

TITLE: GENETIC VARIABILITY OF *CONIDIOBOLUS LAMPRAUGES* FUNGI ISOLATES FROM SHEEP BY RAPD

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ABSTRACT:

Conidiobolus coronatus, *C. incongruus* and *C. lamprauges* fungi, the Entomophthorales order, have been described as the principal agents of conidiobolomycosis. This disease is characterized by granulomatous mycosis and is important in human and veterinary medicine due to its disabling potential and high lethality in the affected species, which can cause serious socio-economic. Conidiobolomycosis in sheep has been reported in tropical and subtropical climates with high humidity and is associated with high lethality and economic losses. In Brazil, outbreaks of this disease have been described in the Northeast, Midwest and South regions, mainly in ovine with two clinical forms: rhinopharyngeal and rhinofacial. In addition to occurring in regions of Brazil in different clinical forms, no data about the genetic diversity of *Conidiobolus lamprauges* is available. Thus, the aim of this study was to evaluate seven isolates of *C. lamprauges* from ovine clinical cases of conidiobolomycosis using five primers with the random amplified polymorphic DNA (RAPD) technique. Amplicons were observed in all isolates and ranged from 200 to 2,500 bp, with primer p50 leading to the most polymorphic amplicons. In this study, it was possible to evaluate the genetic diversity of *C. lamprauges* isolates from three different Brazilian geographic areas using five different primers. Phylongenetic analysis detected four groups (A, B, C and D) based on their geographical origin with 36% similarity between isolates. Mato Grosso isolates were in groups A and B, and the rhinofacial form was present only in group B. Differed from other regions (C and D) and both animals were affected with the rhinopharyngeal form. Genetic variability in Brazilian isolates of *Conidiobolus lamprauges* is likely related both to the clinical form of the disease and the geographic location.

Keywords: *Conidiobolus* sp., RAPD, sheep, zygomycosis.