GENETIC DIVERSITY OF *Meloidogyne* spp. FROM IRRIGATED RICE AND INTEGRATIVE TAXONOMY FOCUSING ON ENZYMATIC AND MOLECULAR MARKERS IN BRAZIL. Diversidade Genética e taxonomia integrativa de *Meloidogyne* spp. do arroz irrigado focando marcadores enzimáticos e moleculares no Brasil Mattos, V.S. [1]; Cares, J.E. [2]; Castagnone-Sereno, P. [3]; Carneiro, R.M.D.G. [1]. [1]Embrapa Cenargen, Brasilia, DF. [2]UNB, Brasilia, DF. [3]INRAE, Sophia Antipolis, France. Email: vsmattos.agro@gmail.com.

Recently, a *Meloidogyne* species complex was detected parasitizing and causing damage to irrigated rice in southern Brazil, highlighting the need to study the genetic diversity of these nematodes in order to select resistant genotypes. Studies compared the Brazilian species and established enzymatic and molecular markers for their identification. Genetic variability was assessed using RAPD and AFLP markers. *M. graminicola* and *M. ottersoni* showed high intraspecific variability: 83.76% and 41.14%, respectively. Cluster analysis revealed a clear separation among rice root-knot nematodes (RKNs) into subclades according to their esterase phenotypes with 100% bootstrap support. Studies have shown that species can be classified according to their esterase phenotypes, and for some species, there is more than one phenotype, as seen in *M. graminicola* (Est G1, Rm: 0.70; G2, Rm: 0.88 and G3, Rm: 0.77), *M. oryzae* (Est O1, Rm:1.2), and *M. ottersoni* (Est O0, without enzyme phenotype). Phylogenetic relationships complemented and confirmed the other studies. In maximum likelihood analysis of ITS, D2-D3 rRNA, and COXII-16S rRNA sequences, all populations of *M. graminicola* from different esterase phenotypes clustered together with the same species. The same pattern was observed for *M. ottersoni*. Considering molecular markers, there are specific primers for *M. graminicola*, *M. oryzae* and *M. salasi*. More studies are required to establish molecular markers for *M. ottersoni* and to validate the markers with more populations.