Abstract

The ultimate goal of this project is to identify peptides that mimick the immunodominant epitopes of the Neisseria meningitides (NM) to be used as the basis for development of the peptide vaccine for NM. To achieve this goal, a panel of monoclonal antibodies (mAbs) specific for NM were generated. Western blot analyses revealed that the specificities of the mAbs generated in this study almost cover all surface antigens including capsular polysaccharide, outer membrane proteins, lipopolysaccharide, and pilus. Among the anti-OMP antibodies, only 210-06 possesses a good complement-dependent bactericidal activity. MALDI-TOF analysis, and recombinant genetic analysis indicated that the antigen recognized by 210-06 is PorA, a class I OMP of N. meningitidis. By using phage display technology and sequence analysis of porA from 210-06 reactive and non-reactive strains, we conclude that 210-06 is specific to P1.2 PorA and the epitope contains the segment QTPK. The third amino acid residue within the tetrapeptide may not participate in the direct interaction with the antibody combining site of 210-06. The feasibility of using the mimotope isolated from the phage display peptide library to elicit antibodies against N. meningitidis expressing P1.2 PorA (NMY) was evaluated by generating antisera against the recombinant phage (phage-S) and the recombinant protein composed of 4.5 copies of the corresponding peptide. While the anti-phage-S bound weakly to NMY, no antibody response was obtained from mice immunized with the recombinant protein. The poor immunogenicity of the recombinant protein probably is due to its small size and low complexity.

Keywords：Neisseria meningitidis；phage display；Monoclonal antibody