

Assessing plant diversity and composition in grasslands across spatial scales: the standardised EDGG sampling methodology

Jürgen Dengler^{*,1,2}, Steffen Boch³, Goffredo Filibeck⁴, Alessandro Chiarucci⁵, Iwona Dembicz^{6,1}, Riccardo Guarino⁷, Benjamin Henneberg⁸, Monika Janišová⁹, Corrado Marcenò¹⁰, Alireza Naqinezhad¹¹, Nina Y. Polchaninova¹², Kiril Vassilev¹³ & Idoia Biurrun¹⁴

1) Plant Ecology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Universitätsstr. 30, 95447 Bayreuth, GERMANY; juergen.dengler@uni-bayreuth.de

2) German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Deutscher Platz 5e, 04103 Leipzig, GERMANY

3) Institute of Plant Sciences, University of Bern, Altenbergrain 21, 3013 Bern, SWITZERLAND; steffen.boch@ips.unibe.ch

4) Department of Agricultural and Forestry Sciences, University of Tuscia, 01100 Viterbo, ITALY; filibeck@unitus.it

5) Department of Biological, Geological and Environmental Sciences, Alma Mater Studiorum University of Bologna, Via Irnerio 42, 40126 Bologna, ITALY; alessandro.chiarucci@unibo.it

6) Department of Plant Ecology and Environmental Conservation, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, ul. Żwirki i Wigury 101, 02-089 Warsaw, POLAND; iwodem@op.pl

7) Dept. STEBICEF – Botanical Unit, University of Palermo, via Archirafi 38, 90123 Palermo, ITALY; guarintoro@hotmail.com

8) Animal Ecology II, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Universitätsstr. 30, 95447 Bayreuth, GERMANY; ben_henneberg@web.de

9) Institute of Botany, Slovak Academy of Sciences, Ďumbierska 1, 974 00 Banská-Bystrica, SLOVAKIA; monika.janisova@gmail.com

10) Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, 61137 Brno, CZECH REPUBLIC; marcenocorrado@libero.it

11) Department of Biology, Faculty of Basic Sciences, University of Mazandaran, P.O. Box 47416-95447, Babolsar, Mazandaran, IRAN; a.naqinezhad@umz.ac.ir

12) V.N. Karazin Kharkiv National University, 4 Svobody Sq., 61077 Kharkiv, UKRAINE; polchaninova_n@ukr.net

13) Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 23 Acad. G. Bonchev Str., 1113 Sofia, BULGARIA; kiril5914@abv.bg

14) Department of Plant Biology and Ecology, University of the Basque Country UPV/EHU, PO. Box 644, 48080 Bilbao, SPAIN; idoia.biurrun@ehu.es

*) Corresponding author

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Abstract: This paper presents the details of the EDGG sampling methodology and its underlying rationales. The methodology has been applied during EDGG Research Expeditions and EDGG Field Workshops since 2009, and has been subsequently adopted by various other researchers. The core of the sampling are the EDGG Biodiversity Plots, which are 100-m² squares comprising, in two opposite corners, nested-plot series of 0.0001, 0.001, 0.01, 0.1, 1 and 10 m² square plots, in which all terricolous vascular plants, bryophytes and lichens are recorded using the shoot presence method. In the 10-m² plots, species cover is also estimated as a percentage and various environmental and structural parameters are recorded. Usually the EDGG Biodiversity Plots are complemented by the sampling of additional 10 m² normal plots with the same parameters as the 10-m² corners of the first, allowing coverage of a greater environmental diversity and the achievement of higher statistical power in the subsequent analyses for this important grain size. The EDGG sampling methodology has been refined over the years, while its core has turned out to generate high-quality, standardised data in an effective manner, which facilitates a multitude of analyses. In this paper we provide the current versions of our guidelines, field forms and data entry spreadsheets, as open-access Online Resources to facilitate the easy implementation of this methodology by other researchers. We also discuss potential future additions and modifications to the approach, among which the most promising are the use of stratified-random methods to *a priori* localise the plots and ideas to sample invertebrate taxa on the same plots and grain sizes, such as grasshoppers (*Orthoptera*) and vegetation-dwelling spiders (*Araneae*). As with any other method, the EDGG sampling methodology is not ideal for every single purpose, but with its continuous improvements and its flexibility, it is a good multi-purpose approach. A particularly advantageous element, lacking in most other sampling schemes, including classical phytosociological sampling, is the multi-scale and multi-taxon approach, which provides data that allow for deeper understanding of the generalities and idiosyncrasies of biodiversity patterns and their underlying drivers across scales and taxa.

Keywords: biodiversity; bryophyte; EDGG Biodiversity Plot; invertebrate; lichen; methodology; multi-taxon study; relevé; scale-dependence; species richness; vegetation-environment relationship; vegetation sampling.

Abbreviations: EDGG = Eurasian Dry Grassland Group; GIS = geographic information system; QA = quality assessment; SAR = species-area relationship.

This article contains Online Resources, which are available from the EDGG homepage (<http://www.edgg.org>) as well as from the ResearchGate account of the first author (https://www.researchgate.net/profile/Juergen_Dengler).

Introduction

Understanding the unequal distribution of species diversity is one of the greatest challenges in ecology. Standardized sampling protocols for diversity assessments are therefore essential to reflect diversity patterns across spatial scales and to compare the diversities of different ecosystems. Palaeartic grasslands harbour a high diversity of various taxa (Allan et al. 2014) and hold the majority of world records in vascular plant species richness for grain sizes smaller than 100 m² (Wilson et al. 2012; Dengler et al. 2014; Chytrý et al. 2015). In addition, bryophyte and lichen diversity can also be high in these habitats (Dengler 2005; Müller et al. 2014; Boch et al. 2016; Dengler et al. 2016). However, there are also particularly species-poor grassland types in the Palaeartic (Dengler 2005; Dengler et al. 2016), making Palaeartic grasslands as a whole suitable as a model system to analyse diversity patterns and their underlying drivers. The acquisition of knowledge on these topics is of great importance in the development of appropriate conservation measures and in order to maintain these highly diverse ecosystems and the ecosystem functions they provide (Soliveres et al. 2016).

The majority of studies analysing the effects of abiotic, biotic and historical factors on species diversity implicitly assume that these factors are universal, and thus studying biodiversity patterns at one grain size provides answers for all grain sizes. On the basis of the nowadays readily available and relatively standardised coarse-grain data, most such studies, and thus general ecological knowledge, are based on coarse-grain analyses. These typically rely on data collected at grain sizes of hundreds or thousands of square kilometres, while fine-grain analyses across large spatial extents are largely lacking (Beck et al. 2012). However, it has long been hypothesized that the prevailing drivers of biodiversity vary strongly between grain sizes (Shmida & Wilson 1985). This assumption has indeed found strong support in several recent meta-analyses (Field et al. 2009; Siefert et al. 2012). Studying patterns and drivers of biodiversity at small grain sizes over several orders of magnitude can be particularly insightful, as at this level, (plant) individuals of different species interact with each other and their environment (see examples in Reed et al. 1993; Dupré & Diekmann 2001; de Bello et al. 2007; Giladi et al. 2011; Turtureanu et al. 2014). However, such studies are still rare and mainly restricted to the local, or very rarely to the regional scale. Often comparisons of studies, or even joint analyses of their combined data, are impeded by the idiosyncrasies of the plot sizes and sampling schemes used. The situation is even worse for phytosociological data that are available in large quantities and are suitable for many purposes (Dengler et al. 2011; Chytrý et al. 2016), as plot sizes (Chytrý & Otýpková 2003), as well as sampling quality (Chytrý 2001), vary greatly. Thus, such phytosociological legacy data are a complex source for studies on diversity patterns and their scale dependence.

