LESSONS LEARNED AFTER APPLICATION OF THE GENOMIC IMMUNIZATION SCREENING PROTOCOL TO *NEISSERIA MENINGITIDIS* SEROGROUP B

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Genetic immunization offers an excellent opportunity to quickly discover new antigens and to handle the antigenicity of the protein at the sequence level without requiring protein production and purification. A very interesting application of DNA vaccination, termed Expression Library Immunization (ELI), is based on immunization with an expression library constructed with the genomic DNA of the pathogen. We have shown firstly that ELI is a viable alternative approach to induce protective immunity against *Neisseria meningitidis* serogroup B. Few rounds of library screening allowed identification of a protective pool of 20 individual antigens that induced protective immune response in mice against *N. meningitidis* infection, and the observed protection was associated with the induction of functional antibodies. This DNA immunogen codified for a group of outer membrane antigens as well as a pool of cytoplasmatic proteins. In parallel, during the present work, we also employed a prime-boost regimen in combination with the expression library immunization screening protocol to improve the protective efficacy of the genomic library used as immunogen. This combined method proposed here, could be applied to the identification of sub-immunogenic antigens during vaccine candidate screening by ELI. During our work we developed new and improved expression vectors to optimize this genomic methodology. In summary, we have demonstrated that the total genome of the pathogen *N. meningitidis*, can be screened by ELI using serological correlates of protection and in the mouse infection model to identify the components of multivalent vaccines. In addition, we added new tools to the general ELI platform.

Key words: Genomic library; *Neisseia meningitidis*; prime-boost; plasmids; vaccine