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Quantitative vs qualitative vegetation sampling methods: a lesson from a grazing experiment in a Mediterranean grassland

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Nomenclature
Feinbrun-Dothan & Danin (1991)

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Abstract

Question: How well does a time-saving, qualitative sampling method compare with an intensive, quantitative sampling method in identifying the effects of reduction and cessation of cattle grazing on compositional change in a Mediterranean grassland?

Location: Upper Galilee, northern Israel.

Methods: Experimental treatments involved two levels of grazing intensity and protection from grazing for different time periods. Sampling methods included a quantitative method, involving harvesting of vegetative biomass from small (25 × 25 cm) quadrats within 10 × 10 m exclosures, and a qualitative method, involving recording presence only of plant species within the same exclosures.

Results: Both sampling methods revealed differences between protected vegetation and grazed vegetation; however they were not comparable in the way they described differences in species composition between grazed and ungrazed vegetation, and neither method could discriminate between the two levels of grazing intensity. The discrepancy between the two methods in the number and identity of species recorded ranged from 37% to 51% per plot for species recorded by both methods.

Conclusions: Qualitative sampling highlighted species that are indicative of protection from grazing; however it did not satisfactorily describe alteration in community composition, since the studied grassland is characterized by changing dominance of common species among treatments, instead of major species turnover. Suitable methods of data collection and monitoring will depend primarily on manpower and the specific characteristics of the studied community.

Introduction

In grazed rangelands, extensification (i.e. reduction of grazing pressure) and cessation of grazing may cause significant changes in vegetation composition (Peco et al. 2005, 2006; Golodets et al. 2010), with important consequences for ecosystem functioning (e.g. productivity, nutrient cycling) and services (e.g. water catchment, species diversity and amenity value) (Marriott et al. 2004). Policy development for rangeland management requires easily accessible, yet comprehensive data on the target system (Ramsay et al. 2006). Appropriate methods of data collection and monitoring will depend primarily on the specific management aims, but may also depend on time, manpower and cost constraints (Bouxin 1975).

Vegetation sampling can be performed by quantitative and/or qualitative methods. Quantitative methods involve intensive sampling with small sampling units. They provide exhaustive and exact information about abundance of the most common species, suitable for detailed monitoring of community dynamics and ecosystem function (Marchant et al. 1995). However, less common and rare species may not to be recorded, due to the small total sampled area and limitations to sampling effort. This approach, therefore, may not be feasible for conservation of rare species. In contrast, qualitative sampling methods involve larger and fewer sampling units where presence of all species is recorded. The total sampled area is much larger than

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that of quantitative sampling methods, enabling recording of less frequent and rare species, and providing a better estimate of species' distributions throughout the target area. Qualitative methods are suitable for monitoring of large areas (Marchant et al. 1995), for developing management plans for conservation of rare species, and can save valuable time and money. However, they lack the small-scale detail required for understanding community dynamics and ecosystem functioning.

We compared qualitative and quantitative sampling methods to determine the preferred method for assessing the response of species composition to reduced grazing pressure and cessation of grazing in a Mediterranean grassland in the Galilee region of Israel. Cattle grazing has been practiced for millennia in this region and the vegetation responds rapidly to changes in grazing conditions (Perevolotsky & Seligman 1998; Sternberg et al. 2000; Golodets et al. 2010), via shifts in dominance of functional groups, from short annual grasses and thistles in grazed vegetation to tall perennial and annual grasses in ungrazed vegetation (Noy-Meir et al. 1989; Sternberg et al. 2000; Golodets et al. 2010). Here, we asked whether qualitative or quantitative sampling methods would be better at capturing changes in herbaceous vegetation composition in grasslands responding to grazing mainly by changes in species dominance, paying specific attention to differences between grazing intensities.

Methods

Site description

The research was carried out at the Karei Deshe Experimental Station (32°55′N, 35°35′E, 150 m a.s.l., 567 mm annual rainfall) in the northeast Galilee region of Israel. The vegetation is Mediterranean semi-steppe batha (Zohary 1973), with hemicryptophytic forbs (*Bituminaria bituminosa*, *Echinops gaillardotii*, *E. adenocaulos*, *Ferula communis*), perennial grasses (*Hordeum bulbosum*) and annual species, including grasses (*Avena sterilis, Alopecurus utriculatus, Bromus* spp.), legumes (*Medicago* spp., *Trifolium* spp.), several composites, crucifers and umbellifers (Noy-Meir et al. 1989; Sternberg et al. 2000). The growth and development of the vegetation depends almost entirely on seasonal rainfall, from mid-October/late November to late April/early May. Productivity is strongly dependent on the amount and distribution of rainfall within the growing season.

