## Poster (Painel)

2207-1 SELECTION OF INTER-SIMPLE SEQUENCE REPEAT (ISSR) MARKER FOR MOLECULAR DIVERSITY OF Fusarium decemcellulare FROM GUARANÁ-TREE

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## Resumo

Guaraná plant (Paullinia cupana var. Sorbilis (Mart.) Ducke) is originated in the Amazon region and have high industrial value due to the caffeine content in its seeds. Brazil is practically the only commercial producer of guaraná tree and about 70% of the national supply of seed is consumed by the soft drink industry. The Amazon weather with high temperatures and humidity contribute to proliferation of diseases caused by fungi that are a major problem in decreased production of guaraná seeds in the state of Amazonas. The disease named "supersprouting" caused by Fusarium decemcellulares (teleomorphic Albonectria regidiuscula) is characterized by symptoms such as floral hyperplasia, galls on the trunk and witch broom in vegetative buds. In recent years supersprouting has become one of the most important diseases of the crop, causing losses of up to 100% of production. The goal of this work was to select ISSR markers to characterize the diversity and population structure of F. decemcellulare. For screening of ISSR marker, 93 primers from UBC set list were tested using DNA of the isolated F001 extracted by CTAB method. The PCR reactions were performed in a 15 μl volume containing 50ng of DNA from F. decemcellulare, 1X Buffer [20mM Tris-HCl pH 8.0, 0.1 mM EDTA, 1.0 mM DTT, 50% (v / v) glycerol]; 1.5 mM MgCl2, 0.8 mM dNTPs, 0.3 µM of primer, 1U Taq DNA Polymerase (Fermentas). The amplification products were separated by electrophoresis on agarose gel 1.5%. The results indicate that 22 of 93 tested primers showed no amplification and others 71 produced of one to 17 bands, to analyze molecular diversity of F. decemcellulare 19 primers presenting 6-17 bands were selected. High number of bands was obtained with AG repeats (primer UBC 808, UBC 809) and GA (UBC 811, UBC812) that produced of 14 to 17 fragments indicating a greater abundance of this microsatellite in the genome of F. decemcellulare