#### **Biotic stability mechanisms in Inner Mongolian grassland**

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*Proceedings of the Royal Society B: Biological Sciences, 2020, dio:10.1098/rspb.2020.0675*

# **Supplementary Information**

Appendixes: Appendix 1-2

Supplementary References

Supplementary Tables: Table S1-S3

Supplementary Figures: Figure S1-S10

### **Appendix 1**

### **Mathematical derivation**

# **1.1 Relating the community temporal coefficient of variation to the species synchrony and the weighted average species temporal coefficient of variation**

In this part, we briefly introduce the mathematical derivation for relating the community temporal coefficient of variation (abbreviated as CV, inverse of temporal stability) to the species synchrony and the weighted average species temporal CV used in the current study and refer readers to papers of Loreau and de Mazancourt [1] and Thibaut and Connolly [2] for further details. We used the superscript *C* and *S* to designate the communitylevel and the species-level quantities. Following previous theoretical works [2–4], we consider a community which includes *n* species and reached a stationary state. Thus, this community can be described with a vector of temporal mean species abundances with elements  $u(s_i)$ , i.e. the temporal mean abundance of species  $i$ , and a temporal variance– covariance matrix of species abundances with elements  $v(s(i, j) = cov(u(s(i), u(s(j))),$  i.e. the covariance between temporal abundances of species *i* and *j*. We next define the temporal mean of the community abundance (*uC*) and the temporal variance of total community abundance (*vC*) as follows:

$$
u^{C} = \sum_{i} u^{S}(i)
$$
 (eqn. S1a)  

$$
v^{C} = \sum_{i,j} v^{S}(i,j)
$$
 (eqn. S1b)

Thus, the community temporal CV can be described as follows:

$$
(CV^{C})^{2} = \frac{v^{C}}{(u^{C})^{2}} = \frac{\sum_{i,j} v^{S}(i,j)}{(\sum_{i} \sqrt{v^{S}(i,i)})^{2}} \left(\sum_{i} \frac{u^{S}(i)}{u^{C}} \frac{\sqrt{v^{S}(i,i)}}{u^{S}(i)}\right)^{2}
$$
(eqn. S2)

Referenced to more recent theoretical works, two terms on the far right-hand side of eqn. S2 were defined as the species synchrony and the weighted average species temporal CV [1,2], which have the following descriptions:

$$
\varphi = \frac{\sum_{i,j} v^S(i,j)}{\left(\sum_i \sqrt{v^S(i,i)}\right)^2} \tag{eqn. S3}
$$

$$
\left(\widetilde{CV}^S\right)^2 = \left(\sum_i \frac{u^S(i)}{u^C} \frac{\sqrt{v^S(i,i)}}{u^S(i)}\right)^2 = \left(\sum_i \frac{u^S(i)}{u^C} CV^S(i)\right)
$$
\n(eqn. S4)

Thus, the community temporal CV can also be described as follows:

$$
(\mathcal{C}V^{\mathcal{C}})^2 = \varphi \left(\widetilde{\mathcal{C}V}^S\right)^2 \tag{eqn. S5}
$$

# **1.2 Relating the weighted average species temporal coefficient of variation to the mean**– **variance scaling effect and the overyielding effect**

Here, we briefly review the derivations for relating the weighted average species temporal CV to the mean–variance scaling effect and the overyielding effect and refer readers to theoretical work of Thibaut and Connolly [2] for further details. These derivations base on two assumptions. The first assumption is that species temporal variances scale with their temporal means according to the Taylor's power law [5], which represents the mean–variance scaling effect and can be described as the following:

$$
v^{S}(i,i) = a (u^{S}(i))^{Z}
$$
 (eqn. S6)

Here, *a* and *z* are parameters relating variance to mean abundance of species *i*. The second assumption is that species and community mean may vary as a function of species richness, which represent the overyielding effect and can be modeled with the following description

[2,3]:

$$
u^C = \sum_i u^S(i) = \sum_i \frac{u_1^S(i)}{n^x}
$$
 (eqn. S7)

Here,  $u_1^s(i)$  is the abundance of the *i*th species in monoculture, *n* is the total species in the community, and *x* describes how the total community abundance changes with the species richness. If  $0 < x < 1$ , the total community abundance increases with increasing species richness, resulting in the overyielding effect. If  $x > 1$ , the total community abundance decreases with the increasing species richness (underyielding) [2,3].

