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Periodontal Health Status Of Patients With Maxillary Chronic Rhinosinusitis(Part 2: Microbiological Study)

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Abstract:
Background: *Periodontal diseases are inflammatory disorders result in damaged periodontium caused by bacterial plaque can be classified into gingivitis and periodontitis. The inflammation of maxillary sinuses which is of at least 12 consecutive weeks duration is Maxillary Chronic Rhinosinusitis (MCRS). MCRS related bacteria: Haemophilus influenzae(H. influenza),Streptococcus pneumonia (S.pneumoniae), Staphylococcus aureus (S.aureus), Moraxella catarrhalis (M.catarrhalis),Pseudomonas aeruginosa (P.aeruginosa) andStreptococcus pyogenes (S.pyogenes).*
Aims of the study*: Detection and comparing types and numbers of MCRS related bacteria from plaque samples in patients with and without MCRS. Determine the similarity in types of MCRS related bacteria from middle meatus swabs and plaque samples in patients with MCRS.*
Materials and methods: *Males and females patients (25-45 years), divided into two groups 1st group: 150 patients suffer from MCRS, 2nd group: 130 patients without MCRS. Clinical periodontal parameters recorded for four sites per tooth except third molars for all patients. Groups were divided into four subgroups: clinically Healthy periodontium, Gingivitis, Chronic periodontitis (CP.1) when probing pocket depth mean is (4-6 mm) and (CP.2) when it is (> 6mm). Middle meatus swabs taken from maxillary sinuses of patients with MCRS then, plaque samples from the two groups were obtained, then using of Blood Agar and Mac Conkey Agar for culturing of bacteria from each swab and plaque sample. Identification of MCRS related bacteria by using morphological appearance, light microscope, biochemical test or Viteck-2 machine as well as, manual counting method.*
Results: *In patients with MCRS, and S.pyogenes detected in highest percentages in Healthy and Gingivitis subgroups respectively, while, M.catarrhalis and P.aeruginosa presented in highest percentages in Gingivitis and CP.1 subgroups respectively. S.pneumoniae was the only type which found in CP.2 subgroup and with highest percentage. All types of MCRS bacteria detected in Gingivitis and CP.1 subgroups. In comparisons among subgroups of patients with MCRS there were highly significant differences regarding to S.aureus, S.pyogenes, M.catarrhalis and P.aeruginosa bacteria. While, 3 types only of MCRS related bacteria found in (22.3%) of plaque samples in patients without MCRS with highly significant differences among subgroups regarding to S.aureus, S.pneumoniae and S.pyogenes bacteria. The patients with MCRS had higher mean values than patients without MCRS concerning S.pyogenes and S.aureus at Healthy and Gingivitis subgroups, S.aureus and S.pneumoniae at CP.1 subgroup.51patients with MCRS of total 95 of patients with MCRS related bacteria had similar types of bacteria in middle meatus swabs and plaque samples at the same time.*
The greatest number of patients (22) with same type of bacteria which was S.aureus. While P.auroginosa had no similarity.
Conclusion: *63.33% of patients with MCRS had MCRS related bacteria in their plaque samples; the same types of MCRS related bacteria found in the same patient in plaque samples and middle meatus swabs at (54%) of patients with MCRS group. May be there is a causal relationship between periodontal diseases and maxillary chronic rhinosinusitis*

Key words: *Periodontal diseases, Maxillary chronic rhinosinusitis related bacteria.*

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I. Introduction

Periodontal diseases (PD) are inflammatory disorders cause damaged periodontal tissues by interactions between periodontopathic bacteria and the host defense system that affect the gingiva, the periodontal ligament and the alveolar bone (1) .The main cause of the PD is bacterial plaque, a sticky colorless microbial film that constantly forms on clean surfaces of teeth and hard surfaces in the oral cavity (2).PD can be classified into gingivitis and periodontitis. Gingivitis is inflammation of the gingiva which is reversible with improved and maintained oral hygiene (3). Periodontitis in which the inflammation extends into the tooth-supporting tissues, which results in periodontal ligament destruction and resorption of the alveolar bone, with

