



Overview of Microbiological Profile of NOMA

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Abstract

Noma is a destructive gangrenous stomatitis and polymicrobial infection that generally affects children in developing countries. Our review listed the different microorganisms, in particular anaerobic bacteria found in the case of Noma.

Keywords: Noma; Cancrum oris; Microorganisms

Introduction

Noma, also known as cancrum oris or gangrenous stomatitis is an opportunistic infection, that typically affects soft as well as hard tissues of the maxillo-facial region [1-3]. The worldwide prevalence of Noma is unknown estimates range from 30 000 to 140 000 cases [4]. It mainly affects children aged 2 to 5 years, but there are rare cases in adolescents and adults. Noma is a disease of extreme poverty and malnourishment, mainly in sub-Saharan Africa [5]. This disease begins with inflammation of the gums causing rapid destruction of hard and soft facial tissue, usually within one week. Noma is known to be non-recurring and is not transmissible [6,7]. The initiation of antibiotic treatments, wound debridement, and nutritional support in the early reversible stages of the disease significantly reduce mortality and morbidity [8]. The etiology of Noma remains an unsolved mystery. Recent studies suggested that an imbalance in the oral microbiota with an overall loss of bacterial diversity appeared to be associated with the presence of Noma disease [9-11].

Microbiology

Bacteria

Noma is an opportunistic and polymicrobial infection, the exact role of microorganisms in pathogenesis is not

well defined. Studies have shown that a number of potential pathogens have been found in abundance at Noma sites which include *Prevotella melaninogenica*, *Corynebacterium pyogenes*, *Fusobacterium nucleatum*, *Bacteroides fragilis*, *Bacillus cereus*, *Prevotella intermedia* and *Fusobacterium necrophorum* [12]. In a comparative study *Prevotella intermedia*, was more present in the mouths of the malnourished than of the healthy children [5].

Other studies showed the presence of *Borrelia vincenti* and *Fusiformis fusiformis* in biopsy samples taken from the transitional zone between the gangrene and healthy tissue, which suggested an important infiltrating role for these two microorganisms [4]. Advances in molecular biology have enabled studies to suggest that Noma lesions have a greater bacterial diversity than healthy sites in control and Noma individuals. Interestingly, these lesions also exhibited a greater abundance of anaerobic bacteria capable of fermentation [7]. Recent reports reported the detection of 67 bacterial species or phylotypes in advanced Noma lesion of four Nigerian patients [13]. The genera *Eubacterium*, *Flavobacterium*, *Kocuria*, *Microbacterium*, *Porphyromonas*, *Streptococcus (salivarius)*, *Sphingomonas*, and *Treponema* were unique to Noma infections [13]. In this same study, twenty-five species had not yet been cultured in vitro, 19 phylotypes, including *Propionibacterium acnes*, *Staphylococcus*, and the opportunistic pathogens *Stenotrophomonas maltophilia* and *Ochrobacterum anthropi* were found in samples of one of the

four patients. According to the author, bacteria not associated with the oral microbiota may be due to contamination from the environment [14].

Viruses

Studies in South Africa and Zimbabwe on the pathogenesis of Noma have shown that HIV infection may play an important role in these countries [15]. Viruses such as human cytomegalovirus, measles virus, herpes simplex virus are associated with necrotizing ulcerative gingivitis and Noma [16,17].

Conclusion

Our review indicates the different bacteria and viruses found in the lesions of Noma. We mainly find anaerobic bacteria in these pathologies.

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