We substitute the right-hand sides of eqn. S6 and eqn. S7 for  $v_s(i, i)$  and  $uc$  in eqn. S4. Then, we have the following descriptions and derivations:

$$
\widetilde{CV}^S = \frac{\sum_i \sqrt{v^S(i,i)}}{\sum_i u^S(i)} = \frac{\sum_i \sqrt{a(u^S(i))^Z}}{\sum_i u^S(i)} = \frac{\sum_i \sqrt{a(\frac{u_1^S(i)}{n^X})^2}}{\sum_i \frac{u_1^S(i)}{n^X}} = \frac{\sqrt{\left(\frac{1}{n^X}\right)^2}}{\frac{1}{n^X}} \frac{\sum_i \sqrt{a(u_1^S(i))^2}}{\sum_i u_1^S(i)}
$$
(eqn. S8)

For the far right-hand side of eqn. S8, we simplify its left fraction and derive its right fraction to have the following descriptions:

$$
\widetilde{CV}^S = \frac{n^{\frac{-xz}{2}}}{n^{-x}} \sum_{i} \frac{u_1^S(i)}{\sum_i u_1^S(i)} \frac{\sqrt{a(u_1^S(i))^z}}{u_1^S(i)} = \sqrt{n^{(2-z)x}} \sum_{i} \frac{u_1^S(i)}{\sum_i u_1^S(i)} \frac{\sqrt{v_1^S(i,i)}}{u_1^S(i)} = \sqrt{n^{(2-z)x}} \widetilde{CV}_1^S \qquad \text{(eqn. S9)}
$$

Then, we substitute the right-hand side of the eqn. S9 into eqn. S5 to obtain the following equation:

$$
(CV^{c})^{2} = \varphi \left(\sqrt{n^{(2-z)x}} \widetilde{CV}_{1}^{S}\right)^{2}
$$
 (eqn. S10)

Eqn. S9 and S10 suggest that the mean–variance scaling effect and the overyielding effect can interactively influence the dependences of the weighted average species temporal CV and the community temporal CV on the species richness. These two equations also

suggest that the effect of species richness on the weighted average species temporal CV will be eliminated if the *z* is close to 2.

## **1.3 Partitioning the species synchrony into different abundances species groups**

Eqn. S2 (eqn. 1a of the main text) showed that the *v<sup>C</sup>* can be descripted with the covariance between species *i* and *j*, which facilitates estimations of the effects of different abundance groups on species synchrony. Here, we introduce three vectors, *dS*, *c<sup>S</sup>* and *rS*, to represent the dominant species, common species and rare species of the community, respectively. We used *d<sup>S</sup>* as example to explain these vectors. The length of *d<sup>S</sup>* is same to the species number of the community (*n*) and has elements *dS*(*i*), i.e. the *i*th species of the community. The *dS*(*i*) was set to 1 if the *i*th species of the community is a dominant species, otherwise, it was set to 0. Similar procedures were used to conduct the *c<sup>S</sup>* and *rS*, in which common species and rare species were set to 1, respectively, otherwise they were set to 0. With these vectors, the species synchrony (eqn. S3) can be described as follows:

$$
\varphi = \frac{\sum_{i,j} d^{S}(i) d^{S}(j) v^{S}(i,j)}{\left(\sum_{i} \sqrt{v^{S}(i,i)}\right)^{2}} + \frac{\sum_{i,j} d^{S}(i) c^{S}(j) v^{S}(i,j)}{\left(\sum_{i} \sqrt{v^{S}(i,i)}\right)^{2}} + \frac{\sum_{i,j} d^{S}(i) r^{S}(j) v^{S}(i,j)}{\left(\sum_{i} \sqrt{v^{S}(i,i)}\right)^{2}} + \frac{\sum_{i,j} c^{S}(i) c^{S}(j) v^{S}(i,j)}{\left(\sum_{i} \sqrt{v^{S}(i,i)}\right)^{2}} + \frac{\sum_{i,j} c^{S}(i) r^{S}(j) v^{S}(i,j)}{\left(\sum_{i} \sqrt{v^{S}(i,i)}\right)^{2}} + \frac{\sum_{i,j} r^{S}(i) r^{S}(j) v^{S}(i,j)}{\left(\sum_{i} \sqrt{v^{S}(i,i)}\right)^{2}} \tag{eqn. S11a}
$$

