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Preoperative evaluation of micro-organisms in non-operated cleft in soft palate: impact on use of antibiotics

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Abstract

To identify the pathogenic micro-organisms that had colonised preoperatively in clefts in the soft palate and oro-nasopharynx, we retrospectively studied the preoperative microbiological profiles of 200 infants who had had primary repair of all types of cleft in the soft palate. Data from a private practice that specialises in the repair of facial clefts were extracted randomly from patients' files. We analysed the results of the culture of preoperative swabs taken from clefts in the soft palate and oro-nasopharynx, and the resistance profile of organisms towards various antibiotics. A total of 23 different pathogenic micro-organisms were isolated from 115 (57%) of the sample. *Klebsiella pneumoniae* most commonly colonised clefts in the lip, alveolus, and palate. This was considerably higher than in other groups. The second most common micro-organism was *Staphylococcus aureus*, which was found most often in patients with isolated clefts in the hard palate. Those with complete cleft lip and palate presented with more pathogenic micro-organisms in preoperative cultures than those with other types of cleft. We need to find a way to control pathogenic micro-organisms in the oral and oro-nasopharyngeal region preoperatively to limit postoperative complications.

Keywords: Cleft palate; Micro-organisms; Antibiotics; Resistance; Oro-nasal fistula

Introduction

A report from 1937 states that infection is the most common reason why operations fail.[1] Clinicians constantly evaluate the role of microbial infections related to complications after the repair of clefts in the soft palate, and the authors of two studies, which reported the presence of *Staphylococcus aureus* in unrepaired clefts in the lip and palate,[2,3] concluded that it inhabits the nasopharyngeal and nasal cavity and colonises the oral cavity through the cleft. In a study of 100 infants, 15 different pathogenic organisms were identified in the oro-nasopharyngeal cavity of patients with a cleft lip and palate and those with a cleft palate (CP) during the perioperative stage of primary palatal repair.[4]

In our unit between 1984 and March 2015, 4183 patients were treated for facial clefts. Of them, 3261 (78%) had a cleft in the soft palate, 1597 (38%) a cleft lip, alveolus and palate (CLAP), 715 (17%) a cleft in the hard and soft palate (hPsP), 773 (19%) an isolated cleft in the soft palate (sP), and 171 (4%) a COMBI cleft (CL + hPsP or sP). The protocol for repair starts with primary reconstruction of the cleft in the soft palate.

Abbreviations: CP, cleft palate; CLP, cleft lip and palate; CLAP, cleft lip, alveolus and palate; bCLAP, bi-lateral cleft lip, alveolus and palate; uCLAP, uni-lateral cleft lip, alveolus and palate; COMBI, cleft lip + cleft hard palate or soft palate; hPsP, cleft hard palate and soft palate; sP, cleft soft palate.

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Table 1
Pathogens identified in 115 patients.

Pathogen	No. of patients
Klebsiella pneumoniae	35
Staphylococcus aureus	25
Escherichia coli	20
Streptococcus pneumoniae	14
Haemophilus influenzae	13
Moraxella catarrhalis	12
Enterobacter cloacae	10
Serratia marcescens	8
Acinetobacter baumannii	4
Enterobacter agglomerans	4
Pseudomonas aeruginosa	4
Alpha-haemolytic streptococcus	3
Klebsiella oxytoca	3
Aeromonas hydrophila	2
Enterobacter aerogenes	2
Aeromonas sobria	1
Enterobacter gergoviae	1
Enterococcus faecalis	1
Kluyvera cryocrescens	1
Staphylococcus epidermidis	1
Streptococcus anginosus	1
Streptococcus pyogenes	1
Streptococcus viridans	1

Pathogenic micro-organisms that are found preoperatively might influence outcome. After a search of PubMed, Ovid, and EBSCOhost, we found 12 publications on the oral flora in infants and toddlers with clefts, seven of which identified micro-organisms found preoperatively.[2–8] One compared the oral types of micro-organisms found in relation to the type of cleft,[8] four referred to *Streptococcus mutans* and lactobacilli, which are involved in dental caries, but do not apply in infants,[6,9–11] and one analysed the prevalence and composition of bacteraemia associated with operations to repair a cleft lip and palate.[12] Others compared the association of postoperative complications with pathogenic organisms found perioperatively.[3,4,7,8]

With the misuse of antimicrobials in mind, we have therefore reported the variety of species of micro-organisms found in different types of cleft in the posterior soft palate and oro-nasopharyngeal region before primary repair.

Patients and methods

This retrospective study was designed and approved by the Faculty of Health Sciences Research Ethics Committee (297/2014) of the University of Pretoria. Data were randomly collected from the files of 3261 infants (aged between 5 and 7 months) who were treated between January 1992 and March 2015. A total of 200 patients who had had primary repair of clefts in the soft palate were included. They had been admitted to the hospital from all over the country, and a paediatrician had deemed them healthy before the operation. To ensure reliability, one researcher selected every sixteenth file that contained all the inclusion criteria, and recorded all the data. All patients had had microbial swabs taken preoperatively from clefts in the soft palate and oro-nasopharyngeal region after induction of anaesthesia and orotracheal intubation, but before they had been surgically prepared. During the operation, a nasogastric tube was inserted for postoperative feeding for six days to prevent contamination of the wound. Antimicrobial drugs given postoperatively were adjusted as soon as the sensitivity results were available. Data on the type of cleft, type of micro-organisms cultured and identified from preoperative swabs, and the report of the sensitivity of micro-organisms to specific antimicrobials, were recorded on a Microsoft Access Database and Excel spread sheet. Statistical tests used was ANOVA (Analyses of variance) between the different groups.

Results

We matched the microbiological reports with the type of cleft, and divided the patients into four groups according to the type: patients with an isolated cleft in the soft palate (sP group, n = 52), those with clefts in the hard and soft palate (hPsP group, n = 63); those with clefts in the lip, alveolus, and hard and soft palate (CLAP group), who were subdivided into unilateral (n = 54), and bilateral (n = 22) groups; and those with a CL and hPsP or sP (COMBI group, n = 9).

A total of 23 different pathogenic micro-organisms were isolated from 115 patients (58%) (p = 0.003). In the remaining 85 (43%), oral flora was normal. Table 1 shows the pathogens identified, and Table 2 the pathogens in the different groups. Fig. 1 shows the pathogens found in the sP and hPsP groups, and Fig. 2 those found in the unilateral and bilateral CLAP groups and the COMBI group. Fig. 3 shows the anti-microbial resistant profile of the seven most common pathogens. We compared the largest number cultured in 10 or more patients using the layout of previously published resistance profiles of the perioperative organisms.[4]

Table 2
Cleft groups: normal compared with pathogenic micro-organisms.

	Group										Total	p value
	sP	p value	hPsP	p value	uCLAP	p value	bCLAP	p value	COMBI	p value		
Normal	26		31		19		6		3		85	
Pathogenic	26	1.00	32	0.87	35	0.002	16	0.003	6	0.16	115	0.003
Total	52		63		54		22		9		200	