Comprehensive Isoaltion Frequencies Of Selective Bacteria After Meta-Analysis

BACTERIA	ISOLATION FREQUENCIES
Enterobacter spp.	16.8 (Table: 2)
Klebsiella spp.	11 (Table: 3)
Staphylococcus spp.	21.3 (Table: 4)
Streptococcus spp.	53.3 (Table: 5)
Pseudomonas spp.	6.1 (Table: 6)
E. coli	5.5 (Table: 7)

Table: 3 Representing the Forest Plot of Enterobacter spp.

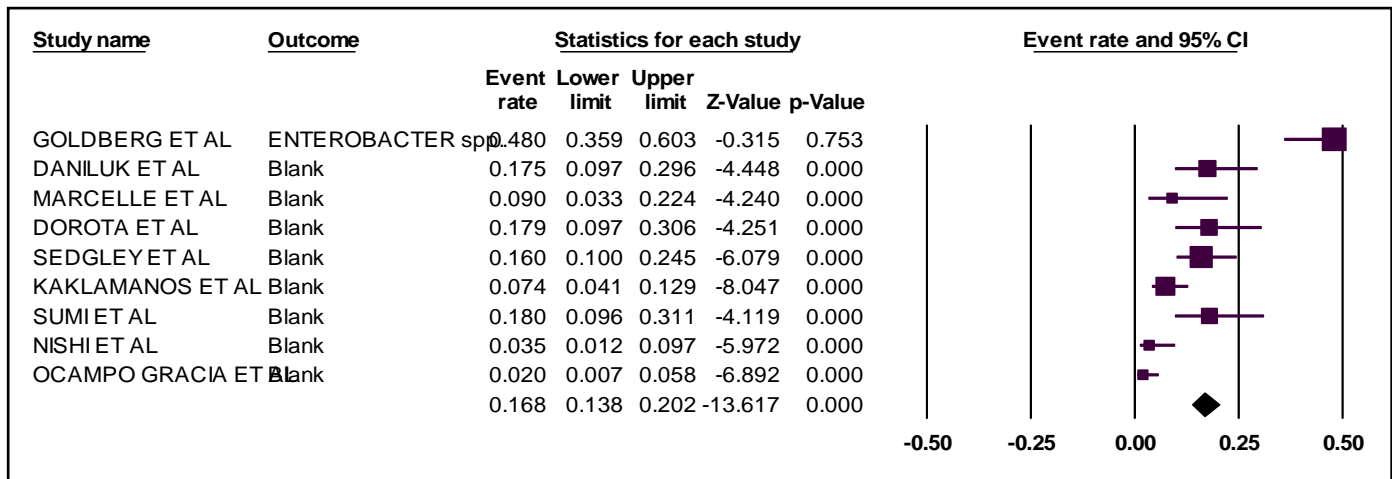


Table: 4 Representing The Forest Plot Of Klebsiella spp.

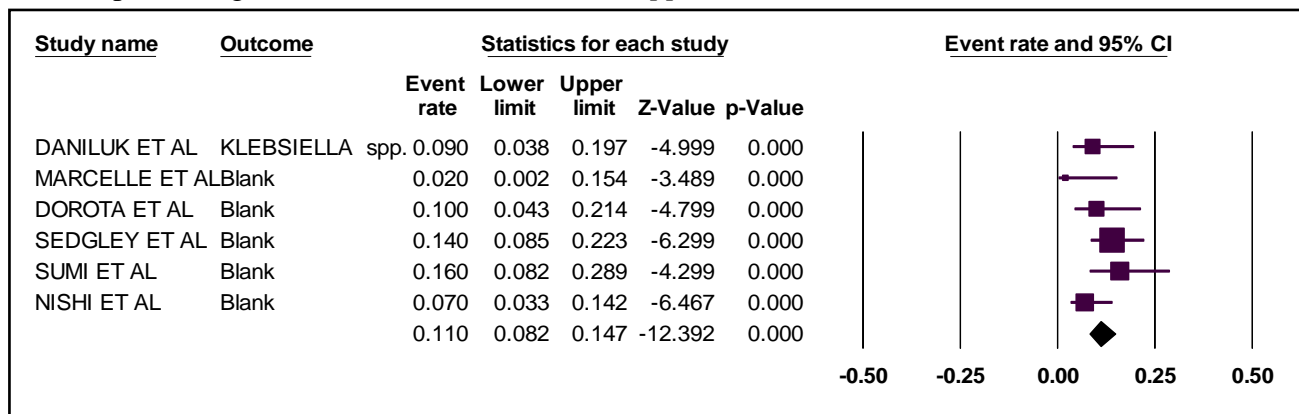


Table : 5 Representing The Forest Plot Of Staphylococcus spp.

