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**Successful plant establishment under different
trait attributes of the resident community**

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Supervision: Verena Cordlandwehr (Ph.D student), Dr. Jan Bakker (professor)

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Introduction

Increasing emphasis is given to grouping species in non-taxonomic classifications in the attempt to describe and explain ecosystem functioning. The new way of grouping is based on the ecological role of species and several terms have been given either according to the resource use or the response to perturbation. The first groups include terms like structural- or functional guild and clique whereas the second functional type, -group and league. It is also argued that the term functional should be given to groups that do not only share the same resource or have the same response to a disturbance effect but share also the same responding mechanisms (Smith *et al.*, 1997). This approach is based on the idea of identifying modules that are considered as the target of major ecological and evolutionary drives in levels higher than the individual and thus produce simplified rules of species assemblages. Some examples of those classifications are the life forms (Raunkiaer, 1934) or the C-S-R triangle (Grime, 1974) or the early and late forbs, perennials and grasses (Tilman *et al.*, 1997) or low-flexibility, gearing down and switching strategy (Grubb, 1998). Those groupings are not only easily made but are also very well stated in literature, fact which make them of great use in current research.

Further steps have been taken after this first trial of analyzing species abundances from a functional perspective. The basic underlying idea is that systems of great complexity should be deformed so as to be comprehended. The emergent properties from one level to the other should be somehow summarized and kept in the analysis. As a result a clear distinction between plant adaptations and responses to environmental changes was made. According to this approach, plant traits could indicate simple assembly rules. Several arguments were formed like "Species in a plant community

have similar trait attributes as a response to the environmental factors forming the community niche. Differences could occur in competition and dispersal traits" (Van der Maarel & Sykes, 1993). Consequently variation in species composition in a plant community, where species share the same niche, is a result of varied individual ability to establish in appearing microsites in a dynamical fluctuating environment. The niche theory (Hutchinson, 1957) on the contrary predicts that every species will take a specific place according to the community it is found and its actual potential of occupying a niche is limited from biotic factors such as competition. These two seemingly contrasting hypotheses were merged by the idea of guild proportionality, which explains ecosystem stability due to several ecologically similar species. They can be interchanged and as a result a loss of one or in some cases more species does not necessarily deform the ecosystem structure. Furthermore both theories are explaining occurring differences in plant abundances by competition, whereas the idea of dispersal limitation as a factor explaining varying plant abundances has been less thoroughly examined. Several arguments have been made about the truly existence of ecological similar species and their ability to be interchanged without harming the community form. Other authors indicate that certain assembly rules do exist and the missing information is to identify the underlying mechanisms of these rules (Wilson, 2007).

Nowadays a stronger effort is given in merging plant traits and assembly rules in communities and as a result species are not only considered as targets of ecosystem changes, but also as drivers of them. The individual level traits are a surrogate of organismal performance. A functional trait is defined as any morpho- physio- and phenological trait, which impacts fitness indirectly, via its effects on individual performance by affecting growth, reproduction, and survival. An attribute is a particular value or modality taken by the trait at any place and time (Violle *et al.*, 2007). Species traits are defined at the individual level and are distinguished in soft if they have an indirect effect on plant fitness and in hard traits if they have direct effects on fitness (Hodgson *et al.*, 1999). Soft traits are often measured more easily. Moreover traits can be distinguished into traits responding to habitat conditions and ecosystem changes (response traits) and those summarizing the effects of a species in ecosystem functioning (effect traits) (Cornwell *et al.*, 2006; Lavorel & Garnier, 2002). Previously the traits were defined in different levels ranging from the individual level to the population even to the community and ecosystem conditions. Currently focus is given to the individual level so that a scaling up method can be applied leading to predictions of the

ecosystem functioning and the probabilities of species occurrence under known environmental conditions (Fig.1).

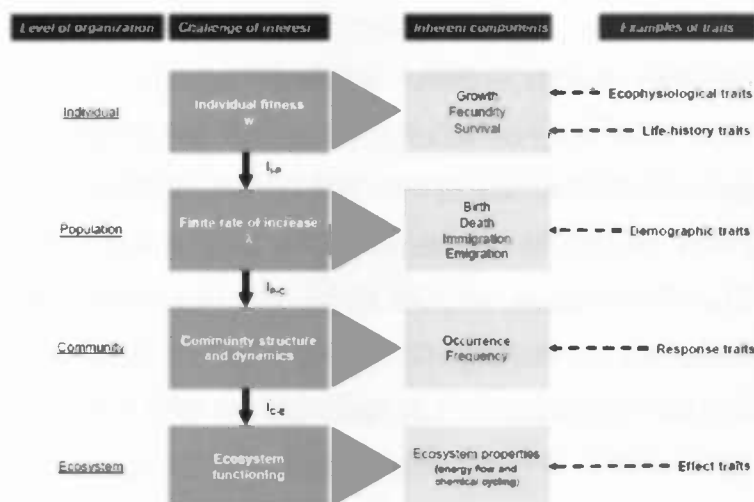


Fig.1: Trait based information provides an easy tool for scaling up from the individual to the ecosystem level. If this information is not available complex model assumptions have to be made so as to produce an ecosystem model. Thus fitness components of an individual determine the components of the finite rate of increase (λ) of the population ($I_{i,p}$). Occurrence and frequency of species at the community level encompass components of I through complex integration (e.g. biotic interactions) ($I_{p,c}$). Finally, scaling-up to ecosystem properties can be done by combining functional property of each species of the community ($I_{c,e}$). (Violle *et al.*, 2007)

The traits are used as markers of species functions and are often weighted according to the species abundances in the site of interest, trying to impose an integrated approach in predicting community assemblages under multiple ecosystem driving processes (Garnier *et al.*, 2004). It is striking that most of the trends are consistent across floras and major phylogenetic groups (Diaz *et al.*, 2004). Quite some studies have focused on testing the mass ratio hypothesis (Grime, 1998) along secondary succession and in different biogeographical regions and revealed that certain patterns can be explained by individual traits and a possible up scaling could be applied in cases of global ecosystem drivers. A new idea of trait filtering processes is formulated as an extension of the mass ratio hypothesis according to which ecosystem properties should depend on species traits and on species contribution to the total community biomass. The new idea splits the processes affecting plant distribution in two major categories. The first is competition and the second habitat filtering, which can be thought as a reduction in the range of successful strategies among coexisting species (Cornwell

et al., 2006). The difference with the mass ratio hypothesis is that species are not divided into different abundance classes and information deriving from traits is the only element explaining varying abundance and richness patterns.

Further research indicated that weighing traits according to plant abundances produces more reliable results, than studies taking into account species absence/presence. The best way of incorporating the influence of abiotic factors is through standardized indices (Garnier *et al.*, 2007). Moreover a way of incorporating intra specific variation in relation to trait attributes is discussed. Some studies indicate that generally inter specific variation is quite larger than the intra specific one, thus its incorporation to the analysis will not significantly change the outcome (Cingolani *et al.*, 2007). However there are suggestions that disturbance and fertility effects will cause highly significant inter specific or inter-site variation that had to be included in the analysis. There is a need for standardized protocols in collecting information from plant traits and analyzing them, using abiotic factors as covariates, so that certain traits that show clear responses to major environmental changes emerged (Garnier, 2008). In the attempt to include site variation by weighing plant traits according to some species properties such as abundance, a suggestion to include species distribution has been made (Naeem & Wright, 2003). Great effort is given in developing models predicting how biodiversity will vary across environments, which plant traits determine community assembly and which plant species from a species pool will be found in which relative abundances in a given environment (Cornwell *et al.*, 2006; Kerkhoff & Enquist, 2006; Shipley *et al.*, 2006). There are also studies, trying to assess the strength of the existing habitat filters, indicating that the first allowing the presence of a species in a habitat is stronger than the second allowing its dominance (Cingolani *et al.*, 2007). Studies based on structural equation modeling in order to explain changes in species abundance according to species traits support allometric relationships (Vile *et al.*, 2006). It is clearly indicated from the majority of the studies in this field that certain trends do exist and could be produced with the appropriate testing of models with global applicability.

Some other researchers explain differences in plant abundances across sites due to two basic factors: competition and habitat filtering. The idea of existing dispersal limitation resulting in differing plant communities was introduced by Zobel (1997) and it has not been thoroughly examined, although it has already been a decade since it was developed. According to this hypothesis local environmental conditions act as a filter removing all species that belong to the local flora, but lack the traits required to survive

in local conditions. Landscape fragmentation creates dispersal barriers for many species and thus, influences species richness. Generally the differences in local and regional species composition and diversity are controlled by dispersal efficiency of the species (Fig.2).

The functional diversity is analyzed in a similar way as species diversity and is split into richness and evenness (Petchey & Gaston, 2002). There is a strong argument that it is not necessary to summarize the whole community diversity in a single number, but on the other hand it is easier to compare one number per community than multiple (Mason *et al.*, 2003; Mason *et al.*, 2005; Mouillot *et al.*, 2005). There are quite some functional diversity (FD) indices developed that are easily calculated for single traits in every community, but the final combination of several coexisting traits in one community still remains a point of discussion (Petchey & Gaston, 2006). The development of FD indices is based on the idea of weighing the traits according to the relative abundance of the species present in the community or taking into account their distribution patterns, thus summarizing the existing patterns combining species and trait data (Bady *et al.*, 2005). Current research also indicates that the trait values could be used to predict the abundance of the species (Mouillot *et al.*, 2007). Nevertheless relations are not automatically seen and hard traits (e.g. growth rate, carbon needed to produce a leaf, resistance to pathogens) are expected to show more easily distinguishable patterns than soft traits (specific leaf area, leaf dry matter content, concentration of secondary metabolites).

Research questions

Taking into account the current approach in community ecology, where the plant species are considered to be drivers and targets of ecosystem processes and where traits are only defined at the individual level, the aim of this project is to test, to what extent can trait information separate community types. We want to know, if trait information can result in defining community fingerprints and, if this separation would be more informative than taxonomic community descriptions. Additionally we investigate correlations of the community fingerprints with abiotic factors. The question will be addressed whether above-ground persistence of species is influenced by the identified community fingerprints. We are also interested in identifying a certain combination of

traits that could explain differences in persistence. Moreover existing differences in survival time will be modeled to indicate general community assembly rules.

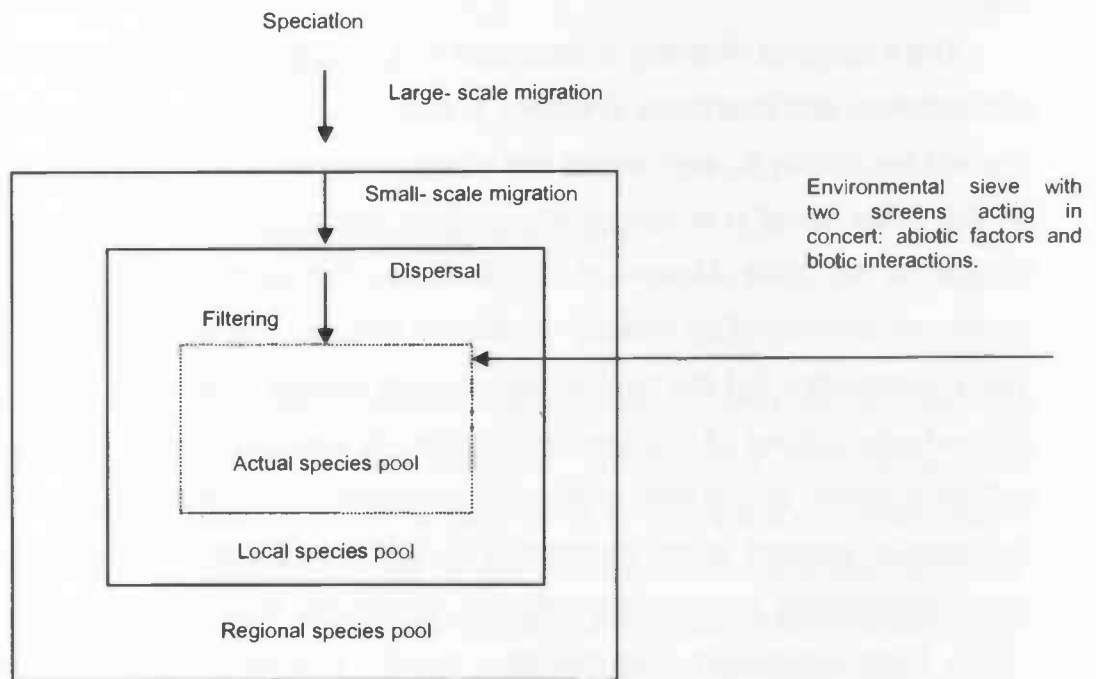


Fig.2: The role of large and small scale processes determining species richness (Zobel, 1997).

