
Revermann, R. & Finckh, M. (2013): Okavango Basin - Vegetation. - Biodiversity & Ecology 5.

Revermann, R., Maiato, F., Gomes, A., Lages, F. & Finckh, M. (2013): Cusseque - Vegetation. - Biodiversity & Ecology 5.

Revermann, R. & Finckh, M. (2013): Caiundo - Vegetation. - Biodiversity & Ecology 5.

Murray-Hudson, M., Finckh, M., & R. Revermann (2013): Seronga - Vegetation. - Biodiversity & Ecology 5.

Electronic Appendix: Methods used in the investigation of vegetation patterns in the Okavango basin

Introduction

The vegetation of the upper reaches of the Okavango basin harbours a largely unknown biodiversity. There are no recent studies on the distribution patterns of plant species and vegetation communities. The first comprehensive work on the Flora of Angola, including a vegetation map, dates back to 1939 (Gossweiler and Mendonça 1939). The most recent vegetation map was produced by Barbosa (1970) and some regional studies at the provincial level were carried out (Monteiro 1970, dos Santos 1982). However, the impact of land use on the vegetation during the last five decades, and detailed knowledge on patterns and processes governing the distribution and regeneration of the vegetation, is lacking. In order to understand ecosystem functioning and to predict future delivery of ecosystem services, a sound knowledge of the vegetation is fundamental. Therefore, a baseline inventory of the vegetation has been carried out in the initial phase of The Future Okavango project. In the following, we present the underlying methodol-

ogy. The first results are given in the fact sheet chapters.

Objectives

- Inventory of vegetation: species composition and vegetation communities
- Vegetation mapping: creating a vegetation map for the core sites and the catchment
- Pattern and processes: governing factors of the distribution of plant species
- Regeneration: successional pathways and regeneration after shifting cultivation
- Provisioning ESS based on vegetation: the usage of plant resources by local land users
- Woody biomass: timber provisioning of the woodlands

Field methods

Biodiversity patterns are strongly scale dependent. Therefore, vegetation plots are based on a nested design encompassing

two sizes of vegetation plots: 100 m² and 1000 m². The location of the plots within the core site is based on a random stratified sampling design to ensure statistical independence of sampling plots and even sampling of major vegetation units. Based on a first classification of a Landsat 7 scene, seven major vegetation units per core site were derived. Within these vegetation units, random sample points were selected and their coordinates transferred to a handheld GPS unit.

In each plot, all vascular plants present were recorded and herbarium collections were made if plants could not be identified in the field. Furthermore, the estimated cover of each species was noted as well as the coverage of the vegetation strata: upper tree layer >20 m, medium tree layer 10-20 m, lower tree layer 5-10 m, upper shrub layer 2-5 m, lower shrub layer 0.5-2 m and herbal layer 0-0.5 m. Every vegetation plot was accompanied by soil sampling with an Edelmann corer and soil samples at three depths (0-10 cm, 45-55 cm and 70-90 cm) were taken and analysed in the laboratory using standard soil parameters.

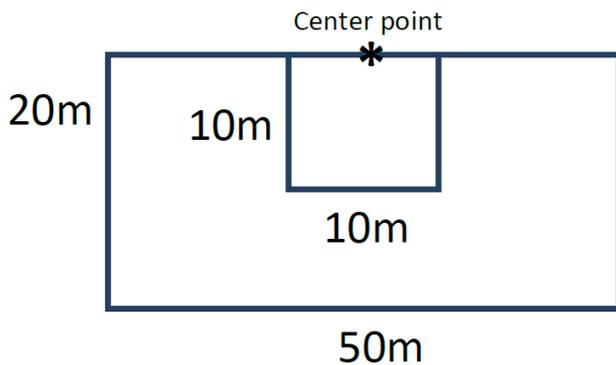


Figure 1: Design of sampling plots.

A regionalization of the sampling to enable predictions at the catchment scale is under way. Plots are selected based on the land cover units derived by the MODIS time series analyses (see fact-sheet on earth observation) to ensure coverage of all major vegetation types. However, sampling is largely restricted by access, i.e. a limited road network and the presence of land mines. The vegetation data feed into a classification of vegetation and the identification of habitat types as spatially explicit entities of ESS delivery.

