

## **Appendix S1** Justification for studying lineage compositions of habitat types within a region

Studying differences in lineage compositions among habitat types within a relatively small and geologically young region under strong impact of recent anthropogenic environmental changes may seem hardly justified. It is obvious that within any small geographic region most or all Angiosperm lineages have not originated in situ but have immigrated from outside, excluding any maintenance of lineages since their origin in that particular region and in its regional habitats. One could even argue that floras of habitat types within such a region are too small, unique, and ephemeral to differentially sort among the immigrant lineages and differ in the outcomes of macroevolutionary diversification across geological time scales.

This argument is based mostly on assumption that lineage composition of habitat types is determined hierarchically from global to regional and from regional to local levels. According to this point of view, lineage composition of local habitat patches within a region is defined mainly by composition of regional species pool. Lineage composition of regional species pools is determined by long-term geologic, climatic and biogeographic processes, while lineage composition of local habitat patches is determined by recent environmental filtering from regional species pool and local interspecific interactions (Guisan & Rahbek, 2011). In analyses of differences in species richness among regions each region is considered as an evolutionary unit with more or less uniform environments within it (i.e., Hawkins *et al.*, 2006). Climatic environmental gradients and barriers between biogeographic regions are thus assumed more likely to show macroevolutionary patterns, than environmental gradients within regions.

However, patches of a given habitat type form networks that extend beyond regions and may be characterized by their specific species pools. As a consequence, differentiation between species pools from habitats within the same biogeographic region might be no less important than differentiation between species pools of a given habitat type in different regions (Ricklefs, 2004). In that case the lineage composition of a habitat type may differ in composition of lineages just as much as the species pool of a biogeographic region does (Fig. S1). Lineages need not have originated within these habitats, but still be a representative part of their species pools today, similar to different regions containing different lineages, including many that did not originate within the respective regions. Different lineages in different habitats may then represent different geological epochs of origin. We see the following evidence for species pools of habitat types containing different lineage compositions.

First, habitats within a given region may in some respects represent a similarly wide range of environments as different regions. For instance, our study system, The Netherlands, may seem a small region with almost absent climatic gradients across its whole area, and therefore with very narrow representation of environmental gradients. Nevertheless, in reality this region represents surprisingly wide gradients for most abiotic factors important for existence of plants, except temperature. Submerged habitats and sand dunes are characteristic elements of the Dutch landscape that represent the extremes of a moisture gradient. There are no wetter places than submerged habitats. Also, moving sand dunes are among the dryer habitats worldwide, and all these habitats are present in the region. Similarly, among the globally most acidic and most calcareous, most fertile and most nutritionally poor, very dark and completely open environments all are represented. Bartish *et al.* (2010) reported ranges of indicator values of the five abiotic (luminosity; soil moisture, nitrogen, and pH; temperature) and one biotic factor (grazing pressure) for Dutch angiosperm flora. Their data demonstrate that with exception of extremes of temperature (and to some extent of very dark and very dry environments) most other extreme abiotic environments and correspondent habitat types are well represented in the region, just like many biotically extreme habitats such as heavily grazed grasslands.

Second, species often use similar habitats on different continents. Niinemets & Valladares (2006) reported that the same species tend to grow in the same habitat environments on different continents ( $R^2 = 0.68\text{--}83$ ). Petitpierre *et al.* (2012) found that even after introduction of species to new continents, habitat niches rarely shift. Species with wide Eurasian ranges can provide corresponding examples. For instance, *Hippophae rhamnoides* (L.) is an equally successful colonizer of moving dune communities in The Netherlands and British Islands, or in Italy and Romania, as in the desert areas south of Zaisan Lake at the border between Kazakhstan and China, or in Nubra valley in Ladakh, India (IVB, personal observation). Environmental filtering into different habitat types likely operates in relatively similar ways in different regions across the globe.

Third, as a likely consequence of such globally consistent filtering of many species into habitats, species often do not shift habitats from ancestors to descendants. Although niche shifts within evolutionary lineages across biomes do exist (Donoghue & Graham, 2014), Crisp *et al.* (2009) found that in the vast majority of cases, descendants maintain the habitat types of their ancestors, even while changing among Southern Hemisphere continents. These global patterns of habitat conservatism within lineages appear to be reflected within regions (Petersen, 2011; note that in terminology of Losos (2008) we refer to ‘phylogenetic signal’). Ortega *et al.* (1997), for instance, reported that across the Canary archipelago in the Atlantic Ocean lineages seem to be more capable of colonizing different islands than different habitat types within an island, *i.e.* vegetation zones.

