27. Roderick, G. K. & Navajas, M. Genes in new environments: genetics and evolution in biological control. *Nature Rev. Genet.* **4,** 889–899 (2003).

28. Macey, J. R., Larson, A., Ananjeva, N. B. & Papenfuss, T. J. Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards. *J. Mol. Evol.* **44,** 660–674 (1997).

29. Huelsenbeck, J. P. & Ronquist, F. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* **17,** 754–755 (2001).

30. Nylander, J.A.A. MrModeltest v1.0b (Department of Systematic Zoology, Uppsala University, 2002).

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Ecosystem stability and compensatory effects in the Inner Mongolia grassland

Yongfei Bai[1], **Xingguo Han**[1], **Jianguo Wu**[1,2], **Zuozhong Chen**[1] **& Linghao Li**[1]

[1]*Laboratory of Quantitative Vegetation Ecology, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China*
[2]*Faculty of Ecology, Evolution and Environmental Science, School of Life Sciences, Arizona State University, Tempe, Arizona 85287-4501, USA*

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Numerous studies have suggested that biodiversity reduces variability in ecosystem productivity through compensatory effects[1–6]; that is, a species increases in its abundance in response to the reduction of another in a fluctuating environment[1,7]. But this view has been challenged on several grounds[8–10]. Because most studies have been based on artificially constructed grasslands with short duration, long-term studies of natural ecosystems are needed. On the basis of a 24-year study of the Inner Mongolia grassland, here we present three key findings. First, that January–July precipitation is the primary climatic factor causing fluctuations in community biomass production; second, that ecosystem stability (conversely related to variability in community biomass production) increases progressively along the hierarchy of organizational levels (that is, from species to functional group to whole community); and finally, that the community-level stability seems to arise from compensatory interactions among major components at both species and functional group levels. From a hierarchical perspective, our results corroborate some previous findings of compensatory effects[1,4,7,11]. Undisturbed mature steppe ecosystems seem to culminate with high biodiversity, productivity and ecosystem stability concurrently. Because these relationships are correlational, further studies are necessary to verify the causation among these factors. Our study provides new insights for better management and restoration of the rapidly degrading Inner Mongolia grassland.

The role of compensatory interactions between species[6,7] has been a key issue in the debate concerning the diversity–stability relationship of an ecosystem. In particular, because different species respond to environmental fluctuations differently, the reduction in biomass of a certain species is more likely to be recompensed by the increased biomass of other species in a species-rich rather than species-poor community[1,4,6]. Such compensatory effects have been reported for both plant and animal communities[1,7,11–14]. However, others have argued that plant diversity has no consistent effect, or even a negative effect, on biomass production and ecosystem stability[10,15,16]. Undoubtedly, ecosystem stability depends not only on community composition but also on disturbance, nutrient supply and climatic conditions[3,4,9,13,15,17], and long-term studies of natural ecosystems are needed for better understanding of compensatory effects and thus the diversity–stability relationship.

Here we present the results of a long-term (1980–2003) study of two natural steppe communities in the Inner Mongolia grassland. The first (site A) is a rhizome-grass-dominated community, and the second (site B) is a bunchgrass-dominated community (see Methods). We classified species into the following five plant functional groups (PFGs) primarily on the basis of life forms: perennial rhizome grass (PR), perennial bunchgrasses (PB), perennial forbs (PF), shrubs and semi-shrubs (SS), and annuals and biennials (AB). PFGs also differ in plant stature, rooting depth, root-to-shoot ratio, water use efficiency, nutrient use efficiency and C:N:P stoichiometry[18–21] (Supplementary Information). Our study addresses the following three questions: first, what are the most important climatic drivers for the aboveground biomass production of steppe communities? Second, how does biomass production respond to precipitation fluctuations at different levels of organization (that is, at the species, plant functional group and community level)? And third, are there detectable compensatory effects reducing the variability in biomass production and thus increasing ecosystem stability?