Bearing this in mind, standardised multi-scale diversity sampling schemes, often combined with the sampling of abiotic

factors and sometimes also non-plant taxa, have been proposed, among them the *Whittaker plots* (Shmida 1984), the plots of the *Carolina Vegetation Survey* (CSW; Peet et al. 1998) and the *BIOTA South Observatories* (Jürgens et al. 2012). Inspired by these, as well as by similar attempts by colleagues (Hobohm 1998; Dolnik 2003), students of the first author tested these ideas in their theses (Löbel 2002; Boch 2005; Allers 2007). On the basis of these studies, Dengler (2009) then proposed the so-called *flexible multi-scale approach for standardised recording of plant species richness patterns*, which can be seen as a methodological framework that allows many different implementations, but with a common core. Starting in the same year, this sampling approach gave rise to the Research Expeditions of the European Dry Grassland Group (EDGG; <http://www.edgg.org>; Vrahnakis et al. 2013), which were meanwhile renamed as *Field Workshops of the Eurasian Dry Grassland Group* (Venn et al. 2016). Here we use the term “field pulse” to refer to both types, inspired by the Carolina Vegetation Survey (Peet et al. 1998), “pulse” implying an intensive event of relatively short duration, but repeated over time. The first event in Transylvania in 2009 (Dengler et al. 2009; Dengler et al. 2012a; Turtureanu et al. 2014) was followed by eight more internationally attended field pulses conducted from Spain in the west to Siberia in the east and from Sicily in the south to Poland in the north (Vrahnakis et al. 2013; Venn et al. 2016). These field pulses created a huge common data pool for joint analyses (Dengler et al. 2016) and yielded a whole series of papers on diversity patterns (Turtureanu et al. 2014; Kuzemko et al. 2016; Polyakova et al. 2016), and also on species composition and syntaxonomy (Dengler et al. 2012a; Pedashenko et al. 2013; Kuzemko et al. 2014). While the sampling approach generally turned out to be very effective for a wide range of different research questions, the joint fieldwork also led to numerous small modifications and additions. Moreover, participants in the field pulses adopted the sampling methods in their own projects (e.g. Baumann et al. 2016; Cancellieri et al. 2017; M.J. and colleagues in Ukraine, unpublished) and even researchers not related to the EDGG started to use this approach (e.g. Mardari & Tănase 2016; A.C. and colleagues in Italy, unpublished).

The EDGG sampling approach, with the EDGG Biodiversity Plots as its core element, is thus evidently effective and attractive. To date, however, no complete in-depth and up-to-date description of this approach has been published. Accordingly this paper presents the current version of our approach, with the latest modifications, subsequent to the 9th EDGG Field Workshop 2016 in Serbia, critically assessing its pros and cons as well as potential extensions and demonstrating potential applications. We believe that our proposal and rationales can also contribute to a better standardisation of other sampling approaches, for example, in phytosociology (compare Mucina et al. 2000). To facilitate the adoption or modification of our approach in other studies, we provide the sampling forms and spreadsheets for data handling in conjunction with this article.

Description of the EDGG sampling methodology and its rationale

The ***description of the methodology*** is always indicated in ***bold-italics***, followed by the justification in normal font. The outlined methodology has been applied in the EDGG field pulses since 2009 (Dengler et al. 2009), unless indicated otherwise. Where appropriate, the methodological explanations are concluded with *practical hints* for their implementation in *italics*.

A. Location and arrangement of the plots

A.1 In each study site, the EDGG Biodiversity Plots (100 m²) are selected subjectively in quasi-homogenous stands of ad-hoc recognizable different vegetation types regarding both site conditions and floristic composition (Photos 1–6). This approach aims at encompassing as much as possible the geographic and ecological heterogeneity within the *a priori* defined “study universe” (e.g. all wet grasslands of a region). Unlike the practice of some phytosociologists (see Glavac 1996), the occurrence of diagnostic species or concurrence

with recognised syntaxa are explicitly excluded as selection criteria. Our approach on the one hand ensures that ecological gradients are representatively covered with a limited sample size, i.e. spatially rare types are relatively over-represented, which is important for analyses of diversity-environment relationships. On the other hand, limiting the number of biodiversity plots per site avoids the risk of over-sampling and pseudo-replication. With the implicit philosophy of relating the number of biodiversity plots per site to its ecological heterogeneity, our approach mimics *ad hoc* the *post-hoc* heterogeneity-constrained random resampling (Lengyel et al. 2011).

A.2 The study-plot sizes are 1 cm²; 10 cm², 100 cm², 1000 cm², 1 m², 10 m² and 100 m² (Fig. 1). Using plot sizes always differing by one order of magnitude is also the philosophy of other widespread multi-scale approaches. For example, Shmida (1984), Peet et al. (1998) and Jürgens et al. (2012) use the same set of plot sizes, excluding only the smallest ones and adding 1000 m². These plot sizes also include three of the most frequently used plot sizes in phytosociology, namely 1, 10 and 100 m² (Chytrý & Otýpková 2003). Having the plot sizes on a geometric scale is beneficial for many ana-



Photo 1. EDGG Biodiversity Plot during the EDGG Field Workshop in Sicily, Italy, 2012 (Photo: T. Becker).



Photo 2. EDGG Biodiversity Plot during the EDGG Research Expedition in Khakassia, Russia, 2013 (Photo: J. Dengler).



Photo 3. EDGG Biodiversity Plot during the EDGG Field Workshop in Navarre, Spain, 2014 (Photo: J. Dengler).



Photo 4. EDGG Biodiversity Plot during the EDGG Field Workshop in Serbia, 2016 (Photo: J. Dengler).

lytical purposes, while the tenfold area increase from one plot to the next largest one is less sampling-intensive and avoids unusual sizes (like 256 m²), which occur in area-doubling approaches (e.g. Chiarucci et al. 2006). We did not include 1000 m² in our standard procedure because complete sampling of such an area in species-rich Palaearctic grasslands can be extremely time-consuming. For example, Dolnik (2003), who is a very experienced field botanist, needed up to seven hours to sample nested plots of up to 900 m² (without replication of subplots) in not particularly rich grassland types of the Curonian Spit (Russia). In contrast, adding smaller grain sizes compared to the other standard sampling schemes, requires only minimal extra effort but is highly beneficial for analyses such as species-area relationships (SARs).

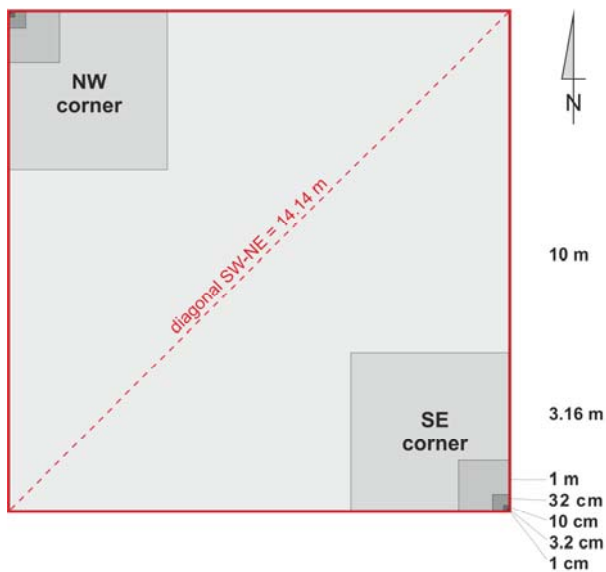


Fig. 1. General arrangement of a 100-m² EDGG Biodiversity Plot and the two series of nested subplots in its NW and SE corners. To establish the 100 m² as a precise square, first the NE-SW diagonal of 14.14 m is delimited (Drawing: I. Dembicz).



