

B-3 The relationship between periodontal disease severity and *Actinobacillus actinomycetemcomitans* serotype & genotype distribution

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The present study was performed to evaluate the relationship between the serotype or the genotype of *Actinobacillus actinomycetemcomitans* (A.a.) and the severity of periodontal disease. Total 64 A.a. clinical isolates were sampled from 46 sites of 20 subjects classified into the group I (1 periodontally healthy subject (H), 2 gingivitis patients (G), 5 early adult periodontitis patients (E), group II (3 moderately adult periodontitis patients (M) and group III (1 advanced adult periodontitis patient (A) 8 RPP patients (R). Southern blot hybridization (fingerprinting) patterns of the five reference strains, A.a. strain ATCC 29523 (serotype a), ATCC 29522 (serotype b), ATCC 43719 (serotype c), IDH 781 (serotype d) and IDH 1705 (serotype e), were used as the five basic genotypic patterns (A, B, C, D, E). NT type was designated as one which did not represent any of those five basic types. The serotypes were determined by ELISA technique with the serum samples from pre-immunized rabbit.

On subject-basis analysis, genotypes A and C, NT, and B, D, E were significantly related to the disease groups I, II, and III respectively. However, serotypes a and c, b and nd were significantly related to the disease groups I & II, and III respectively.

On site-basis analysis, genotypes A, and C were frequently isolated in sites with slight loss of attachment level (LA) ($LA < 4\text{mm}$), and moderate attachment loss ($4\text{mm} \leq LA < 6\text{mm}$) respectively. And genotypes B, D, E, NT were also frequently isolated in sites with severe attachment loss ($LA \geq 6\text{mm}$). And also serotypes a and c were frequently found in sites with slight to moderate attachment loss ($LA < 4\text{mm}$ & $4\text{mm} \leq LA < 6\text{mm}$), and serotypes b, nd were frequently found in sites with severe attachment loss ($LA \geq 6\text{mm}$).

The results indicated that genotyping can provide more detailed information on its relationship with the disease severity both on the patient-basis and the site-basis analysis.