

**MGV007** - EPIGENETIC ENHANCEMENT AND DROUGHT STRESS TOLERANCE IN MAIZE: SELECTION TO ANTHESIS-SILKING INTERVAL. DURÃES, F.O.M.; SANTOS, M.X.DOS; GAMA, E.E.G.; GUIMARÃES, C.T.; PAIVA, E.; OLIVEIRA, A.C. (Embrapa Milho e Sorgo, C.P. 151, 35701-970 Sete Lagoas, MG, Brasil. E-mail: [fduraes@cnpms.embrapa.br](mailto:fduraes@cnpms.embrapa.br))

Drought tolerant genotypes utilization is an efficient strategy for increasing yield and reducing cropping risks in areas under water stress problems. Anthesis-silking interval (ASI) in maize has been shown an important phenotypic index for drought tolerance evaluation. In this work there are presented the main strategies of a maize breeding program focusing on drought tolerance, some results on phenotypic evaluations of secondary traits and genotypic evaluation using molecular markers. Using molecular markers, it will be possible to identify maize genomic regions responsible for tolerance (low ASI) and susceptibility (high ASI) to drought, considering ASI as one of the main phenotypic markers. Using the trait ASI there were obtained contrasting endogamic lines (L1170 and L1147 - high ASI, and L13.1.2, L6.1.1, L8.3.1, L10.1.1 - low ASI), which were crossed to obtain a selected  $F_1$  (L1147 x L13.1.2). This hybrid was self-pollinated in order to generate  $F_2$  segregant population. Individuals from this population were evaluated under controlled water stress during the flowering period. It was observed genetic variability and tendency to normally distributed frequency for the trait ASI for this population, suggesting a quantitative inherited trait. These results pointed out a possibility of selection of individuals with extremes phenotypes for this character, allowing mapping some QTL's related with drought tolerance, by using molecular markers associated with *bulk segregant analysis*.