Photo 5. EDGG Biodiversity Plot in an alpine steppe of Mt. Damavand, Iran, 2016 (Photo: A. Talebi).

A.3 All plots have a square shape. Some widespread multi-scale recording schemes use different plot shapes depending on grain size (e.g. Shmida 1984; Stohlgren 1995; Peet et al. 1998). However, since plot shape significantly influences species richness (Stohlgren 2007; Bacaro et al. 2015; Güler et al. 2016), constant shape is important for cross-scale studies and analyses of SARs. Among all the possible shapes (squares, rectangles, circles, hexagons, irregular forms), squared plots have a multitude of advantages: (a) apart from circles and hexagons, they are the most compact form, and thus, on average, reflect the least pronounced abiotic gradient and therefore the closest link between environmental conditions, species composition and richness; (b) unlike circles and hexagons, square plots can easily and precisely be delimited in the field with little effort and (c) small squares can be aggregated to larger ones, which is not possible for circles or hexagons. While circles (e.g. Jonsson et al. 1992; Olano et al. 1998; Szwagrzyk et al. 2001) and hexagons (e.g. Jurasinski & Beierkuhnlein 2006) might be beneficial for very specific sampling purposes, we consider the square to be the most practical shape for multi-purpose phytodiversity sampling approaches, also considering that the great majority of legacy data has also been recorded on plots of that shape. *In practice, the 100-m² plot is established first by measuring a diagonal (14.14 m), marking the two corners not to be used for the nested-plot series, fixing a fibreglass measuring tape at 0 m and at 20 m at these two corners and pulling it at the 10-m mark until both sides are straight lines (Fig. 1).* According to our experiences, we do not recommend metal measuring tapes as they are too stiff to allow precise delimitation of the squares in the corners. Also the 10-m² plots (3.16 m edge length) are best delimited using fibreglass measuring tapes and metal pegs, while for 1 m² (1 m edge length) and 0.1 m² (0.32 m edge length) it is more convenient to bend a 2-m folding rule at a right angle and to lay it on the ground. For the three smallest grain sizes, 0.01 m² (0.1 m edge length), 0.001 m² (0.032 m edge length) and 0.0001 m² (0.01 m edge length), in many cases the best way is not to lay-out the inner margins, but just directly measure the position of plants that



Photo 6. EDGG Biodiversity Plot during an advanced student field course in NE Brandenburg, Germany, 2016. The student group in the background is determining grasshoppers that just have been collected on the diagonal of the 100-m² plot (Photo: J. Dengler).

are presumably close to the non-marked inner margins from the outer margins that are marked with the measuring tape anyway.

A.4 The plots < 100 m² are nested and replicated twice in two opposite corners of the 100-m² plot (Photo 6). Since relative variability of species richness and of practically any other relevant parameter increases towards smaller plot sizes (see Dengler 2006), it is important to replicate the grain sizes below the largest ones. For analyses of species-area relationships, it is beneficial to use the average values of the replicates, while using just one plot per grain size (e.g. Löbel 2002; Dolnik 2003) can significantly distort results (Dengler & Boch 2008). While the standard error of the estimates for grain-size richness values decreases with the number of replicates, it turned out during the EDGG field pulses that using only two replicates is a good compromise between precision and time efficiency. *Practically, the two subseries of nested plots are placed in the NW and SE corners of the 100 m² plot.*

A.5 The plots are normally oriented along the cardinal directions (deviations are recorded); GPS coordinates are recorded in decimal degrees (WGS 84) from the NW and SE corner of the 100-m² plot, using the averaging function to achieve the best-possible precision (since 2009), and these corners are permanently marked with buried magnets (introduced after field pulse 2016). These measures are aimed at enabling future re-visitation with precise re-location of the same plots. With this minimal additional “investment” of time and material, the EDGG Biodiversity Plots become real permanent plots, making them the best possible solution to study vegetation dynamics without any distortions (i.e. pseudo-turnover) through inaccurate re-location (see Chytrý et al. 2014).

A.6 In addition to the EDGG Biodiversity Plots (100 m²), “normal plots” of 10 m² are sampled with the same parameters as the 10-m² subplots of the Biodiversity Plots (see below), but with no nesting. These plots are much less time-consuming than EDGG Biodiversity Plots and the additional sampling of “normal plots” allows higher replication and better coverage of environmental gradients for this major grain size. Since the normal plots are in every respect identical to the 10-m² subplots from the corners of the EDGG Biodiversity Plots, they can be combined in one analysis, which improves the statistical power of the analyses at 10 m² (see examples in Turtureanu et al. 2014; Kuzemko et al. 2016; Polyakova et al. 2016), and ensures that, despite limited sampling time, enough plots are recorded for meaningful vegetation classification (Dengler et al. 2012a; Pedashenko et al. 2013; Kuzemko et al. 2014).

B. Species recording

B.1 All living terricolous (i.e. soil-dwelling) vascular plants, bryophytes, lichens and macro-“algae” are recorded. Besides vascular plants, we also record all other photoautotrophic terricolous taxa that are macroscopically visible, meaning that we aim at generating a complete picture of the vegetation. Bryophytes and lichens can contribute very substantially to the overall “phytodiversity” (acknowledging that lichens taxonomically are not plants but symbioses of fungi with photoautotrophic partners) of grasslands (Dengler 2005; Müller et al. 2014; Boch et al. 2016; Dengler et al. 2016). Moreover, multi-taxon studies are generally very insightful (e.g. Zulka et al. 2014; Manning et al. 2015) and the three main taxonomic groups of vegetation: vascular plants, bryophytes and lichens, show quite contrasting relationships to environmental drivers (Löbel et al. 2006; Lenoir et al. 2012; Polyakova et al. 2016). *In practice, dead material of perennial plants is not considered, while dead annuals from the same year are recorded when present. We do this because we consider that a record of a plant community should reflect a complete year, not just a season (Dengler 2003). Theoretically, a better solution would be two recordings per year in communities with a pronounced spring-ephemeroïd aspect and combining both relevés into one (Dierschke 1994), but this is impractical for a one-time field pulse.*

B.2 Presences-absence recording with the shoot-presence system for all plot sizes. There are two common ways to record plant species presence in plots, *rooted presence* (similar to but not identical with the grid-point system) and *shoot presence* (any-part system) (Williamson 2003; Dengler 2008). While for larger grain sizes the results of both methods differ only negligibly, the richness recorded with rooted presences deviates more and more negatively from shoot presence values with decreasing plot sizes, which is theoretically obvious (Williamson 2003), but has recently also been demonstrated empirically for grasslands (Güler et al. 2016; Cancellieri et al. 2017). Therefore, data derived from both methods cannot be directly compared. We decided to use shoot presence because (a) this method is advantageous when analysing SARs as both ways of recording necessarily show deviations from a power law at small spatial scales, but these distortions are much stronger and occur at a far larger grain size for rooted presence than for shoot presence (Williamson 2003; Dengler 2008) and (b) shoot presence, i.e. assuming an individual as occupying an area and not only the point where it penetrates the soil surface, better reflects which species are interacting in the studied plot. *In practice, recording shoot presence is challenging for the three smallest grain sizes of 1 cm², 10 cm² and 100 cm². Here it is important that the observer is very careful not to distort the original arrangement of the vegetation when placing the pegs in the corners and establishing the plots. For these smallest plots, a single observer should do the*



Photo 7. Using a preliminary version of the disc for standardised assessment of vegetation height during the EDGG Field Workshop in Serbia 2016 (Photo: I. Dembicz).

recording. The observer should always look from the same angle into the plot and start recording plants from the highest to the lowest layers, without recording additional plants of the higher layer after they have been bent away to sample plants of the lower layers, nor after the plots have been affected by wind, etc. Our experience suggests that representative results can be achieved with the shoot presence method if one observer works fast and thoroughly.

