

日本において分離された*Borrelia burgdorferi*
sensu lato の菌体表層蛋白 OspC 遺伝子の解析

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Outer Surface Protein C Gene Sequence Analysis
of *Borrelia burgdorferi* Sensu Lato Isolates of Japan

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The nucleotide sequences of the outer surface protein C gene (*ospC*) from *Borrelia burgdorferi* sensu lato isolates representing six different restriction fragment length polymorphism (RFLP) ribotype groups were determined and the deduced amino acid sequences were aligned in comparison with the previously published OspC protein sequences. The sequence similarity analysis revealed the high sequence variability of OspC protein, and the degree of amino acid similarity ranged from 53.8 to 100% among 25 isolates. It has been reported that the representatives belonging to the three species of *B. burgdorferi* sensu lato showed a species-specific amino acid sequence motif at positions 23 to 35 (B. Wilske, S. Jauris-Heipke, R. Lobentanzer, I. Pradel, V. Preac-Mursic, D. Rossler, E. Soutschek, and R.C. Johnson, J. Clin. Microbiol. 33: 103-109, 1995). Alignment with the OspC sequences of RFLP-ribotype groups IV, V and VI isolates revealed that a sequence motif of all the isolates was quite similar to that of *Borrelia garinii*. A phylogenetic analysis based on OspC protein sequences also showed that most of the Japanese isolates were closely related to the species *B. garinii*. The RFLP-ribotype group IV species is predominant among clinical isolates of Lyme disease patients, reservoir rodents, and adult ticks in Japan. Although the isolates differed from type strains of the three delineated genospecies in genetic and immunological characteristics, it is likely that the spirochetes diverged within the species level. Therefore, the representatives of ribotype groups IV, V and VI appear to have evolved within *B.*

garinii and to have adapted to Asiatic habitat, and there appeared to be a sufficient ecological pressure to allow bacterial species level development.

日本において分離された *Borrelia burgdorferi sensu lato* の菌体表層蛋白 (OspC) 遺伝子の塩基配列を決定し、その推定アミノ酸配列を欧米分離株と比較した。その結果、この OspC の推定アミノ酸配列は多様でその相同性は 53.8~100% であった。また、推定アミノ酸配列の比較から、日本における分離株のリボタイプ IV、V、VI のグループは *B. garinii* に近縁であるが、欧米の *B. garinii* とは異なったアジア地域に適応した遺伝種であることが明らかとなった。