Assessment of the standing woody biomass was carried out in the same plots. Tree height and diameter at breast height (DBH) were measured. In the 100 m² plot, all trees with a DBH > 5 cm were recorded; in the 1,000 m² plot, all trees exceeding a DBH of 63 cm were mapped. Additionally, the state of the regeneration of locally dominant or important tree species was assessed by measuring all individuals of those species - disregarding their size - in the 100 m² plot. In Cusseque these species were: *Brachystegia spiciformis*, *Brachystegia bakeriana*, *Burkea africana*, *Cryptosepalum exfoliatum* ssp. *pseudotaxus*, *Erythrophleum africanum*, *Julbernardia paniculata*, and *Pterocarpus angolensis*; in Caiundo: *Baikiaea plurijuga*, *Burkea africana*, *Guibourtia coleosperma*, *Schinziophyton rautanenii*, and *Pterocarpus angolensis*.

How to read the core site fact-sheets on vegetation

Table 1 in the factsheets gives a general overview of the vegetation of the core sites and the sampling carried out. Sampling was generally undertaken during the vegetation period starting in October and

extending as far as May. The number of plots per scale may differ. The designation of the ecoregion refers to the classification of terrestrial ecosystems by Olson et al. (2001). The vegetation units in turn refer to the classification based on the MODIS time series analysis (see Stellmes et al. 2013 in this issue). The classes representing most of the area of the core site are displayed.

The four dominant families are denoted according to cover and according to species richness based on all plots within the site. Three measures of vascular plant diversity are presented at both spatial scales; for all measures the median of all plots is given and their range is displayed in brackets:

- species richness, i.e. the number of different species of vascular plants recorded in the plot; often regarded as the “common currency” in biodiversity studies.
- cover based version of Shannon evenness J' (Magurran 2004), ranging from 0 to 1. A value of 0 denotes very unequal distribution of cover values of the species whereas 1 means that all species occur with the same cover.
- Simpson diversity index D_{Si} (Maarel 1997), also based on estimated cover. D_{Si} ranges from 0 to 1 where higher values indicate higher diversity.

Furthermore, the species richness within the different vegetation units is displayed in boxplots. The boxplots provide information on the average and range of the data. The line in the middle of the boxplot refers to the median of the species richness; the length of the box resembles 50% of the vegetation plots, whereas the points lying outside the so called “whiskers” represent outliers.

Classification of vegetation units of the Caiundo core site

The classification is based on all woody species recorded in the 1000 m² plots. Vegetation data were first Hellinger transformed as recommended by Dufrêne & Legendre (1997). In a next step a Bray Curtis dissimilarity matrix was calculated; this is advantageous to avoid the double zero problem, common in vegetation data (McCune et al. 2002). Subsequently, the dissimilarity matrix was subject to a principal coordinate analysis (PCoA). In order to derive vegetation units the first three axes of the PCoA were clustered based on the Diana algorithm (DIVisive ANALysis clustering, Kaufman and Rousseeuw 1990).

In vegetation ecology, the analysis of diagnostic or indicator species serves as a tool to characterize vegetation units. We calculated Pearson’s *phi* coefficient of association to study the strength of association of species to the derived vegetation units (Chytrý et al. 2002). The *phi*-value ranges between -100 and 100 with high values proving high fidelity. A species with a *phi*-value > 50 can be regarded as diagnostic, and >75 as highly diagnostic. The *phi*-value analysis was corrected for unequal group sizes. Furthermore, associations to more than one group, e.g. combinations of two or more groups, were allowed. We defined the optimal cluster depth as the one resolution yielding the maximum number of species with a significant *phi*-value, resulting in four vegetation units for the Caiundo core site.

All statistical analysis was carried out in R (R Development Core Team 2013) using the libraries *vegan* (Oksanen et al. 2011), *labdsv* (Roberts 2012) and *in-*

dicspecies (De Cáceres & Legendre 2009).

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