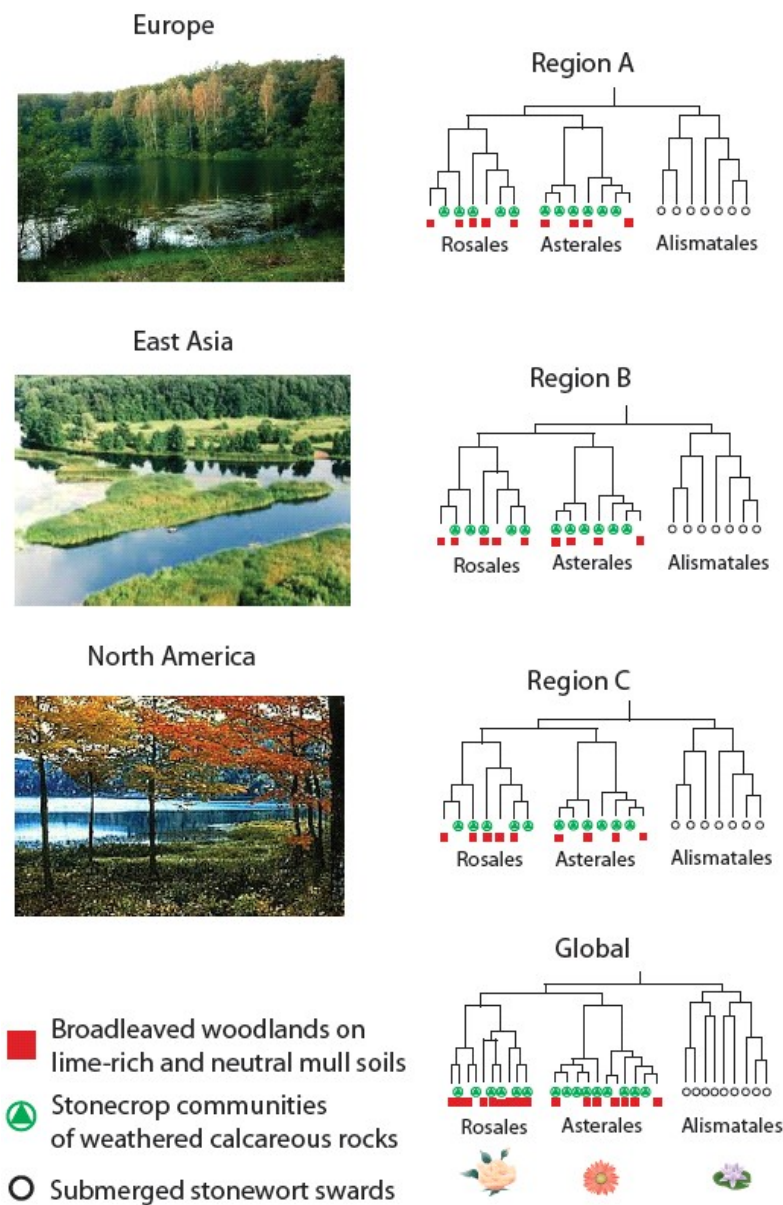
Fourth, stochastic or transient ecological factors that may control the species composition of local habitat patches might average out at the scale of entire species pools of habitat types. A species eliminated by a local competitor, by dispersal limitation or by random environmental fluctuation from one patch of a habitat may still be present in other patches of the same habitat type. Hence, while these factors may erase signals of macroevolutionary diversification at the scale of communities within local habitat patches, they are much less powerful at the scale of entire species pools of habitat types.

An exploratory analysis of the flora of the Netherlands in fact confirms such differentiation of species pools between habitat types which can be on a par to differentiation between regions (Table S1a). We found that in species pools of three habitat types representative of three main biomes, a considerable fraction of species have wide Eurasian ranges: 64%, 38%, and 39%, for ‘Submerged stonewort swards’, ‘Stonecrop communities of weathered calcareous rocks’, and ‘Broadleaved woodlands on lime-rich and neutral mull soils’, respectively. Correspondingly, habitat types of submerged stonewort swards in the Netherlands contain a large fraction of angiosperm species with ranges across the whole Northern Hemisphere (49%), but they share only 3% of species with stonecrop communities of weathered calcareous rocks within the country (Table S1a).

