R-27. The detection of subgingival plaque microflora using 16S rRNA analysis in Korean adult Periodontitis

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Introduction & object

The 16S rRNA analyzing method is a bacterial identification method that is useful in identifying bacteria which is difficult to do by other means. The following 7 types of bacteria which are *Treponema, A. actinomycetemcomitans, P. gingivalis, Fusobacterium, B. forsythus, P. intermedia, P. micros* were evaluated in order to study their distribution among patients with adult periodontitis.

Material & methods

The 16S rRNA analyzing method was used to compare bacterial distribution among 3 groups. Subgingival plaque acquired from the affected sites(pocket depth ≥6mm) of 29 patients with adult periodontitis were grouped as the experimental group while plaque from the non-affected sites(pocket depth≤3mm) were grouped as control 2 and finally plaque acquired from students with healthy periodontal tissues were grouped as control 1.

Results

1. The distribution of *Treponema* was 12.5% for group1, 21.4% for group2 and 75.4% for the experimental group. For *A. actinomycetemcomitans* the distribution was 0.5%, 19.0%, 44.4% in respect to the order of groups mentioned above. *P. gingivalis* showed 10.5%, 43.1%, 94.0% distribution, *Fusobacterium* 33.0%, 48.3%, 81.0% distribution, *B. forsythus* 9.5%, 17.2%, 65.9% distribution, *P. intermedia* 1.0%, 12.1%, 26.3% distribution and finally *P. micros* 5.0%, 19.0%, 48.7% respectively. In all 7 types of bacteria, the experimental group showed higher bacterial distribution compared to the other two groups with statistically significant difference.
2. In the case of *Treponema, A. actinomycetemcomitans, P. gingivalis, Fusobacterium, B. forsythus, P. intermedia, P. micros* showed significant difference between control 1 and 2.

Conclusion

These results suggest that the 16S rRNA analyzing method which was applied on Koreans for the first time could be utilized and useful in finding potential pathogens of periodontal disease.