Materials and Methods

Study site

The study site is located in the Drentsche Aa reserve (53°05'N, 6°40'E, 21m maximum altitude), which has been established in 1965. Sandy soils are predominant on the plateau, but boulder clay is present in the subsoil, a fact which results in the increase of the water holding capacity of the soil. The Drentsche Aa plateau was used for hay making by slightly drainage of the marshes. The sandy soils were covered with heathland, where cattle and sheep grazed and sod-cutting took place. Wooded hedgerows were erected at the transition between meadows and heathland to prevent acid water from heaths inundating the meadows. *Salix sp.* shrubs and *Alnus sp.* were probably more abundant in the pastures, than grass species. No fertilization occurred in

the meadows until the last century and artificial flooding was applied to increase their productivity. The application of fertilizers drastically changed the system by converting the heathlands into pastures or arable fields during the early 1930s. Consequently heavy flooding of the fields took place, resulting in large-scale interferences with the hydrology in the 1960s and the complete disappearance of all natural water courses and in deep drainage of all peaty soils.

The goal after 1965 was to preserve and restore the semi natural landscape with its characteristic heathlands, species-rich meadows, hedgerows and small villages. Until recently the approach was rewetting the less intensively used grasslands and applying a regular mowing regime without fertilizing. Nowadays restoration measures not only affect the classical target areas in the centre of the reserve, where species diversity has dramatically increased in the meadows, heathlands and water courses, but its effects stretches out to the infiltration areas, where attempts are made to restore local and regional hydrological systems, which supply the wetland area with clean groundwater. Sod-stripping in former agricultural areas on the valley flanks is a recent approach to restore the nutrient poor heathlands (Grootjans, 2002).

The vegetation has been monitored for 35 years and recent and historical regional species composition pool will be used (Bakker, 1989)

Trait table and trait selection

Trait attributes related to dispersability, persistence and regeneration were derived from the LEDA trait database (www.leda-traitbase.org) (Knevel *et al.*, 2003) and trait describing clonal growth were extracted from the CLO-PLA project (<http://clopla.butbn.cas.cz/index.php?page=intro>). The dispersability traits are seed production, seed weight, seed releasing height, terminal falling velocity, external and internal animal dispersal and lateral spread of the clonal growing organ. The persistence traits are specific leaf area, canopy height, plant growth form, woodiness, root depth, -spread and the time of connection between the clone and the mother plant. The regeneration traits are plant life span, age of first flowering, seed weight -shape,-size and -longevity and the ability to resprout.

Missing values of the trait table were filled out using information from Floras and internet sources. For leaf distribution, plant life form, canopy height, woodiness, root

depth and root spread and checking synonyms for the existing species in our communities the following internet sites were used:

- <http://ip30.eti.uva.nl/BIS/flora.php?selected=beschrijving&menuentry=soorten&id=3862>
- <http://www.plant-identification.co.uk/skye>
- <http://www.judywoods.dial.pipex.com/>
- <http://montana.plant-life.org>
- <http://www.floraweb.de/pflanzenarten/pflanzenarten.html>
- <http://plants.usda.gov/checklist.html>

The Floras that were used for filling missing data were FLORA EUROPÆ and OLDENBURG ATLAS (Kutschera & Lichtenegger, 1992). The Oldenburg Atlas (Kutschera & Lichtenegger, 1992) was mainly used to fill in root traits and plant growth forms, whereas the Flora Europæ for canopy height, leaf distribution and plant life form. The canopy height is defined as the distance between the highest photosynthetic tissue and the base of the plant in the LEDA trait database. So in cases where pictures and data for stem height and leaf distribution were available, the canopy height was calculated. These calculations were conducted for the species: *Dactylorhiza majalis*, *Agrostis stolonifera*, *Carex otrubae*, *Poa trivialis*, *Juncus bufonius*, *Bromus hordaceus*, *Anemone ranunculoides*, *Cerastium brachypetalum*, *Elytrigia repens*, *Festuca rubra*, *Rumex crispus* X *obtusifolius*, *Bromus racemosus*, *Dactylorhiza maculata*, *Montia Fontana* and *Iva xanthifolia*.

Missing data for the specific leaf area, releasing height, seed mass, leaf dry matter content, leaf mass, leaf size were filled using raw data from people participating in the BIOPOP project. Woody species traits referring to trees were excluded from the analysis, because these species appear in the communities as seedlings and the trait values were referring to adult species.

The percentage of available trait data was calculated for every trait for the total species list. For further analysis only traits covering more than 80% of the species were used. Those were canopy height, leaf dry matter content, leaf distribution, seed mass, epizoochory (dispersal on animals), endozoochory (dispersal in animals), seed longevity, woodiness, releasing height, plant life span, specific leaf area, plant growth form, clonal growth persistence and lateral spread of clonal growth. The traits were also

weighed by the relative abundance of the species present in every relevé and functional diversity indices $FDvar=2/\pi*\arctan(5V)$ (Mason *et al.*, 2003) were calculated for the quantitative data and for the categorical data according to Shannon-Wiener (H). The formulae are shown in the box. The Shannon-Wiener index weighs the logarithmic values of the traits by the relative abundance of the species, whereas the Fdvar index by Mason *et al.* (2003) takes into account the difference of a single logarithmic trait values from the mean of logarithmic value and weighs that difference by the relative abundance of the species. So the FDvar index is also incorporating the distribution of a trait in a community apart from weighing it according to the relative abundance of the species present in that community. The weighted averages were also standardized by dividing with the maximum value per trait and the categorical data were merged by summing up non-woody and semi-woody species, annuals with biennials, rosette-leaved, tufts, semi-rosette leaved and scarcely foliated species, species with no lateral spread of clonal growth and species with spread less than 0.01, species with lateral spread more than 0.25m with those with 0.01-0.25m and species with clonal growth persistence of 1 year with those of 2. In the same way FD indices were merged. That merging was done in order to reduce the effect of variables with many categories that would pull the analysis stronger towards one direction, compared with variables that had fewer categories.

Mason *et al.*, 2003

$$V = \sum_{i=1}^N w_i (\ln x_i - \overline{\ln x})$$

$$\overline{\ln x} = \sum_{i=1}^N (w_i * \ln x_i)$$

$$w_i = \frac{a_i}{\sum_{j=1}^N a_j}$$

Shannon - Wiener

$$H = - \sum_{i=1}^N p_i \ln x_i$$

w_i or p_i = relative abundance

a_i = abundance

x_i = trait value

As abiotic factors, we used Ellenberg indicator values for temperature, light, moisture, acidity, nitrogen and resistance to mowing. These values were calculated from the present species in every relevé that had an Ellenberg indicator value and as a final relevé attribute the weighted median was used.

In total 14 traits from 190 species distributed in 5105 relevés (180 plots monitored for more than 30 years) were suitable for the analysis.

Defining the community fingerprints

The weighted values of the traits and the FD indices were analyzed separately by ordination techniques so as to define community fingerprints. The length of the gradient in every case was checked via DCA analysis. In cases linear relations could be

assumed, PCA analyses were used. Correlations of the ordination axes with habitat characteristics were tested for an ecological interpretation. Correlation coefficients were calculated for the axes scores and Ellenberg indicator values. Sociological clustering of the relevés was used to compare means for every trait among the different types of the communities. The total number of community types was 25 identified by ASSOCIA (Schaminee *et al.*, 2007). Table 7 in the Appendix indicates the codes used for every community type. Some of the resulting types were excluded prior to ordination techniques. The ones excluded were the ones being represented by less than 40 relevés and the ones that couldn't be classified to a specific community type (excluded: *Asplenietea trichomanis* (code:21), *Artemisietea vulgaris* (code:31), *Stellarietea mediae* (code:30), *Molinio-Arrhenatheretea* (code:16), basal community (BC) *Carex disticha*-[*Calthion palustris*] (code:16RG06)).

The vegetation data were also analyzed with ordination techniques using both a relative abundance and a presence/absence matrix excluding species existing in five or less relevés. A DCA analysis indicated non linear relations and the score axes were correlated with Ellenberg values.

The clustering in community types was used to compare mean values of weighted averages and FD indices per trait by One-way Anova, thus identifying which of the variables explain this classification best and as a consequence define the community fingerprint. Variables, that is weighted averages and FD indices of the traits, distinguishing the community types in more than 10 groups by a Tukey test were selected.

The percentage of occurrence of every species in every community (none of them was excluded) was calculated so as to see in how many different communities a species occurred and also which are the dominant species of every community type.

Survival analysis

Presences/Absences of species of interest were analyzed with survival techniques, thus producing hazard ratio estimates in time intervals for those species (Kleinbaum & Klein, 2005; Zens & Peart, 2003). Such an analysis deals well with missing data and unknown actual starting or ending time of an individual (censored data) and it can produce accurate estimates for the survival of a species in a time range (Ozinga *et al.*, 2007). For all the types of analysis a species is considered as 'disappeared' from a site,

if it is also absent the year after its first absence. This will be applied to correct for human mistakes of not distinguishing species in a site due to either their small size or their growth along another species or even other unpredictable factors. The species of interest were selected according to the following criteria: a) the mean survival time had to be at least 2 years, b) the number of observations per species had to be more than 35 and c) the percentage of non-censored data needed to be more than 0.45. The criteria b) and c) are imposed by the survival analysis, whereas the criterion a) was imposed by us according to the nature of our data. In total 68 species were suitable for the survival analysis and we refer to them as focal species. From those focal species a smaller number was selected according to their distribution and abundance in the communities and separate models for each one were built. Those species were *Caltha palustris*, *Crepis paludosa*, *Dactylorhiza majalis*, *Filipendula ulmaria*, *Glyceria fluitans*, *Juncus articulatus*, *Myosotis scorpioides*, *Ranunculus flammula*, *Rhinanthus angustifolius*.

For the survival analysis we firstly prepared Kaplan Meier curves per species and then proceeded by building Cox regression models using as independent variables the merged weighted averages and the merged FD indices of the traits separately. The analysis was conducted separately for the year that a focal species appeared and for the year that it disappeared. As the year appeared or disappeared for a focal species the year before or after its actual occurrence was used. Thus in the first case the influence of the surrounding vegetation was analysed at the beginning of a focal species establishment and in the second case the influence of the surrounding vegetation after its occurrence period. A mean survival curve including all the focal species was produced and every species was compared to that one by a Log-rank test. For the species that were statistically significant different from the mean either higher or lower, we proceeded by analyzing their traits by Generalized Linear Model using as dependent variable the grouping in higher or lower than the mean curve and as explanatory variable every trait separately. So we could find out if there are certain traits explaining the observed differences.

