

Antoine Lecerf, Guillaume Marie, John S. Kominoski, Carri J. LeRoy, Caroline Bernadet, and Christopher M. Swan. 2011. Incubation time, functional litter diversity, and habitat characteristics predict litter-mixing effects on decomposition. *Ecology* 92:160-169.

Appendix B. Quantification of functional litter diversity.

Specific litter degradability

Specific litter degradability (k) was estimated as the exponential daily decay constant for each litter species decomposing in isolation from each experiment.

$$MR = MR_0 e^{-kt} \quad , \text{ with } MR = \text{observed litter mass remaining at any time, } MR_0 \text{ the value at day 0 (theoretically equal to 1) and } t \text{ is the incubation time in days.}$$

Note: k -values were taken directly from studies or recalculated from litter mass remaining data using nonlinear regression.

FRci

Functional richness (FRci) was calculated as the range of trait values ($\ln k$) (Mason et al. 2005). It was scaled by the largest range for co-occurring riparian plants in natural habitats. We estimated the largest range of \ln -transformed degradability values to be 4.6, which corresponds to a two orders of magnitude difference between the highest and lowest exponential decay constants reported by Hladysz et al. (2008).

$$FRci = \frac{\max(\ln k) - \min(\ln k)}{4.6}$$

FRO

Functional regularity (FRO) is a measure of functional evenness for continuous traits (Mouillot et al. 2005). FRO reaches the maximal value of 1 when litter species are equally spaced along the $\ln(k)$ axis and have equal initial mass. Low FRO values denote uneven mixtures and/or irregularly spaced species.

$$FRO = \sum_{i=1}^{S-1} \min(PEW_{i,i+1}, \frac{1}{S-1})$$

$$\text{with } PEW_{i,i+1} = \frac{EW_{i,i+1}}{\sum_{i=1}^{S-1} EW_{i,i+1}} \quad , \quad EW_{i,i+1} = \frac{|\ln(k_{i+1}) - \ln(k_i)|}{(M_{i+1} + M_i)}$$

$PEW_{i,i+1}$ and $EW_{i,i+1}$ = weighted difference (for percentage and absolute value, respectively) in trait values of the nearest species along the trait axis.

S = species number

M_i = initial mass of litter species i in mixture

Note: FRO is not applicable to assemblages made with less than three species.

FDvar

Functional divergence (FDvar) is the homologue of the sum of squared deviations from the mean $\ln(k)$ values weighted by the relative litter mass prior to incubation in-stream (V). An arctangent transformation constrained the variation of FDvar within a 0-1 range (Mason et al. 2003).

$$FDvar = 0.5 \pi \arctan(5V)$$

$$\text{with } V = \sum_{i=1}^S MR_i (\ln k_i - \overline{\ln(k)})^2, \quad \overline{\ln(k)} = \sum_{i=1}^S M_i \ln(k_i)$$

FLD1 and FLD2

Because FRci, FRO, and FDvar were not independent of each other ($r = 0.14-0.90$, $P < 0.05$), we condensed information contained in these variables into two composite, orthogonal Functional Litter Diversity indices (FLD1 and FLD2) using Principal Components Analysis (PCA). A PCA was computed using Non-linear Iterative Partial Least Squares (NIPALS) algorithm in order to interpolate non-existing FRO values for two-species mixtures using least square fit. As a correlate of functional diversity indices, litter species richness was incorporated into the NIPALS PCA to optimize the interpolation process. This analysis was performed using the ‘ade4’ package in *R* (Dray and Dufour 2007).

FLD1 and FLD2 were the scores of the two first principal components summarizing most of information from the four diversity indices ($54.3 + 35.9 = 90.2\%$ of total variance). FLD1 captured cross-mixture variation in functional richness (loading = 0.97) and functional divergence (loading = 0.89) whereas FLD2 was consistent with cross-mixture variation in functional regularity (loading = 0.92). Litter species richness contributed equally to the definition of FLD1 (loading = 0.65) and FLD2 (loading = -0.64). Loadings indicate that litter species richness was correlated positively to FRci and FDvar (and thus FLD1) and negatively to FRO (and thus FLD2).

LITERATURE CITED

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