increased Probing Pocket Depth (PPD), recession or both. The clinical feature that distinguishes periodontitis from gingivitis is the presence of clinically detectable attachment loss [(4)]. Maxillary rhinosinisitisis inflammation of the maxillary sinuses. Maxillary Chronic Rhinosinusitis (MCRS) is the inflammation of at least 12 consecutive weeks duration [(5)]. Common bacteria found in MCRS include: *Haemophilus influenzae, Streptococcus pneumoniae, Staphylococcus aureus, Moraxella catarrhalis, Pseudomonas aeruginosa and Streptococcus pyogenes*[(6)].Dental plaque acts as reservoir for colonization of respiratory pathogens which can be shed into saliva, as well as oral bacteria can be cultured from lung fluid in a significant proportion. A good harmony was found between respiratory pathogens colonization in dental plaque and the presence of the same pathogen in the tracheal aspirate culture[(7)].It was proven that there is a relation between PD and MCRS clinically in the first part of this study[(8)]. This research was conducted to find the correlation between MCRS and PD microbiologically.

II. Materials & Methods

Following of the same steps in part 1[(8)] of this study which were as follows: Males and females patients at age (25-45) years collected from ENT out patients clinic in AL-Karama Teaching Hospital in AL- KUT \ Wasit\ Iraqdivided into 2 groups, the first group consisted of 150 patients with MCRS examined endoscopiccally by ENT specialist, while the second group consist of 130 patients without MCRS. Inclusion criteria include patients with bilateral MCRS ≥12 weeks duration and at least 20 teeth present. While the exclusion criteria included smokers or alcohol drinkers, pregnant ladies, on contraceptive pills or hormonal medication, on anti-inflammatory or anti-microbial therapy and who have undergone periodontal treatment during 3 months prior to the study, presence of removable or fixed appliances, patients without maxillary posterior teeth or patients complaining of unilateral MCRS and systemic diseases. Assessment of clinical periodontal parameters was performed by using Michigan O periodontal probe on four surfaces (mesial, buccal/labial, distal and lingual/palatal) of all teeth except third molars. These included: Plaque Index (PL.I)[(9)], Gingival Index (G.I) [(10)]Bleeding on Probing (BOP)[(11)], Probing Pocket Depth (PPD) and Clinical Attachment Level (CAL).According to this examination the periodontal health status of each subject fit into one of the four subgroups: 1. **Healthy** subgroup: patients with clinically healthy periodontium, this was defined by absence of any signs and symptoms of gingival inflammation and without periodontal pockets or clinical attachment loss.2. **Gingivitis** subgroup: patients with gingivitis which defined by presence of signs and symptoms of gingival inflammation and without periodontal pockets or clinical attachment loss. 3. Chronic Periodontitis (**CP.1)** subgroup: patients with chronic periodontitis and the mean of PPD is (4-6 mm).Mean= Sum of PPD/No of pockets. 4. Chronic Periodontitis (**CP.2)** subgroup: patients with chronic periodontitis and the mean of PPD is (> 6mm). Note: Chronic periodontitis (CP) defined as the presence of at least four sites with PPD ≥ 4 mm and clinical attachment loss of (1-2) mm or greater [(12)].Middle meatus swabs were taken from patients with MCRS then, plaque sample was obtained from maxillary first molar if extracted from second molar and if not available the second premolar and then first premolar from patients of both groups. Hence after using air sprays to dry the teeth and cotton rolls to isolate the area and prevent contamination from saliva and other tissues. Periodontal Universal curette was used to remove supragingival plaque (above the marginal gingiva) from one site of maxillary tooth to obtain plaque samples from patients with clinically healthy periodontium, and from patients with gingivitis. Plaque collected from the base of periodontal pocket in case of chronic periodontitis patients, from one pocket measures (4-6mm) in CP.1 subgroup, and from one pocket measures (>6mm) in CP.2 subgroup. Hence; we should avoid touching adjacent tissue to get pure plaque, and then transferred directly to swab [(13)]. Using transport media to maintain the growth and provide nutrition for bacteria while transporting to lab, using of Blood Agar and Mac Conkey Agar for culturing of each swab or sample of bacteria by streaking then, incubation for 24 hours at 37 ^{o}C. Identification of MCRS related bacteria from plaque samples and middle meatus swabs which include: *H. influenzae, S. aureus, S. pyogenes, S.pneumoniae,* M. catarrhalis *and P. aeruginosa* by morphological appearance, light microscope, biochemical tests or vitech-2 machine. Counting of each type of colonies of MCRS related bacteria manually to find colony forming unit. Statistical analysis by using of means, percentages, t-test and one way ANOVA. Graphical presentation by using: Column and pie charts. All the statistical analysis are significant (S) at P-value ≤0.05, highly significant (HS) at P-value ≤0.01 and non-significant (NS) at P-value > 0.05.We certify that this study involving human patients is in accordance with the Helsinky declaration of 1975 as revised in 2000 and that it has been approved by the relevant institutional Ethical Committee.