In total four different models were built, two for the year appeared and two for the year disappeared. The selection of the variables was done by five different combinations: a) continuous data and Ellenberg values b) only Ellenberg values c) the variables identified from the ordination d) one category per trait and the mean values from the continuous data e) the same as d but using the other category per trait. At last

all the significant variables from those combinations were chosen and another Cox regression model was run, thus allowing for the final identification of the variables explaining the differences in survival time of the focal species. Generally, we proceeded by building models with all the possible significant variables also trying different combinations of them, thus resulting in the best fitting model with the least possible explanatory variables. Survival curves were prepared separately for every model including the mean values of all the variables and also for each variable separately.

Another two models were built for the year appeared and the year disappeared separately using as explanatory variables the sociological groups.

The separate models for each of the selected focal species were built only for the year appeared combining the merged FD indices and weighted averages and significant variables were selected the same way as for the models for the year appeared and disappeared.

The variable codes used for the weighted averages and the FD indices are explained in the appendix at Table 6.

Results

Community fingerprints

The One-Way Anovas using as dependent variable either the weighted averages or the FD indices separately and as categorical predictor the sociological grouping, indicate the traits, which are significantly distinguishing the communities. From those we selected the variables distinguishing at least 10 groups of community types by a Tukey test (Table 1).

Table 1: Variables (weighted averages or FD indices of traits) identified by One-Way Anovas as distinguishing the community types in at least 10 groups.

Variables identified by using the weighted averages of the traits	Variables identified by using the FD indices of the traits
Leaves along the stem	Non-woody
Rosettes	Rosettes
Epizoochory	Non-epizoochory
Non-endozoochory	Non-endozoochory

Annual & biennial	Endozoochory
Therophytes	Hemicryptophytes
Persistence of clonal growth for 1-2 years	Lateral spread of clonal growth more than 0.01m
Minimum Canopy Height	Mean Specific Leaf Area
Mean Lead Dry Matter Content	Minimum Specific Leaf Area
Mean Seed Mass	Maximum Specific Leaf Area
Minimum Seed Mass	Mean Seed Mass
Maximum Seed Mass	Minimum Seed Mass
Seed Longevity	Seed Longevity
Minimum releasing height	
Maximum Specific Leaf Area	

The variables indicated by the one-way Anovas are the ones defining the community fingerprints. The weighted averages and the FD indices show different results. Only 17 % of the traits defining the community fingerprints are similar in both analyses and 60 % of the similarity is based on continuous traits (seed mass, seed longevity, specific leaf area, canopy height, leaf dry matter content). The same number of categorical variables (epizoochory, endozoochory, leaf distribution, woodiness, plant life span and plant life form) was indicated from both analyses. The analysis based on the weighted averages indicated more continuous traits than the one based on the FD indices. These variables and the Ellenberg indicator values were then used to ordinate the community types.

The ordination of the communities, using the mean values of the weighted averages, by performing a principal component analysis (PCA) indicated five axes explaining 89 % of the total variance [1→(40.1%), 2→ (16.99%), 3→ (12.82%), 4→(9.7%), 5→(9.3%)] (Fig.1), whereas the PCA using FD indices for the functional diversity of the relevés indicated three axes explaining 88 % [1→(38.73%), 2→(32.44%), 3→(16.76%)] (Fig.2). The Ellenberg indicator values were also used to ordinate the groups and two axes explained 81 % of the total variance [1→(62%), 2→(19.13%)] (Fig.3). At the first two PCA analyses the Ellenberg values and the total number of species per community were used as supplementary variables and for the ordination based only on Ellenberg values the total number of species per community was used as supplementary variable. Thus their correlation with the axes was checked without affecting the axes scores of the rest of the variables. In both cases the total number of species was not correlated with any of the axes and could not explain any differences in

the observed ordination of the communities. Moreover, in both cases the Ellenberg indicator values for moisture and nitrogen were correlated with the second PCA axes negatively and positively respectively and the indicator value for resistance to mowing was correlated positively with the third axis. The correlation coefficients were higher for the PCA based on the weighted averages.

Based on the weighted averages and the FD indices of the traits defining the community fingerprints pair wise comparisons were done using Tukey tests. The percentage of the communities belonging to different groups was calculated separately for the weighted averages and the FDvar indices. Results are shown at Table 2. The higher the percentage indicated in Table 1 the more dissimilar the two communities are. The codes for the sociological groups are shown at Table 7 in the appendix. The communities with the codes 16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]), 16AB06 (*Angelico-Cirsietum oleracei*), 16RG02 (BC *Holcus lanatus*-*Lychnis flos-cuculi*-[*Molinietalia*]), 16AB01 (*Crepido-Juncetum acutiflori*), 16BC01 (*Lolio-Cynosuretum*) and 16RG05 (BC *Carex panacea*-*Succisa pratensis*-[*Junco-Molinion*]) are representing 70% of the relevés with the communities 16RG01 and 16AB06 representing 24% each.

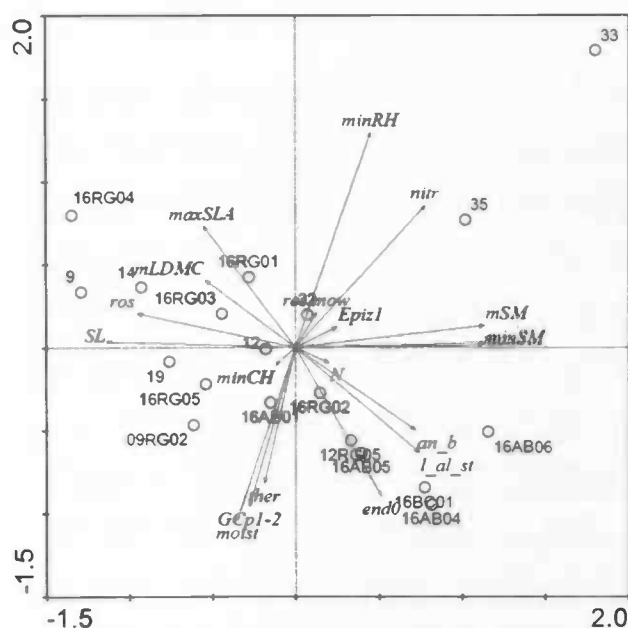


Fig.1: Ordination of the sociological groups in the first 2 PCA axes (57% explained) (89 % of the total variance explained by five axes). The ordination is based on weighted averages of the traits.

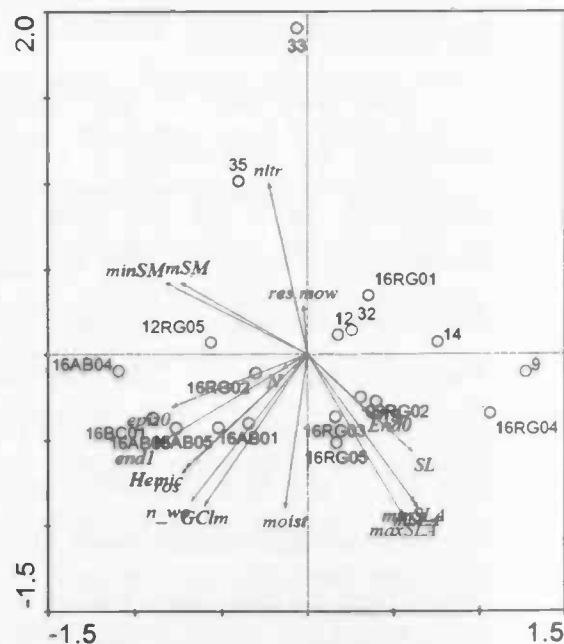


Fig.2: Ordination of the sociological groups in the first 2 PCA axes (71% explained) (88 % of the total variance explained by three axes). The ordination is based on indices of the traits.

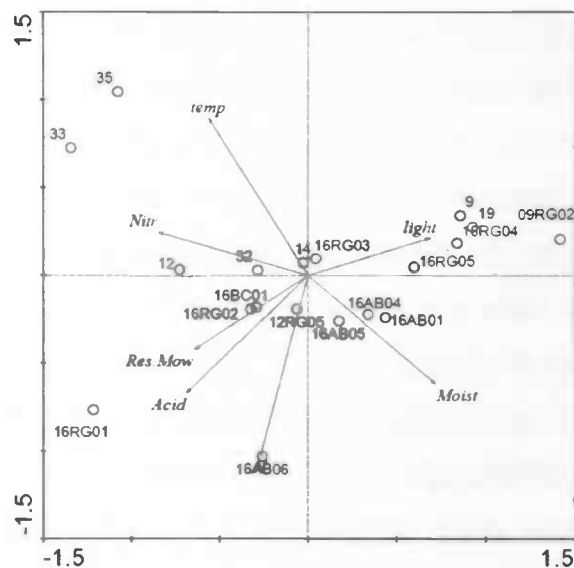


Fig.3: Ordination of the sociological groups in the first 2 PCA axes (81 % of the total variance explained). The ordination is based on Ellenberg values of the communities.

The communities' fingerprints are defined by the ordination of the weighted averages and the FD indices of two regeneration, five dispersability and seven persistence traits. In general the grouping of the sociological communities is based on six continuous (Canopy height, LDMC, Seed Mass, Seed longevity, release height and SLA) and eight categorical traits (leaf distribution, dispersal with animals internally, dispersal with animals externally, woodiness, plant life span, plant growth form, persistence of clonal growth and lateral spread of clonal growth), but if one would count the single categories then grouping is based on 50% of categorical and 50% of continuous traits. Despite the fact that the persistence traits are over represented in our analysis compared with the rest of the traits' classes, both analyses indicate traits that are associated with all of the traits' classes and the traits Seed Mass, Specific Leaf Area and Seed Longevity are common in both. The similarity of the analyses is also shown by the fact that there are common traits to all of the traits' classes used in our research. One can state that the community types are split in both ordinations and generally similar communities like 09RG02 (BC *Carex nigra*-*Agrostis canina*-[*Caricion nigrae*]) and

16RG05 (*Scirpetum sylvatici*) (the dominant species in those are *Anthoxanthum odoratum*, *Carex nigra* and *Festuca rubra*) are placed together (Table 3).

Both analyses indicate the same number of categorical traits, whereas the one based on the weighted averages indicates as significant traits more continuous than the one based on the FD indices. These differences could be due to the fact that the FD indices are double weighting the continuous traits (FDvar index) and only once the categorical traits (Shannon-Wiener index). Thus the selection for the continuous traits is far more stringent using the FD indices compared to the weighted averages and as a result the FD indices indicate the continuous traits that would possibly be twice as strong as from those indicated from the weighted averages analysis. The results though from both the analyses are not contrasting. The continuous traits indicated from the FD indices analysis are also indicated in the weighted averages analysis.

Taking into account the categorical traits the same number of traits distinguishing the communities is indicated by the analyses using either the weighted averages or the FD indices. The differences between the traits are small if one would count a trait as being similar independently of the category indicated. For example four traits (36%) are similar in both analyses (Plant growth form, Epizoochory, Endozoochory and leaf distribution) but if one would count the similar categories then only two (14%) (rosettes and non- endozoochorous species) are similar. This could be explained by the fact that the FD indices are taking into account the relative abundance of species per relevé twice compared to the analysis with the weighted averages. Though one could argue that the results are contrasting due to the fact that when the same trait is indicated as significant in distinguishing the communities' fingerprints dissimilar categories are shown from the analyses. This should not be interpreted as contrasting results but as complementary information, since double weighting the traits will also influence the outcome and probably produce more stringent results for the FD indices.