Using  $\varphi_{dd}$ ,  $\varphi_{dc}$ ,  $\varphi_{dr}$ ,  $\varphi_{cc}$ ,  $\varphi_{cr}$  and  $\varphi_{rr}$  to represent the six components on the right-hand side of the eqn. S11a, this equation can be described as follows:

$$
\varphi = \varphi_{dd} + \varphi_{dc} + \varphi_{dr} + \varphi_{cc} + \varphi_{cr} + \varphi_{rr}
$$
 (eqn. S11b)

Considering that these six components have the same denominator, we use the numerator to explain them. For example, the first term,  $\sum_{i,j} d^S(i) d^S(j) v^S(i,j)$ , will only contribute the species synchrony if both species *i* and *j* are dominant species. Thus, this term represents the contributions of the dynamics between dominant species to the communitywide species synchrony. Similar explanations can also be used for the other components. For the following five terms, they represent the contributions of the dynamics between dominant species and common species, between dominant species and rare species, between common species, between common and rare species and between rare species to the community-wide species synchrony.

# **1.4 Partitioning the weighted averaged species temporal coefficient of variation into**

# **different abundances species groups**

Using the vectors, *dS*, *c<sup>S</sup>* and *rS*, mentioned previously, we can rewrite the eqn. S4 as follows:

$$
\widetilde{CV}^S = \sum_i d^S(i) \frac{u^S(i)}{u^C} \frac{\sqrt{v^S(i,i)}}{u^S(i)} + \sum_i c^S(i) \frac{u^S(i)}{u^C} \frac{\sqrt{v^S(i,i)}}{u^S(i)} + \sum_i r^S(i) \frac{u^S(i)}{u^C} \frac{\sqrt{v^S(i,i)}}{u^S(i)} \qquad \text{(eqn. S12a)}
$$

Here, we use  $\widetilde{CV}_d^S$ ,  $\widetilde{CV}_c^S$  and  $\widetilde{CV}_r^S$  to represent the three components on the right-hand side of the eqn. S12a, and thus, this equation can be rewritten as follows:

$$
\widetilde{CV}^S = \widetilde{CV}_d^S + \widetilde{CV}_c^S + \widetilde{CV}_r^S \tag{eqn. S12b}
$$

For the first term on the right-hand side of the eqn. S12, the non-zero elements are composed of only temporal CV of dominant species. Thus, it represents the contribution of the dominant species group to the weighted average species temporal CV of the community. For the following two terms, they represent contributions of the common and rare species groups to the weighted average species temporal CV of the community.

## **Appendix 2**

# **Statistical analyses for constructing the initial Structure Equation Model**

Based on a-priori hypotheses, the exploration of the correlation matrix of directly measured and derived variables and results of multiple linear regressions, we constructed Structure Equation Models (SEMs). We deliberately stayed as close as possible to a-priori hypotheses about causal relationships and fitted models even if they included non-significant relationships but reflected pathways proposed to be essential biotic stability mechanisms (for example see models presented in Thibaut & Connolly [2] and Hallett et al. [6]). Model-fit statistics such as Chi-square tests or goodness-of-fit index (GFI), which compare the deviation of a current SEM to a full SEM without residual degrees of freedom, were only used as an additional guide to avoid searching for a best model post hoc. Symbols and their descriptions can be found in the following box (Box 1).



The following statistical analyses were used to relate the community temporal CV to biotic stability mechanisms, climatic factors and species diversity indices. Based on the results shown in the correlation matrix and simple linear regressions, we investigated the effects of multiple explanatory variables reflecting biotic stability mechanisms on community temporal CV (*CVC*) with two general linear models. Model 2.1.1 showed that growing-season precipitation (*MGP*), mean-variance scaling power (*z*), weighted average species temporal CV  $(\widetilde{CV}^s)$  and species synchrony ( $\varphi$ ), fitted in this sequence, all significantly affected the community temporal CV (*CVC*). All these variables were also part of the initial a-priori SEM model (Table S3, Figure S6). In model 2.1.2, the growing-season precipitation (*MGP*) and the mean-variance scaling power (*z*) were fitted after the weighted average species temporal CV  $(\widetilde{CV}^s)$  and the species synchrony ( $\varphi$ ), which explained their effects such that they lost significance. In terms of path analysis this means that the growing-season precipitation (*MGP*) and the mean-variance scaling power (*z*) affected the community temporal CV (*CVC*) indirectly via the weighted average species temporal CV ( $\widetilde{CV}^s$ ) and species synchrony ( $\varphi$ ), which in turn had direct effects on the community temporal CV.

