

THE ROLE OF RECOMBINATION IN OSPC VARIATION IN LYME DISEASE BORRELIA

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ABSTRACT

The OspC protein of Lyme disease *Borrelia* (*Borrelia burgdorferi* sensu lato) is highly immunogenic and is a protective antigen, thus an ideal candidate for a subunit vaccine. However, this protein is extremely heterogeneous. This study was undertaken to analyze the variability of the OspC protein at the genetic level. The *ospC* gene was amplified by the polymerase chain reaction (PCR) from 76 *Borrelia burgdorferi* sensu lato strains. PCR products were subjected to restriction fragment length polymorphism (RFLP) analyses and genes from different RFLP types were sequenced. A total of 33 *ospC* RFLP types were identified, and two additional RFLP types were deduced from published *ospC* sequences. Genes from different RFLP types were found to be extremely divergent, while within a given RFLP type, no sequence differences were detected. The majority of amino acid changes are localized to the central, highly variable portion of the mature OspC. Pairwise sequence comparisons indicate a mosaic structure of *ospC*. These results suggest that OspC variation is based on frequent recombination between *ospC* alleles; this genetic exchange is proposed to be mediated by lateral transfer of *ospC* sequences between strains.

KEY WORDS

Lyme disease, *Borrelia*, *ospC*, recombination

INTRODUCTION

The OspC protein of Lyme disease (LD) *Borrelia* is highly immunogenic in the natural infection (1-3) and is a protective immunogen in animal models (4, 5). This protein is thus a good candidate for a subunit vaccine and may be of value in the serological diagnosis of LD. OspC is a surface-localized lipoprotein with a molecular weight of approximately 22kD. The protein is encoded by a single gene located on

a circular plasmid (6,7); expression of OspC correlates inversely with that of OspA and OspB (8), and is regulated by environmental factors (9,10). Comparisons of OspC proteins from different strains of *Borrelia burgdorferi* (*Bb*) indicate this protein is antigenically extremely heterogeneous (11-13). To investigate the nature and extent of this variation at the genetic level, we have analyzed and compared *ospC* genes from a large collection of LD *Borrelia* strains.