III. Results

From table (1), in patients with MCRS the Gingivitis and CP.1 subgroups, all types of MCRS related bacteria can be found and the highest percentages of *S.pyogenes* and *M.catarrhalis* were in Gingivitis subgroup, while the highest percentage of *S.aureus* was in Healthy subgroup, *S.pneumoniae* found in all subgroups with highest percentage in CP.2 subgroup that revealed only this type of bacteria. On the other hand, *M.catarrhalis*

in Gingivitis and CP.1 subgroups had nearly identical percentages. While, *P.aeruginosa* found in high percentage in CP.1 subgroup and less in Gingivitis subgroup. *H.Influenzae* not found in all subgroups therefore it was ignored in the results. The highest total number was demonstrated by *M.catarrhalis*. The least one was *S.pneumoniae*. From 150 patients with MCRS, there were 95 (63.33%) of them had MCRS related bacteria in their plaque samples and 55 (36.67%) of them these types of bacteria not present in their plaque samples, as shown in figure (1).Table (2) demonstrated highly significant differences regarding to *S.pyogenes, S.aureus, M.catarrhalis* and *P.aeruginosa* bacteria, but a non-significant difference about *S.pneumonuiae* bacteria. In table (3), there were non-significant differences regarding *S.pneumoniae*, between all pairs of subgroups. Furthermore, the comparison between CP.1 with Healthy subgroups revealed marginal significant difference regarding *S.pyogenes*. While, CP.1 with Gingivitis subgroups demonstrated highly significant differences about *S.aureus, M.catarrhalis* and *P.aeruginosa* bacteria, also Healthy with Gingivitis subgroups demonstrated highly significant difference about *S.pyogenes* bacteria, and the same result was revealed in the comparison between Healthy with CP.1 subgroups regarding *S.aureus*. Hence, *M.catarrhalis* and *P. aeruginosa* not found in Healthy subgroup, in addition at CP.2 subgroup detected only *S.pneumoniae* in their plaque samples, thus no comparisons could be made. In table (4), *M.catarrhalis* and *P.aeruginosa* were not found in the plaque samples of any subgroup of patients without MCRS, while *S.pyogenes, S.aureus* and *S.pneumoniae* detected in highest percentages at Healthy subgroup. The highest total number was demonstrated by *S.pneumoniae*. From 130 patients without MCRS, the MCRS related bacteria found in plaque samples of 29 (22.3%) patients and not found in plaque samples of 101(77.7%) patients, as demonstrated in figure (2).Table (5), demonstrated highly significant differences regarding to *S.pyogenes, S.aureus* and *S.pneumonuiae* bacteria. Table (6), showed significant differences regarding *S.pyogenes* and *S.aureus* in the comparison between Healthy with Gingivitis subgroups, *S.pneumoniae* in the comparison between Healthy with Gingivitis and each of them with CP.1 subgroups. While, CP.1 with both Healthy and Gingivitis subgroups revealed highly significant differences regarding *S.aureus*. In table (7), highly significant differences were demonstrated in Healthy and Gingivitis subgroups about *S.pyogenes*. Regarding *S.aureus* comparison revealed highly significant difference in Healthy subgroup, while, it was marginal significant difference in Gingivitis subgroup. Moreover highly significant difference was demonstrated in CP.1 and marginal significant difference in Healthy subgroups concerning *S.pneumoniae*. Figures (3,4,5) illustrated that the patients with MCRS had higher mean values than patients without MCRS concerning *S.pyogenes* and *S.aureus* at Healthy and Gingivitis subgroups, *S.aureus* and *S.pneumoniae* at CP.1 subgroup. Table (8), from 150 patients with MCRS group, there were 51patients had similar types of MCRS related bacteria in middle meatus swabs and plaque samples at the same time and 99 patients did not have this similarity. The greatest number of patients (22) with same type of bacteria which was *S.aureus*, followed by (17) for *S.pyogenes*, then (10) for *M.catarrhalis* and lastly only (2) for *S.pneumoniae*. Regarding *S.pyogenes*, the highest percentage of patients with similarity (47.06%) found in Gingivitis subgroup, while *S.aureus* demonstrated the highest percentage of patients with similarity (45.45%) in Healthy subgroup. Hence, *S.pneumoniae* similarity found only in CP.1 subgroup. *M.catarrhalis* similarity found in both Gingivitis and CP.1 subgroups. There were no similarity about *P.aeruginosa* and in CP.2 subgroup. Figure (6), showed the highest percentage of similarity was (43.13%) demonstrated by patients had *S.aureus* type of MCRS related bacteria, followed by patients had *S.pyogenes*, then *M. catarrhalis* and the least percentage revealed by patients had *S. pneumoniae*. From total (150) patients with MCRS group, (95) of them had MCRS related bacteria, while, 51 (from 95) was the total number of patients with MCRS group demonstrated similarity that represent (54%) regarding all types of MCRS related bacteria from plaque samples and middle meatus swabs, as illustrated in figure (7)