Experimental treatments

The rangeland at the station is grazed by cattle under a controlled grazing system (Sternberg et al. 2000) set up in 1993. The four experimental treatments used in the present study include two grazing treatments – continuous heavy (CH), and continuous moderate (CM), with 1.1 and 0.55 cows ha^{-1} yr^{-1}, respectively, and plots protected from grazing for 3 yrs short-term protection (SP) and for 30–40 yrs long-term protection (LP). In the continuous grazing treatments, the cattle grazed for about 8 months, from mid-January to late August (as opposed to shorter seasonal – i.e. spring and summer – grazing practiced in other plots on the station; Sternberg et al. 2000). During the autumn, cattle are supplemented with poultry litter. Each grazing treatment included two replicate plots making a total of eight plots for the experiment. Within each grazed plot, 10 × 10 m exclosures were established in February–March 2003, separated from each other by 50–100 m. The exclosures were set up to monitor short-term recovery of the vegetation after protection from grazing, and to compare it with the vegetation in the protected plots. The grazed plots are relatively large compared to the protected plots (*ca.* 20–30 ha vs 0.4–2.0 ha), but the actual sampled area was very similar between treatments. In the protected plots, five 2.5-m long stakes were located randomly within each plot, with each stake marking the centre of the 100-m^2 area for sampling (Golodets et al. 2009).

Sampling

Biomass production and functional group composition were determined immediately after setting up exclosures, to identify effects of grazing on the vegetation (Golodets et al. 2010). Data presented in this paper were collected in 2004 from three exclosures in each plot. One plot in the SP treatment was destroyed prior to sampling in 2004, however we retained the second plot in this treatment for the comparison, since our aim here is to compare sampling methods, not to analyse statistical differences between treatments.

For the quantitative method, five small quadrat (25 × 25 cm) vegetation samples were taken within each of the three exclosures in grazed plots (excluding vegetation within 1 m of the fence, which may be accessible to cattle), and within a 4.5-m radius of each of the three stakes in protected plots, for a total of 105 samples (5 samples × 3 exclosures/stakes × 7 plots). Vegetation was sampled randomly within the sample area, avoiding rocks and large perennial hemicryptophyes but including the dominant perennial grass *Hordeum bulbosum* (23% cover) Above-ground plant material was removed within the sampling quadrat, sorted by species, oven-dried at 70 °C for 48 h and weighed. Biomass per species was used as the quantitative measure of species abundance, based on Grime's (1998) biomass ratio hypothesis, which states that ecosystem functioning is primarily determined by the species that dominate plant biomass production. This

quantitative method adequately represents changes in diversity, plant traits and ecosystem function between grazed and ungrazed vegetation (Golodets et al. 2009, 2010, 2011).

For the qualitative method, we surveyed the entire area in which we conducted the quantitative sampling. Thus, all herbaceous species (i.e. excluding dicotyledonous hemicryptophytes) appearing within an 8 × 8 m quadrat within exclosures in each grazed plot and in the protected plots were recorded. Sampling by the two methods was done simultaneously. Nomenclature follows Feinbrun-Dothan & Danin (1991).

Data analysis

Discrepancy analysis

We calculated the percentage discrepancy in recording of species using the two methods, with the equation of Nilsson & Nilsson (1985) for pseudo-turnover:

$$\frac{A+B}{S_A+S_B}\times 100$$

where A and B are the numbers of exclusive species for each method and S_A and S_B are numbers of species recorded by each method. Discrepancy was calculated per exclosure (grazed plots) or sampling location (protected plots), by pooling species lists for the five 25 × 25 cm quadrats sampled by the quantitative method, for both the full species list and for the subset of species recorded with both sampling methods. The two different discrepancy calculations were compared using a paired t-test in JMP 7.0.2 (SAS Institute Inc., Cary, NC, USA).

Ordination

We used principal components analysis (PCA) to analyse the data. In order to enable paired analysis of data from both sampling methods, quadrat data from the quantitative sampling were pooled per exclosure. We built a combined data set, using the 62 species that were recorded by both methods, encoding each species twice – once for the quantitative sampling, and once for the qualitative sampling, for a total of 21 samples × 124 species (each species appears twice). PCA was conducted in CANOCO for Windows 4.5 (Microcomputer Power, Ithaca, NY, USA). Species data were centered and standardized, to enable analysis of both data types in the same PCA. Since the first two PCA axes explained similar amounts of variation, we calculated the correlation coefficient between species scores of quantitative vs. qualitative sampling methods on each axis to determine whether the two methods captured variability of species composition in a comparable way.