*Model 2.1.1:*  $CVc \sim MGP + z + \widetilde{CV}^s + \omega$ 

Analysis of variance table for Model 2.1.1:								
	Df	Sum Sq	$P$ -value					
MGP		0.1248	0.1248	39.2071	$0.001$ ***			
Z.		0.1475	0.1475	46.3239	$0.001$ ***			
$\tilde{CV}^s$		0.0286	0.0286	8.9845	$0.008**$			
$\varphi$		0.1338	0.1338	42.0269	$0.001$ ***			
Residuals	18	0.0573	0.0032					
Significance level: '***' $P < 0.001$ , '**' $P < 0.01$								

Analysis of variance table for Model 2.1.2:									
	Df	Sum Sq $F$ -value $P$ -value Mean Sq							
$\widetilde{CV}^s$		0.2440	0.2440	76.6494	*** < 0.001				
$\varphi$		0.1851	0.1851	58.1417	*** < 0.001				
MGP		0.0040	0.0040	1.2449	0.279				
		0.0016	0.0016	0.5064	0.486				
Residuals	18	0.0573	0.0032						
Significance level: '***' $P < 0.001$									

*Model 2.1.2:*  $CVc \sim \widetilde{CV}^s + \omega + MGP + z$ 

We then explored explanatory variables predicted to affect the weighted average species temporal CV ( $\widetilde{CV}^s$ ) (Model 2.1.3 and Model 2.1.4). Biodiversity has been proposed as one such explanatory variable (see e.g. Thibaut & Connolly [2]) and we therefore included it as either the species richness (*n*) or the effective species richness (*D*). We also included the growing-season precipitation (*MGP*) as it can be expected to positively affect the species richness (*n*) or the effective species richness (*D*) (see e.g. studies of Ma et al. [7] and Hallett et al. [6] and Table 1). Comparing model 2.1.3 with model 2.1.4, we found that the effective species richness (*D*) had stronger explanatory power than the species richness (*n*). Thus, we only used the effective species richness (*D*) as biodiversity measure in SEMs. Furthermore, we found that changing the fitted sequence of growing-season precipitation (*MGP*), effective species richness (*D*) and mean-variance scaling power (*z*) (Model 2.1.4 and Model 2.1.5) results in a non-significant effect of effective species richness (*D*) on the weighted average species temporal CV ( $\widetilde{CV}^s$ ), suggesting that the effective species richness (*D*) is less important than growing-season precipitation (*MGP*) and mean-variance scaling power (*z*) in affecting the weighted average species temporal CV ( $\widetilde{CV}^s$ ).

Analysis of variance table for Model 2.1.3: Df Sum Sq Mean Sq *F*-value *P*-value *MGP* 1 0.1003 0.1003 6.4786 0.02 \* *n* 1 0.1798 0.1798 11.6164 0.003 \*\* *z* 1 0.3089 0.3089 19.9628 < 0.001 \*\*\* *Residuals* 19 0.2940 0.0155 Significant level: '\*\*\*' *P* < 0.001, '\*\*' *P* < 0.01, '\*' *P* < 0.05

*Model 2.1.3:*  $\widetilde{CV}^s \sim MGP + n + z$ 

*Model 2.1.4:*  $\widetilde{CV}^S \sim MGP + D + z$ 

Analysis of variance table for Model 2.1.4:										
	Df	$F$ -value Sum Sq $P$ -value Mean Sq								
MGP		0.1003	0.1003	7.4247	$0.013*$					
		0.2147	0.2147	15.9015	*** < 0.001					
		0.3115	0.3115	23.0645	*** < 0.001					
Residuals	19	0.2566	0.0135							
Significant level: '***' $P < 0.001$ , '*' $P < 0.05$										

