



Antimicrobial resistance in oral microbiota: Straightforward explanation

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ABSTRACT

The microbial content of the oral cavity is one of the most complicated communities with a large number of different organisms living in symbiosis. Disturbance of such peaceful correlation by external or internal factors may encourage the conversion of some oral microbiota into pathogens. Many genes with information to encode antimicrobial resistant proteins are increased the pathogenesis of oral microbiota. Description of oral community and development of antimicrobial resistant is discussed in this review.

Keywords: Microbiota, Oral cavity, Antimicrobial, Resistance.

INTRODUCTION

The oral cavity is a reservoir for a large number of microbiota with varying distribution at different sites in the mouth. There are around 500 bacterial species identified with 22 genera [1-4]. A further large number of oral microbiota still needs to be identified [4]. The oral microbiota is generally in a state of equilibrium with one another and any disturbance in this equation will provide an opportunity for some species to become pathogens [1, 5-6]. Several types of oral diseases can be caused by oral microbiota. The treatment of these diseases may be a major issue today because of the development of antimicrobial resistance in oral microbiota [6-7]. Transposable genes in members of microbiota, which encode several factors associated with antimicrobial resistance, are the main reason for advancing resistance development [6,8]. The resistance mechanism in the oral microbiota is no different from that used by other organisms, which is frequently included the activation of the drug efflux, reduce antibiotic uptake, change of drug target, and inactivation of drug [9].

Oral normal flora

Microbiota or normal flora is a term with the same meaning that refers to organisms that live symbiotically with the human body [1-2]. It could be found in many parts of the human body with differing levels of density and diversity. The oral cavity is the second major part of the human body containing microbial communities of bacteria, fungi and viruses [1,3]. A colonization of about 700 species in over 500 bacterial taxa and about 22 identified genera has been identified in different parts of the oral cavity [1-4]. Initiation to oral microbiota starts first with contact with the birth canal during birth, then with breastfeeding of the parents, and later from other sources such as water, food and from surrounding environment [3-5]. The density and diversity of microorganisms in the oral cavity increases with time, from some facultative species in childhood to different species in adults [4].

The oral flora of bacteria is not fully identified, even their distribution location has been determined on various surfaces of the oral cavity such as the tooth and tongue [4]. Many advanced technologies are trying to form a clear picture of the complexity of oral microflora and its role in diseases [1]. The

environmental conditions of the site of occurrence have an effect on the type of oral organism that later affects the metabolic activities of that organism [4-5]. However, differences in the distribution of micro flora between oral sites are clearly identified in healthy and may have no effect on the organism types and density, especially in indigenous bacteria [4].

The balance between the different types of oral flora is an indication of the healthy state of the mouth and any change in such correlation will allow pathogenic bacteria to overgrow causing oral diseases [1,5]. Many types of diseases caused by the normal flora of the oral cavity may develop resulting from such disturbances as with tooth decay, gingivitis and periodontitis [1].

Antimicrobial resistance in oral normal flora

Over prescription and misuse of antibiotic for a long period in the treatment of microbial infection enforce bacterial normal flora to develop a resistant evolution to protect itself from antimicrobial action of such antibiotics [10]. Today, antimicrobial resistance is one of the most important public health issues, where it is associated with a high rate of morbidity and mortality [6-7]. Orally treatment of 35 children with six types of antibiotics, who had not received antibiotics during the previous 3 months, showed that a total of 432 antibiotic-resistant isolates were recovered, in which it comprised 18 genera and 47 species [11]. A further 47 children from another study who received no antibiotics for 3 months showed resistance to tetracycline and 56% of these are resistant to at least another antibiotic such as erythromycin as with oral *Streptococcus* spp. (65%), *Veillonella* spp. (10%) and *Neisseria* spp. (9%) [12].

Destruction of normal flora, as in the oral cavity, will stimulate the multiplication of pathogenic microorganisms that cause serious diseases [6]. One other factor associated with the more rapid development of antimicrobial resistance is the transfer of resistance elements within the bacterial population [10]. The resistance gene may easily be a horizontal transfer from normal flora to pathogenic bacteria after improper use of antibiotics [6,8]. According to a recent study, a single oral dose of antibiotic may encourage an increase in the number of resistance genes [8]. In addition, biofilm formation by different species of oral microbiota on teeth and mucous membranes is another factor in association

with the development of bacterial resistance to antibiotics and also facilitate transferring of resistance gene between bacterial compositions of biofilm [8].

Mechanism of antimicrobial resistant

The microorganism has a capacity for adaptation and evolution against the harmful effects of various toxic substances, including antimicrobial agents, by the development of many resistant mechanisms [9, 13]. This type of resistance plays a major role in increasing the complications of treatment of microbial infection and increasing the threat to human health worldwide [13-14]. Generally, antibacterial agents like the most typical antibiotics, can inhibit or kill several species of bacteria by interfering with the different metabolic process in the bacterial cell, including the synthesis of nucleic acid (eg. fluoroquinolones, rifampin), protein (eg. Macrolides, tetracyclines), cell wall (eg. β -lactams, glycopeptide agents), and other metabolic substances (eg. trimethoprim-sulfamethoxazole), and also effects on the structure of bacterial membranes (eg. polymyxins) [14]. Thus, the bacteria have been developed several strategies aimed at limiting or resisting the toxic effects of these antibacterial agents include; activation of drug efflux, reduce antibiotic uptake, change of drug target, and inactivation of drug [9].

Acquired antibiotic-resistance by bacteria generally comes from two different major sources. The first is related to bacteria and considers intrinsically which give resistance to at least one of the antibacterial agents [9, 14]. It is typically developed through mutation in antibiotic genetic targeting [13]. The second source of resistance is the acquisition of a resistance gene from an extrinsic source or other microorganisms through horizontal gene transfer [9,13-14]. Three processes may be used by bacteria to acquire external genetic material, including phage mediated transduction, naked DNA transformation, and pili-connected conjugation [13].

In conclusion; the oral cavity contains a large number with various species distribution in different areas. Disruption of the balanced oral community can result in various diseases. Pathogenic species in the oral cavity can become resistant to a variety of antibiotics by having resistant genes. Resistance of the oral

microbiota may develop through a number of mechanisms.

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