

of IgA secretion, modulation of inflammatory responses to pathogens and stabilization of the gut mucosal barrier. Additionally, prebiotics with enhanced function have been designed. These oligosaccharide derivatives contain sugars that are specific epithelial cell receptors to which pathogens adhere and they, therefore, provide „decoy” adhesion sites and cause pathogens to adhere to luminal contents rather than to epithelial cells. [14]

## **Oral microbiota in health and disease**

More than 700 species have been detected in the human mouth and the resident microbiota of an individual may comprise 30 to >100 species.<sup>15</sup> A wide variety of sites in the mouth are heavily colonized. Supragingival and subgingival plaque form through sequential and specific adhesive interactions that result in a complex climax community. [16] The tongue is heavily colonized and micro-organisms on the dorsum of the tongue are reservoirs for supragingival and subgingival plaque and salivary microbial populations. [17] Many oral bacteria, especially streptococci, also survive within buccal epithelial cells. [18]

## **Functions of the resident microbiota**

Resident microbiota does not play merely a passive role, but actively contributes to the maintenance of health. The large, diverse resident microbial communities that colonize mucosal sites co-exist with a host, producing harmful effects only if the host becomes immunocompromised, if the resident microbial populations are suppressed or if micro-organisms reach sites to which they do not normally have access (i.e. through trauma). Resident microbial populations contribute to host protection through development of the immune system, [19] the maintenance of healthy oral tissue by influencing expression of mediators such as intracellular adhesion molecule 1 (ICAM-1), E-selectin and IL-8, [20] modulating immune responses and enhancing cellular homeostatic mechanisms. [21]

## **Defining the resident microbiota**

Resident oral microbial populations are site- specific as well as highly diverse. Kilian et al. [22] list the following species as „true” oral commensal microorganisms: *Streptococcus mitis*, *Streptococcus oralis*, *Actinomyces naeslundii*, *Fusobacterium nucleatum*, *Haemophilus parainfluenzae*, *Eikenella corrodens* and some species of *Prevotella*.

## **Microbial populations associated with oral disease**

The most common oral diseases are caries and periodontitis, which result from a shift in the balance of the resident microbiota at a site. In caries, there are increases