

GENETIC DIVERSITY EVALUATION OF OAT PROMISE GENOTYPES BY MEANS OF FORAGE PRODUCTION VARIABLES

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The oat (*Avena sativa* L.) is an interesting annual forage species. It belongs to the Poaceae family and it has increase exploitation directly by grazing or by use as hay or silage. In this context, the exploration of the forage potential of this species requires more knowledge about the agronomic performance of different genotypes under field conditions. Therefore, this study aims characterizing agronomically 10 oat breeding lines (09Q11002-2, 09Q11002-1, 09Q11003-3, 09Q11003-1, 09Q11004-1, 09Q11004-3, 09Q7019-2, 09Q7019-1, 09Q9022-3 and 09Q9016-1) of Universidade Federal do Rio Grande do Sul with three additional controls (FAPA 43, Iguazu and IPR 126) through the evaluation of total dry matter (TDM) and leaf dry matter content (LDM). The experiment established in May 2012 in Bagé – RS – Brazil, being carried out in 2012 growing season. The plots were installed in a randomized complete block design (RCBD), comprising 8 lines 5 meter long, spaced 20 cm between lines, being the data collected in the four central rows. The plants were cut back to a height of 10 cm above ground level when plants achieved around 25 cm above the ground. The data analyses encompass both (RCBD) for the accumulated matter of all cuts and split plot arrangement considering genotypes as plots and cuts as subplots. The means were tested by Scott Knott 5% significance. The experiment resulted in six cuts during the growing season. The first cut was performed in June 27, 2012 and the last one in October 16, 2012. The accumulated data of all cuts ranged from 5574.762 to 3905.968 kg ha⁻¹ and 4811.0489 to 3392.969 kg ha⁻¹ for TDM and LDM, respectively. Considering the data of all cuts together, no significative difference was observed in both traits. Whereas, analyzing the split plot arrangement genotypes x cuts, significant effects occurred in the interaction genotypes x cuts, as well as, in the cuts effect. In this way, the means was compared between genotypes along each cut and between cuts along each genotype. Interestingly, the genotypes start differentiating within each cut, by Scott Knott, just from the fourth cut and on. Especially attention should be given to genotypes 09Q11003-1, 09Q11004-1, 09Q11004-3, 09Q7019-1 and 09Q9016-1, being remarkable genetic resources in terms of dry matter production in Bagé-RS.

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