Table (1): Descriptive statistics of different types of MCRS related bacteria from plaque samples at each subgroup of patients with MCRS

Patients with MCRS subgroups	S.pyogenes		S.aureus		S.pneumoniae		M.catarrhalis		P.aeruginosa	
	CFU	%	CFU.	%	CFU	%	CFU	%	CFU.	%
Healthy	3575	33.8%	2979	47.7 %	396	21.66%	0	0	0	0
Gingivitis	6320	59.7%	2543	40.7 %	472	25.82%	5471	51.5%	964	33.8 %
CP.1	678	6.5%	725	11.6 %	370	20.24%	5150	48.5%	1885	66.2 %
CP.2	0	0	0	0	590	32.27%	0	0	0	0
Total	10573	100%	6247	100%	1828	100%	10621	100%	2849	100%

Table (2): Comparisons among subgroups of mean values of MCRS related bacteria from plaque samples of patients with MCRS by one way ANOVA test

Statistics	S.pyogenes	S.aureus	S.pneumoniae	M.catarrhalis	P.aeruginosa
F-test	7.52	7.10	1.85	11.25	18.75
p-value Sig.	0.000 HS	0.001 HS	0.152 NS	0.000 HS	0.000 HS

Table (3): Intersubgroups comparisons of mean values of MCRS related bacteria from plaque samples of patients with MCRS

Patients with MCRS subgroups	S.pyogenes		S.aureus		S.pneumoniae		M.catarrhalis		P.aeruginosa	
	t-test	p-value Sig.	t-test	p-value Sig.	t-test	p-value Sig.	t-test	p-value Sig.	t-test	p-value Sig.
Healthy×Gingivitis	6.93	0.003 HS	1.25	0.22 NS	0.53	0.60 NS	-	-	-	-
Healthy×CP.1	2.17	0.050 Marginal S	3.68	0.005 HS	0.27	0.76 NS	-	-	-	-
Healthy×CP.2	-	-	-	-	0.15	0.88 NS	-	-	-	-
Gingivitis×CP.1	0.18	0.861 NS	3.96	0.007 HS	0.51	0.59 NS	2.62	0.01 HS	4.7	0.009 HS
Gingivitis×CP.2	-	-	-	-	1.03	0.24 NS	-	-	-	-
CP.1×CP.2	-	-	-	-	1.74	0.33 NS	-	-	-	-

Table (4): Descriptive statistics of different types of MCRS related bacteria from plaque samples at each subgroup of patients without MCRS

Patients without MCRS subgroups	S.pyogenes		S.aureus		S.pneumoniae		M.catarrhalis		P.aeruginosa	
	CFU	%	CFU	%	CFU	%	CFU	%	CFU	%
Healthy	265	59.6 %	540	59.47 %	1052	60.9%	0	0	0	0
Gingivitis	180	40.4 %	278	30.6 %	218	12.6%	0	0	0	0
CP.1	0	0	90	9.93%	458	26.5%	0	0	0	0
CP.2	0	0	0	0	0	0	0	0	0	0
Total	445	100%	908	100%	1728	100%	0	0	0	0

Table (5): Comparisons among subgroups of mean values of MCRS related bacteria from plaque samples of patients without MCRS by one way ANOVA test