B.3 Additional percentage cover estimations for the 10-m² plots. Traditionally, phytosociologists recorded plant performance in a plot with the combined cover-abundance scale of Braun-Blanquet (1964) or one of its many modified/refined versions (e.g. Wilmanns 1998). This approach has multiple shortcomings, in particular the combination of two different criteria, cover and abundance which, in the strict sense, precludes most mathematical analyses but which is often ignored. Furthermore, most numerical approaches do not calculate with the cover-abundance scale, but back-transform each cover-abundance class to the mean of its range, introducing a double-error of transformation: first from what is seen in the field to an abstract category and then back to a real cover value, which in some cases can be quite different from the original value. Imagine, for example, a cover of 5%, which belongs to the traditional Braun-Blanquet cover-abundance category “2”, which then usually is back-transformed to a cover value of 15% (because 2 stands for 5–25%), meaning that this step introduced a three-fold error. Last but not least, the Braun-Blanquet scale and almost all similar scales are too coarse for recording species-rich grasslands of high evenness (where almost all species are in the category 2m or 2a) or in very sparse vegetation (where most species have less than 1% cover. However, it is a big difference, i.e. a factor of 10,000, whether the cover is 0.0001% or 1%, which is not reflected in traditional scales). To facilitate realistic cover estimates, we (a) use “estimation aids” such as the calculation to which fully filled square typi-

cal cover percentages within a 10-m² plot would correspond (Table 1) and (b) advise participants that they should always double-check that the cumulative cover of species of one group is at least as high as the independently estimated cover of that group.

Table 1. Areas of completely filled squares that correspond to certain percentage cover values in 10-m² plots.

Percentage cover value	Area in m ²	Area in cm ²	Edge length of square in cm
5	0.5	5000	70.7
4	0.4	4000	63.2
3	0.3	3000	54.8
2	0.2	2000	44.7
1	0.1	1000	31.6
0.5	0.05	500	22.4
0.1	0.01	100	10.0
0.05	0.005	50	7.1
0.01	0.001	10	3.2
0.005	0.0005	5	2.2
0.001	0.0001	1	1.0

C. Structural and environmental variables (in each 10-m² plot)

C.1 Cover of vegetation layers: Cover of the tree (woody > 5 m), shrub (woody 0.5–5 m), herb (woody < 0.5 m and herbaceous) and cryptogam layers are estimated as percentages (since 2009). Additionally, the herb layer is subdivided into the functional groups phanerophytes, chamaephytes, graminoids, legume forbs and other forbs, allowing for overlap between these (adopted after 2016). This last step does not only provide valuable data in itself, but also allows for cross-checking the consistency of species cover data (see B.3).

C.2 Maximum height of tree, shrub and herb layers.

C.3 Measurement of “standard height” of the vegetation (since 2016; prototype during field pulse, improved version afterwards; Photo 7): At five random points in the plot, a circular plastic disc with a central borehole (22.5 cm diameter, 117 g) is released along the inverted penetrometer (see below), the handle of which is placed on the ground. The height where the falling disc is stopped by the vegetation is measured at the borehole. The five measurements provide a reproducible measure of the height at which the vegetation becomes dense, as well as of its spatial variability.



Photo 8. Clipping biomass during the EDGG Field Workshop in Serbia 2016 (Photo: J. Dengler).

C.4 Aboveground biomass (first variants during field pulse 2015; current version after the field pulse 2016; **Photo 8**): Within each 10-m² plot, we clip the aboveground biomass within two random areas of 20 cm × 20 cm to the soil surface. We then pool both samples, i.e. a total surface of 800 cm², after which we dry and weigh them. Sampling two separate areas allows a much better estimate of the mean biomass per 1 m² within the 10 m² plot than a single plot would do (as in 2015). Due to the relatively small total surface, the amount of biomass is still practicable, even during longer field pulses, i.e. the material can be transported and pre-dried. While in 2015, we separated the three fractions into living vascular plants, living non-vascular plants and litter, since 2016 we have taken just one combined sample for biomass s.l. because the previous approach was too time-consuming. *Practically, the area to be sampled can be delimited by a specifically manufactured steel frame or more easily by a frame created by bending a folding ruler four times. The inner edge is 19 cm, but since it is impossible to fix the position 100% during biomass cutting, this is a good approximation of the intended size. Drying is done in an oven at 65 °C until the weight remains constant.*

C.5 Cover of litter and deadwood: Percentage cover after virtually removing all vegetation. Note that the widespread approach of phytosociologists to estimate only that part of the litter that is visible from above, i.e. not covered by living vegetation, precludes using litter cover as a predictor of vegetation attributes, because the two variables would then not be independent of each other.

C.6 Fractions of abiotic soil surface: Percentage cover of the three texture classes: stones and rocks (diameter > 63 mm), gravel (2–63 mm) and fine soil (< 2 mm) at the soil surface after virtually removing all vegetation, litter and deadwood, thus, summing up to 100% cover. Note that the widespread approach of phytosociologists to estimate only that part of the soil surface that is visible from above, i.e. not covered by

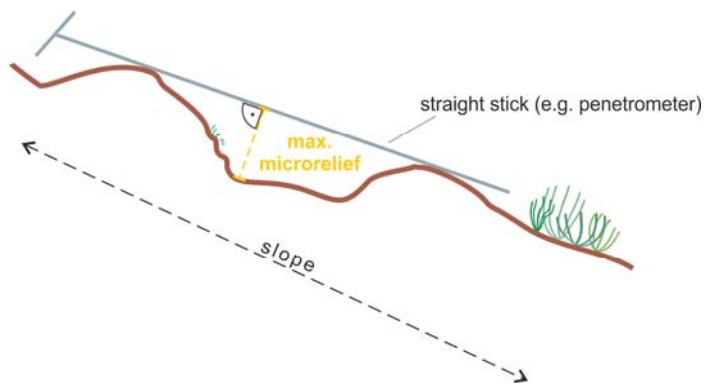


Fig. 2. Illustration of how to measure the maximum microrelief (orange line) in a plot (in our case the 10 m² plots) (Drawing: I. Dembicz).

living or dead vegetation, precludes using these fractions as predictors of vegetation attributes because they would then not be independent.

C.7 Slope aspect and inclination: Practically measured by placing the penetrometer (see below) on the ground along the slope line. Aspect is measured in degrees with a compass and (mean) inclination in degrees with an inclinometer. Nowadays, smartphone apps are available that do both in a very convenient way when placing the smartphone on the 85 cm long penetrometer.

C.8 Microrelief: Is defined as the maximum distance to the ground when placing the penetrometer (see below) to the ground in the most rugged part of the plot, measured perpendicular to the device (since 2014; **Fig. 2**). Formerly, we took this measurement plumb-vertical, but this approach strongly confounded measurements of microrelief by slope inclination.

C.9 Soil depth: Is measured at five random points (to allow calculation of mean and standard deviation) using our soil depth indicator (penetrometer; **Photo 9**). This is a steel pole of 85 cm length and 1.0 cm diameter, pointed at one end and with a handle at the other. It is pushed into the ground until it hits a rock or the soil becomes so dense that it cannot be pushed further. Each depth measurement is noted separately, even if it is “0 cm” (rock at the surface) or “>80 cm” (no resistance at any depth). It is obvious that this measurement should preferably always be done by the same person of average weight and strength. The “odd” length of the penetrometer is because this was the length of our first device. However, it turned out that a device of this length still can be reasonably well carried in checked-in luggage during air travel, while a length of 1 m would already cause problems.

