GENETIC DIVERSITY OF *Colletotrichum graminicola* ISOLATED FROM SORGHUM CULTURED IN TROPICAL AGROECOSYSTEM AS REVEALED BY SDS-PAGE, RAPD AND SEQUENCING ANALYSIS OF 18S rDNA AND 18S-28S INTERGENIC SPACER. Paoli HC, Quintão PL, Coelho VTS, Fonseca PC, Ferreira AS, Casela CR, Guimarães CT, Gomes EA, Figueiredo JEF. Faculdades Metodistas Integradas Izabela Hendrix, Belo Horizonte, MG, Brazil, Escola Superior de Agricultura e Ciências de Machado, Machado, MG, Brazil, Embrapa Milho e Sorgo, Sete Lagoas, MG, Brazil. rike77@hotmail.com

Sorghum is one of the most important cereal crop for subsistence farmers in arid and semi-arid portions of the world. This crop is essential for human life on marginal lands throughout the poorest regions of the world. In developed countries, sorghum is increasingly important as feed crop and as crop that can be grown on marginal lands as part of a sustainable agroecosystem. Anthracnose of sorghum caused by *Colletotrichum graminicola* is a serious disease in Brazil. *C. graminicola* attacking sorghum is highly variable pathogenically and many races have been identified. It has been shown that pathogen changes rapidly and may do so even while attempts are being made to define protocols for classification of the pathotypes. We are interested in developing molecular methods based on SDS-PAGE, RAPD, RFLP, rDNA and sequencing analysis for identifying pathotypes of *C. graminicola* attacking cultured sorghum in Brazilian fields. Five races of *C. graminicola* identified by their ability to cause symptoms of anthracnose in shorgum were used in the present work. Total protein of each pathotype was extracted from micelia and electrophorosed in 12,5% SDS-PAGE. Protein profile of the five pathotypes was very similar but differences could be noted in the pattern of protein expression as well as in relation to the presence or absence of some protein bands in the gel. DNA profile of the arbitrary amplified products by RAPD-PCR using ten random primers (Operon) showed different pattern for the five races while the restriction fragment lenght of the amplified products of rDNA (ITS region and 18S) using six different enzimes that recognize four or six bases showed the same pattern. However, sequencing data of the rDNA product amplified by PCR revealed differences among all five races. The above results showed that different molecular techniques are useful for identifying races of *C. graminicola*. Órgão Financiador : Embrapa/ FAMIH