Statistics	S.pyogenes	S.aureus	S.pneumoniae
F-test	288.65	62.36	61.65
p-value Sig.	0.000 HS	0.000 HS	0.000 HS

Table (6): Intersubgroups comparisons of mean values of MCRS related bacteria from plaque samples of patients without MCRS

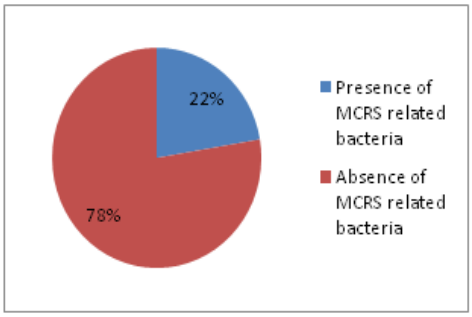
Patients without MCRS subgroups	S.pyogenes		S.aureus		S.pneumoniae	
	t-test	p-value Sig.	t-test	p-value Sig.	t-test	p-value Sig.
Healthy×Gingivitis	2.38	0.020 S	2.72	0.012 S	5.02	0.04 S
Healthy×CP.1	-	-	4.86	0.008 HS	2.65	0.049 S
Gingivitis×CP.1	-	-	4.47	0.01 HS	2.21	0.05 Marginal S

Table (7): The significance of differences in mean values of MCRS related bacteria from plaque samples between patients with MCRS and patients without MCRS subgroups.

Subgroups	S.pyogenes		S.aureus		S.pneumoniae	
	t-test	p-value Sig.	t-test	p-value Sig.	t-test	p-value Sig.
Healthy	5.87	0.002 HS	3.80	0.004 HS	2.09	0.05 Marginal S
Gingivitis	6.18	0.000 HS	2.15	0.05 Marginal S	0.76	0.62 NS
CP.1	-	-	0.68	0.565 NS	6.21	0.000 HS

Table (8): Descriptive statistics of patients with MCRS subgroups according to similarity of each type of MCRS related bacteria from middle meatus swabs and plaque samples

Patients with MCRS subgroups	S.pyogenes		S.aureus		S.pneumoniae		M.catarrhalis.		P.aeruginosa	
	Patient No.	Patient %	Patient No.	Patient %	Patient No.	Patient %	Patient No.	Patient %	Patient No.	Patient %
Healthy	3	17.65 %	10	45.45 %	0	0%	0	0%	0	0%
Gingivitis	8	47.06 %	7	31.83 %	0	0%	6	60%	0	0%
CP.1	6	35.29 %	5	22.72 %	2	100%	4	40%	0	0%
CP.2	0	0%	0	0%	0	0%	0	0%	0	0%
Total	17	100%	22	100%	2	100%	10	100%	0	0%



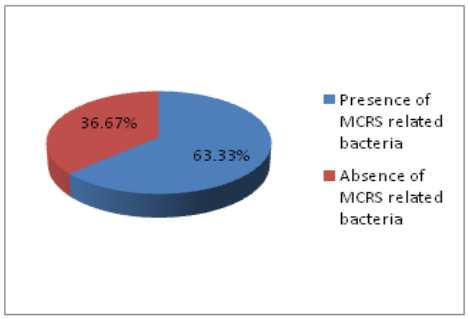


Figure (1): Pie chart for percentages of patients with MCRS group according to MCRS related bacteria from plaque samples

Figure (2): Pie chart for percentages of patients without MCRS group according to MCRS related bacteria from plaque samples

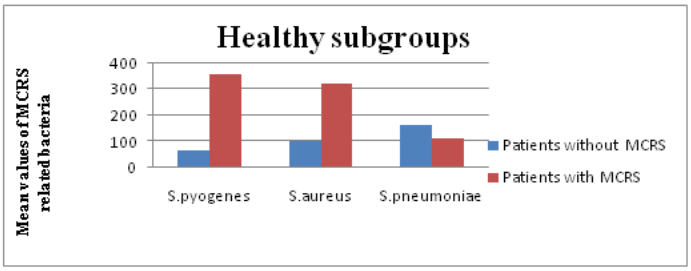


Figure (3): Bar chart for differences in mean values of MCRS related bacteria between patients without MCRS and patients with MCRS at Healthy subgroups.