C.10 Soil samples: A mixed soil sample of the uppermost 10 cm of the mineral soil is taken from five random locations within the 10-m² plot (**Photo 10**). This sample is air-dried during the field pulse (**Photo 11**) and afterwards dried at 65 °C. From this sample, we determine as a minimum the following parameters: **(a) skeleton content** (i.e. mass fraction of particles > 2 mm), **(b) texture class** (mostly estimated with a finger test – see Schlichting et al. 1995; Ad-hoc-AG Boden 2005 – sometimes measured, which is time-consuming and costly); **(c) pH** (in a suspension of 10 g dry soil in 25 g aqua dest.); **(d1) humus content** (as loss at ignition at 430 °C until constancy) or, if resources allow, **(d2) C and N contents** (with a C/N analyser), including correction for C from carbonates.

C.11 Land-use: Is problematic to assess during a one-off visit. We try to categorize each plot based on traces, such as faeces, grazing marks, presence/absence of pasture weeds, into **pasture** (i.e. livestock grazed), **meadow** (i.e. mown) or **un-used** in recent years (abandoned semi-natural grassland or natural grassland) (e.g. Turtureanu et al. 2014). Additionally, we use burning traces to decide whether the plot was **burned during the current year** or not. Any more precise information on land-use, the management regimes, their timing and duration (e.g. livestock type, number of animals, combination of mowing, grazing and fertilization, peculiarities in grassland history, etc.) that is available is recorded. Unfortunately, our experience is that during a one-off visit such data can hardly be gathered consistently, so that in none of the field pulses so far were we able to use more detailed land-use parameters for analyses.

D. Data management

To facilitate and standardise data collection and management, the EDGG provides and regularly updates a series of documents, i.e. instructions, templates for printed forms and spreadsheets, the currently up-to-date versions of which accompany this article. All these documents are open access and can be modified according to personal needs. Online Resource 1 contains a detailed list of equipment needed for sampling like that done during EDGG field pulses, depending on the duration and number of participants (**Photo 12**). Online Resource 2 provides detailed practical instructions on how to implement the EDGG sampling in the field, while Online Resource 3 describes the data handling and recording after the fieldwork. Online Resources 4 and 5 are the current templates for biodiversity plots and for normal plots. Online Resources 6 and 7, finally, are spreadsheets (*.xlsx format) for the efficient data entry of species data and header data, respectively. They include some embedded functions that facilitate work and provide some simple data checks (filling in the species list for 100-m² plots automatically based on the two corners, checks of consistency of cover values, calculation of mean and standard deviation for parameters with multiple measurements, descriptive statistics for parameters across all plots to check for



Photo 9. Applying the penetrometer to determine the accessible soil depth during the EDGG Field Workshop in Navarre, Spain, 2014 (Photo: J. Dengler).

outliers/entry errors). From these two spreadsheets, the relevant datasets for the multiple analyses, be it in R or any other statistical software, can be derived with a few clicks.

The data of the EDGG field pulses and some related sampling schemes are stored in a common database, registered in the Global Index of Vegetation-Plot Databases (GIVD; Dengler et al. 2011) as EU-00-003 (Dengler et al. 2012b). These data are available for common data analyses by the contributors and their partners. Moreover, the field pulse data of the 10-m² plots are contributed to existing national or regional partner databases of the European Vegetation Archive (EVA; Chytrý et al. 2016) and the global counterpart “sPlot” (Purschke et al. 2015) so that they are available for continental or global analyses.

E. Possible extensions of the methodology

E.1 Other spatial scales: The most meaningful additional scale would be 1000 m² (31.62 m × 31.62 m) since this is a common grain size in many biodiversity sampling schemes worldwide, albeit mostly realised as 50 m × 20 m (e.g.



Photo 10. Taking a soil sample during the EDGG Field Workshop in Khakassia, Russia, 2013 (Photo: J. Dengler).



Photo 11. Drying and sorting of soil samples during the EDGG Field Workshop in Navarre, Spain, 2014 (Photo: J. Dengler).



Photo 12. Equipment needed for the EDGG sampling methodology, spread to be packed by the different teams during the EDGG Field Workshop in Serbia, 2016 (Photo: C. Marcenò).

Shmida 1984; Peet et al. 1998; Jürgens et al. 2012). There are several ways to arrange nested plots within 1000 m² in a way that is compatible with the EDGG Biodiversity Plots: (a) place one EDGG Biodiversity Plot in the centre of the 1000 m² plot; (b) place two EDGG Biodiversity Plots in two opposite corners; (c) place single nested series of 0.0001–100 m² in two corners or (d) the variant shown in Dengler (2009: Fig. 1). One should be aware that adding 1000 m² drastically increases the time needed for sampling (compare the times for a single nested-plot series up to 900 m² as reported by Dolnik 2003). Therefore, one should only opt for this addition when there are adequate resources available to sample the 1000 m² as comprehensively as the 100 m². Most conveniently this can be done in relatively species poor vegetation with low cover values, e.g. in some open herbaceous vegetation of Southern Africa (Jürgens et al. 2012) or in transitions from steppes to semi-deserts in Iran (where a group including A.N. is currently doing this). Sampling smaller grain sizes than 1 cm², i.e. 1 mm² and 10 mm², is also possible, but requires a special device (Dengler et al. 2004). Finally, it can make sense to “insert” additional plot sizes with full sampling (including cover values and environmental data), such as 16 m² or 25 m², if this is a national standard for sampling herbaceous vegetation for phytosociological purposes. In this case, however, this additional plot size should not be used in SAR analyses, to avoid bias.

E.2 Higher replication at smaller scales: Since the coefficient of variation of species richness strongly increases with decreasing plot size (Dengler 2008 and references therein), increasingly more replicates would be necessary for smaller plots to estimate mean species richness with the same precision. Thus, the original approach of Dengler (2009) proposed that towards each smaller scale within the 100-m² plots, and down to 0.01 m², the number of sub-plot replicates is doubled. Due to time constraints and because it is hardly possible to arrange such an increasing replication that is both nested and unbiased with respect to the 100-m² area (i.e. does not have higher sampling intensity in some regions than in others), this approach was never adopted during the EDGG field pulses. However, Dengler et al. (2004) and Boch (2005; see Dengler & Boch 2008) used four and five series of nested plots (0.0001–10 m²) within the 100-m² plot. Recently Cancellieri et al. (2017) adopted the idea of Dengler (2009: Fig. 2), although with a limited nested series composed of only three spatial scales.

