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Original Research Article

Bacteriological profile of suppurative cervico-facial cellulitis of dental origin at the Lomé-CHU campus

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ABSTRACT

Background: Cervico facial cellulitis is mainly complications of oral infections. A better knowledge of the main germs involved and their susceptibility to antibiotics is necessary for their treatment.
Methods: Three-year prospective study, carried out in the odontostomatology department of the CHU-Campus of Lome, fifty-five patients were included. The pus was taken by suction in a sterile single-use syringe and then directly seeded on agar. The incubation was carried out for 48 h.
Results: The sample consisted of 28 men and 27 women. Fifty-four point fifty percent of patients were between 14 and 40 years of age. Forty-four cultures (80%) were positive. The main germs isolated were *Staphylococcus aureus*, *Streptococci*, *Escherichia coli*, and *Klebsiella pneumoniae*. The study showed good susceptibility of staphylococcus to quinolones, from *streptococcus* to aminoglycosides, quinolones, and amoxicillin-clavulanic acid, and *Enterobacteria* to cephalosporins, aminoglycosides and quinolones. In the same way, the total resistance of all these germs to tetracyclines was proved.
Conclusions: The resistance of *Staphylococci* and *Streptococcus* to betalactamins is a real public health problem.

Keywords: Cervical-facial cellulitis, Dental infection, Microbial flora, Susceptibility to antibiotics

INTRODUCTION

Cervico-facial cellulitis are known as primarily dental cause affections. These are complications of dental pathology including carious ones. These infections range from simple localized dental abscesses to infections in the deep lining of the face and neck, which can lead to the patient's prognosis or the functional prognosis of certain noble organs such as the eyes.[1-3] They constitute medico-surgical emergencies, the management of which associates the suppression of the causal dental drainage of the purulent collection, and adapted antibiotherapy. There is a commensal bacterial flora specific to the oro-facial region. This one evolves during the lifetime according to several factors.[4] The aim of the present work was to identify the main germs responsible for cervico-facial cellulitis of dental origin at the CHU-Lome Campus and to assess their sensitivity and/or their resistance to the various antibiotics commonly used as first-line antibodies. This should make it possible to update the

bacteriological data and thus guide practitioners in the choice of probabilistic antibiotics.

METHODS

We conducted a prospective study over three years (January 2013 to December 2015) in the odontostomatology department of the CHU-Campus of Lome, out of fifty-five (55) patients with suppurative cervico-facial cellulitis of dental origin. In this sample, patients who were not on antibiotic medication before the early stage of the infectious pathology. Those who had done any self-medication were excluded from it.

The pus was taken by aspiration in a disposable sterile syringe of 5 ml and an 18/22 gauge needle percutaneously or endobuccally. All samples were directly seeded on agar (blood, chocolate, purple bromocresol) and on nalidixic acid. The incubation lasted 48 hours. In addition these patients were not under antibiotic medication before the onset of the infectious pathology. Different antibiotics were tested on the basis of the agar diffusion of antibiotic-impregnated disks. At the end of this stage, an antibiogram was performed. The parameters exploited in our patients were sex and age. These patients had not taken any antibiotics since the beginning of the infection. Interpretation of the results was done according to the rules and recommendations of the antibiogram committee of the French Society of Bacteriology. Our data has been entered and used on a PC equipped with the Microsoft Office, the Word 2010 and the statistical calculations by Excel 2010 and EPI-INFO-6.

RESULTS

Our sample consisted of 55 patients including 28 men and 27 women as shown in Figure 1 below. The sex ratio was 1.03.

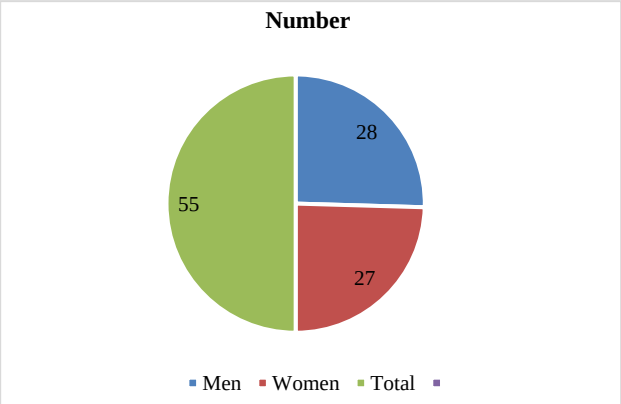

Figure 1: Sex distribution of patients.

The distribution of patients by age indicated that 54.50% of patients had an age between 10 and 40 years illustrated in Figure 2.

