

Standardization of Polymerase Chain Reaction for Molecular Identification of Ixodidae Ticks

Santos, N.F.¹, Agostini, M.M.¹, Mourão, L.C.¹, Malta, T.M.¹, Silva, W. G.¹, Galvão, M.A.M.², Mafra, C. L.^{1†}, Moraes, G.H.K.¹

¹Departamento de Bioquímica e Biologia Molecular, Universidade Federal de Viçosa, Minas Gerais, Brazil; ²Departamento de Nutrição Clínica e Social, Universidade Federal de Ouro Preto, Minas Gerais, Brazil

Ticks, haematophagous arthropod ectoparasites, have a great parasitological importance not only due to its action on the host, but also by acting as vectors of several pathogens. However, it is known that the study of the life cycle of these arthropods and the epidemiology of the diseases transmitted by them are very hampered by difficulties related to the correct taxonomic identification. Traditionally, only morphologic characteristics are used for such identification (taxonomic keys), nevertheless, they are ambiguous, open to doubt, used only in particular stages of the development of the specimen and depends on the state of preservation of the animal. These facts transform ticks' identification in a very laborious activity. Thus, PCR (Polymerase Chain Reaction), using specific primers, was proposed as a molecular strategy to identify some different genera and species of ticks. Looking for the standardization of the procedure, tests to improve the functionality and the specificity of the PCRs are been developed. Actually, satisfactory results were obtained for many genera and species with standard reactions. Tests for other genera and species are in progress, but the correct result obtained, using as control specimens from reference laboratories, already indicates the success of the strategy proposed for molecular identification of Ixodidae ticks.

Key words: *Ticks, molecular taxonomy, PCR*

Financial support: CNPq and FAPEMIG

[†] mafra@ufv.br