

Appendix S7 The phylogenetic age structure of habitat species pools of Dutch angiosperms does not correspond to their mean lineage ages

If standardized mean lineage ages (*stMLAs*) captured variation in phylogenetic age structure in habitat species pools, we should expect habitats with highest *stMLAs* to show highest diversities of lineages (*stELDs*) dating back to the oldest epoch. We should also expect habitats with lowest *stMLAs* to show highest *stELDs* dating back to the youngest epoch. Indeed, we found that highest *stMLAs* of habitat species pools corresponded to highest *stELDs* from the oldest epoch (from root of the tree to 126 Ma; $r = 0.76$; Fig. S7(a)). However, for the second-oldest epoch (126 – 100 Ma) this very abruptly shifted to the strong negative relationship between *stMLAs* and *stELDs* ($r = -0.61$; Fig. S7(b)). For the following two epochs (100 – 33.9 Ma) there is no correlation between *stMLAs* and *stELDs* ($r = -0.03$ and 0.11 , respectively; Fig. S7(c) and Fig. S7(d)). During the remaining three epochs (33.9 Ma – present) high *stMLAs* again corresponded to low *stELDs*, however in an inverse order compared to the expectation ($r = -0.54$, -0.53 , and -0.38 , respectively). Obviously, phylogenetic age structures are much more complex than can be grasped from *stMLAs*. A habitat type can contain a species pool with lineages, which on average diversified early but nevertheless show distinct peaks of diversities of lineages dating back to much younger epochs and vice versa.

Figure S7 Relationship between standardized mean lineage ages (*stMLAs*) of habitat species pools of Dutch Angiosperms and the standardized epoch-specific lineage diversities (*stELDs*) during the first four geological epochs studied. *Epoch-specific lineage diversities* characterize the diversity of lineages a habitat harbours from a given epoch: (a) 164 – 126 Ma; (b) 126 – 100 Ma; (c) 100 – 66 Ma; (d) 66 – 33.9 Ma. Regressions (solid lines) are given. Note that the relationship between both variables does not change systematically from old to young epochs. Mean lineage age of a habitat type does not predict its phylogenetic structure, i.e. the *stELDs* across different epochs.

