Analysis of Cystatin Sequences and Prediction of Cross-Antigenic Regions for a Tick Vaccine

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INTRODUCTION: Cystatins are inhibitors of cysteine proteases involved with blood uptake and digestion, and there is evidence of their potential use as a tick vaccine. Cystatins have conserved motifs that can block the enzymatic site of target proteinases. The aim of this work was to analyze the cystatins of the ticks *Ixodes persulcatus* (JpIpcys2a, JpIpcys2b, JpIpcys2c) *Ixodes ovatus* (Jplocys2a) and *Rhipicephalus appendiculatus* (QnRacys2a), concerning the conserved motifs, the sequence similarities and antigenic regions.

MATERIALS AND METHODS: Deduced amino acid sequences were aligned with twenty-three amino acid sequences of tick cystatin obtained from Genbank using ClustalW algorithm. The conserved motifs of tick cystatins and the similarity between their amino acid sequences were analyzed. The antigenic regions of cystatins were predicted using Jameson–Wolf algorithm to select sequences that could be useful in a multi specie vaccine.

RESULTS AND DISCUSSION: The N-terminal glycine and the motif QxVxG are conserved in JpIpcys2a, JpIpcys2b, Jplocys2a and QnRacys2a, and the PW motif in JpIpcys2b, Jplocys2a and QnRacys2a. The amino acid sequence of JpIpcys2a shares 89.4% of similarity with the Sialostatin L of *Ixodes scapularis*, suggesting a similar inhibition activity in cathepsin L. The amino acid sequence of QnRacys2a showed 92.3% and 94.9% similarity with *Rhipicephalus pulchellus* and *Rhipicephalus microplus* cystatins, respectively, both without known functions. The Jplocys2a and JpIpcys2b shared 99.1% similarity between them, but showed low similarity with other cystatins. Five similar regions between Jplocys2a and JpIpcys2b amino acid sequences, and three similar regions among QnRacys2a, *R. pulchellus* and *R. microplus* amino acid sequences showed high antigenicity.

CONCLUSION: The high similarity among the amino acid cystatin sequences suggest that these proteins play similar functions. Also, the presence of regions with high similarity and antigenicity suggests that these proteins could be useful in a cross protection tick vaccine.

Keywords: Cystatin, sequence analysis, tick, vaccine.

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