Journal of Oral Microbiology

co-action PUBLISHING

Pg London 2015

The commensal microbiota and the development of human disease – an introduction

Philip D. Marsh[1,2]

[1]Public Health England, Salisbury, UK; [2]Department of Oral Biology, School of Dentistry, University of Leeds, Leeds, UK

Humans have co-evolved with microorganisms, and both exist in a symbiotic or mutualistic relationship. We are colonised by a diverse, resident microbiota, which develop into structurally and functionally organised biofilms. The resident microorganisms gain a secure, warm, nutritious habitat from the host and, in return, contribute to the development of many important host functions. The resident microbiota of each habitat is natural and provides important benefits for the host including immunological priming, down-regulation of excessive pro-inflammatory responses, regulation of gastrointestinal and cardiovascular systems, and prevention of colonisation by exogenous microbes. The biological properties of each habitat determine which microorganisms can colonise and grow, and dictate which will be major or minor components of the resident microbiota of a site. This results in different surfaces having distinct but characteristic microbiotas. This relationship between the resident microbiota and the host is dynamic and, on occasions, this symbiotic relationship breaks down due to, for example, changes in lifestyle, immune status or following broad spectrum antibiotic therapy. This 'dysbiosis' can result in previously minor components of the microbiota out-competing the normally dominant and beneficial bacteria, thereby increasing the risk of disease. Such perturbations have been associated with a number of clinical disorders such as obesity, allergy, and a variety of inflammatory diseases, including periodontal diseases. A better understanding of the delicate balance between the host and its resident microbiota could lead to novel approaches to the promotion of health and the prevention of dysbiosis.

Citation: Journal of Oral Microbiology 2015, **7**: 29128 - http://dx.doi.org/10.3402/jom.v7.29128