

Nutritive value of perennial ryegrass (*Lolium perenne* L.) with special reference to genotype- and ploidy-related effects

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Perennial ryegrass is known to be the most prevalent forage grass species in Northwestern Europe based on its high digestibility and good herbage yield. Ruminant livestock production generates vast quantities of ammonia which contribute to environmental N pollution. This could be attributed to the imbalance between fast nitrogen degradation and insufficient available energy resulting from slow carbohydrate fermentation in the rumen. This problem could be solved by reducing the N output through animal excretion, through improving its utilization by the animal.

Objectives of the current project were to (1) investigate the genotype-related variations in the proteolytic activity of perennial ryegrass, (2) provide information whether the observed genetic variation might be used as a tool in future breeding programs for increasing forage quality in order to support high N-use efficiency in the soil-plant-animal system, (3) use the Cornell Net Carbohydrate and Protein System to evaluate the variations in the composition of crude protein and carbohydrate fractions and provide information about the variability in the rumen kinetics of a set of early-intermediate heading perennial ryegrass genotypes, as well as between closely related diploid and tetraploid genotypes. The data base of the project comprised two 2-yr (2006-2007) field experiments, conducted at three experimental sites in Northern Germany.

In the first study, a decline in protein content along the incubation period was detected, which confirmed that plant-mediated proteases are involved in the process of proteolysis under rumen-like conditions. In addition, evaluation of the protein degradation characteristics showed that the large subunit of Rubisco contributed to the major proportion to the protein decline. Screening of the tested genotypes did not reveal any significant variability in the proteolytic activity. Thus, this quality aspect should be further investigated in order to identify genetic variability, which could be included in future breeding programs. In the second and third studies, significant variations were, generally, detected among the 20 tested genotypes, as well as, among the closely related diploids and tetraploids, concerning the carbohydrate and protein fractions. The variations were, however, few and of little impact. Despite of that, the Cornell Net Carbohydrate and Protein System (CNCPS), proved to be a vital tool in achieving detailed information about feed fractionation and ruminal kinetics. The CNCPS screening proved that introducing high-sugar genotypes to the diet, would positively contribute in improving the carbohydrate/protein balance and thus decreasing the risk of high ammonia excretion and environmental pollution. Nonetheless, despite of the close genetic relationship between the tested diploids and tetraploids within the ploidy families, only few variations could be detected. The detected small variations among the genotypes suggest that the tested genetic material was similar, and highlights the need of introducing more variation to the genetic base of selection for the investigated quality parameters.