## Supplementary materials

Table S1: Activity of B-glucosidase (GLU), cellobiosidase (CEB), chitinase (CHI), and leucine-aminopeptidase (LAP) as well as decomposition rate constant $(k)$ and stabilization factor $(S)$ in unplanted soils exposed to three different flooding frequencies (monthly, weekly and daily), values are means and $S E(n=4)$. Values not connected by the same letter within one column are significantly different at $\mathbf{p} \leq 0.05$ based on Tukey's HSD tests. Corresponding one-way ANOVA results are included below ( $\mathbf{p}$-values bold typed at $\mathbf{p} \leq 0.05$ ).

| Flooding | GLU | CEB | CHI | LAP | $k$ | $S$ |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Monthly | $27.20 \pm 2.67 \mathrm{a}$ | $14.24 \pm 2.37 \mathrm{a}$ | $12.21 \pm 2.09 \mathrm{a}$ | $63.97 \pm 3.61 \mathrm{a}$ | $0.016 \pm 0.003 \mathrm{a}$ | $0.17 \pm 0.02 \mathrm{a}$ |  |  |
| Weekly | $24.26 \pm 4.93 \mathrm{a}$ | $12.30 \pm 1.86 \mathrm{a}$ | $11.32 \pm 2.51 \mathrm{a}$ | $55.09 \pm 10.53 \mathrm{a}$ | $0.012 \pm 0.003 \mathrm{a}$ | $0.17 \pm 0.01 \mathrm{a}$ |  |  |
| Daily | $32.32 \pm 10.78 \mathrm{a}$ | $12.29 \pm 3.48 \mathrm{a}$ | $11.95 \pm 2.65 \mathrm{a}$ | $56.40 \pm 8.16 \mathrm{a}$ | $0.010 \pm 0.000 \mathrm{a}$ | $0.10 \pm 0.02 \mathrm{a}$ |  |  |
| One-way ANOVA results |  |  |  |  |  |  |  |  |
|  | F | p | F | p | F | p |  |  |
|  |  |  |  |  |  |  |  |  |
| Flooding | 0.338 | 0.722 | 0.179 | 0.839 | 0.036 | 0.965 | 0.362 | p |

Table S2: Correlations between soil microbial C- and N-enzyme activities and litter-breakdown parameters. Shown are Pearson correlation coefficients ( $\mathbf{r}$ ). Significant ( $\mathbf{p} \leq 0.05$ ) correlations are highlighted in bold font.

|  | C activity | N activity | $\Delta$ C activity | $\Delta \mathrm{N}$ activity |  |
| :--- | ---: | ---: | ---: | ---: | :---: |
| Decomp. rate $(k)$ | $\mathbf{0 . 4 9}$ | 0.20 | $\mathbf{0 . 5 2}$ | $\mathbf{0 . 2 9}$ |  |
| Stabilization $(S)$ | -0.10 | -0.08 | -0.04 | -0.04 |  |
| $\Delta k$ | $\mathbf{0 . 3 9}$ | 0.04 | $\mathbf{0 . 4 1}$ | 0.20 |  |
| $\Delta S$ | -0.22 | $\mathbf{- 0 . 3 4}$ | -0.22 | -0.27 |  |

Notes: C activity = sum of C-acquisition enzyme activities ( $\beta$-glucosidase + cellobiosidase); N activity $=$ sum of N -acquisition enzyme activities (aminopeptidase + chitinase); Decomp. rate ( $k$ ) = decomposition rate constant (sensu Keuskamp et al. 2013); Stabilization ( $S$ ) = stabilization factor (sensu Keuskamp et al. 2013); $\Delta=$ activity values in relation to the unplanted control (i.e. percentage change of planted vs. unplanted mesocosms) reflecting plant effects independent of direct (i.e. non-plant mediated) flooding effects.


Figure S1: NMDS plot showing prokaryotic (bacterial + archaeal) community composition in soils planted with intolerant and tolerant plant genotypes of Elymus athericus exposed to three different flooding frequencies (monthly, weekly, and daily). Plot shows all technical replicates (i.e. two samples from $\mathbf{n}=\mathbf{3}$ mesocosms). The ID showing labels (1-18) and technical-replicate labels (1 or _2).


Figure S2: Activities of the exo-enzymes B-glucosidase (A) and cellobiosidase (B) (microbial C acquisition) as well as chitinase ( $C$ ) and leucine-aminopeptidase ( $D$ ) (microbial $\mathbf{N}$ acquisition) in mesocosms containing soils without plants exposed to three different flooding frequencies (monthly, weekly and daily). Values are means and $\mathrm{SE}(\mathrm{n}=4)$ ). No significant differences at $\mathbf{p} \leq 0.05$ based on Tukey's HSD were detected.


Figure S3: CCA plot showing the relation of microbial community composition to plant biomass, microbial enzyme activity, and litter decomposition parameters. Notes: $\mathbf{A G B}=$ aboveground biomass, BGB $=$ belowground biomass, GLU $=$ Bglucosidase, $\mathrm{CEB}=$ cellobiosidase, $\mathrm{CHI}=$ chitinase, $\mathrm{LAP}=$ leucine-aminopeptidase, $k=$ initial decomposition rate constant, $S=$ stabilization factor. ANOVA-like permutation tests for Constrained Correspondence Analysis: AGB: $F=1.72, p=0.001$; BGB: $F=1.70, p=0.001 ;$ GLU: $F=1.41, p=0.003 ;$ CEB: $F=1.18, p=0.073 ;$ CHI: $F=1.44, p=0.001 ;$ LAP: $F=1.35, p=$ $0.005 ; k: \mathrm{F}=1.31, \mathrm{p}=0.015 ; S: \mathrm{F}=1.42, \mathrm{p}=0.003$




Figure S4: Relative abundance of different microbial lineages. Along the horizontal axis samples are arranged according to tolerant (TG) and intolerant (IG) plant genotypes of the Elymus athericus exposed to three different flooding frequencies. The rank order along the vertical axis is shown for the class (A), order (B) and phylum (C).


Figure S5: NMDS plot showing prokaryotic (bacterial + archaeal) community composition in mesocosms containing soils without plants exposed to three different flooding frequencies (monthly, weekly and daily). One-way PERMANOVA results are included.