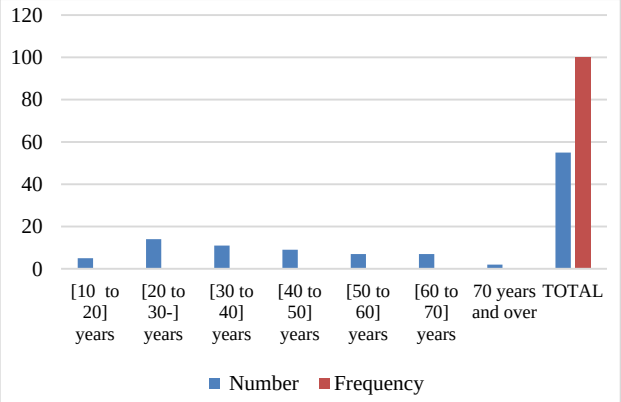

Figure 2: Age distribution of the patients.

The identification process of the main causative organisms found 44 essentially monomicrobial positive cultures, of which *Staphylococcus aureus* (34.10%) and *Streptococci* (25.00%) were the most represented as shown in the Table 1.

Table 1: Nature and number of main isolated germs.

Germs	Number	Frequency (%)
Staphylococcus aureus	15	34.10
Streptocci	11	25.00
Escherichia coli	06	13.63
Entérobacteria	06	13.63
Klebsiella pneumoniae	04	09.10
Proteus mirabilis	01	02.27
Y pseudotuberculosis	01	02.27
Total	44	100

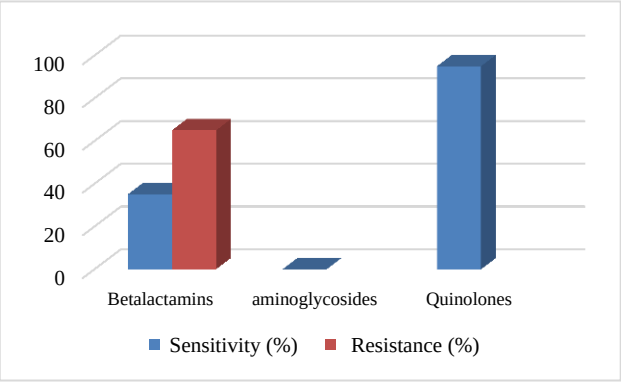

Figure 3 : Sensitivity and/or resistance of *Staphylococcus aureus* to the various antibiotics.

The sensitivity and/or resistance of the main germs to the various antibiotics have been demonstrated as illustrated in Figures 3-5.

Staphylococcus aureus was resistant to betalactamins in 65% of cases, while it was sensitive to aminoglycosides

in 80-90% of cases, and to quinolones in 95% of cases (Figure 3).

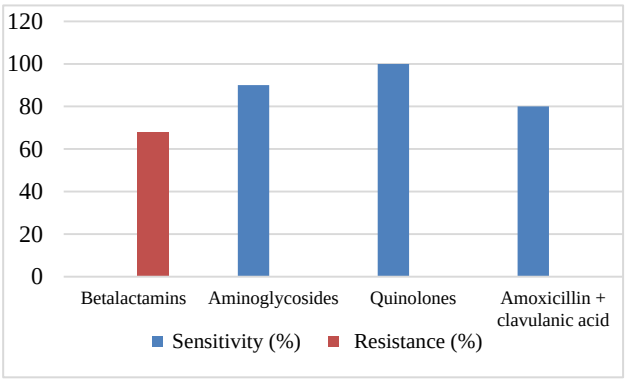

Figure 4 : Sensitivity and/or resistance of *Streptococci* to the various antibiotics.

Streptococci were resistant to betalactamins in 68% of cases, whereas they were sensitive to the combination of amoxicillin and clavulanic Acid in 80% of cases, to aminoglycosides in 90% of cases, and to quinolones in 100% of cases as shown in the Figure 4.

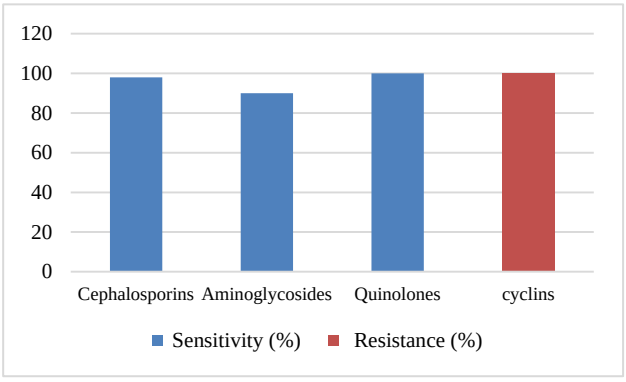

Figure 5 : Sensitivity and/or resistance of *Echerichia coli* to the various antibiotics.

Escherichia coli was resistant to cyclins in 100% of cases, while it was sensitive to aminoglycosides in 90% of cases, to cephalosporins in 98% of cases, and to quinolones in 100% of cases as shown in Figure 5.