*Model 2.1.5:*  $\widetilde{CV}^S \sim z + D + MGP$ 



Furthermore, we investigated explanatory variables predicted to affect  $\varphi$ . Besides biodiversity (effective species richness, *D* and species richness, *n*) we expected a positive influence of the interannual variation in precipitation ( $CV<sub>MGP</sub>$ ) on the species synchrony ( $\varphi$ ). We found that species synchrony was significantly affected by effective species richness (*D*) (Model 2.1.7), but independent of the species richness (*n*) (Model 2.1.6). In addition, we founded that changing the fitted sequence of interannual variation in precipitation (*CVMGP*)

and effective species richness (*D*) (Model 2.1.7 and Model 2.1.8) had no effects on their significances in influencing the species synchrony  $(\varphi)$ . Therefore, we used the interannual variation in precipitation (*CVMGP*) and the effective species richness (*D*) in SEMs.

*Model 2.1.6:*  $\varphi \sim CVMGP + n$ 

Analysis of variance table for Model 2.1.6:										
	Df	Sum Sq <i>F</i> -value Mean Sq $P$ -value								
$CV_{MGP}$		0.1668	0.1668	10.1484	$0.005**$					
n		0.0186	0.0186	1.1334	0.300					
Residuals	20	0.3287	0.0164							
Significant level: '**' $P < 0.01$										

*Model 2.1.7:*  $\varphi \sim CVMGP + D$ 

Analysis of variance table for Model 2.1.7:							
	Df	Sum Sq	Mean Sq	$F$ -value	$P$ -value		
$CV_{MGP}$		0.1668	0.1668	14.3938	$0.001**$		
		0.1156	0.1156	9.9742	$0.005$ **		
Residuals	20	0.2317	0.0116				
Significant level: '**' $P < 0.01$							

*Model 2.1.8:*  $\varphi \sim D + CVMGP$ 



Owing to the interannual variation in precipitation (*CVMGP*) and the effective species richness (*D*) have not been included in Model 2.1.1 and Model 2.1.2, we furtherly examined whether they only have indirect effects on the community temporal CV (*CVC*) via the species synchrony  $(\varphi)$  with Model 2.1.9–2.1.11. These three models showed non-significant effects of the interannual variation in precipitation (*CVMGP*) and the effective species richness (*D*) and significant effect of the species synchrony on the community temporal CV (*CVC*) no matter with the fitted sequence. In addition, our correlation (Figure 1) and regression (Figure 2) analyses also showed that the interannual variation in precipitation (*CVMGP*) and the effective species richness (*D*) had non-significant effects on the community temporal CV (*CVC*) but significant effects on the species synchrony  $(\varphi)$ , suggesting their indirect effects on the community temporal CV  $(CVc)$  via the species synchrony  $(\varphi)$ .

*Model 2.1.9:*  $CVc \sim \varphi + CV_{MGP} + D$ 

Analysis of variance table for Model 2.1.9:									
	Df $P$ -value Sum Sq Mean Sq $F$ -value								
$\varphi$		0.1449	0.1449	8.230	$0.010**$				
CV <sub>MGP</sub>		0.0055	0.0055	0.311	0.583				
		0.0070	0.0070	0.397	0.536				
Residuals	19	0.3346	0.0176						
Significant level: '**' $P < 0.01$									

*Model 2.1.10:*  $CVc \sim CV_{MGP} + D + \varphi$ 

Analysis of variance table for Model 2.1.10:								
	Df Sum Sq $F$ -value Mean Sq $P$ -value							
$CV_{MGP}$		0.0243	0.0243	1.382	0.025			
		0.0187	0.0187	1.059	0.316			
$\varphi$		0.1144	0.1144	6.497	$0.020*$			
Residuals	19	0.3346	0.0176					
Significant level: "*' $P < 0.05$								

*Model 2.1.11:*  $CVc \sim D + CV<sub>MGP</sub> + \varphi$ 





Above analyses were carried out with all species or only the dominant species

included in biodiversity measures and derived explanatory variables.