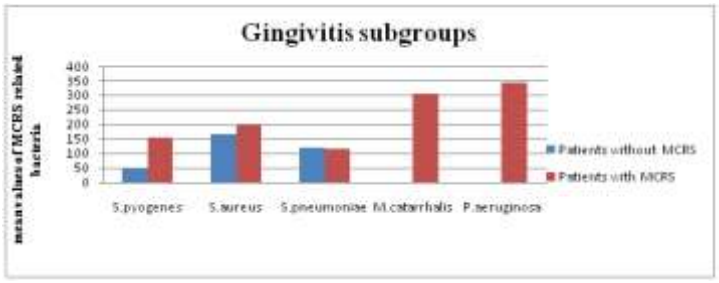


Figure (4): Bar chart for differences in means of MCRS related bacteria between patients without MCRS and patients with MCRS at Gingivitis subgroups

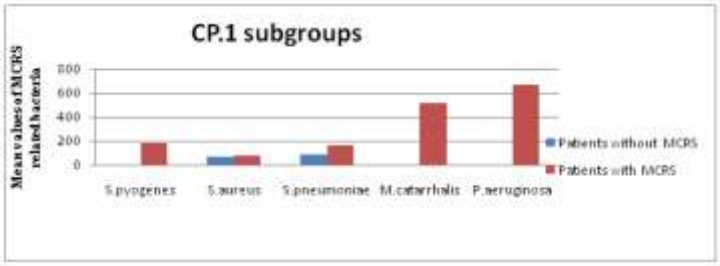


Figure (5): Bar chart for differences in mean values of MCRS related bacteria between patients without MCRS and patients with MCRS at CP.1 subgroups

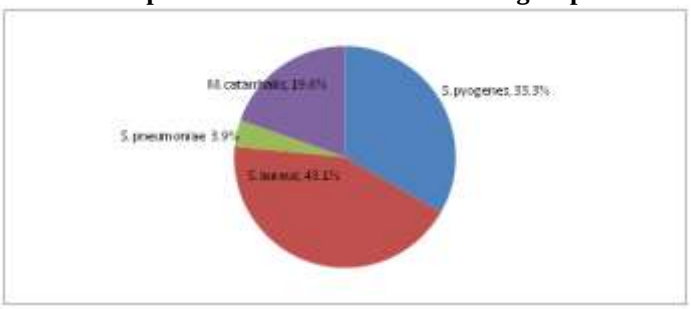


Figure (6): Pie chart for the percentages of patients with MCRS group according to similarity of each type of MCRS related bacteria in middle meatus swabs and plaque samples

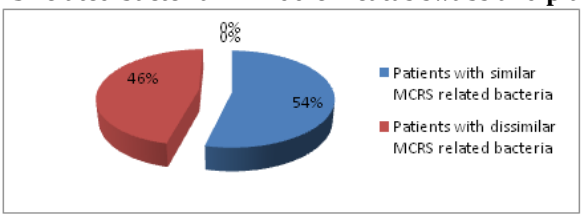


Figure (7): Pie chart for the percentages of patients with MCRS group according to similarity of MCRS related bacteria from plaque samples and middle meatus swabs

IV. Discussion

The *S.aureus* and *S.pneumoniae* were considered as normal oral flora [(4)], but these two bacteria among many other types of aerobic bacteria which are associated with MCRS [(6)]. The *S.aureus* and *S.pyogenes* found in greater percentages in Healthy and Gingivitis subgroups respectively and less percentages in CP.1 and not found in CP.2 subgroups inpatients with MCRS because, they are aerobic bacteria and difficult to live in anaerobic condition of deep pockets, this is agreed with **Egwar in 2009**[(14)] who found that *S.pyogenes* represents (20.6%) from plaque microorganisms in patients with gingivitis, while, S.aureus percentage was (11.8%). *S.pneumoniae* detected in all subgroups in almost identical values because it is facultative and can live in deep pockets. While, *M.catarrhalis* and *P.aeruginosa* were not found in Healthy subgroup but they can be detected in Gingivitis and CP.1 subgroups, hence, no identical other studies to this study so, we cannot compare the results. On the other hand *S.pyogenes* and *S.aureus* decreased in percentages with progression of periodontal diseases. But, *M.catarrhalis* and *P.aeruginosa* increased in percentages with progression of periodontal diseases and this was demonstrated by significant and highly significant differences respectively between Gingivitis and CP.1 subgroups which referred to specific relation between these 2 types of MCRS related bacteria and periodontal disease severity, this is agreed with **(Silva, 2014)**[(15)] who found that *P.aeruginosa* was associated with periodontal diseases. While, *M. catarrhalis* has the ability to compete with the normal flora and overcome the stiff environmental conditions, such as limitation of nutrition hence, this will lead to severe infection of periodontal tissue [(16)].In addition, **Andrea et al.**in **2013**[(17)]who found that the proportions of *S. aureus* and *P. aeruginosa* were significantly higher in plaque samples of patients with periodontitis when compared with healthy individuals also found that *P. aeruginosa* were detected in 50 % of patients with PPD ≥6 mm and clinical attachment loss .**Mehra** in **2004**[(18)]concluded that perforation of the Schneidarian membrane because of periodontal infection lead to MCRS. Hence, according to **Janneret al.**in **2011**[(19)] the range of thickness of the Schneiderian membrane is (0.16 mm) to (34.61 mm), so, it will be easily perforated in people with minimum thickness.

