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How to simplify tools for natural grassland characterisation based on biological measures without losing too much information?

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Introduction In marginal areas, such as the Pyrenees, natural grasslands are the only available resource for livestock feeding. Despite this, there is a lack of simple and efficient tools for advisers to aid the management of the complex vegetation of these grasslands. Therefore, we tested an approach derived from functional ecology, to construct such tools: using biological traits to inform on the agronomic characteristics and the way farmers' practices act on them (Ansquer *et al.*, 2004). Nevertheless, the required protocol of measurement is still time-consuming and difficult. In this paper, we test different ways of simplifying this protocol by reducing the number of species measured and not considering specific abundances.

Materials and methods The experimental design, located in the French Pyrenees (Ariège), consisted in 6 "treatments" derived from two factors corresponding to the farmers' practices: the fertility level (N and P) and the intensity of mowing and/or grazing. Three biological traits were measured: height of the plant, specific leaf area (SLA) and leaf dry matter content (LDMC). Measurements were made at the vegetative stage, as described by Cornelissen *et al.* (2003), on each species contributing at least 80% of the grassland standing biomass. The first level of simplification tested corresponds to comparisons between traits values calculated at 3 different levels of the grassland community: all the measured species, the grass community and the 2 dominant grass species only. At a second level, comparisons were made between traits values weighted (w) or not (nw) by the specific abundances of the species considered. Spearman rank correlation tests and one-way Anova were used respectively to compare the different levels of simplification and the capacity of traits to separate the treatments.

Results Table 1 shows that the weighted trait values obtained at the whole community level are well correlated with those calculated using the grass community and both dominant grass species. The order of SLA values is the best conserved. The weighted and not weighted values are also well correlated at the 2 "grass levels" (Table 2); no correlation between w and nw LDMC was obtained for the whole community. Significant differences among treatments for each trait were found, weighting or not by abundances, at the "grass levels" (p<0.05) but not for LDMC calculated on all species. These results can be explained by the different ranges of LDMC values between growth forms so mixing different growth forms as for the "all species" value is not relevant.

Table 1 Rank correlations (r and level of significance[#]) between weighted traits values calculated at the grassland level (All species) and on the grass community (Grasses) and between All species and the 2 dominant grass species together (2 dom. Grasses).

Trait	SLA	Height	LDM
All sp. vs grasses	1.00***	0.94 **	0.83 *
All sp. vs 2 dom. grasses	0.94 *	0.83 *	0.83 *

Table 2 Rank correlations (r and level of significance[#]) between w and nw traits values calculated at the grassland level (All species), on the grass community (Grasses) and on the 2 dominant grass species (2 dom. Grasses).

Trait	SLA	Height	LDMC
All species	1.00 ***	0.94 **	ns
Grasses	0.94 **	1.00 ***	0.94 **
2 dom. grasses	1.00 ***	1.00 ***	0.94 **

* *P*<0.05; ** *P*<0.01; *** *P*<0.001; ns, not significant

Conclusions Our results emphasize the possibility of measuring functional traits of the grass community or even only of the 2 dominant grasses without taking into account the specific abundances. Thus, tools for characterising grasslands, using a simple protocol of trait measurement, can be constructed.

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