Large study identifies DNA sections responsible for gum disease

The largest-ever study into the genetics of severe forms of periodontitis (gum disease), conducted by an international research network led by researchers from Charité – Universitätsmedizin Berlin, has identified certain DNA sequence variants which demonstrate highly significant associations with an increased risk of developing different types of periodontitis. Results from this study have been published in the current issue of the journal Human Molecular Genetics.*

Gum disease is a very common inflammatory condition that is caused by bacteria. Severe periodontal disease is estimated to have a worldwide prevalence of approximately 11 percent. Gum disease is considered a complex condition because individual susceptibility is determined by interactions between the oral microbiome and the immune system, smoking and diet, but also by metabolic disorders such as diabetes. The way in which the body responds to these factors is, to a large degree, determined by an individual’s genetic makeup.

The research group led by Prof. Dr. Arne Schäfer of the Institute of Dental, Oral and Maxillofacial Medicine conducted a genome-wide association study (GWAS) to investigate the link between gene sequence variations and the incidence of gum disease. As part of this study, the researchers tested several thousand patients with aggressive and chronic gum disease, comparing them with healthy controls. “This type of study is very systematic in nature. It aims to identify the genes that have an effect on a person’s risk of developing a specific disease, and does so directly, i.e. without having to first develop a hypothesis,” explains Prof. Schäfer, who designed the study. Large groups of patients and controls are required in order to study millions of DNA sequence variations, which occur across the entire genome, and represent the majority of a person’s genetic information. Prof. Schäfer adds: “DNA sequence variations can have an effect on a person’s risk of developing a particular disease. By comparing frequencies of variants in patients and in healthy controls, it is possible to find which areas of a chromosome are associated with the disease.”

The researchers found two areas which appeared to be associated with an increased risk of developing different forms of gum disease. One of these two areas is responsible for the synthesis of alpha-defensins – antimicrobial peptides which are produced in specialized immune cells. Referred to as ‘neutrophils’, these immune cells form part of the body’s natural immune response, and are involved in the identification and destruction of microorganisms. The second area (Siglec-5) identified by the researchers is responsible for inhibiting the activation of these immune cells.

“Our results show that the different forms of gum disease share a common genetic origin,” explains Prof. Schäfer. He stresses: “This means that there are groups of patients who are susceptible to developing gum disease, but whose susceptibility is independent on other risk factors, such as smoking, oral hygiene, or aging.”

Links

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