The communities 16AB06 (*Angelico-Cirsietum oleracei*) and 16RG01(*BC Holcus lanatus-Lolium perenne-[Molinio-Arrhenatheretea]*) are always positioned at different quartiles considering both axes in both analyses, and their relative positioning in the ordination axes is the same in both analyses (Fig. 1-2). The by their biomass weighted species of community 16AB06 have on average a higher seed mass but lower seed longevity, a higher Ellenberg indicator value for nitrogen and moisture, more annuals and biennial plants, more species with leaves distributes along the stem, more non-endozoochores and more therophytes, a lower maximum SLA and mean leaf dry matter

content and are also more persistent in their clonal growth for 1-2 years than in community 16RG01 (Fig.1). The communities 16AB01 (*Crepido-Juncetum acutiflori*) and 16RG05 (BC *Carex panicea-Succisa pratensis*-[*Junco-Molinia*]) are quite similar and the same holds for the communities 16BC01 (*Lolium-Cynosuretum*) and 16AB06 (*Angelico-Cirsietum oleracei*). The communities 16BC01 and 16AB04 (*Ranunculo-Senecionetum aquatici*) are almost identical and that applies to the communities 12RG05 (BC *Agrostis canina-Ranunculus repens*- [*Lolium-Poten. anserinae/Molinietalia*]) and 16AB05 (*Scirpetum sylvatici*). These similar pairs of communities are distinct from the communities 16RG01 (BC *Holcus lanatus-Lolium perenne*-[*Molinio-Arrhenatheretea*]), 16RG03 (BC *Festuca rubra-Lotus uliginosus*-[*Molinietalia*]), 16RG04 (BC *Juncus effusus*-[*Molinietalia/Lolium-Potentillion*]) and 9 (*Parvocaricetea*). The latter are characterized by plants with higher maximum SLA and mean LDMC, more rosette plants and generally species which have higher seed longevity (Fig.1). They are less moist and have slighter higher Ellenberg indicator values for nitrogen.

The ordination based on the FD indices generally distinguishes the communities in a more compact way than the one based on the weighted averages (Fig.2), but the observed relations are the same. Axis 1 is positively correlated with the weighted averages for the traits rosette plants, hemicryptophytes and endozoochore species, which means that the communities with higher absolute values for the FD indices of the same traits are also characterized by higher values in the weighted averages. It is shown that communities (16RG04 (BC *Juncus effusus*-[*Molinietalia/Lolium-Potentillion*]), 9 (*Parvocaricetea*), 09RG02 (BC *Carex nigra-Agrostis canina*-[*Caricion nigrae*]), and 16RG03 (BC *Festuca rubra-Lotus uliginosus*-[*Molinietalia*]) with species with higher values for seed longevity and lower values for seed mass are also characterized by low Ellenberg indicator values for nitrogen. The communities with higher values for SLA are also showing higher values for indicator values for moisture, which is contrasting with the results from the ordination based on the weighted averages of the traits. This could possibly be due to the fact that the indicator Ellenberg value for moisture cannot distinguish the communities as strict as in the ordination based on the weighted averages. The same applies for all the Ellenberg indicator values used in the ordination based on the FD indices of the traits. The communities 09RG02 (BC *Carex nigra-Agrostis canina*-[*Caricion nigrae*]) and 19 (*Nardetea*) are almost identical and the same holds for the communities 16BC01 (*Lolium-Cynosuretum*) and 16AB06 (*Angelico-Cirsietum oleracei*). The first are characterized by species with high SLA, seed mass

and more non- endozoochore species, whereas the latter by more endozoochore and non-epizoochore species, more hemicryptophytes and species with high lateral spread of their clonal growth. However, the differences among these traits are small if the two similar groups are compared and the trait that distinguishes them well is the seed mass with the first group having lower values than the second. The traits that mostly distinguish the community 16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]) from the community 16AB06 (*Angelico-Cirsietum oleracei*) are seed mass, hemicryptophytes, endozoochore and rosette species with high lateral spread of their clonal growth with the latter having lower values for those traits and only higher values for SLA.

The ordination based on the Ellenberg indicator values (Fig. 3) is distinguishing the communities well but not as stringent as the one based on the weighted averages of the traits (Fig.2). It could be stated that the separation of the communities is as stringent as the separation based on the FD indices and it can be explained from the fact that the variability in the Ellenberg indicator values of the community types is not that high as the one for the weighted averages of the traits. From Fig.3 one can see that the communities representing most of the relevés (16AB06 and 16RG01) are positioned in the same quartile of the graph and are mainly distinguished by the Ellenberg indicator values of moisture and nitrogen with the first being more moist with less nitrogen. The rest of the Ellenberg indicator values are also indicating differences between these two communities with 16RG01 being more acid and more resistant to mowing than 16AB06. The Ellenberg indicator values for moisture, nitrogen and acidity are distinguishing most of the communities. The communities 16BC01 (*Lolio-Cynosuterum*) and 16RG02 (BC *Holcus lanatus*-*Lychnis flos-cuculi*-[*Molinietalia*]) are almost identical and the same applies for the communities 14 (*Koelerio-Coryneporetea*) and 16RG03 (BC *Festuca rubra*-*Lotus uliginosus*-[*Molinietalia*]) with the first group having higher Ellenberg indicator values except for light and temperature than the second group.

Table 2: Pair wise comparison of communities using weighted averages and FD indices of traits

Community types in Chronosequence																				
		Parvocaricetea	Plantagineetea majoris	Koeleno-Corynephoretea	Nardetea	Convolvulo-Filipenduletea	Gallo-Urticetea	Lonicero-Rubetea plicati	Lolio-Cynosuretum	Crepidulo-Juncetum acutiflori	Scirpetum sylvatici	Angelico-Cirsietum olivacei	Ranunculo-Senecionetum aquatili	BC Holcus lanatus-Lolium perenne- [Molinio-Arrhenatheretea]	BC Festuca rubra-Lolus uliginosus- [Molinietalia]	BC Holcus lanatus-Lychnis flos-cuculi- [Molinietalia]	BC Juncus effusus- [Molinietalia/Lolio-Potentillon]	BC Carex panacea-Succisa pratensis- [Junco-Molinion]	BC Agrostis canina-Ranunculus repens- [Lolio-Poten. anserinae/Molinietalia]	BC Carex nigra-Agrostis canina- [Carcion nigrae]
		33.4	36.5	13.4	33.4	46.7	61.6	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
		33.4	36.5	13.4	33.4	46.7	61.6	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
		46.7	61.6	23.1	73.4	26.7	30.8	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.4
		53.4	26.7	33.4	46.7	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
		23.1	0.0	7.7	15.4	46.7	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
		60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
		53.9	61.6	53.9	92.4	53.9	92.4	53.9	92.4	53.9	92.4	53.9	92.4	53.9	92.4	53.9	92.4	53.9	92.4	53.9
		66.7	46.7	60.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
		77.0	84.7	69.3	84.7	61.6	77.0	73.4	77.0	73.4	77.0	73.4	77.0	73.4	77.0	73.4	77.0	73.4	77.0	73.4
		86.7	66.7	80.0	66.7	80.0	84.7	61.6	86.7	66.7	80.0	61.6	86.7	66.7	80.0	61.6	86.7	66.7	80.0	61.6
		92.4	77.0	80.0	53.4	60.0	84.7	61.6	86.7	66.7	80.0	61.6	86.7	66.7	80.0	61.6	86.7	66.7	80.0	61.6
		33.4	80.0	53.4	60.0	26.7	80.0	61.6	86.7	66.7	80.0	61.6	86.7	66.7	80.0	61.6	86.7	66.7	80.0	61.6
		84.7	69.3	69.3	38.5	38.5	92.4	61.6	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2
		60.0	40.0	53.4	40.0	20.0	88.7	46.7	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4
		84.7	30.8	53.9	30.8	30.8	77.0	53.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
		66.7	66.7	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4
		100.0	77.0	77.0	69.3	46.2	92.4	40.0	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5
		80.0	60.0	66.7	73.4	40.0	66.7	40.0	26.7	73.4	20.0	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1
		92.4	77.0	92.4	77.0	69.3	84.7	53.9	23.1	46.2	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1
		53.4	26.7	46.7	86.7	40.0	80.0	46.7	26.7	86.7	80.0	100.0	73.4	26.7	86.7	80.0	100.0	73.4	26.7	86.7
		53.9	30.8	30.8	89.3	15.4	77.0	46.7	92.4	69.3	36.5	69.3	69.3	26.7	86.7	33.4	53.9	30.8	30.8	30.8
		33.4	20.0	13.4	33.4	13.4	60.0	46.7	13.4	40.0	40.0	60.0	73.4	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		53.9	23.1	7.7	23.1	0.0	77.0	69.3	69.3	7.7	7.7	61.6	69.3	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		66.7	26.7	66.7	66.7	13.4	80.0	46.7	26.7	73.4	20.0	80.0	66.7	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		84.7	30.8	61.6	30.8	7.7	84.7	77.0	61.6	38.5	0.0	53.9	61.6	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		40.0	73.4	40.0	66.7	60.0	66.7	66.7	100.0	80.0	86.7	100.0	100.0	73.4	86.7	33.4	53.9	30.8	30.8	30.8
		7.7	23.1	15.4	23.1	23.1	93.4	80.0	100.0	92.4	61.6	100.0	100.0	73.4	86.7	33.4	53.9	30.8	30.8	30.8
		66.7	80.0	40.0	20.0	40.0	100.0	80.0	33.4	46.2	33.4	80.0	93.4	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		77.0	53.9	46.2	15.4	23.1	100.0	77.0	33.4	46.2	15.4	92.4	77.0	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		66.7	46.7	66.7	46.7	40.0	80.0	53.4	33.4	73.4	0.0	73.4	40.0	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		84.7	46.2	69.3	46.2	15.4	69.3	61.6	15.4	30.8	0.0	46.2	46.2	46.2	86.7	33.4	53.9	30.8	30.8	30.8
		53.4	73.4	40.0	20.0	66.7	93.4	80.0	53.4	66.7	33.4	80.0	66.7	73.4	46.7	66.7	73.4	13.4	46.7	46.7
		69.3	38.5	46.2	0.0	15.4	92.4	84.7	77.0	38.5	23.1	69.3	84.7	61.6	30.8	30.8	69.3	15.4	38.5	38.5

The numbers on the first rows are based on the weighted averages and on the second on the FD indices of the traits. Values above 50% are indicated with a grey background.

Results based on weighted averages and FD indices are not generally contrasting. The comparison based on the FD indices shows more extreme similarities and dissimilarities for the community types than the comparisons based on the weighted averages. Even though the dissimilarity indicated for completely similar groups by the FD indices comparison is never more than 20 % for the comparison with the weighted averages. For community pairs with significant differences for all the trait FD indices, the dissimilarity after the weighted averages is generally 20% lower than that indicated by the FD indices.

The community types with codes including both numbers and letters in Table 1 are arranged in a chronosequence, which shows the transition from one type of habitat to another due to management shifts. Generally the less moist and nutrient-rich communities are preceding the more moist and nutrient-poor communities. The community types that contain the letters BC (basal community) are still developing and thus are only classified at the end. The clear order in the chronosequence is the one indicating that the community 16BC01 (*Lolio-Cynosuretum*) can change to community types 16AB04 (*Ranunculo Senecionetum aquatici*) or 16AB06 (*Angelico Cirsietum oleracei*) under increased moisture and to communities 16AB01 (*Crepido Juncetum acutiflori*) and 16AB05 (*Scirpetum sylvatici*) under dryness and grazing. One can see that the dissimilarities of the community 16BC01 (*Lolio-Cynosuretum*) with the communities 16AB01 (*Crepido Juncetum acutiflori*) and 16AB06 (*Angelico Cirsietum oleracei*) are higher than the dissimilarities with the communities 16AB05 (*Scirpetum sylvatici*) and 16AB04 (*Ranunculo Senecionetum aquatici*), since the first are the primary stages of transition and the latter the climax stages. One can easily see that the dissimilarity with the last stages does not exceed 30% independently of the weighted averages or the FD indices of the traits.

