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Microbial microarray analysis of gingival crevicular fluid in periodontitis

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Background. Gingival crevicular fluid (GCF) contains a variety of host-derived substances, but the bacterial composition is less known. Bacteria in GCF may represent planktonic forms released from subgingival plaque biofilms.

Materials and methods. The pilot included 11 patients (range 43-56 years) with chronic periodontitis. GCF was collected by paper strips and preserved at -80°C until DNA extraction. Periodontal examination included all teeth. Bacterial identification was performed using a microarray (HOMIM). Blood samples were collected and analyzed for CRP and IgG antibodies against certain *Porphyromonas gingivalis* bacteria-associated molecular patterns (BAMPs), LPS and OMP.

Results. Twelve to 50 (median 30) bacterial taxa, of which 4 to 10 (median 9) classical periodontitis-associated bacterial species, were found per sample. The most common of the latter were *P. gingivalis* (64%), *Tannerella forsythia* (73%), *Filifactor alocis* (82%) and *Parvimonas micra* (100%). Species of *Dialister*, *Eubacterium*, *Fusobacterium*, and *Selenomonas* were also frequently detected (55-100%). Total number of taxa correlated negatively to age. Number of periodontitis-associated taxa correlated positively to mean pocket depth and attachment level of the sampled sites and all periodontal sites measured. Serum antibody levels against LPS and OMP were significantly higher in patients with *P. gingivalis*, while those against LPS correlated positively with CRP concentrations.

Conclusions. Bacterial composition of the GCF samples concurred with previous knowledge of periodontal pocket microbiota and reflected periodontal status. *P. gingivalis* detection correlated to elevated systemic immunoinflammatory response to *P. gingivalis* BAMPs.