Additional background information to

Reconciling complexity with stability in naturally assembling food webs

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This information is provided to facilitate the calculation of the (Jacobian) community matrices analysed in the Letter.

In the Supplementary Information of this Letter[1], no biomass data were given of the two basal food-web compartments: Roots and Detritus. These were not measured in the soil samples (see also ref 2). Following ref 2, we used values for Root biomass of 900 kg ha^{-1} in all webs with roots present. We used values for Detritus biomass of 4, 25, 250 and 2500 kg ha^{-1} for the successional stages 1 to 4 respectively, of both series (roughly corresponding to the increase in organic matter along the productivity gradients). We assumed the same values for the replicates within each stage. (Exception: in the one replicate in stage 1 (Schiermonnikoog) where phytophageous nematodes were present, basal values of stage 2 were used.) The choice of these particular values by no means affects our key findings.

The data to do the stability analyses are either directly provided in the Letter or the Supplementary Information to the Letter, or they can be obtained through references in the Letter (ref 2 and 17). To make this latter information easier accessible, we here present the estimated physiological parameter values (Added Table 1), the matrix of feeding relations and prey preferences (Added Table 2), and formalisation of detritus feedbacks. We also provide the Jacobian matrix of one of the food webs, as an example (Added Table 3).

Added Table 1 gives the estimated values of specific natural (i.e. non-predatory) death rates, assimilation efficiencies, and production efficiencies. The conversion efficiency used to calculate feeding rates (see Methods of our Letter[1]) and interaction strengths, is the product of the assimilation efficiency and production efficiency: $e_i = e_i^{ass} e_i^{prod}$. Assimilation efficiencies were used to determine the fraction of unassimilated food in each predator-prey interaction, needed to calculate the feedbacks to detritus (see below).

Added Table 2 specifies the diet choice in terms of prey preferences p_{ij} of predators (columns) for their prey (rows). For the use of these preference factors in the calculation of feeding rates, see Methods of our Letter[1]. Note that in Fig. 1 of the Letter an arrow is missing between Bacterivorous Nematodes (nr. 5) and Predatory Collembolans (nr.17). This is a typographic error. Supplementary Table 1 of the Letter[1] (biomass data of the observed groups) can be used to determine the structure of each web; for groups not present the corresponding rows and columns in Added

Table 2 are to be deleted. Biomass densities of Detritus and Roots are not given in Supplementary Table 1; Detritus was present in all webs, and Roots were present in the webs where Phytophageous Nematodes were present (see for illustration also Figure 1 of the Letter[1]).

The parameter values given in Added Table 1 and 2 are those as used by De Ruiter *et al.*[2].

Added Table 3 presents an example of a community matrix. The procedure for deriving the matrix element values referring to the effects of predators on their prey and vice versa (the interaction strengths in the food web) is explained in Methods. Biomassses of the trophic groups are given in Supplementary Table 1. Note that the diagonal elements referring to intra-specific competition of the organisms were not determined from the observations, but modelled as a fraction (s) of total natural mass-specific death (d_i), where s was determined in the stability calculations. In the example in Table 3, the total mass-specific death rates are given as the (baseline) diagonal elements (i.e. $-d_i$).

Feedbacks to detritus were modelled as in De Ruiter *et al.*[2], with a modified Lotka-Volterra equation for detritus[3], sensu DeAngelis *et al.*[4]:

$$\frac{dX_D}{dt} = R_D + \sum_{i=1}^{n} d_i X_i + \sum_{i=1}^{n}\sum_{j=1}^{n}(1 - e_j^{ass})\, c_{ij} X_i X_j - \sum_{j=1}^{n} c_{Dj} X_D X_j\,, \qquad (1)$$

where X_i is the density of species i, R_D is the input of allochtonous material, e_j^{ass} is the assimilation efficiency of group j ($0 < e_j^{ass} < 1$), c_{ij} is the coefficient of predation on group i by group j, d_i is the specific non-predatory death rate of group i, $i \neq j$ and all parameters are defined to be positive. Elements of the community matrix referring to the feedbacks to detritus are the partial derivatives of equation (1) with respect to this trophic group, near equilibrium.

In terms of mass-specific predation rates in equilibrium f_{ij} and observed biomass densities B_i (see Methods), the effect of a population i on detritus is $\alpha_{Di} = d_i + \sum_{j=1}^{n}\left(1 - e_i^{ass}\right) f_{ji} + \sum_{j=1}^{n}\left(1 - e_j^{ass}\right) f_{ij} \frac{B_j}{B_i} - f_{Di}$. The effect of detritus on itself (diagonal element) is $\alpha_{DD} = -\sum_{j=1}^{n} e_j^{ass} f_{Dj} \frac{B_j}{B_D}$.

References

1. Neutel A. M., Heesterbeek, J.A.P., van de Koppel, J., et al. Reconciling complexity with stability in naturally assembling food webs. *Nature* **449** (7162): 599-602 (2007).