Based on the weighted averages of the traits the communities 16AB06 (*Angelico Cirsietum oleracei*) and 16RG01 (BC *Holcus lanatus-Lolium perenne*-[*Molinio-Arrhenatheretea*]) and the communities 16RG04 (BC *Juncus effusus*-[*Molinietalia/Lolio-Potentillion*]) and 16BC01 (*Lolio Cynosuretum*) are always distinct from each other independently of the trait used for the comparison, whereas the communities 12RG05 (BC *Agrostis canina- Ranunculus repens- [Lolio-Potentillion. anserinae/Molinietalia]*) and 16AB05 (*Scirpetum sylvatici*) are 100% similar. Based on the FD indices of the traits the communities 16AB06 (*Angelico-Cirsietum oleracei*) and 9 (*Parvocaricetea*), 16RG05

(BC *Carex panicea*-*Succisa pratensis*-[*Junco-Molinion*]) and 33 (*Galio-Urticetea*), 16RG04 (BC *Juncus effusus*-[*Molinietalia/Lolio-Potentillion*]) and 16BC01 (*Lolio-Cynosuretum*)- 16AB06 (*Angelico Cirsietum oleracei*)- 16AB04 (*Ranunculo Senecionetum aquatici*) are never belonging to the same group independently of the FD indices for the traits used, whereas the communities 32 (*Convolvulo-Filipenduletea*) and 12 (*Plantaginetea majoris*), 09RG02 (BC *Carex nigra*-*Agrostis canina*-[*Caricion nigrae*]) and 19 (*Nardetea*), 16RG03 (BC *Festuca rubra*-*Lotus uliginosus*-[*Molinietalia*]) and 33 (*Galio-Urticetea*), 16AB05 (*Scirpetum sylvatici*) and 16RG02 (BC *Holcus lanatus*-*Lychnis flos-cuculi*-[*Molinietalia*])-16BC01 (*Lolio-Cynosuretum*), 16AB06 (*Angelico Cirsietum oleracei*) and 16AB05 (*Scirpetum sylvatici*) are completely similar.

The community 16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]) belongs more than 70% of the weighted averages of traits compared to a different group from the communities 33 (*Galio-Urticetea*), 16RG05 (BC *Carex panicea*-*Succisa pratensis*-[*Junco-Molinion*]), 16RG02 (BC *Holcus lanatus*-*Lychnis flos-cuculi*-[*Molinietalia*]), 16BC01 (*Lolio-Cynosuretum*), 16AB04 (*Ranunculo-Senecionetum aquatici*), 16AB01 (*Crepido-Juncetum acutiflori*), 16RG04 (BC *Juncus effusus*-[*Molinietalia/Lolio-Potentillion*]), 09RG02 (BC *Carex nigra*-*Agrostis canina*-[*Caricion nigrae*]), whereas it is for more than 70% of the traits similar to the communities 12 (*Plantaginetea majoris*) and 16RG03 (BC *Festuca rubra*-*Lotus uliginosus*-[*Molinietalia*]). Applying the same criteria to the FD indices of the traits the community 16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]) belongs more than 70% of the traits to a different group from the communities 33 (*Galio-Urticetea*), 35 (*Lonicero-Rubetea plicati*), 16RG05 (BC *Carex panicea*-*Succisa pratensis*-[*Junco-Molinion*]), 16RG02 (BC *Holcus lanatus*-*Lychnis flos-cuculi*-[*Molinietalia*]) and 12RG05 (BC *Agrostis canina*- *Ranunculus repens*- [*Lolio-Potentillion anserinae/Molinietalia*]); and is more than 70% similar with the communities 32 (*Convolvulo-Filipenduletea*), 12 (*Plantaginetea majoris*), 14 (*Koelerio-Corynephoretea*) and 16RG03 (BC *Festuca rubra*-*Lotus uliginosus*-[*Molinietalia*]).

The community 16AB06 (*Angelico-Cirsietum oleracei*) for the same criterion based on the weighted averages as for the community 16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]) belongs to a different group of the communities 12 (*Plantaginetea majoris*), 14 (*Koelerio-Corynephoretea*), 19 (*Nardetea*), 33 (*Galio-Urticetea*), 16RG05 (BC *Carex panicea*-*Succisa pratensis*-[*Junco-Molinion*]), 16RG02 (BC *Holcus lanatus*-*Lychnis flos-cuculi*-[*Molinietalia*]), 16AB01 (*Crepido-Juncetum*

acutiflori), 12RG05 (BC *Agrostis canina*- *Ranunculus repens*- [*Lolio-Poten. anserinae*/Molinietalia]), 09RG02 (BC *Carex nigra*-*Agrostis canina*-[*Caricion nigrae*]) and 16RG04 (BC *Juncus effusus*-[Molinietalia/*Lolio-Potentillion*]), whereas it is more than 60% similar with the communities 32 (*Convolvulo-Filipenduletea*), 35 (*Lonicero-Rubetea plicati*), 16AB05 (*Scirpetum sylvatici*) and 16AB04(*Ranunculo-Senecionetum aquatici*). Based on the FD indices the community 16AB06 (*Angelico-Cirsietum oleracei*) is more than 70% similar with the communities 16AB05 (*Scirpetum sylvatici*) and 16AB04 (*Ranunculo-Senecionetum aquatici*) and dissimilar from the communities 9 (*Parvocaricetea*), 12 (*Plantaginetea majoris*), 14 (*Koelerio-Corynepherea*), 33 (*Galio-Urticetea*), 35 (*Lonicero-Rubetea plicati*), 16RG05 (BC *Carex panicea*-*Succisa pratensis*-[*Junco-Molinion*]) and 16RG04 (BC *Juncus effusus*-[Molinietalia/*Lolio-Potentillion*])

One can see that by comparing the dissimilarity results for the two communities representing the majority of the relevés that the results are not that contrasting and generally the FD indices indicate less dissimilarities, whereas the number of similar groups is almost the same for 16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]). The similarities indicated by the FD indices of the traits are only half of those indicated by the weighted averages for the community 16AB06 (*Angelico-Cirsietum oleracei*).

Table 3 indicates the percentages of occurrence of species in the different community types.

[illegible]

Survival analysis

The comparison of every focal species with the mean survival curve indicated that 60 % of the species were different from the mean. These were classified in two groups according to their position of their Kaplan Meier curve in comparison with the mean curve, that is "+" if their curve was higher than the mean and "-" if their curve was lower than the mean curve and were tested by GLZ models. Species that had curves crossing the mean curve were excluded from the analysis. Differences between the two groups were indicated for the following traits seed longevity, mean releasing height, minimum releasing height and mean specific leaf area. Figure 4 shows the comparison of six example species with the mean curve.

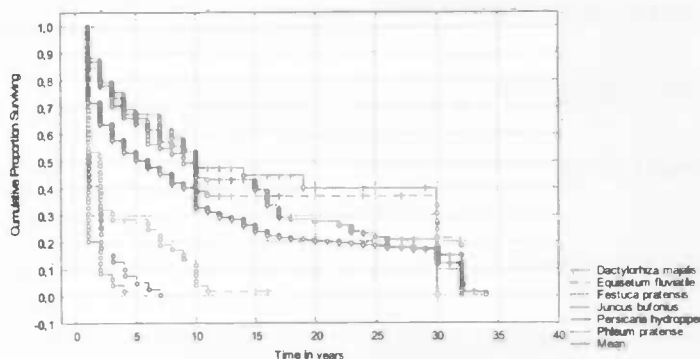


Fig.4: Comparison of some species with the mean survival curve. Species below the mean curve were coded as (-) and species above the mean

One can clearly see (Fig.4) that the mean survival curve separates the species in two groups; one showing higher survival probability (*Dactylorhiza majalis*, *Festuca pratensis*, *Equisetum fluviatile*) and another showing lower survival probability than the mean (*Juncus bufonius*, *Persicaria hydropiper*, *Phleum pratense*). We were only interested in identifying the single traits that can explain these differences and thus we did not proceed in building a model containing all these traits and checking their interactions. We only checked graphically the relations of these traits with the "+" and the "-" group. We could see that the group "-" has higher values for seed longevity and mean SLA and lower for mean and minimum release height compared to the group "+".

An overview for the models built for selected focal species for the year appeared is shown at Table 4. Some of the p values are marginal, but the model indicated is the best fitting one.

Table 4: Overview of the Cox proportional models built for the selected focal species. The variables in the formulae are stated in descending order of significance based on the Wald statistic.

Species name	Number of observations and censorship percentage	Cox proportional model formula	Total Hazard Ratio	P
<i>Caltha palustris</i>	62 (20,97)	$h=h_0 e^{*32,985[WA_maxSM]-41,4537[WA_minSM]-4,9716[WA_mSLA]-7,5571[WA_maxLDMC]}$	0,003	0,007
<i>Crepis paludosa</i>	51 (3,92)	$h=h_0 * e^{-8,57265[WA_maxCH]+7,19335[WA_end1]}$	0,252	0,005
<i>Dactylorhiza majalis</i>	68 (47,06)	$h=h_0 * e^{0,643736[nitr]+2,608129[F_maxSLA]}$	25,839	0,001
<i>Filipendula ulmaria</i>	70 (21,43)	$h=h_0 * e^{3,30649[WA_ther]-4,85229[H_l_st]+20,87018[H_vasc]}$	246871866	0,044
<i>Glyceria fluitans</i>	92 (10,87)	$h=h_0 * e^{-0,386821[moist]+5,588056[F_mCH]}$	181,497	0,028
<i>Juncus articulatus</i>	66 (7,58)	$h=h_0 * e^{-5,48164[WA_GCP1-2]-2,55116[WA_Hydr]}$	0,001	0,023
<i>Myosotis scorpioides</i>	111 (2,7)	$h=h_0 * e^{-5,93423[WA_mCH]-4,05386[H_Geop]+3,58593[WA_mRH]}$	0,002	0,028
<i>Ranunculus flammula</i>	66 (15,15)	$h=h_0 * e^{-31,6355[WA_minSM]+21,6768[WA_maxSM]+2,5299[F_mSM]}$	0,001	0,0497
<i>Rhinanthus angustifolius</i>	187 (34,22)	$h=h_0 * e^{1,891254[F_mSLA]}$	6,628	0,001

In the appendix the simple Kaplan Meier and the corrected ones for each of the selected focal species are displayed in Figures 8-15. One can see that the corrected curves are generally showing slightly lower survival times. The differences though are not that striking and generally are observed after the first decade of the vegetation recordings and explained by the variables included in the Cox models. For *Filipendula ulmaria* and *Crepis paludosa* the two curves coincide after the first decade of vegetation recordings. For other species like *Juncus articulatus*, *Myosotis scorpioides*, *Ranunculus flammula*, *Glyceria fluitans* and *Dactylorhiza majalis* the two curves are almost parallel after the first decade, whereas a great difference between the two curves is observed for *Caltha palustris*.

The selected focal species are observed with the highest frequency at five different communities. The species *Caltha palustris*, *Juncus articulatus*, *Myosotis scorpioides*,

Ranunculus flammula and *Rhinanthus angustifolius* belong to the community 16AB04 (Ranunculo-Senecionetum aquatici) and the species *Crepis paludosa* and *Filipendula ulmaria* to the community 16AB06 (Angelico-Cirsietum oleracei). *Dactylorhiza majalis* belongs to 16AB01 (Crepido-Juncetum acutiflori) and *Glyceria fluitans* to 12RG05 (BC Agrostis canina- Ranunculus repens- [Lolio-Poten. anserinae/Molinietalia]). The community 16AB04 (Ranunculo-Senecionetum aquatici) is characterized by wet and acid environment relatively rich in nutrients. The ordination indicates that this community is characterized by species with high seed mass but short longevity, high nitrogen, species with low mean leaf dry matter content and low SLA results that are perfectly correlating with the general description of this community and variables correlated with these traits are also reflected at the models built for the single species belonging to this community.