Results

Labour and time requirements

Combined labour and time requirements for the quantitative method were nearly ten times higher than those for the qualitative method (Table 1), mainly due to the need for sorting, identification and weighing of the biomass samples in the laboratory.

Species occurrence

The total area sampled by the quantitative method comprising 105 samples, was 6.56 m^2, which was 0.49% of the area sampled by the qualitative method (2112 m^2). The quantitative method recorded just over half the number of species recorded by the qualitative method (68 vs 124). Species lists for the quantitative and qualitative sampling methods are presented in Appendices S1 and S2, respectively. The combined total number of species recorded was 130. Of these, just over half (62 species) were recorded by both methods.

The number of species recorded per plot (Table 2) ranged from 19 to 31 species for the quantitative method, and from 37 to 70 species for the qualitative method. The discrepancy between the two methods in the number and identity of species recorded ranged from 45% to 62% per plot for the full species set, and from 37% to 51% for the subset of species recorded by both methods. This difference was significant (t = 8.95; P < 0.0001).

PCA ordination

The first two PCA axes represented 13.7% and 13.0%, respectively, of the variation in species composition. They differentiated between short-term (positive values on Axis 1) or long-term (positive values on Axis 2) protected

Table 1. Comparison of labour and time requirements for quantitative and qualitative sampling methods.

	Quantitative method		Qualitative method	
	Days	No. people	Days	No. people
Sampling (field)	2	5	4	2
Species sorting and classification (laboratory)	2	5	Conducted in the field	
Weighing biomass samples (laboratory)	3	1	Not applicable	
Total[1]	7	11	4	2
Total manpower days	77		8	

[1]Does not include 2 days for drying of biomass samples.

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Table 2. Discrepancy in species richness and identity per exclosure (mean ± SE), between quantitative and qualitative sampling methods, for all species and for the subset of species recorded with both methods. Species lists for the quantitative method were the pooled species lists from the five quadrats in each exclosure. Discrepancy values calculated for the latter were significantly lower ($P < 0.0001$, paired *t*-test) than those calculated for the former. Experimental treatments: heavy grazing (CH1, CH2), moderate grazing (CM1, CM2), long-term grazing protection (LP1, LP2), short-term grazing protection (SP).

Plot	All species (130)	Shared species (62)
LP1	62.0 ± 2.73	51.2 ± 3.28
LP2	58.1 ± 4.07	49.8 ± 1.98
SP	48.1 ± 5.28	44.6 ± 5.99
CM1	53.3 ± 1.60	43.6 ± 1.45
CM2	44.9 ± 2.61	37.3 ± 5.07
CH1	58.4 ± 5.79	50.8 ± 8.62
CH2	61.3 ± 5.15	50.2 ± 8.55

vegetation vs recently grazed vegetation (neutral or negative scores on both axes). Species scores from the two methods on the first and second PCA axes (Table 3) were significantly and positively correlated, however the correlation coefficients were relatively low ($R = 0.486$ and $R = 0.367$ for Axis 1 and Axis 2, respectively) and not biologically meaningful. When examining effects of sampling method on species scores, we found that a difference of $\geq$ 0.5 units (*ca.* 20% of axis length) between species scores on the PCA axes reflected differences between sampling methods in describing species' distributions across experimental plots. In total, species scores of 35 species (22 and 25 species, respectively, for Axis 1 and Axis 2), were found to differ by $\geq$ 0.5 units along the PCA axes. Fifteen such species (Table 3) were recorded more often by the qualitative method than by the quantitative one, while the opposite was true for *Brassica nigra*. Six common species (*Alopecurus utriculatus, Avena sterilis, Bromus lanceolatus, Hordeum bulbosum, Lolium rigidum, Triticum dicoccoides*) and one less common species (*Scandix verna*) were recorded at a similar frequency with both methods, however their abundance differed markedly between plots. Twelve additional species were recorded in different plots by the two methods (Table 3).

Discussion

The comparison between quantitative and qualitative sampling methods presented here emphasizes important differences in the abilities of the two sampling methods to accurately represent changes in species composition of this Mediterranean grassland in response to grazing. Although we expected that the qualitative method would differentiate more efficiently between different levels of grazing intensity, our expectations were not met. The qualitative method recovered nearly twice the number of species that were recorded by the quantitative method, using just over one-tenth of the manpower and resources required by the quantitative method. However, the analyses presented here show that the two methods were not comparable in their description of the plant community.

