Funcional and Structural Characterization of the Mps1 kinase protein in the hard tick *Rhipicephalus (Boophilus) microplus*

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The Spindle Assembly Checkpoint (SAC) is a cell cycle control mechanisms. This pathway monitors the correct anchoring of microtubules of the mitotic spindle to the sister chromatids and one of the major cell cycle control elements of SAC is the MPS1 protein (MonoPolar spindle 1). Mps1 exist in most eukaryotes organisms and since its discovery in yeast has been identified and characterized in humans, fish, amphibians, insects and plants. Due to its importance for proper functioning of Spindle Assembly Checkpoint (SAC), Mps1 was placed as a promising target for anti-tumoral drugs. One of the major problems in livestock is tick control, which can be extremely expensive only with chemical control. *Rhipicephalus (Boophilus) microplus* is the most important tick of bovine herd in Brazil. The aim of this work is to characterize structurally and functionally the kinase protein Mps1 from *R. microplus* (RmMps1). Our results show that primary sequence of RmMps1 is well conserved not only among invertebrates, but also among others eukaryotes. The kinase domain of RmMps1 has highly similar homologs with human Mps1 (hMps1) and RmMps1can interact with SP600125 inhibitor the same way hMps1 does. Using prediction tools we identified several phosphorylation sites in RmMps1 well conserved in others eukaryotes. Motifs analyse show that RmMps1 can interact with others cell cycle proteins, such as CDKs, APC and ciclyns and serines related to energy metabolism such as GSK-3, 14-3-3 and CK. Our results suggest that RmMps1 protein has as important function in tick cell cycle control and may be an important target for synthetic molecules to control *R. microplus*.