DISCUSSION

For many years, few meaningful studies of microbiology have been carried out in Togo, in connection with dental infections. Moreover, the plurality of methods of investigation, combined with the variety of materials used, made it difficult or even impossible to compare them.[5] Our sample included 55 patients on whom samples were taken. Thus, 44 cultures have been used to isolate various pathogenic germs. This sample is more consistent than that of Walia et al which included 42 patients, Patankar et al, with 35 patients and Fating et al, with 26 patients but lower than that of Kityamuwesi et al, with 130 patients, and Bahl et al, with 100 patients.[4,6-9] Our specimens were taken by aspiration of the pus in the abscessed box, before the surgical drainage, after careful local asepsis. This made it possible to avoid contamination by commensal germs. This approach has been found in almost all previous studies.[4,6,8,9] Approximately half of the sample (54.55%) was between 14 and 40 years of age with an average of 32.50. This is a relatively young population and this trend is found in the studies of Walias et al, Patankar et al, Fating et al, Kityanuwesi et al, Bahl et al.[4,6-9] In our series, the male patients were 28 and the female patients were 27, a sex ratio of about 1. This non-significant difference in exposure by sex can be explained by an almost equal risk of exposure to potentially infectious dental diseases in both sexes. It is not the same in Walia et al, which found 78.57% of men against only 21.43% of women, Fating et al, and Kityamuwesi et al who found 53.8% of men respectively, compared with 46.2% of women, and 47.7 women.[4,7,8] Intrabuccal microbial flora is one of the most diverse in the human body. This diversity is explained by the existence of several microenvironments in the oral cavity such as the different facets of the teeth, the gingival pockets, the tongue and the oral mucosa. Each microorganism requires specific conditions for its residence and development, including receptors for its adhesion, suitable nutrients, oxygen content or simply physical protection against adverse conditions. For these reasons a good understanding of the nature of the oral flora and its dynamics is important in infections of the orofacial sphere.[10] Of the 55 patients in our series, 44 cultures were positive and isolated mainly mono-microbial flora. This result is consistent with that of Kityamuwesi et al who found a mono-microbial flora in 84.8% of the cases in his study.[8] However, this result contrasts with those found in other studies where polyfloride flora is often reported.[6,7,9]

Among the germs isolated in our series, the *Cocci* gram positive were the most represented, in particular the *Staphylococcus aureus*, followed by the streptococci. Indeed these two germs are those found in the initial stage of infection for *Staphylococcus aureus*, and quasi associated with oral infections for the streptococcus. These results are superimposed on those of Walia et al who found a predominance of *Staphylococcus aureus* in 17.50% of cases followed by *Streptococci* in 15% of cases.[4] However, Patankar et al found in their series a predominance of *Streptococci* in 17% of cases followed by *Staphylococcus aureus* in 11% of cases.[6] The gram-negative aerobic germs found in our series were represented by *Escherichia coli* and *Klebsiella pneumoniae*. The same trend was reported by Walia et al and Patankar et al.[4,6] *Pseudomonas aeruginosa* was found as a minor percentage in our study, as in that of Patankar et al.[6] *Streptococcus* and *Staphylococci* were resistant to betalactamins in 65% and 68%, respectively, while both germs were sensitive to aminoglycosides in 90% of cases and quinolones were more resistant to antibiotics of 95% of cases. The sensitivity of the Streptococci to the

combination of amoxicillin and clavulanic acid was 80%. The resistance of *Staphylococcus aureus* to betalactamins is linked to the production of betalactamases, but also to the presence of a gene, the DLP2a protein, which has a poor affinity for betalactamins. Walia and Al found staphylococci resistance to penicillin and erythromycin in 71.42%, and 100% sensitivity to gentamycin, ciprofloxacin and cephotaxime.[4]

In the same study, sensitivity of *Streptococci* to penicillin, erythromycin and gentamycin was found in 75%, while sensitivity was 100% with ciprofloxacin and cephotaxime. In the Fating et al series all aerobic germs were sensitive to gentamycin, vancomycin and imipenam, but also 80% were sensitive to penicillin G, amoxicillin, amoxicillin-clavulanic acid combination.[7] In addition, the sensitivity of *Enterobacteria* is added. In our study, Gram-negative *Escherichia Coli* were resistant to cyclins in 100% of cases, whereas they were sensitive to aminoglycosides in 90% of cases, to cephalosporins in 98% of cases, and to quinolones in 100% of cases. Walia et al found a sensitivity of *Escherichia coli* and *Klebsiella* to amikacin in 100% of cases.[4]

CONCLUSION

At the end of this evaluation, our study should focus on the good sensitivity of *Staphylococci* to quinolones, that of the streptococcus to aminoglycosides, quinolones, and amoxicillin-clavulanic acid, and that of *Entero-bacteriaceae* to cephalosporins, aminoglycosides and quinolones, as well as the total resistance of all these major germs to tetracyclines. The resistance of staphylococci and streptococcus to betalactamins is a real public health problem due in part to excessive use of the latter in terms of doses and duration of treatment.

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Ethical approval: The study was approved by the Institutional Ethics Committee

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