Discrepancy in species richness and identity was very high (37–51%), even when differences in species richness between the two methods were accounted for by calculating discrepancy only for the 62 shared species. Previous studies reported much lower values of discrepancy between sample methods or observers. In those studies, however, the vegetation was sampled by different observers using the same or different quantitative sampling methods (e.g. Nilsson & Nilsson 1985; Lepš & Hadincová 1992; Kercher et al. 2003; Archaux et al. 2006), thus the discrepancy calculations were a measure of repeatability of the sampling process. We could argue that the high discrepancy is an artefact of the difference in sample area between the two methods, however, further evidence presented below shows that even when we factor out this variable, we still find that the qualitative method cannot adequately describe the studied plant community.

The PCA of species recorded with both methods highlights further differences between the sampling methods, and provides ample evidence that the two methods are not comparable in their description of the vegetation. The low correlation coefficients between species scores (0.367–0.486) for the two methods along the ordination axes, as well as the small amount of variation explained by the first two axes (13.7% and 13.0%) indicate that the two methods are not capturing the same variation in species composition. In a comparison between density and cover estimates of species abundance, Pavlů et al. (2009) were able to identify differences between methods even with correlation coefficients as high as 0.8, therefore a very high correlation (*ca.* 0.9) would be required in order to conclude that two methods are comparable.

Over half of the species recorded with both methods (35 out of 62) were represented differently among experimental plots by the two methods. In particular, some of the most abundant species (*Alopecurus utriculatus, Avena sterilis, Bromus lanceolatus, Hordeum bulbosum, Lolium rigidum, Triticum dicoccoides*), which had variable abundance among the experimental plots and are key species for differentiating between grazing treatments (Golodets et al. 2009, 2010), were not identified as important species by the qualitative method because they were present in all experimental plots. Conversely, several species that were identified by the qualitative plot as being important indicators of long- or short-term protection from grazing (e.g. *Anthemis* spp., *Bellevalia flexuosa*, *Geropogon hybridus*) are relatively rare. It is unlikely that such species are important for ecosystem

Table 3. Species scores along the first PCA axis, based on the 62 species recorded with both quantitative and qualitative sampling methods. Species in bold type are those with a difference of $\geq$ 0.5 units between quantitative and qualitative species scores along the first two PCA axes. Axis 1 differentiates between short-term protected vegetation (positive) and recently grazed vegetation (neutral-negative); Axis 2 differentiates between long-term protected vegetation (positive) and recently grazed vegetation (neutral-negative).

