

Bm86 protein epitope polymorphisms: Is a global vaccine against cattle ticks possible?

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Rhipicephalus (*Boophilus*) *microplus* is a cattle ectoparasite that provoke concern in agribusiness for large economical losses. Its control is mainly based by acaricides application, which are chemical substances that can contaminate products of animal origin, as well the environment. Another bias of this method is the increasing emergence of resistant tick strains to several chemical bases. An alternative method to control ticks is vaccinating animals with tick's antigens. Nevertheless, the two vaccines that have been launched on the market, which both contain gut proteins homologous to Bm86, showed variable efficacy worldwide. Thus, the aim of this study is to use reverse vaccinology tools to predict the main epitopes of Bm86 amino acid sequences, associated with phylogenetic analyses of these predicted epitopes with sequences available on GenBank, from different *R. (B.) microplus* populations, to find conserved antigenic peptides that share enough conservation that can serve as an immunogen for a global commercial vaccine. For this purpose, the Bm86-CG amino acid sequence was analyzed with bioinformatics algorithms available online, and three majority epitopes, sharing several antigenic features, were mapped. Next, the predicted amino acid sequences were subjected to phylogenetic analysis to determine their variability within the Bm86 protein sequences. As results, we shown that exist some polymorphisms within the selected epitopes, and they might be involved in the variability of the efficacy of vaccines composed of proteins homologous to Bm86 worldwide.

Keywords: Bm86, ticks, epitopes, immunobioinformatics, genetic variability

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