### **Supplementary references**

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# **Supplementary Tables**

**Table S1** Site characteristics. The geographical location (LAT for latitude and LON for longitude), vegetation type, mean annual precipitation (*MAP*), mean growing-season precipitation (*MGP*), mean annual air temperature (*MAT*), mean growing-season temperature (*MGT*), mean community biomass, species richness and dominant species with their Latin names, functional groups and relative species biomass (*RSB*) for each site have been shown.









Site <i>F</i> -value	$P$ -value		Site $F$ -value	$P$ -value		Site <i>F</i> -value	$P$ -value
S01 $F_{1,2} = 61.66$	0.02	S <sub>09</sub>	$F_{1,2} = 0.36$	0.61		S17 $F_{1,3} = 3.36$	0.16
S02 $F_{1,1} = 0.46$	0.62	S <sub>10</sub>	$F_{1,3} = 2.64$	0.20		$S18$ $F_{1,3} = 0.11$	0.76
S03 $F_{1,3} = 5.25$	0.11	S11	$F_{1,3} = 1.92$	0.26		S19 $F_{1,3} = 2.60$	0.21
S04 $F_{1,3} = 2.39$	0.22		$S12 \tF_{1,2} = 0.79$	0.47	S <sub>20</sub>	$F_{1,3} = 1.97$	0.26
S05 $F_{1,2} = 0.56$	0.53	S <sub>13</sub>	$F_{1,2} = 0.14$	0.75	S21	$F_{1,3} = 1.12$	0.37
S06 $F_{1,2} = 0.76$	0.48	S <sub>14</sub>	$F_{1,3} = 4.90$	0.11		$S22 \quad F_{1,3} = 0.14$	0.73
S07 $F_{1,3} = 0.34$	0.60		S15 $F_{1,2} = 5.65$	0.14		S23 $F_{1,1} = 45.85$	0.09
S08 $F_{1,3} = 3.11$	0.18		$S16 \tF_{1,2} = 0.03$	0.88			

**Table S2.** Results (*F*-values) of the linear regression between community biomass and the sampling year for each site. No detrending was done because only 1 of the 23 sites showed a significant linear relationship.





# **Supplementary Figures**



Figure S1. Geographical distribution of study sites and vegetation map of the natural temperate steppes of Inner Mongolia. Site numbers are shown in this figure.



Figure S2. Descending order of relative species biomass, based on data of all species recorded in each site during 2012-2016.



**Figure S3.** Time series of plant species biomass in each site.



**Figure S4.** Mean-variance scaling relationship (showed by solid line) in each site.



**Figure S5.** Community biomass in relation to species richness in each site. Results of regression analyses are showed in each subfigure. The solid lines represent significant (*P* < 0.05) linear relationships between variables, and the dashed grey lines represent nonsignificant  $(0.05 < P < 0.10)$  linear relationships between variables.



**Figure S6.** The initial structural equation model. This model considered the effects of abiotic factors, e.g. the growing-season precipitation and its interannual variation (estimated with the temporal coefficient of variation (CV)), biotic factor, e.g. effective species richness, and biotic mechanisms, e.g. the mean–variance scaling, the weighted average species temporal CV and the species synchrony, on the community temporal CV via all pathways derived from correlation matrix, simple linear regressions and statistical analyses in Appendix 2.



**Figure S7.** The weighted average species temporal coefficient of variation (CV) in relation to the weighted average dominant (a), common (b) and rare (c) species temporal CVs. Results of linear regression analyses are showed in each scatter plot. Black solid lines represent significant linear relationships ( $P < 0.05$ ) and grey dashed line represents non-significant linear relationships  $(P > 0.05)$ .



**Figure S8.** The species synchrony in relation to the synchrony between dominant species (a), between dominant and common species (b), between dominant and rare species (c), between common species (d), between common and rare species (e) and between rare species (f). Results of linear regression analyses are showed in each scatter plot. Black solid line represents significant linear relationships  $(P < 0.05)$  and grey dashed lines represent nonsignificant linear relationships  $(P > 0.05)$ .



Figure S9. Biomass (a) of dominant species group and its temporal standard deviation (b) in relation to mean growing-season precipitation. Results of linear regression analyses are showed in each scatter plot. Black solid line represents significant linear relationships (*P* < 0.05).



Figure S10. Relationship between species temporal coefficient of variation (CV) and relative species biomass. Solid line shows a significant linear relationship. Results of regression analyses were showed in this figure.