Species	PCA axis 1		PCA axis 2	
	Quantitative method	Qualitative method	Quantitative method	Qualitative method
Aegilops peregrina	1.11	1.54	0.03	0.29
Ainsworthia trachycarpa[1]	−0.08	−0.31	**−0.32**	**0.35**
Alopecurus utriculatus[2]	0.35	0	**−0.89**	**0**
Ammi majus	−0.07	−0.16	−0.27	−0.53
Anagallis arvensis[1]	**1.20**	**−0.29**	**0.14**	**0.67**
Anthemis bornmuelleri[3]	−0.09	−0.28	**−0.28**	**0.92**
Anthemis palaestina[3]	−0.25	−0.34	**0.053**	**1.04**
Avena sterilis[2]	**1.52**	**0.29**	0.28	0.52
Bellevalia flexuosa[1]	**−0.05**	**0.65**	**−0.21**	**−0.97**
Beta vulgaris	−0.06	−0.32	−0.38	−0.72
Brachypodium distachyon	1.40	0.93	0.21	0.59
Brassica nigra[4]	**−0.34**	**1.54**	**0.88**	**0.29**
Bromus lanceolatus[2]	0.24	0.19	**−0.57**	**0.29**
Bromus madritensis[3]	−0.28	−0.59	**0.92**	**−0.45**
Bromus scoparius	−0.03	−0.05	−0.18	−0.30
Bromus sterilis[3]	−0.41	−0.21	**1.15**	**−0.32**
Carthamus glauca[1]	**1.20**	**0.45**	0.18	0.04
Cephalaria joppensis	−0.34	−0.34	0.92	1.04
Cichorium pumilum	−0.17	−0.09	−0.36	0.14
Convolvulus palaestinus[3]	**0.66**	**1.20**	0.12	0.15
Convolvulus pentapetaloides[3]	−0.20	−0.37	**−0.26**	**−0.78**
Cucsuta brevistylis	−0.16	−0.21	−0.48	−0.45
Cynodon dactylum	1.15	1.37	0.22	0.11
Echium plantagineum[1]	**−0.27**	**0.50**	0	0.14
Euphorbia oxydonta[1]	**−0.28**	**0.46**	0.92	1.04
Geranium molle	−0.34	−0.71	0.92	0.48
Geropogon hybridus[3]	**−0.25**	**0.69**	**0.14**	**1.19**
Hedypnois cretica	−0.11	−0.20	−0.26	−0.74
Hordeum bulbosum[2]	**0.88**	**0.19**	**0.84**	**0.29**
Hordeum spontaneum	−0.14	−0.59	−0.23	0.05
Hymenocarpos circinnatus	1.20	0.73	0.14	−0.45
Isatis lusitanica[1]	**−0.03**	**0.49**	−0.18	0.17
Lamium amplexicaule	−0.34	−0.37	0.92	0.53
Lathyrus aphaca[1]	**−0.19**	**0.36**	0.52	0.89
Lathyrus blepharicarpa	−0.12	−0.09	−0.28	−0.28
Lathyrus gorgonei[1]	**0.68**	**0.08**	**0.20**	**1.00**
Lathyrus marmoratus[3]	**0.66**	**−0.05**	0.11	−0.21
Lavatera punctata[3]	−0.25	−0.21	**0.14**	**−0.45**
Linus pubescens[1]	−0.28	0.06	**0.04**	**0.59**
Lolium rigidum[2]	**0.96**	**0.26**	**−0.02**	**0.52**
Medicago granadensis[3]	−0.21	−0.30	**−0.17**	**0.44**
Medicago polymorpha[1]	−0.20	0.22	**−0.41**	**0.57**
Medicago rotata[1]	**1.20**	**0.63**	0.15	0.32
Morea sisyrinchium	−0.23	−0.32	−0.19	−0.45
Octhodium aegyptiacum	−0.29	−0.67	−0.32	0.08
Phalaris paradoxa[3]	**1.22**	**−0.19**	**−0.08**	**0.52**
Pimpinella cretica[3]	**−0.43**	**0.99**	**1.15**	**−0.10**
Poa bulbosa	−0.04	−0.28	−0.20	−0.37
Polypogon equisetiforme	−0.44	−0.52	1.34	1.38
Polycarpon tetraphyllum	−0.25	−0.40	−0.26	−0.53
Raphanus rostrata[1]	−0.42	−0.62	**0.84**	**−1.00**
Rapistrum rugosum[1]	**−0.26**	**0.26**	−0.73	−0.02
Scandix verna[2]	**1.34**	**0.71**	**0.18**	**−1.00**
Scolymus maculata	0.33	0.10	−0.43	0.06
Senecio vernalis	−0.34	−0.56	0.92	1.05
Thrincia tuberosa	0.65	1.09	0.06	−0.19
Torilis tenella	−0.33	−0.37	1.01	0.58
Trifolium argutum	−0.04	0.41	−0.24	−0.21
Trifolium pilulare[1]	**1.09**	**0.09**	**−0.01**	**−0.77**
Trifolium purpureum	−0.40	0.08	0.75	1.12
Triticum dicoccoides[2]	**1.54**	**0.67**	**0.25**	**1.34**
Vicia peregrina	−0.34	−0.44	0.92	1.33

[1]Species recorded in more plots with the qualitative method.
[2]Species recorded in a similar number of plots with each method, with variable abundance across plots.
[3]Species recorded in different plots with each method.
[4]Species recorded in more plots with the quantitative method.

functioning (Grime 1998), yet they may act as indicators of changes in environmental conditions or biotic interactions (Volis et al. 2011). In addition, many species' distributions were described differently by the two methods because they were either 'overlooked' during the qualitative sampling, or were not detected by the quantitative method due to the limited sample area.

The studied annual grassland is characterized by changes in dominance of functional groups under

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different grazing conditions (Sternberg et al. 2000; Golodets et al. 2010), where the same common species are present under all conditions, however at different abundances. This particular characteristic of the system is the likely reason why the qualitative sampling method did not represent changes in species composition in a way that was comparable to the quantitative method. Rather, this method highlighted less common species that were confined to specific grazing conditions. It is possible that in other systems, where changes in species composition between grazing (or other environmental) conditions are due to more extensive species turnover, qualitative sampling could be a good approximation for quantitative sampling.

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Supporting Information

Additional supporting information may be found in the online version of this article:

Appendix S1. Species recorded by quantitative sampling method per plot in 2004 in the experimental treatments. Values represent pooled biomass (g) for 15 samples (five per exclosure/sampling area) in each plot.

Appendix S2. Species recorded by qualitative sampling method per plot in 2004 in the experimental treatments.

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