It is not surprising to find oral flora in maxillary sinus and MCRS related bacteria in dental plaque if we know that **Ozmen et al.** in **2008**[(20)] detected Pepsin (gastric acid) in nasal lavage fluid. It is believed that the periodontal bacteria detached from the periodontal pockets into the saliva and from there they are breathed into the upper respiratory tract [(21)]. In second way the post nasal drip which is mucosal purulent discharge pass from the nose posteriorly to the oropharynx and mix with saliva [(22)]. This may give an explanation of the presence of MCRS related bacteria in oral cavity and in plaque samples. *H.Influenzae* not found in all subgroups because they need chocolate agar media and it is facultative anaerobic bacteria prefers CO2 enriched incubator to grow [(23)].22% of the patients without MCRS showed 3 types of MCRS related bacteria, this agreed with **Susanna et al.**in **2002**[(24)] who concluded that the direct connection between maxillary sinus and the oral cavity leading to find the MCRS related bacteria in the oral cavity and vice versa, thus oral bacteria may ascend from the mouth through the middle meatus to the maxillary sinus. This can be explained that the bacteria of oral flora can be infectious when reach nasal sinuses and cause sinusitis [(25)].In patients with MCRS group; results explain the effective role of MCRS related bacteria in development of periodontal diseases. Since, *S.aureus* and *S.pyogenes* play an important role in periodontal diseases by production of enzymes, such as proteases and lipases that invade and destroy the periodontal tissues [(26)]. *M.catarrhalis* interact with *S.pyogenes* in order to adhere to epithelial cells and lead to destruction of this tissue, Hence presence of these two types of bacteria together result in more infection and damage to periodontium[(27)]. *P.aeruginosa* uses its flagellum in order to adhere to tissue surfaces; then it leads to tissue damage by releasing of exotoxins and endotoxins, in addition acute diseases caused by *P.aeruginosa* tend to be chronic and life-threatening [(28)]. Since, all these types of MCRS related bacteria release products cause destruction of periodontal tissues lead to gingivitis and with continuous irritation of dental plaque would change to chronic periodontitis [(29)].Results illustrated that 51 patients with MCRS group had the same types of bacteria in middle meatus swabs and plaque samples. These results are in agreement with **Susanna et al.**in **2002**[(24)] who said that some bacterial species in the maxillary sinus found at the same time in the oral cavity. The explanations of how oral bacteria participate in the pathogenesis of respiratory infection were as follows [(30)]:

1. Oral pathogen can be aspirated.
2. The salivary enzymes (as mannosidase, fucosidase) associated with periodontal diseases cause modification of respiratory mucosal surfaces and promote adhesion and colonization by respiratory pathogens.
3. Hydrolytic enzymes from periodontopathic bacteria may destroy the salivary film that protects against pathogenic bacteria. Thus leaving them free to adhere to mucosal receptors in the respiratory tract.
4. The release of a large variety of cytokines from periodontal tissues cause alterations of respiratory epithelium and promote colonization by respiratory pathogens.

The results of this study demonstrated that the highest percentage of similarity was demonstrated by *S.aureus* (43.13%) then *S.pyogenes*, followed by *M.catarrhalis* and the least percentage revealed by *S.*

pneumoniae and no similarity of *P.aeruginosa* was demonstrated. Hence, **Susanna et al.**in **2002**[24] found that *P.aeruginosa* and *S.aureus* found in both dental plaque and maxillary sinus.

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