The community 16AB06 (Angelico-Cirsietum oleracei) has the same attributes as the community 16AB04 (Ranunculo-Senecionetum aquatici)(Fig1-2), but it is more acid and less moist and poorer in nutrients compared to it. The models for the selected focal species are only reflecting connections with this community considering the leaf distribution and the dispersal of the seeds through animals (H_I_al_st and WA_end1). It is striking that these variables are not included in the ordinations (Fig. 1-2) thus defining the community fingerprints but are correlated positively with those used in the ordinations (results not shown).

The community 12RG05 (BC Agrostis canina- Ranunculus repens- [Lolio-Poten. anserinae/Molinietalia]) is characterized by wet and acid environment with short vegetation and these attributes are mirrored in the model built for *Glyceria fluitans* suggesting that this species will survive more in moist sites with short canopy height. *Dactylorhiza majalis* is mostly observed in the community 16AB01 (Crepido-Juncetum acutiflori) which is characterized by moist and acid environment poor in nutrients. The model suggests that this species will survive longer in environments with low SLA and low nitrogen.

Generally the single models should be interpreted using the community fingerprints of the communities where the species are mostly observed (Fig. 1-2). Most species but *Caltha palustris*, *Ranunculus flammula* and *Crepis paludosa* are following the same traits trend as the community where they are mostly observed.

The models built by using the community types, which occurred at the plot in the year of appearance or disappearance of the focal species, as explanatory variables

indicated, which of the communities are mostly explaining the differences in survival time of all the species at the beginning of the vegetation recording and its end. The conditions of co-occurring species in the year of appearance are explained by the communities 16BC01 (*Lolio-Cynosuretum*) and 16AB06 (*Angelico-Cirsietum oleracei*) and both are positively influencing the survival of the species. The survival curves built for the Cox regression models are based on cumulative probabilities, which means that the values are derived by the inverse of the hazard ratios. So the variables with positive coefficients will influence negatively the survival probability and vice versa for the variables with negative coefficients. The conditions of the year of disappearance are positively influenced by the community 16AB04 (*Ranunculo-Senecionetum aquatici*) and negatively by the community 16AB06 (*Angelico-Cirsietum oleracei*). The Cox formulae are shown at Table 4. Figure 5 is showing the Kaplan Meier curves for the year appeared and the year disappeared corrected for the communities explaining the survival times.

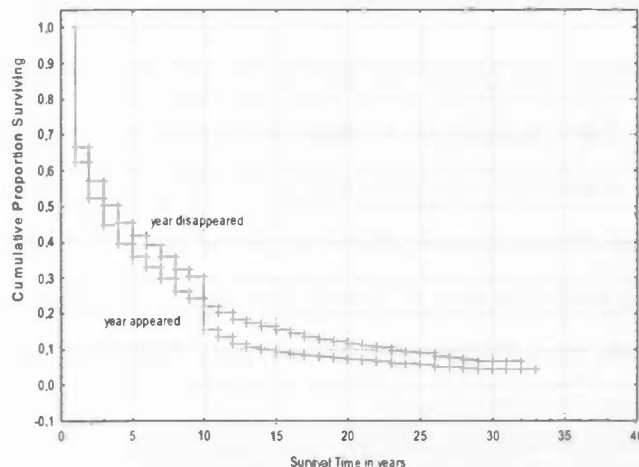


Fig.5: Corrected curves for year appeared and year disappeared. Communities 16BC01-16AB06 and 16AB06-16AB04 are explaining the curves respectively.

The community 16AB06 (*Angelico-Cirsietum oleracei*) shows explanatory power in both models, but it positively influences the survival time when it occurs in the establishing phase and negatively in the disappearing phase. It is striking though that the community 16RG01 (*BC Holcus lanatus-Lolium perenne*-[*Molinio-Arrhenatheretea*]), which is the second one after 16AB06 (*Angelico-Cirsietum oleracei*) in representing the majority of the relevés, is not observed in the models. This could be explained due to the fact that this community has different traits from the community 16AB06 (*Angelico-*

Cirsietum oleracei) and as a result the conditions during the year of occurrence and the year of disappearance of species could be possibly affected more by the more stable and more species diverse (more dominant species present) community 16AB06 (Angelico-Cirsietum oleracei) (Table 3). After all most of the dominant species present in the community 16RG01 (BC Holcus lanatus-Lolium perenne-[Molinio-Arrhenatheretea]) are also presented in the community 16AB06 (Angelico-Cirsietum oleracei) and only *Poa pratensis* is only observed in the first. The rest of the communities included in the models are represented by at least 100 relevés. The influence of the conditions at the year appeared on survival time is explained mostly by two communities that are very close in their attributes (16AB06 (Angelico-Cirsietum oleracei) and 16BC01 (Lolio-Cynosuretum) and the same counts for the year disappeared (16AB06 Angelico-Cirsietum oleracei) and 16AB04 (Ranunculo-Senecionetum aquatici). These communities are characterized by heavy seeds with short longevity and high nitrogen, moisture and acidity. They also have more non-epizoochorous and endozoochorous species with low mean leaf dry matter content and low SLA and contain more annuals and biennials with leaves distributed along the stem and intermediate persistence of clonal growth (Fig 1-2).

Generally higher survival probabilities are observed for the year disappeared and this can be explained by the fact that the Drentsche A reserve follows a trend where species that can survive well under the secondary succession processes are selected.

For the communities explaining the differences in survival times for all the species for the conditions during the year of appearance and of disappearance; bar plots for the weighted averages and the FD indices describing the community fingerprints were prepared and are shown at Figures 6 and 7 respectively.

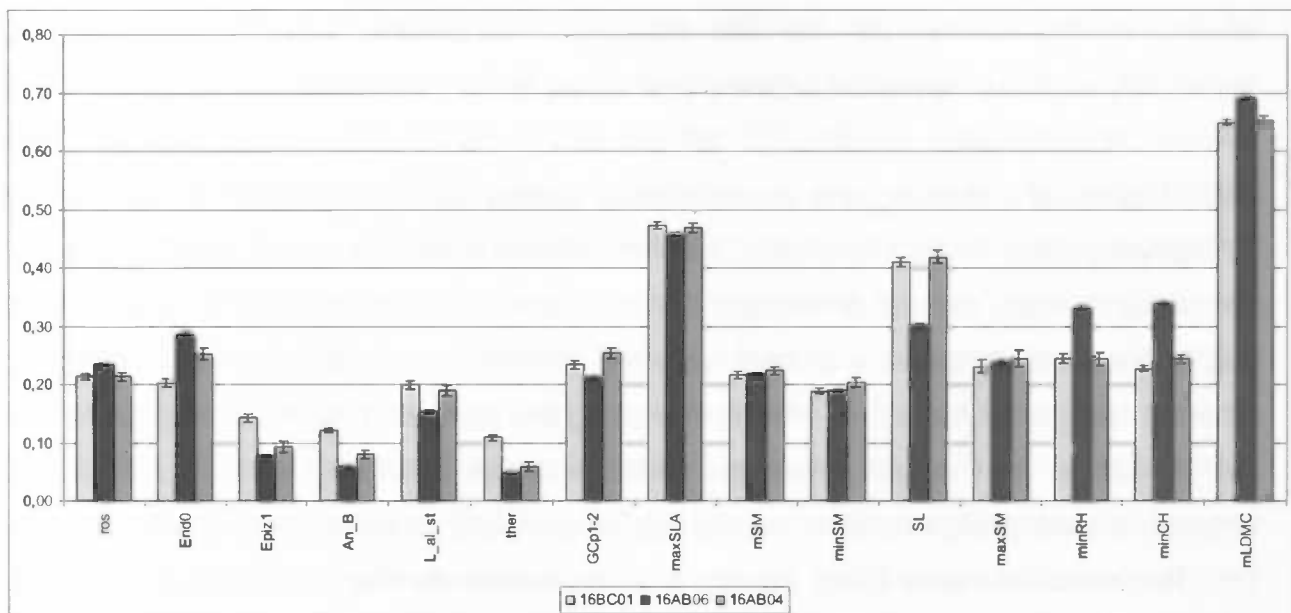


Fig.6: Mean weighted averages for the communities explaining the survival curves for the year appeared and the year disappeared. The error bars are indicating the standard errors. Light blue color corresponds to the community 16BC01(Lolio-Cynosuretum), purple represents the community 16AB06 (Angelico -Cirsietum oleracei) and red the community 16AB04 (Ranunculo-Senecionetum aquatici).

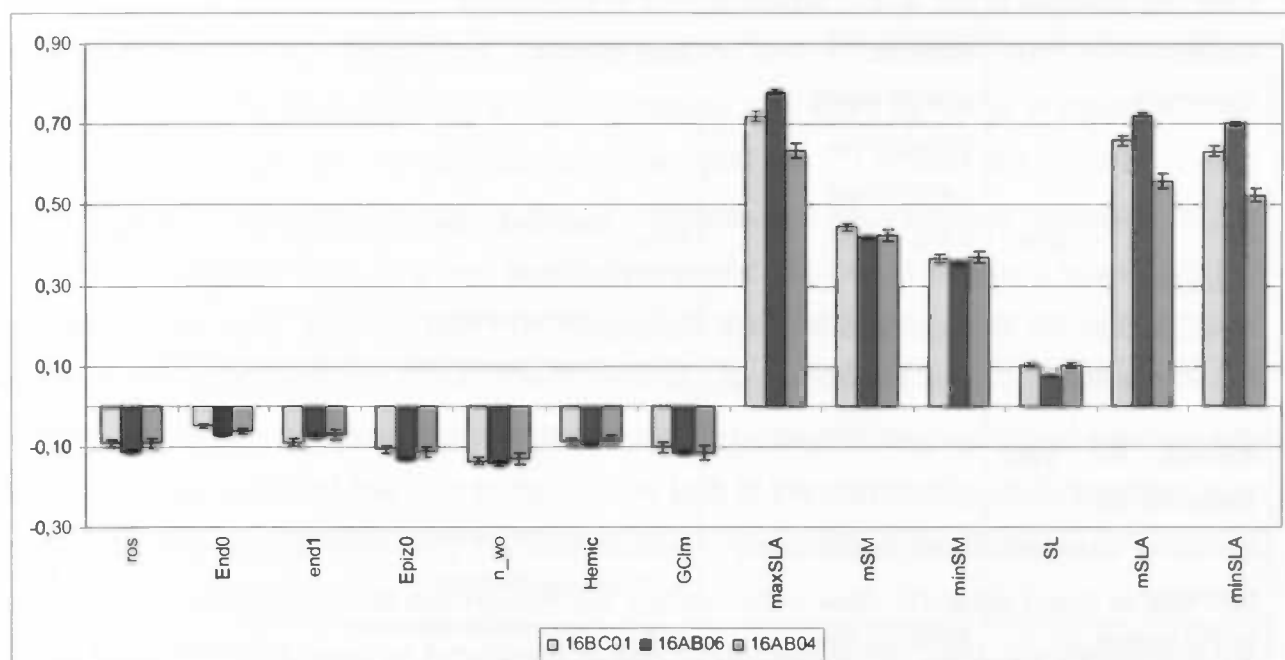


Fig.7: Mean FD indices for the communities explaining the survival curves for the year appeared and the year disappeared. The error bars are indicating the standard errors. Light blue color corresponds to the community 16BC01(Lolio-Cynosuretum), purple

represents the community 16AB06 (Angelico -Cirsietum oleracei) and red the community 16AB04 (Ranunculo-Senecionetum aquatici).