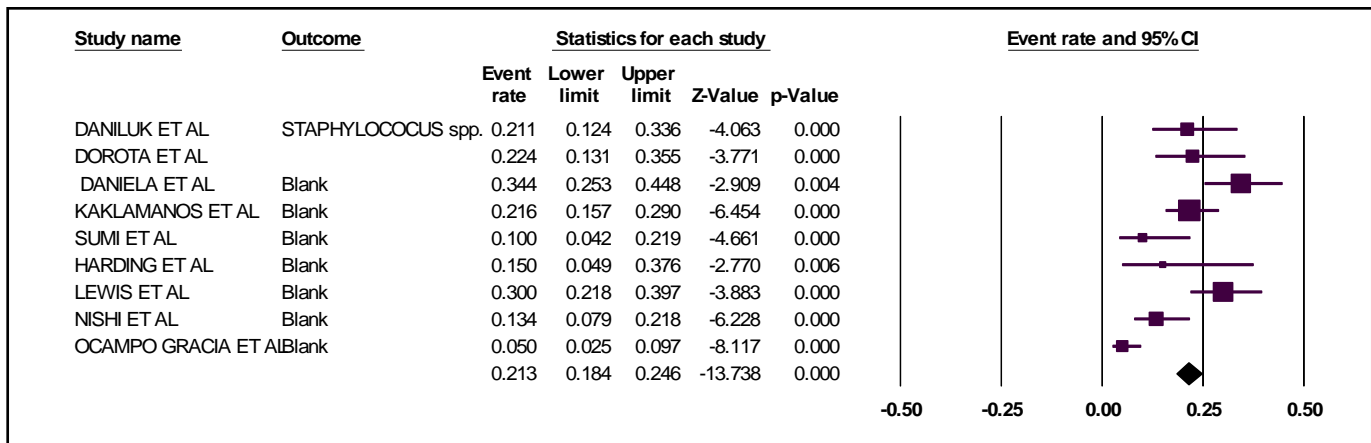


Table :6 Representing The Forest Plot Of *Streptococcus spp.*

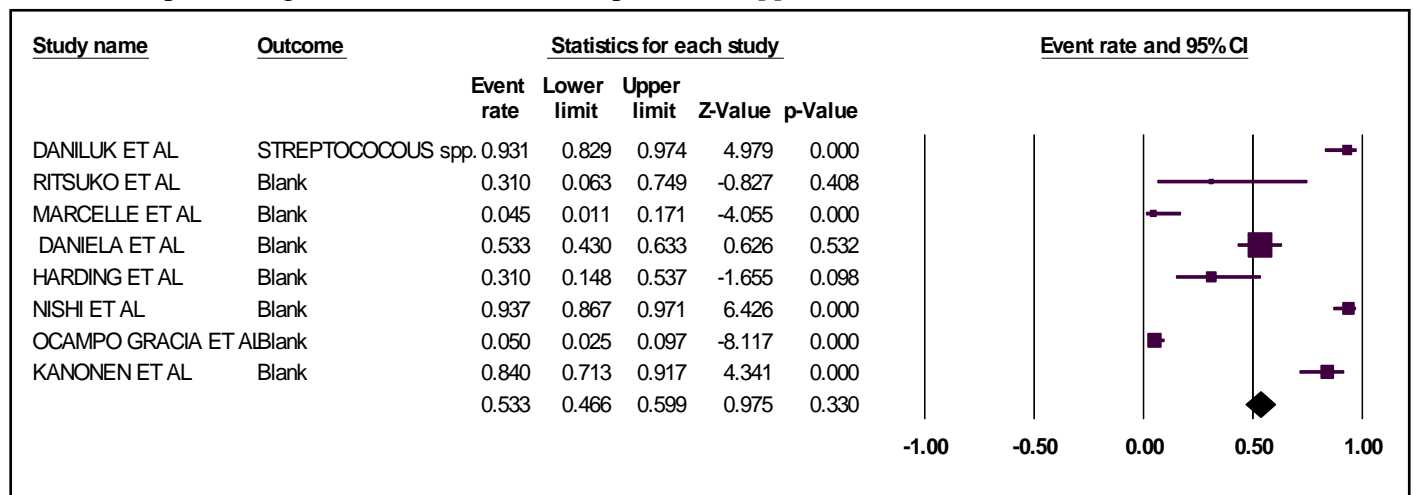


Table :7 Representing The Forest Plot Of *Pseudomonas spp.*

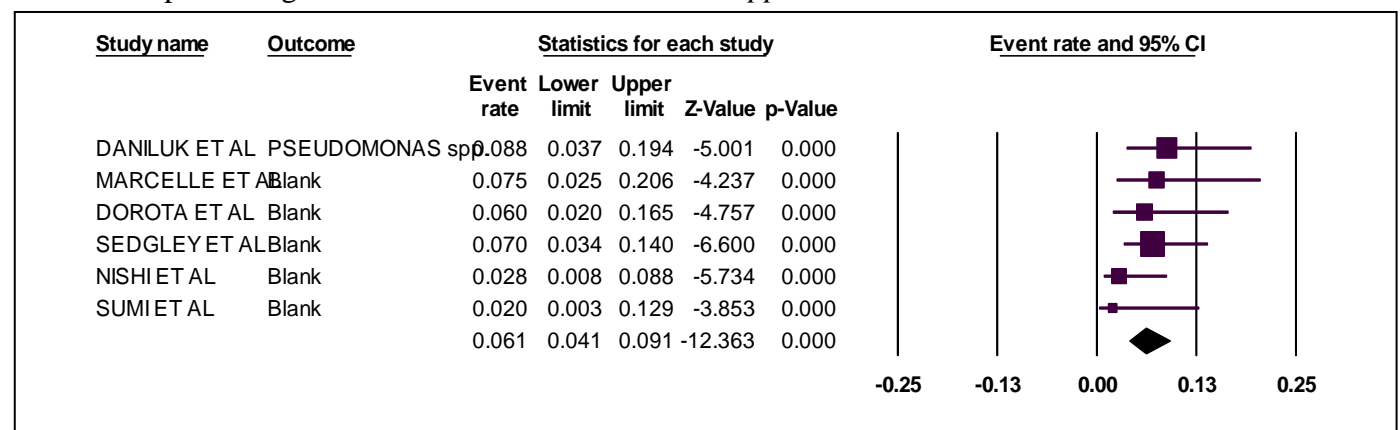
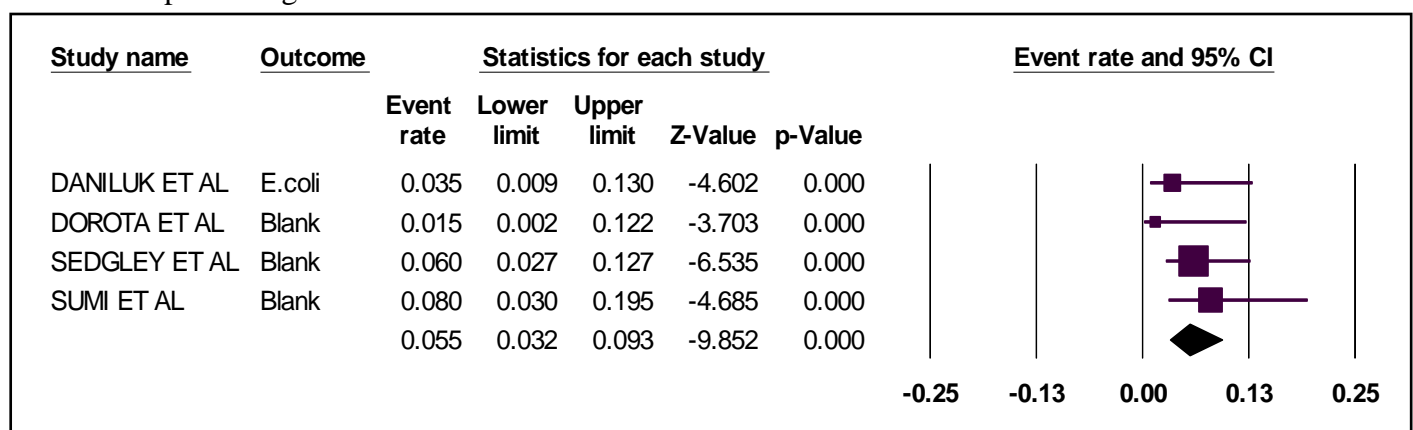
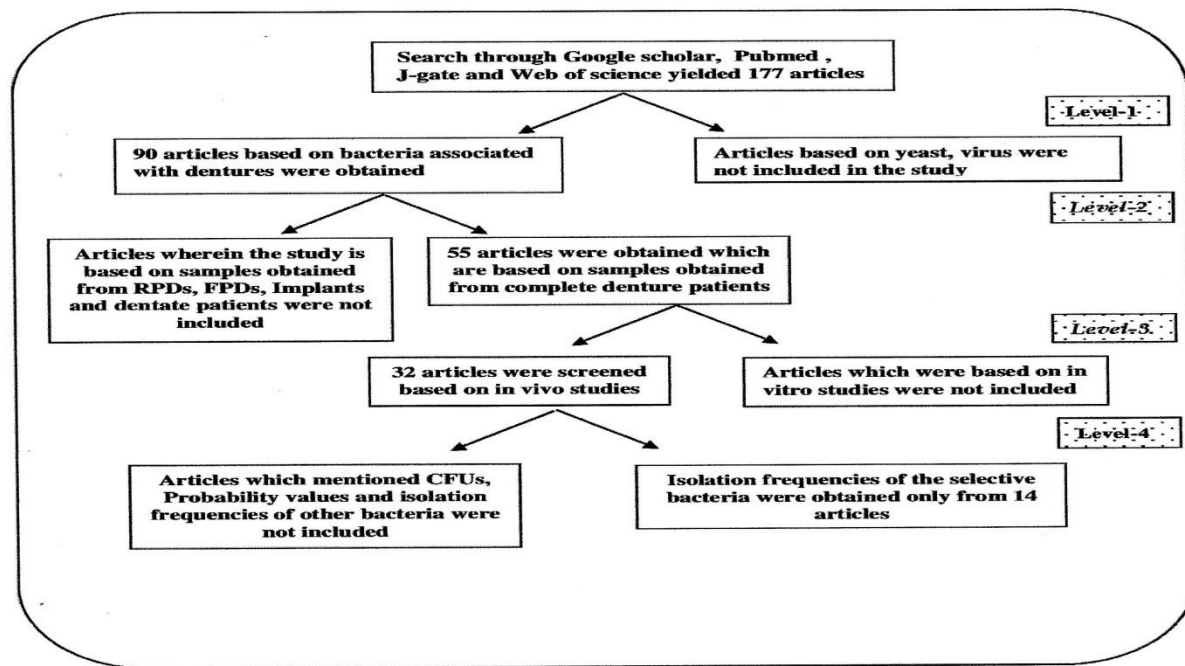


Table: 8 Representing The Forest Plot Of *E.Coli*





FLOWCHART : 1

Conclusion

From the meta-analysis it was found that several pathogenic bacteria were present in the complete dentures as evident from their isolation and microbiological examination. But the isolation frequencies of these selective pathogenic differed remarkably. The isolation frequencies of the selective bacteria from the highest to the lowest are as follows: *Streptococcus spp.*, *Staphylococcus spp.*, *Enterobacter spp.*, *Klebisella spp.*, *Pseudomonas spp.* and *E.coli*. Now that the isolation frequencies of these bacteria are known, the various disinfection procedures targeting these pathogenic bacteria have to be implemented to prevent possible aspiration/engulfment that could be an etiological factor for systemic conditions such as endocarditis, respiratory infections as well as gastrointestinal infections.

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