E.3 Stratified-random sampling: Step A.1 of the EDGG sampling methodology is aimed at approximating a dataset similar to one gained with stratified random sampling, but when such an *a priori* stratification is not feasible due to time constraints or lack of suitable information layers for use in a Geographic Information System (GIS). Basically, the sampling approach of Dengler (2009) is applicable in subjectively delimited habitat types, with stratified random sampling (or an

approximation of it) or with fully random sampling (for the pros and cons of these sampling approaches, see Wildi 1986). Only fully random sampling allows calculation of true spatial means of attributes, such as species richness (e.g. Dengler & Allers 2006; see also the grid-based random approach by Cancellieri et al. 2017, which was inspired by Chiarucci et al. 2012), but this usually leads to a strong underrepresentation of rare habitat types (Diekmann et al. 2007). Stratified-random sampling theoretically allows one to get a dataset that is more balanced with regard to environmental gradients (than fully random sampling would) and even to approximate spatial means (when taking the fractional extent of the strata into account), while avoiding the potential biases of subjectively locating the plots. However, stratified-random sampling requires that the main environmental gradients are rather clear *a priori* and available as GIS layers for the study region, which is not usually the case for EDGG field pulses, one of whose main aims is to study undersampled regions. If the prerequisites are met, we recommend considering a stratified-random approach (and aim to implement it in the Field Workshop 2017 in Central Italy; see Filibeck et al. 2016). This approach means that random coordinates within each level of one or several crossed main environmental factors are generated within a GIS and then sampled in the field. For example, one could stratify the region by elevation and bedrock type or by land-use type and slope position. It is self-evident that one needs to decide for one, two or a maximum of three gradients, each subdivided into a small number of categories, because otherwise the number of plots necessary would soon become unrealistic. One should however be aware of the potential problems of a stratified-random approach, even when these prerequisites are met. On the one hand, the *a priori* assumption about the main gradient(s) might turn out to be wrong and then the sampling would not be optimal. For example, Baumann et al. (2016) used EDGG Biodiversity Plots with elevational stratification, only to find out that the elevational gradient in their case was of subordinate importance for the species richness patterns. On the other hand, stratified-random sampling significantly increases the time needed to find and reach the plots in the field, which in some cases might even turn out to be impossible due to inaccessibility.

E.4 Better assessment of beta diversity: Through the multi-scale sampling, the EDGG Biodiversity Plots provide a straightforward tool to assess beta diversity at the smallest scales (i.e. within 100 m²). As Polyakova et al. (2016) demonstrate, the z-values of the power-law SARs are a measure of standardised, multiplicative beta diversity, which allows comparisons of within-plot species turnover between EDGG Biodiversity Plots of different ecological conditions or regions (see also Dengler & Boch 2008; Turtureanu et al. 2014). Assessing beta diversity across larger spatial extents than 100 m², for example across 1 km² or 1000 km² in a comparable manner, is not straightforward with the EDGG sampling methodology because beta diversity values are largely determined by the spatial (and ecological) extent of the study universe (Chiarucci et al. 2009). The approach of constrained-rarefaction offers a way to make data from study regions of different spatial ex-

tent comparable (Chiarucci et al. 2009). However, even this would not account for potentially different ecological/syntaxonomical delimitations of the “study universe” in different field pulses (if, for example, in one only *Festuco-Brometea* were sampled and in another all types of semi-natural grasslands). Therefore, if the assessment of landscape-scale beta diversity is a major aim of a study, one should consider the appropriate placement of the EDGG Biodiversity Plots. One should decide on the landscape scale of interest, e.g. 200 km² (a circle with a radius of 7.98 km), in which the plots should be located randomly. In this respect E.4 can well be combined with E.3. If a less formal, *ad hoc* solution is required, one could think of placing a set of five (or another fixed number) EDGG Biodiversity Plots within the survey perimeter haphazardly, with the only restriction that each of these should represent a different grassland type or, if only one type is considered, come from a different grassland patch.

E.5 Non-terricolous taxa of the vegetation: Also saxicolous (species growing on rocks), lignicolous (species growing on deadwood) and epiphytic taxa (species growing on the bark or evergreen leaves of other plants) belong to the overall phytodiversity. Therefore, we recommend to sample also these taxa. Particularly, saxicolous bryophytes and lichens can contribute significantly to the overall richness in rocky grasslands (e.g. Boch 2005; Boch et al. 2016). Unfortunately, such sampling requires specific equipment (e.g. a knife to collect lignicolous and epiphytic species as well as a hammer and a chisel to collect samples of saxicolous lichens that cannot be identified in the field) and special expertise in the identification of these species. For non-experienced observers aiming at sampling non-vascular plants, one possibility might be the sampling of so called macro-cryptogams, which are easily discernible in the field (e.g. excluding crustose lichens and very small bryophytes). Their richness can be used as an indicator for the overall richness of cryptogams (Bergamini et al. 2005).

E.6 Animal taxa: Given the high potential value of multi-taxon studies to understand patterns and drivers of biodiversity (e.g. Allan et al. 2014; Zulka et al. 2014; Manning et al. 2015; Soliveres et al. 2016), it is highly desirable to also sample animal taxa, for which sampling at the given spatial scales makes sense and can be performed during a single visit. In any case, it must be decided which of the grain sizes can be sampled meaningfully, given that animals, unlike plants, are on the one hand mobile and on the other hand not always discernible even if they are present (i.e. records usually represent activity, not presence). In contrast to plants, typically only one or perhaps two of the standard grain sizes can be sampled and matched with the phytodiversity data. Vegetation structure and, in some cases, plant species composition and richness, have a strong influence on species composition, richness, activities and abundances of many above and belowground invertebrate taxa (Lawton 1983; Borges & Brown 2001; Birkhofer et al. 2011; Simons et al. 2014). For example, spiders as predators are influenced indirectly by



Photo 13. Sampling vegetation-dwelling spiders on a 100-m² EDGG Biodiversity Plot during the EDGG Field Workshop in Navarre, Spain, 2014 (Photo: J. Dengler).

changes in microclimatic conditions, prey abundance, sites for building webs, sheltering and/or oviposition (Gunnarsson 1990; Halaj et al. 1998; McNett & Rypstra 2000). Therefore, collaboration of botanists and zoologists in biodiversity assessments is highly desirable.

During the Field Workshop in Navarre, Spain, vegetation-dwelling spiders (*Araneae*) were sampled by N.Y.P. on the 100-m² plots with standard sampling methods, such as sweep-netting and hand collecting (Duffey 1974; **Photo 13**). As the biodiversity plots are relatively small for sweep-netting, one sample of 15 sweeps was taken inside a given plot and three samples adjacent to it. Using repeated sweeps at the same plot is ineffective for spiders, as they fall on the ground and do not ascend into the vegetation again immediately. Some biodiversity plots could not be sampled because of an extremely low sward. Spider diversity data have not been analysed yet, but this sampling has led to the description of a new spider species (Kastrygina et al. 2016). Where it is possible (but this is evidently not the case during EDGG field pulses with only one visit per site), we recommend to start in early spring with pitfall trapping, using at least five traps per each EDGG Biodiversity Plot. The trap exposition may vary from 5–10 days monthly to a month. Spiders are recommended to be collected during the whole vegetation period because of the different seasonal activities and maturation times. If there is no opportunity to conduct such long-term studies, it is possible to limit them to spring and early summer. Sweep-netting is effective from late spring until mid-summer. The suction method using a Tullgren funnel is effective for plots with low vegetation in the same period. In general, it is preferable to add one autumnal sample. Quadrat samples (hand-collecting in 25 cm × 25 cm plots on the ground and/or litter layer) can reveal less mobile ground-dwelling species. This method can be particularly well combined with the vegetation data, as one can take as many samples as required inside a vegetation plot. To estimate the complete spider community in a given EDGG Biodiversity Plot, one would need to combine all the above-described methods.