Both Figures are showing the same pattern among the communities if the different categories belong to the same traits; for instance the pattern in seed mass is the same no matter if mean, minima or maxima are compared. For the categorical traits like leaf distribution similar patterns are observed if the FD indices are used when comparing the different categories like plants with leaves along the stem with rosette plants. Generally the FD indices for the categorical data indicate similar values for all the communities, whereas the weighted averages show a higher variability concerning those traits.

Results of the best fitting models built separately for the year appeared and the year disappeared using the weighted averages and the FD indices of the traits are indicated at Table 5.

Table 5: Models for the year appeared and the year disappeared using as explanatory variables the weighted averages or the FD indices of the traits and the community types. The variables in the formulae are ordered descending according to their significance in the model based on the Wald Statistic.

Models for year appeared	Number of observations - censorship percentage	Cox formula	Total Hazard Ratio	p
by weighted averages	5320 (15,36)	$h=h_0 \cdot e^{-0,465755[WA_GCp>2]+0,549030[WA_mCH]+0,292045[WA_mSM]}$	1,456	<0,001
by FD indices	5320 (15,36)	$h=h_0 \cdot e^{-0,065719[res.mow]}$	0,936	0,003
by communities	5320 (15,36)	$h=h_0 \cdot e^{0,20064[16AB06]+0,142509[16BC01]}$	1,409	<0,001
Models for year disappeared				
by weighted averages	5966 (24,52)	$h=h_0 \cdot e^{4,04409[WA_maxSM]+4,75171[WA_mSM]+0,10799[res.mow]-0,07668[nitr]}$	2,094	<0,001
by FD indices	5966 (24,52)	$h=h_0 \cdot e^{0,113832[res.mow]-0,06531[nitr]}$	0,897	<0,001
by communities	5966 (24,52)	$h=h_0 \cdot e^{-0,126878[16AB06]+0,179314[16AB04]}$	1,054	<0,001

The model based on the weighted averages for the year appeared shows that species surrounded by communities with high mean seed mass and mean canopy

height will survive less than the rest of the species and species surrounded by communities with persistence of clonal growth for more than 2 years will survive longer than the rest. The same model based on the FD indices suggests that species surrounded by communities with higher resistance to mowing will survive more than the rest. The models for the year disappeared based on the weighted averages suggest that species belonging to environments with high nitrogen will survive more and species belonging to more moist sites will survive less than the rest. The model based on the FD indices also indicates that species that are less diverse in their resistance to mowing with a high diversity in their Ellenberg indicator values for nitrogen will survive longer than the rest. It is worth noting that some of the variables are common (seed mass and resistance to mowing) in the models of year appeared and year disappeared but their effects are opposite (resistance to mowing).

Discussion

Community Fingerprints

It can generally be stated that by using trait information the attributes of communities can be identified in a more compact way than by using vegetation data. The differences between the weighted averages and the FD indices are not that striking and by checking the correlation of the FD indices and the weighted averages of the traits we could see that they are positively correlated. The ordinations based on the weighted averages and on the FD indices of the traits (Fig. 1-2) do not indicate contrasting results and the small differences can be explained by the fact that the FD indices apart from weighing traits according to the relative abundance of species are also taking into account the distribution of the trait in the community, thus resulting in a more compact way of ordinating the communities. Generally seed mass, seed longevity and specific leaf area could distinguish the communities well. Thus we could argue that these traits could be used as functional markers (Garnier *et al.*, 2004) for describing the management shifts in the Drentsche A reserve. We have also checked the correlation of the ordination axes with the Ellenberg values and we have shown that correlations exist on the second and third axes. This means that the trait information is quite strong in

defining community fingerprints and relations with "abiotic factors" exist at the secondary gradients of the ordinations.

The vegetation's data ordination (excluding species that were present in less than five relevés) by presence/absence or by relative abundance of the species by DCA indicated distinct differences between the species of the acid communities from the rest and small differences between the species of the wet and the dry communities (Results not shown). By combining the vegetation ordination with the traits distinguishing the community fingerprints one could think that these traits would be distinguishing the driest from the wettest communities and the acid from the rest.

The two communities representing most of the relevés (16RG01 (BC *Holcus lanatus*-*Lolium perenne*-[*Molinio-Arrhenatheretea*]) and 16BC01(*Lolio-Cynosuretum*) differ in their height and their moisture so we are expecting the analysis independently of the FD indices or the weighted averages used to indicate variables correlating with these differences (Fig.1-2). Consequently seeing the leaf distribution and the plant growth form -though with a different category for each of the analyses- explains these differences. Generally the two communities mostly representing the majority of relevés are distinguished well by traits associated with dispersability and persistence independently of the weighted averages or the FD indices of the traits used. The strength of the regeneration traits is mainly indicated in the one based on the weighted averages. The same counts for the rest of the communities, since the ordinations are revealing distinguishing relationships among the communities mostly due to persistence and dispersability traits.

The traits identified as strong in distinguishing community fingerprints could explain differences in dispersal-establishment (seed mass and seed longevity) of the species and differences in the growth rate and the photosynthetic capacity (specific leaf area) and possibly mirror the different plant strategies developed under the secondary succession processes (Lloret & Vila, 2003). Seed mass has been indicated by other studies (Vile *et al.*, 2006) as a trait having the power to distinguish plant strategies under secondary succession. Our study indicates a trade-off between seed mass and seed longevity- SLA, with heavier seeds surviving for a shorter period and growing slower than the lighter ones. These results can be easily explained by the fact that most of the relevés in the Drentsche A are nutrient poor and the most advantageous strategy for a species is having a slow growth rate and light seeds.

Survival Analysis

It can generally be stated that differences in traits can explain differences in survival time of species and the existing patterns can be modeled. The degree up to which we can understand all the processes taking place under secondary succession and the accuracy of the models, depends on the linkage of the models with basic ecological mechanisms (Vile *et al.*, 2006).

From the models built based on all species we could possibly conclude that the communities included in the models (16AB06 (*Angelico-Cirsietum oleracei*), 16BC01 (*Lolio Cynosuretum*) and 16AB04 (*Ranunculo-Senecionetum aquatici*) are the more stable ones and the traits (seed mass, canopy height, resistance to mowing and nitrogen concentration) used are the stronger ones in indicating differences in survival times of the species. It has been shown that species with wide lateral spread are more abundant in disturbed sites (Lloret & Vila, 2003). Our results indicate that species surrounded by communities with high clonal growth persistence and more resistant to mowing will survive more than the rest, whereas species surrounded by communities with heavy seeds and high canopy height will survive less than the rest.

The effects of the high seed mass are observed both for the year of appearance and of disappearance of a species. This can be explained by the high competitive ability of species with heavier seeds and the higher colonizing ability of species with lighter seeds (Ozinga *et al.*, 2007). A lighter seed can be transferred easier to a beneficial site and since it has established it is easier for a lighter seed to enter the upper soil seed bank and remain there. There are quite some studies showing that the upper soil seed bank mainly reflects and is highly correlated with the established vegetation than with species transferred from tidal perturbations (Wolters & Bakker, 2002). So a species with a low seed mass remains basically on the upper soil layer (0-5cm) and it is easier to sprout and be subjected to disadvantageous conditions and thus disappear rather than transferred deeper and remain protected in the soil.

The effects of resistance to mowing are contrasting for the year appeared and the year disappeared suggesting that species surrounded by communities with high resistance to mowing have a higher probability of surviving at the beginning of their establishment and lower at the end of it. This could be explained by taking into account that at the year of disappearance the increased nitrogen concentrations are

advantageous for the successful establishment of the species. So the model for the year of disappearance is describing communities that are nutrient rich and the species present in them could have higher competitive abilities, thus they are more resistance to mowing and affect negatively the longer survival of species in those sites (Hooper & Vitousek, 1998). The resistance to mowing is advantageous for the year of appearance probably because the communities are under drastic changes and this trait could enable the establishment of species by causing more favorable environmental conditions, but as long as more species have established then competition processes play a more important role and thus this trait has negative effects for the longer survival of species in nutrient-rich communities.

The communities 16BC01 (*Lolio Cynosuretum*) and 16AB06 (*Angelico Cirsietum oleracei*) will influence negatively the survival probability of species when occupying the plot in the year appeared, which means that individuals that grow in these communities have a lower probability of surviving than the species growing in the rest of the communities. Another explanation could be that these communities could have been objected to radical habitat changes during the year of occurrence of species and thus secondary succession processes do not allow high survival probabilities for the species belonging to them. For the year disappeared the community 16AB06 (*Angelico Cirsietum oleracei*) influences positively the survival of the species and the community 16AB04 (*Ranunculo-Senecionetum aquatici*) negatively. That is that species occurring in community 16AB06 (*Angelico Cirsietum oleracei*) have a higher probability of surviving than the rest and species occurring in the community 16AB04 (*Ranunculo-Senecionetum aquatici*) have a lower probability than the rest. It can be stated that the community 16AB06 (*Angelico Cirsietum oleracei*) is the most stable one and as long as species establish in it they can survive longer than the rest.

The comparison of all the focal species with the mean survival curve indicates that differences from the mean survival time can be explained by SLA, seed longevity and release height. It is striking that the group surviving less than the mean has higher values for seed longevity and SLA than the group surviving more than the mean. This can be explained by the fact that the measured survival in our research is actually the aboveground persistence of a species. So this could be interpreted as being absent from above ground but surviving in a seed form (Ozinga *et al.*, 2007). Higher values in SLA are associated with higher relative growth rate, which is disadvantageous in nutrient-poor sites. So the species belonging to the group surviving less than the mean

could be growing faster but also disappearing faster from aboveground. The group that survives less than the mean is characterized by lower values in releasing height and consequently in a shorter dispersal range than the one of the group surviving more than the mean. The inability to disperse over long distances results in the constant dealing of disadvantageous conditions possibly resulting in the disappearance of a species from the established vegetation.

The single models for the selected focal species have indicated a certain group of traits that can explain differences of survival time between each species and the community where it is mostly observed. These traits are seed mass, canopy height and release height and are complying with the traits revealed from other studies dealing with the same questions (Ozinga *et al.*, 2007). Generally traits associated with dispersability and nutrient requirements can indicate differences in survival times. It can be argued that a certain combination of traits can summarize ecosystem processes and describe compactly differences in plant strategies (Garnier *et al.*, 2004; Vile *et al.*, 2006). Most of the species follow the same trait trend as the community where they are mostly observed, which means that their traits are passing through the same environmental filter as the traits of the surrounding vegetation (Zobel, 1997). The species *Caltha palustris*, *Ranunculus flammula* and *Crepis paludosa* are negatively affected by the communities where they are mostly observed, which means that they survive better having contrasting traits with those communities. This means that they are competing with the surrounding vegetation and the reason that they are not observed with higher frequencies in communities that have the same traits could be due to their limited dispersal (Zobel, 1997). We could hypothesize that the management shifts have created certain landscape barriers that these species cannot overcome yet and generally the system will lead to a state where all the species present will survive better in the communities where they are mostly observed.

Conclusions

1. The community fingerprints can be defined by trait values better than by vegetation data. The FD indices of the traits are more stringent in the communities' separation than the weighted averages. In general the continuous

traits such as canopy height, seed mass, seed longevity, leaf dry matter content, specific leaf area are considered better in separating the attributes of the communities if only single categories are counted. If not, then the categorical traits such as plant life span, plant growth form, woodiness, persistence of clonal growth, lateral spread of clonal growth, leaf distribution, epizoochory and endozoochory are considered better and the same number of significant traits is indicated by both analyses using either the weighted averages or the FD indices of the traits.