Taxonomic composition of the three Dutch habitat types is also very different. For example, Alismatales together with Poales are by far the most species-rich orders in submerged stonewort swards (Table S1b). However, not a single species of Alismatales was recorded in stonecrop communities. Similarly, Asterales, Caryophyllales, and Rosales are (together with Poales) the most species rich orders in stonecrop communities and broadleaved woodlands, together accounting for 33% and 25% of all species in these two habitat types, respectively. However, these three orders represent only 6% of the species pool of submerged stonewort swards. Differences in environmental adaptations of species from Alismatales and other taxa are most likely responsible for the observed contrasts in proportional representation of different species-rich orders among the three habitat types (Fig. S1). Poales are seemingly an exception among the five most species-rich orders. However, within this taxon, the most species-rich families Cyperaceae and Poaceae also strongly differ in their representation in different habitat types (Table S1b).

The above considerations suggest altogether that Dutch habitat types of angiosperms are characterised by distinct macroevolutionary signatures in terms of lineage composition. This is consistent with the phylogenetic signal in the habitat distribution of species from the same flora (e.g. Prinzing *et al.*, 2001). The next step is hence to analyse whether differences in lineage composition among Dutch habitats correspond to differences in geological ages of origin of these lineages. The analysis remains regional and it remains to be shown if these regionally-specific patterns will be confirmed for other regions, climatic zones, or for global samples.

**Figure S1** Schematic distribution of species from several species-rich clades (orders Alismatales, Asterales, and Rosales) of Dutch Angiosperms among three habitat types: ‘Submerged stonewort swards’, ‘Stonecrop communities of weathered calcareous rocks’, and ‘Broadleaved woodlands on lime-rich and neutral mull soils’. Phylogenetic patterns and proportions of species from different clades and habitat types correspond approximately to phylogenetic patterns and proportions of species in real habitat types and clades of Dutch Angiosperms. Note that similar habitat types from different continents can share higher proportion of lineages and even species, than different habitat types from the same region (Table S1a).



**Table S1a** Proportion of shared species between species pools of three habitat types of Dutch Angiosperms and proportion of species within each of the habitat types with ranges in East Asia and North America. Habitat types: ‘Submerged stonewort swards’ (SSS); ‘Stonecrop communities of weathered calcareous rocks’ (SWC); ‘Broadleaved woodlands on lime-rich and neutral mull soils’ (BWL) (corresponding to habitat types 4, 13, 43 in Fig. 1 in the main body of the study). Note that in five out of six cases habitat types contain higher proportion of species with ranges around the Northern Hemisphere than they share with two other habitat types from the same region.

	SSS	SWC	BWL	East Asia	North America
SSS		3.2%	39.5%	63.7%	49.2%
SWC	2.6%		52.3%	37.9%	10.5%
BWL	9.9%	16.2%		38.6%	17.4%

**Table S1b** Proportion of the most species-rich orders (and their respective families) in species pools of three habitat types of Dutch Angiosperms. Habitat types: ‘Submerged stonewort swards’ (SSS); ‘Stonecrop communities of weathered calcareous rocks’ (SWC); ‘Broadleaved woodlands on lime-rich and neutral mull soils’ (BWL) (habitat types 4, 13, 43 in Fig. 1 in the main body of the study). For each order, the family that is characteristic of a given habitat type is given in bold.

Taxon	SSS	SWC	BWL
<i>Alismatales</i>	0.274	0	0.016
Alismataceae	0.032	0	0
Araceae	0.048	0	0.008
Butomaceae	0.008	0	0
Hydrocharitaceae	0.032	0	0
Juncaginaceae	0.008	0	0.002
<b>Potamogetonaceae</b>	<b>0.137</b>	0	0.002
Ruppiaceae	0.008	0	0.002
Scheuchzeriaceae	0	0	0.002
<i>Poales</i>	0.282	0.196	0.202
<b>Poaceae</b>	0.057	<b>0.183</b>	<b>0.111</b>
<b>Cyperaceae</b>	<b>0.137</b>	0.013	<b>0.067</b>
Juncaceae	0.048	0	0.020
Typhaceae	0.040	0	0.004
<i>Asterales</i>	0.024	0.150	0.107
<b>Asteraceae</b>	0.016	<b>0.144</b>	<b>0.099</b>
Campanulaceae	0	0.007	0.008
Menyanthaceae	0.008	0	0
<i>Rosales</i>	0.008	0.078	0.075
<b>Rosaceae</b>	0.008	<b>0.078</b>	<b>0.065</b>
Cannabaceae	0	0	0.002
Elaeagnaceae	0	0	0.002
Rhamnaceae	0	0	0.002
Ulmaceae	0	0	0.004
<i>Caryophyllales</i>	0.032	0.105	0.069
Amaranthaceae	0	0	0.010
<b>Caryophyllaceae</b>	0	<b>0.092</b>	0.030
Polygonaceae	0.032	0.013	0.028
<i>Total</i>	0.621	0.529	0.469