GENETIC VARIATION IN PERENNIAL RYEGRASS FOR VOLATILE FATTY ACID PRODUCTION IN RUMEN FLUID

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ABSTRACT

In perennial ryegrass genetic variation was shown not only for *in vitro* organic matter degradation (OMD) in rumen fluid and neutral detergent fibre content (NDF) but also for production of volatile fatty acids (VFAs) upon *in vitro* incubation in rumen fluid. The correlations among concentrations of VFAs in the incubation fluid were high. OMD and NDF, on the other hand, were poorly correlated to the VFA concentrations.

KEYWORDS

Perennial ryegrass, *in vitro* degradation, volatile fatty acids

INTRODUCTION

Extent and rate of degradation of organic matter in rumen fluid largely determine the nutritive value of forages. Both traits can be estimated in *in vitro* assays using rumen fluid (Van Soest et al., 1966; Beuvink and Spoelstra,1992). Application of such methods in genetic studies with maize and forage grass species has shown that a large part of the variation in extent and rate of organic matter degradation (OMD) are genetically determined (Van Loo et al., 1995; Dolstra et al., 1993; Buxton, 1990). In addition to extent and rate of degradation also the fermentation profile of forages, i.e. volatile fatty acids (VFAs) and microbial biomass production, determine the ruminant's ability to produce milk, beef and/or wool and its quality. Fermentation studies with stalk samples of maize indicate that VFA profiles as monitored in *in vitro* assays with rumen fluid depend on the chemical composition of the sample and may be manipulated by plant breeders (Marvin et al., 1995).

In this paper genetic variation was investigated in a set of clones, inbred lines and populations of perennial ryegrass for *in vitro* VFA production in rumen fluid to obtain a better understanding of the impact of genotypic differences.

MATERIALS AND METHODS

The grass samples used in this study were obtained from a field trial with twenty different entries of perennial ryegrass at two locations. The experimental units consisted of 1-row plots of ten spaced plants. The entries included ten clonally multiplicated genotypes, five seed multiplicated inbred families and five open pollinated populations. Each entry was represented by a set of ten plants. In the case of the genotypes these ten plants were genetically the same. In the case of inbred families and populations these ten plants were randomly chosen from the inbred family or population. All plants of each inbred family had a common parent that was selfed three times. The set of ten plants of each entry was clonally duplicated. The two duplicate sets of ten plants were evaluated at the two locations. The rows were cut in late summer and the harvested material was dried at 70°C for 24 h and subsequently ground in a hammer mill over a 1 mm sieve. The ground samples were incubated in rumen fluid for 48 h as described by Beuvink and Spoelstra (1992) and the concentration of the various VFAs (i.e. acetic acid [HA], propionic acid [HP], and butyric acid [HB]) in the rumen fluid after 48 h was measured by gas chromatography as described by Robinson et al. (1986). The neutral detergent fibre (NDF) content of the grass samples was measured by the method of Van Soest et al. (1966). Crude protein content was calculated as 6.25* total N-content (no nitrate was present) and N-content was measured by the Kjeldahl method.

RESULTS AND DISCUSSION

The extent and range of OMD, NDF and VFA productions for clones, lines and populations, respectively, are shown in Table 1. Means of the two locations are presented, since entry x location interactions were much smaller than main effects of entries. In each subgroup of entries the range was large for all traits investigated; the maximal differences between entries were always significant. Coefficients of correlation among entry means for the various VFAs were always higher than 0.8 which is in agreement with earlier studies in maize (Marvin et al., 1995).

The entry means for VFAs were poorly correlated to OMD and NDF, respectively ($r < 0.55$). This finding is in clear contrast to those of similar experiments with stalk samples in maize (Marvin, unpublished results).

The relationship between the production of the various VFAs and OMD or NDF was not improved when organic matter was corrected for crude protein content. Influence of water soluble carbohydrates on the VFA profiles, differences in contents of water soluble carbohydrate and lower ranges for OMD and NDF as compared to maize may have caused the striking difference between grass and maize.

In conclusion, the experiment showed genetic variation in perennial ryegrass not only for OMD and NDF, but also for the production of VFAs upon incubation in rumen fluid, indicating that VFA profiles in the rumen of cattle may be manipulated by plant breeding.

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Table 1
Mean and range of *in vitro* fermentation characteristics in different groups of genetic material of perennial ryegrass. Based on averages of two locations.

		Trait				
		OMD	NDF	HA	HP	HB
Type of entry		(% of OM)			(mmol.g OM^{-1})	
Genotypes	Min	81.8	46.1	4.0	1.5	0.51
	Max	87.2	55.7	5.2	1.8	0.60
Inbred families	Min	82.3	50.7	3.8	1.3	0.39
	Max	87.0	55.8	4.8	1.7	0.55
Populations	Min	79.1	53.1	4.2	1.5	0.48
	Max	84.6	58.8	4.9	1.8	0.61
	LSD(P=0.05)	2.1	4.1	0.8	0.2	0.12
	Mean	82.7	52.7	4.6	1.6	0.54

Abbreviations: OMD: organic matter degradation; NDF: neutral detegerent fibre; HA: acetic acid; HP: propionic acid; HB: butyric acid; OM: organic matter. LSD for pairwise comparisons between entry means.