2. Stable communities can explain differences in survival time of species both during the year of appearance and year of disappearance and are characterized by heavy seeds with short longevity and high nitrogen, moisture and acidity. They also have more non-epizoochorous and endozoochorous plants with low mean leaf dry matter content and low SLA and contain more annuals and biennials with leaves distributed along the stem and intermediate persistence of clonal growth.
3. Certain groups of traits can distinguish community fingerprints and/ or explain differences in survival times.
 - a. Seed mass, seed longevity and SLA can distinguish the attributes of the communities well.
 - b. Seed longevity, SLA and release height explain differences in the survival time of species from the mean survival.
 - c. Canopy height, seed mass and release height can indicate if a species is following the same trait trend with the community where it is mostly observed.
4. Survival models built for individual species are reflecting relations that can be explained by the attributes of the community that mostly represents each species. Some are affected positively by the resident community and some negative. Negative effects are explained by competition and dispersal limitation processes (a species has contrasting traits than the community where is mostly observed and its occurrence in another community having the same traits is may be limited), whereas positive effects are explained by habitat filtering processes (a species is passing through the same environmental filter as the traits of the community where it is mostly observed).

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Appendix

Table 6: Explaining the coded of the variables used

Codes for variables	Explanation
WA_	Weighted averages
F_	FDvar index
H_	Shannon-Wiener index
m	Mean value
min	Minimum value
max	Maximum value
CH	Canopy Height
LDMC	Leaf dry matter content
SM	Seed Mass
SL	Seed Longevity
RH	Releasing Height
SLA	Specific leaf area
L_al_st	Leaves along the stem
Ros	Rosettes
Epiz0	Non-epizoochore
Epiz1	Epizoochore
End0	Non-Endozoochore
End1	Endozoochore
N_wo	Non-woody
Ther	Therophyte
Hemic	Hemicryptophyte
Geop	Geophyte
Hydr	Hydrophyte
Vasc	Vascular-semi parasites
GCp1-2	Clonal growth persistence of 1 or 2 years
GCp>2	Clonal growth persistence of more than 2 years
GCI _m	Lateral spread of clonal growth of more than 0,25m
GCI _l	Lateral spread of clonal growth from less than 0,01m up to 0,25m
An-b	Annuals or biennials

moist	Ellenberg values for moisture (median-presence/absence)
nitr	Ellenberg value for nitrogen (median-presence/absence)
acid	Ellenberg value for acidity (median-presence/absence)
light	Ellenberg value for light (median-presence/absence)
Res.mow	Ellenberg value for resistance to mowing (median-presence/absence)

Table 7: Explanations of the sociological groups

Codes for the sociological groups	Explanation
9	Parvocaricetea
12	Plantaginetea majoris
14	Koelerio-Coryneporetea
19	Nardetea
32	Convolvulo-Filipenduletea
33	Galio-Urticetea
35	Lonicero-Rubetea plicati
16RG05	BC Carex panacea-Succisa pratensis-[Junco-Molinion]
16RG03	BC Festuca rubra-Lotus uliginosus-[Molinietalia]
16RG01	BC Holcus lanatus-Lolium perenne-[Molinio-Arrhenatheretea]
16RG02	BC Holcus lanatus-Lychnis flos-cuculi-[Molinietalia]
16BC01	Lolio-Cynosuretum
16AB05	Scirpetum sylvatici
16AB06	Angelico-Cirsietum oleracei
16AB04	Ranunculo-Senecionetum aquatici
16AB01	Crepido-Juncetum acutiflori
12RG05	BC Agrostis canina-Ranunculus repens-[Lolio-Poten. anserinae/Molinietalia]
09RG02	BC Carex nigra-Agrostis canina-[Caricion nigrae]
16RG04	BC Juncus effusus-[Molinietalia/Lolio-Potentillion]

Survival curves for the selected focal species
(the simple Kaplan Meier curves are indicated with blue color and the Cox corrected curves with red color)

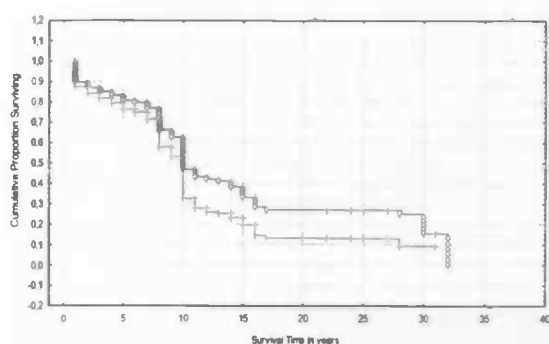


Fig.8: Simple Kaplan Meier and Cox corrected curve for *Rhinanthus angustifolius*

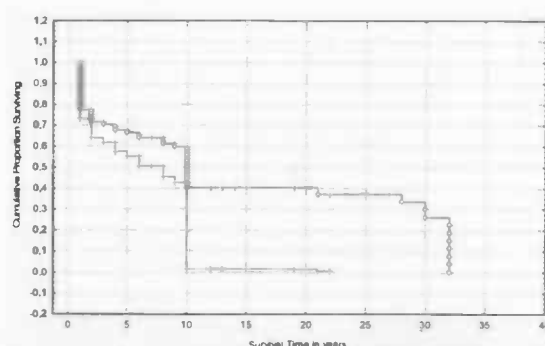


Fig.9 Simple Kaplan Meier and Cox corrected curve for *Caltha palustris*

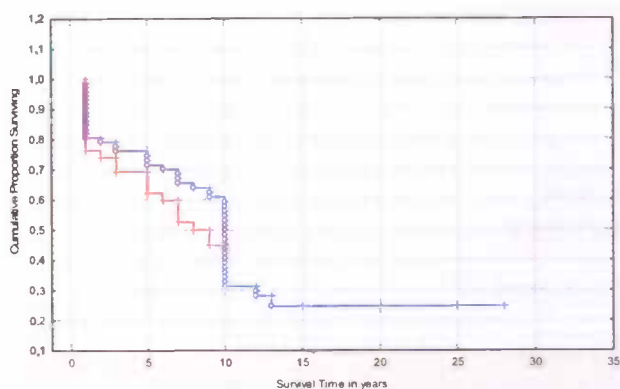


Fig.10: Simple Kaplan Meier and Cox corrected curve for *Crepis paludosa*

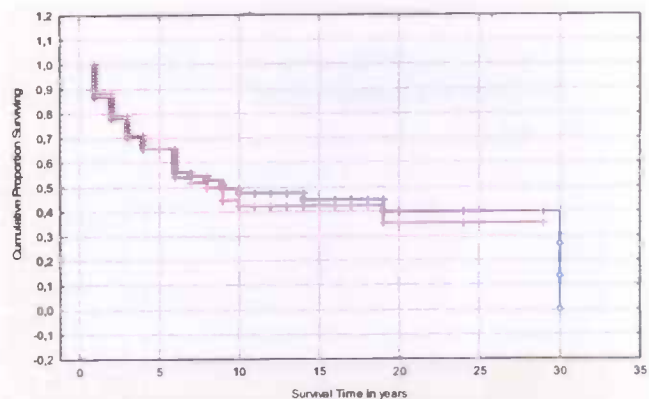


Fig.11: Simple Kaplan Meier and Cox corrected curve for *Dactylorhiza majalis*

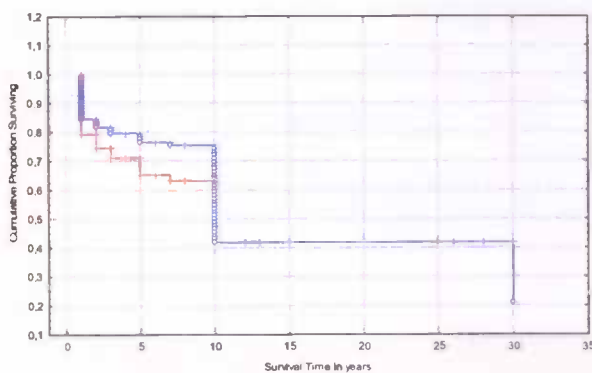


Fig.11: Simple Kaplan Meier and Cox corrected curve for *Filipendula ulmaria*

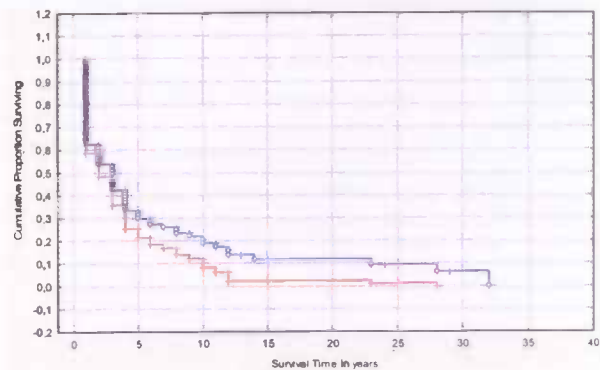


Fig.12: Simple Kaplan Meier and Cox corrected curve for *Glyceria fluitans*

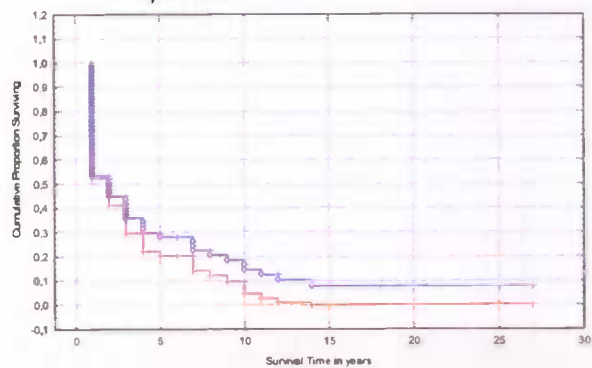


Fig.13: Simple Kaplan Meier and Cox corrected curve for *Juncus articulatus*

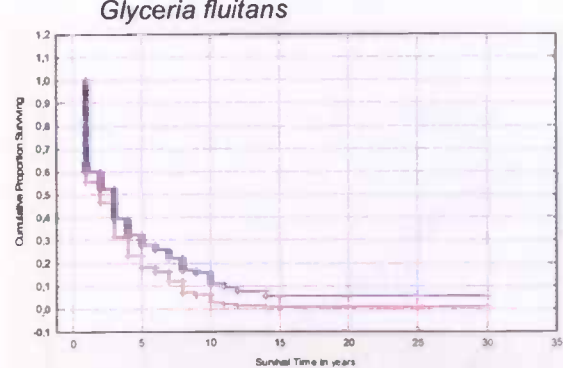


Fig.14: Simple Kaplan Meier and Cox corrected curve for *Myosotis scorpioides*

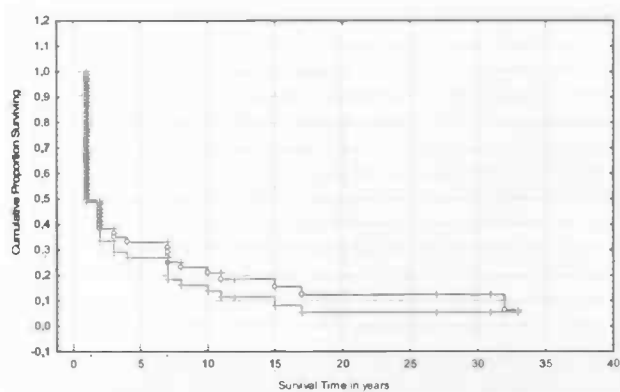


Fig.15: Simple Kaplan Meier
and Cox corrected curve for
Ranunculus flammula