Recently, students of the first author, including B.H., sampled grasshoppers (*Orthoptera*) in EDGG Biodiversity Plots (**Photo 14**). Given the relatively low number of species, *Orthoptera* are easier to identify than many other insect taxa. Phytophagous *Orthoptera* are usually polyphagous, meaning they are not limited to just one family of food plants but rather consume a wide range of plant species across different plant families. Therefore, it can be assumed that the occurrence of certain species of *Orthoptera* will not depend on the occurrence of certain plant species, but will rather follow factors like the microclimate, vegetation structure (Gardiner et al. 2002), plant-cover or land-use. The sampling of *Orthoptera* should take place during warm sunny days in late summer (August – September) to ensure detection of mostly imagines (which are easier to determine than juveniles). Days of sampling should not follow a day of intense rainfall. We used the sweep-netting method because it is the most rapid method in the field and does not require expensive equipment. The most commonly used net size is 38 cm diameter (Bomar 2001; Gardiner et al. 2005). Within each 100-m² EDGG Biodiversity Plot, first the NE-SW diagonal (i.e. the one through the corners without 10-m² vegetation plots) was swept by advancing one step forward after each sweep. By doing so, the sweeping of the diagonal was completed after about 15 consecutive sweeps. In addition, the whole 100-m² plot was sampled again three times by walking around and sweeping within the plot for about five seconds each time to ensure that the whole plot area was sampled. After each sweep the *Orthoptera* caught in the net were transferred into plastic boxes for subsequent identification and counting. While the described method generally worked well, it becomes problematic in vegetation plots with taller vegetation (>50 cm plant height), as the catching efficiency may be impeded by vegetation structure (Gardiner et al. 2005).

In the Swiss Biodiversity Monitoring, apart from vascular plants and bryophytes, also land snails (*Gastropoda*) are sampled on the same 10 m² plots (Koordinationsstelle BDM 2014). Other invertebrate groups that are potentially suitable



Photo 14. Sampling grasshoppers on a 100-m² EDGG Biodiversity Plot during an advanced student field course in NE Brandenburg, Germany, 2016 (Photo: J. Dengler).

for inclusion in the EDGG Biodiversity Plots include **leafhoppers (*Auchenorrhyncha*)** (e.g. Primi et al. in press).

E.7 More and better standardised environmental data:

Clearly, the greater the amount of standardised abiotic data that are associated with the recorded biodiversity data, the more analytical opportunities they offer. The EDGG sampling methodology requires parameters and measurement methods that generate reliable data during a single visit using limited time and resources. Among soil parameters, good candidates that were collected during some field pulses but not fixed as standard yet are electrical conductivity (EC), which is particularly relevant when sampling in arid areas or saline habitats, and H- and S-value, from which cation exchange capacity (CEC) and base saturation (BS) can be derived. If the EDGG Biodiversity Plots are distributed within a relatively narrow region and revisiting all of them within one or a few days of constant dry weather is feasible, also soil water content (volumetric or gravimetric) would be a valuable parameter.

E.8 Quality assessment: There are relatively many studies (see review by [Morrison 2016](#)) that measured the impact of observer-related discrepancies in vegetation sampling and warn against the resulting biases in species richness, cover estimates, and visual estimates of other vegetation features. However, this issue is still surprisingly disregarded or overlooked in the vast majority of published researches based on analysis of plot-based data across spatial and environmental gradients. Nevertheless, most studies on observer-related error found mean values of pseudo-turnover (i.e. of the difference in species composition between two observers, or teams of observers, surveying the same plot) ranging from 10% to 30% ([Morrison 2016](#)). In a study with fine-scale plots in temperate European grasslands, [Klimeš et al. \(2001\)](#) found that the discrepancy in vascular plant richness between individual observers ranged from 10% to 20%. These figures are large enough to potentially bias statistical inference and to flaw the search for correlation between environmental vari-



Photo 16. Collection of reference specimens for comparison during the EDGG Research Expedition in Khakassia, Russia, 2013 (Photo: J. Dengler).

ables and species richness. Many studies underlined that pseudo-turnover figures are much reduced when plots are surveyed by a team of botanists rather than by a single researcher. This is already a standard practice in the EDGG field workshops, where each “corner” of the nested series in an EDGG Biodiversity Plot is always surveyed by at least two people (thus the whole Biodiversity Plot is usually surveyed by 4–6 researchers), and the additional normal plots are similarly surveyed by a team of at least 2–3 people. On the other hand, it is to be taken into account that as the participants in EDGG field pulses typically come from many different countries, they will have very different (though often only moderate) levels of familiarity with the regional flora. This is a well-known source of pseudo-turnover, even if the researchers have a lot of experience in their own region, as shown already in 1972 by Tüxen (quoted in [Klimeš et al. 2001](#)).

We consider that the quality of data obtained from the EDGG field pulses is superior to that obtained in typical phytosociological studies for the following reasons: (a) we use clearly delimited plots and spend much more time on these than phytosociologists usually do; (b) at least two people jointly sample each plot; (c) the composition of sampling teams varies, while all participants sample all subtypes of grasslands in a region, (d) the participants of the field pulses always include several local organisers who are deeply familiar with the flora



Photo 15. Plant determination, preparation of herbarium specimens, data correction and data entry during the EDGG Field Workshop in Serbia, 2016 (Photo: J. Dengler).

of the study region, as well as very experienced field botanists from many countries, with good knowledge also of vegetative traits of grassland plants, and they often participate on a regular basis, and (e) every evening the results of the determination of “critical” specimens, as well as the handling of taxonomically problematic taxa, are discussed among the groups, including a display of such specimens (**Photos 15–16**). These measures reduce errors of incomplete or erroneous species records (but cannot exclude them) and they effectively avoid systematic biases between grassland types or among study regions because the remaining errors should be distributed randomly. Since, however, we are so far not able to quantify how big these estimation errors are, we are planning a pilot project for the field pulse 2017 (Filibeck et al. 2016) to introduce some simple quality assessment (QA) procedures, i.e. to obtain estimates of the average pseudo-turnover in the dataset and include the results of this in the subsequent publications. Although thorough QA procedures may be very time-consuming, a reasonable trade-off could be double-sampling 10% of the 10-m² plots (cf. Kercher et al. 2003; Morrison 2016). The problem is more complex, however, for the smaller plots, where double-sampling procedures are faced with practical issues connected with trampling and specimen collection. In addition, the sampling protocol might be refined with some strategies (see e.g. Archaux et al. 2009; Burg et al. 2015; Morrison 2016) to reduce the potential for observer-related error, such as devoting the first day(s) to a thorough floristic training and “calibration” of the participants, with simulated plots; requiring that all plots > 1 m² have to be sampled by at least three observers; recording the time spent on each plot; frequently changing the composition of survey teams or reducing the number of plots studied per day to reduce the effects of fatigue.

Advantages of the EDGG sampling methodology

The major strength of the methodology is that it provides high-quality data for a multitude of different analytical procedures, namely vegetation classification (Dengler et al. 2012a; Pedashenko et al. 2013; Kuzemko et al. 2014), diversity-environment relationships (Turtureanu et al. 2014; Kuzemko et al. 2016; Polyakova et al. 2016) and species-area relationships (Dengler & Boch 2008; Turtureanu et al. 2014). Other obvious options that have not been explored yet include relationships between species diversity, phylogenetic diversity and functional diversity, studies on assembly rules (environmental filtering vs. limiting similarity) or ecological niches, plus the multitude of possibilities that arise from joint analyses of the various consistent regional datasets across large biogeographic gradients. While the time needed for sampling (typically 1–6 hours for a team of 4–6 people for complete recording of an EDGG Biodiversity Plot) is significantly higher than for normal phytosociological sampling, our experience is that this investment pays off in higher data quality and a much wider range of analytical options.

The methodology can be used to study both the overall diversity of dry grasslands or of all grasslands of a region or to fo-

cus on specific environmental gradients. For example, [Baumann et al. \(2016\)](#) used it to study an elevational gradient in the Italian Alps, while two Bachelor students under the supervision of J.D. are currently analysing semi-natural grasslands along the full hydrological gradient with this approach.

