

Process-oriented evaluation of yield performance and nutritive value of perennial ryegrass (*Lolium perenne* L.) genotypes

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In Europe, perennial ryegrass is considered to be the most important grassland species due to its high nutritive value. Intensive grassland-based dairy production systems in Europe have been identified as a major source of nitrogen (N) losses, which is a principle cause of the environmental pollution. This problem could be effectively solved by reducing the N output through animal excretion by improving N utilization, thus achieving a balanced carbohydrate/protein metabolism.

Objectives of the current project were to (1) quantify genotype-related effects in yield and quality among the early-intermediate heading perennial ryegrass genotypes, (2) assess the ploidy-related variation between closely related diploids and tetraploids, (3) investigate the maturity-related variations in yield and important quality parameters, and (4) use the Cornell Net Carbohydrate and Protein System (CNCPS) to evaluate the genotypic variations in the composition of crude protein and carbohydrate fractions their kinetics in the rumen. The data base of the project comprised two 2-yr (2006-2007) field experiments, conducted at three experimental sites in Northern Germany.

Results revealed significant variability in yield and nutritive performances among genotypes within the same maturity group, as well as, among closely related diploids and tetraploids. However, magnitude of the differences was small, and the trend was inconsistent for the yield performance of the ploidy levels. This result highlights that the genetic makeup of the diploids and tetraploids under comparison should not be ignored while carrying out yield and/or quality comparisons.

The nutritive value of the early-intermediate heading genotypes varied significantly, due to the heading variations within the same maturity group. Accurate determination of the developmental stage of the grass sward is, therefore, important to evaluate genotypic variations in forage quality. The simplified maturity index (SMI8 - expressed as percentage of tillers beginning the boot stage), provided similar correlations to the yield and studied quality attributes as the commonly used Mean Stage by Count (MSC), but was less time consuming and can be applied routinely and easily in the field. Maturity indices like SMI8 should be considered when performing the Value of Cultivation and Use (VCU) trials prior to registration of new genotypes to avoid maturity biased results.

Using the CNCPS, significant variations were detected among the 20 tested genotypes, concerning the carbohydrate and protein fractions and their kinetics in the rumen, which were, however, few and of little impact, especially in case of the protein fractions. The CNCPS screening of the 20 tested genotypes revealed that introducing high-sugar genotypes to the diet, characterized by their low fiber content and high digestibility, would positively contribute in improving the carbohydrate/protein balance and thus decreasing the risk of high ammonia excretion and environmental pollution. The CNCPS proved to be a vital tool in achieving deep and accurate information about feed fractionation and ruminal kinetics.