2. de Ruiter, P. C., Neutel, A. M. & Moore, J. C. Energetics, patterns of interaction strengths, and stability in real ecosystems. *Science* **269**, 1257-1260 (1995).

3. Moore, J. C., de Ruiter, P. C. & Hunt, H. W. Influence of productivity on the stability of real and model ecosystems. *Science* **261**, 906-908 (1993).

4. DeAngelis, D. L., Mulholland, P. J. & Palumbo A. V, Steinman, Huston, A. D. et al. Nutrient dynamics and food-web stability. Ann. Rev. Ecol. Sys. **20**, 71-95 (1989).

Added Table 1. Estimated values of physiological parameters

Functional group	Specific death rate d_i (year^{-1})	Assimilation efficiency e_i^{ass}	Production efficiency e_i^{prod}
Predatory mites	1.84	0.60	0.35
Predatory collembolans	1.84	0.50	0.35
Nematode feeding mites	1.84	0.90	0.35
Predatory nematodes	3.00	0.50	0.37
Amoebae	6.00	0.95	0.40
Collembolans	1.84	0.50	0.35
Cryptostigmatic mites	1.20	0.50	0.35
Noncryptostigmatic mites	1.84	0.50	0.35
Fungivorous nematodes	1.92	0.38	0.37
Bacteriophageous mites	1.84	0.50	0.35
Bacteriophageous nematodes	2.68	0.60	0.37
Flagellates	6.00	0.95	0.40
Phytophageous Nematodes	1.08	0.25	0.37
Saprophytic fungi	1.20	1.00	0.30
Bacteria	1.20	1.00	0.30
Roots	1.00	-	-
Detritus	N/A	N/A	N/A

Added Table 2. Feeding relations and prey preferences

	Prmi	Prco	Nemi	Prne	Amoe	Coll	Cryp	Ncry	Fune	Bami	Bane	Flag	Phne	Fung	Bact	Root	Detr
Prmi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prco	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nemi	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Prne	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Amoe	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0
Coll	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cryp	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ncry	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fune	1	1	1	1000	0	0	0	0	0	0	0	0	0	0	0	0	0
Bami	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bane	1	1	1	1000	0	0	0	0	0	0	0	0	0	0	0	0	0
Flag	0	0	0	10	1	0	0	0	0	0	0	0	0	0	0	0	0
Phne	1	1	1	1000	0	0	0	0	0	0	0	0	0	0	0	0	0
Fung	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0
Bact	0	0	0	1	1	0	0	0	0	1	1	1	0	0	0	0	0
Root	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Detr	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0

For explanation of abbreviated names, see Added Table 1 (The order of the groups is as in Added Table 1).

Added Table 3. Community matrix of Schiermonnikoog, Stage 3, replicate food web nr 2 (example)

	Prmi	Nemi	Prne	Amoe	Coll	Cryp	Ncry	Fune	Bane	Flag	Phne	Fung	Bact	Root	Detr
Prmi	-1.84	0.13	0.063	0	0.13	0.13	0.13	0.063	0.063	0	0.063	0	0	0	0
Nemi	-0.11	-1.84	0.011	0	0	0	0	0.011	0.011	0	0.011	0	0	0	0
Prne	-0.12	-0.78	-3.00	0.0031	0	0	0	0.31	0.31	0.0031	0.31	0	0.00031	0	0
Amoe	0	0	-0.24	-6.00	0	0	0	0	0	0.052	0	0	0.052	0	0
Coll	-2.3	0	0	0	-1.84	0	0	0	0	0	0	0.65	0	0	0
Cryp	-1.4	0	0	0	0	-1.20	0	0	0	0	0	0.30	0	0	0
Ncry	-3.8	0	0	0	0	0	-1.84	0	0	0	0	1.1	0	0	0
Fune	-0.29	-1.8	-3.9	0	0	0	0	-1.9	0	0	0	0.27	0	0	0
Bane	-0.81	-5.1	-11	0	0	0	0	0	-2.68	0	0	0	0.018	0	0
Flag	0	0	-0.073	-0.041	0	0	0	0	0	-6.00	0	0	0.016	0	0
Phne	-0.0011	-0.0068	-0.015	0	0	0	0	0	0	0	-1.08	0	0	0.00000021	0
Fung	0	0	0	0	-14	-10	-14	-28	0	0	0	-1.20	0	0	0.014
Bact	0	0	-2.8	-16	0	0	0	0	-21	-16	0	0	-1.20	0	0.068
Root	0	0	0	0	0	0	0	0	0	0	-33	0	0	-1.00	0
Detr	5.3	2.9	12	6.8	9.0	6.6	9.0	20	12	6.8	27	-41	-3.6	1.0	-0.27

For explanation of abbreviated names, see Added Table 1 (The order of the groups is as in Added Table 1).