One aspect that turned out to be particularly beneficial, albeit at first glance it looks like an inconsistency, is the combination of the EDGG Biodiversity Plots with additional 10 m² normal plots. This allows for a much higher replication at one particularly relevant grain size, resulting in the inclusion of rarer vegetation types and greater statistical power. While one might assume that in a combined analysis of 10 m² plots one should include only one of the two corners of the EDGG Biodiversity Plots, due to the risk of pseudo-replication, this was actually not the case in any of the analyses of biodiversity patterns we have carried out so far ([Turtureanu et al. 2014](#); [Kuzemko et al. 2016](#); [Polyakova et al. 2016](#)). While the richness values of the two corners obviously showed spatial autocorrelation, no significant autocorrelation was present in the residuals of the regression models any more, allowing to use both corners in the final models. This means that if one samples, for example, 30 EDGG Biodiversity Plots and 40 normal plots, 100 10-m² plots with full environmental information become available for analysis.

Starting the sampling always with the smallest grain sizes, forces the researchers to see the grassland from the plant’s perspective and to familiarize themselves with tiny and vegetative specimens, which also should improve the reliability and completeness of species records at larger grain sizes (**Photos 17–20**). This factor together with the option to analyse the data in many different directions makes this sampling design also particularly suitable for student courses at the Bachelor and Masters levels (**Photos 21–22**). For example, the first author regularly employs this method with his Bachelor classes in “Plant ecology” to study and compare grasslands of three different management/disturbance regimes on the campus of the University of Bayreuth. These classes last only 3.5 working days in total, spread over one week. After having developed hypotheses regarding the outcomes they expect, the students typically sample 18 EDGG Biodiversity Plots plus additional trait data, and prepare and analyse them. While they perform the sampling jointly, the analyses are carried out in four groups of four students: (a) scale-dependent species richness and SARs; (b) functional composition (fractions of life forms, community-weighted means of metric traits) vs. disturbance regime; (c) diagnostic species of management types, Ellenberg indicator values and vegetation classification; and (d) intraspecific trait variability between the management regimes (not directly related to the EDGG sampling approach, but sampled on the same plots). At the end of the week, the students present the results of their group’s work to the other groups and discuss them. Overall, the students who at the beginning of the week often hardly knew any of the common grass and forb species, could not only distinguish them with and without flowers, but got deep insights into some of the core methods and theories of plant community ecology.

Limitations of the EDGG sampling methodology

As is true for any other sampling approach, there are always options to improve certain steps, but this usually comes with significant additional effort and might compromise other aspects of the sampling. One always has to weigh the potential benefits of a modification against the “costs”. For example, adding 1000 m² or an increasing replication towards smaller scales would be highly desirable from our perspective (see above), but the additional effort necessary has so far precluded the adoption of these during the field pulses, because otherwise the dataset that could be sampled within the limited duration with a limited team of observers available would get too small for meaningful analyses. The unavoidable “imprecision” of shoot presence sampling has led others to opt for the precise rooted presence sampling (e.g. Peet et al. 1998), but at the cost that SAR analyses become problematic (see Dengler 2008). Methodologically, the biggest limitation is that we sample abiotic parameters only at one spatial scale (10 m²) and use this as a proxy for the abiotic conditions within the smaller grain sizes. This is a reasonable approximation, but still problematic if one of the aims is to explore the

varying drivers of biodiversity across spatial scales. This fact might partly also explain why the explanatory power of our diversity-environment relationships strongly decreases towards the smallest scales (Turtureanu et al. 2014; Kuzemko et al. 2016; Polyakova et al. 2016). However, the sampling of e.g. soil data separately for each grain size would create a prohibitive effort and is practically impossible for the smallest grain sizes. Lastly, one major limitation arises from the fact that during the EDGG Field Workshops we can visit the plots only once, meaning that certain data can only be approximated (e.g. land-use or diversities of the majority of animal taxa), not measured at all (e.g. the important factor: soil moisture regime), or are essentially only comparable within a dataset but not between datasets (e.g. biomass).

Conclusions and outlook

The EDGG sampling methodology was devised to be an effective multi-purpose sampling strategy. Since its first application during the Research Expedition in Transylvania (Dengler et al. 2009, 2012a) it has proven to fulfil this expectation quite well. The experiences of many of the researchers in-



Photo 17. One of the richest 0.1-m² subplots of an EDGG Biodiversity Plot during the EDGG Field Workshop in Navarre, Spain, 2014 (Photo: J. Dengler).



Photo 18. Learning to know the species in one of the first EDGG Biodiversity Plots during the EDGG Research Expedition in Khakassia, Russia, 2013 (Photo: J. Dengler).



Photo 19. Detailed searching for plants in an 1-m² subplot of an EDGG Biodiversity Plot during the EDGG Field Workshop in Serbia, 2016 (Photo: J. Dengler).



Photo 20. Thorough search for tiny plants in an EDGG Biodiversity Plot during the EDGG Field Workshop in Navarre, Spain, 2014 (Photo: J. Dengler).



Photo 21. *Sampling of an EDGG Biodiversity Plot with a Bachelor-level practical course in plant ecology on the lawns of the University of Bayreuth, Germany, 2016 (Photo: J. Dengler).*

involved, both in the field and during data analysis over the years, led to numerous small modifications and additions, while leaving the overall approach untouched. It has been shown to provide high-quality data for a wide range of different research questions at the regional scale, while at the same time accumulating a highly consistent dataset across the Palaearctic biogeographic realm (Dengler et al. 2016) that promises exciting macroecological studies that are yet to be done.

While most of us have a strong phytosociological background, we have to admit that the phytosociological tradition contains many methodological aspects that are not optimal from our present-day knowledge, yet are rarely questioned (e.g. using varying plot sizes, not precisely delimiting the plots, Braun-Blanquet scale instead of direct estimation of percentage cover, etc.). Re-evaluating these, but avoiding throwing the baby out with the bath water, led to our current approach, which in nearly every tiny detail deviates from standard phytosociological practices (e.g. Dierschke 1994). Still our data are perfectly suited for phytosociological classifications (Dengler et al. 2012a, [Pedashenko et al. 2013](#), [Kuzemko et al. 2014](#)), but at the same time also for many other questions, such as vegetation-environment relationships, scaling laws in ecology, relationships between different facets of biodiversity, and many more. The time effort is certainly higher than for classical phytosociological sampling ([Mucina et al. 2000](#); [Dengler et al. 2008](#)), but the additional time pays off, in our experience, which is corroborated by the fact that people outside the EDGG are applying it (e.g. [Mardari & Tănase 2016](#); unpublished studies of A.C.'s group).

One of the major strengths of the approach is certainly its modularity. There is a core set of well-justified elements that can be reduced, augmented or modified, depending on the specific needs and resources, while still keeping full comparability to an increasing body of reference data and published

studies (see [Dengler et al. 2016](#)). We hope that many readers will feel inspired to apply the EDGG sampling methodology, and inform us of their experiences, as well as suggestions for further improvements, and possibly contribute their data to our collaborative database for cross-site studies.

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Author contributions

J.D. proposed the general idea of the sampling in 2008, "invented" the EDGG Field Workshops in 2009 and since then



Photo 22. *A group of "grassland managers" showing some interest in an EDGG Biodiversity Plot during a Master-level field course in NE Brandenburg, Germany, 2016 (Photo: J. Dengler).*

has coordinated them, supported by I.B. as EDGG Deputy Field Workshop Coordinator. C.M. had the idea for this article, the writing of which was led by J.D. S.B. and G.F. contributed significant parts to the manuscript, B.H. and N.Y.P. the information on zoological sampling, while all others made smaller contributions of text and illustrative material and helped revise the text.

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