To address the first question, we used multiple regressions to examine how the aboveground community biomass (B_{comm}) was related to several climatic variables: precipitation (annual, January–July, January–August and May–August); cumulative temperature (°C), that is, the accumulated excess when temperature exceeded 0 °C (January–July and January–August), 5 °C (annual) and 10 °C
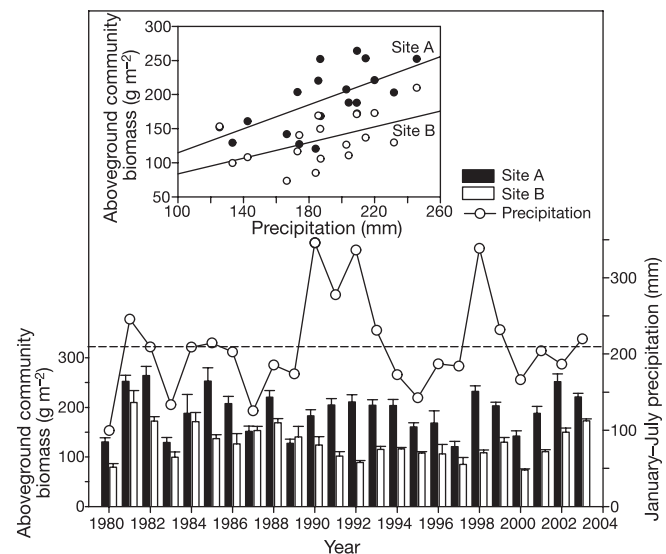

Figure 1 The relationship between January–July precipitation and total community aboveground biomass (B_{comm}) for the *Leymus chinensis* (site A) and *Stipa grandis* (site B) steppe ecosystems of the Inner Mongolia grassland, using data from 1980 to 2003. Bottom panel: B_{comm} was positively correlated to January–July precipitation in site A ($r^2 = 0.25$, $P = 0.01$), but not in site B ($r^2 = 0.003$, $P = 0.81$; $n = 24$). Error bars represent s.e.m., and the horizontal dashed line is the mean January–July precipitation from 1980 to 2003. Top panel: a significant positive correlation was found between B_{comm} and January–July precipitation in both sites after removing the four extraordinarily wet years (1990, 1991, 1992 and 1998). For site A (black dots) $r^2 = 0.49$, $P < 0.001$, $n = 19$; for site B (open circles) $r^2 = 0.35$, $P < 0.01$, $n = 19$.

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(annual); and the number of days on which temperature-dependent plant growth occurred ($\geq 5\,°C$ growing degree days and $\geq 10\,°C$ growing degree days). For site A, only January–July precipitation remained as a significant variable in simplified multiple regressions obtained by backward elimination ($r^2 = 0.25$, $P < 0.01$), whereas no significant variable was found for site B. This lack of statistical significance was due mainly to the influence of four extraordinarily wet years (1990, 1991, 1992 and 1998) to which community biomass did not respond proportionately (Fig. 1). When these four years were excluded, January–July precipitation became a highly significant variable for both site A ($r^2 = 0.49$, $P < 0.001$) and site B ($r^2 = 0.35$, $P < 0.01$), and was highly correlated with B_{comm} (Fig. 1). January–July precipitation alone explained 35–49% of the variation in biomass for the two sites.

To address the second question, we compared the coefficient of variation in biomass at the levels of individual species ($CV_{sp.}$), plant functional group (CV_{PFG}) and the whole community (CV_{comm}) (Fig. 2). We calculated $CV_{sp.}$ for 22 commonly found species in site A and 16 in site B, and the values ranged from 53.56% to 259.06% for site A and from 55.12% to 260.17% for site B. In both sites, species with higher relative biomass tended to have lower $CV_{sp.}$ (Fig. 2a). The coefficient of variation in aboveground biomass varied significantly among certain PFGs in both sites ($F = 38.51$, $P < 0.0001$ for site A; $F = 23.28$, $P < 0.0001$ for site B). Specifically, the values of CV_{PFG} were significantly different among PR, SS and AB ($P < 0.01$) in site A and among PB, PR and AB in site B (Fig. 2b). CV_{PFG} was negatively related to the relative biomass of PFGs (B_{rel}) in both site A

($CV_{PFG} = -2.77 B_{rel} + 159.34$; $r^2 = 0.44$, $P < 0.001$) and site B ($CV_{PFG} = -2.03 B_{rel} + 157.7$; $r^2 = 0.45$, $P < 0.001$).

At the community level, the aboveground biomass (B_{comm}) was significantly different between the two sites over the 24-yr period ($F = 112.99$, $P < 0.0001$, $n = 120$). The average B_{comm} was $192.51\,\mathrm{g\,m^{-2}}$ (s.e.m. = 13.92, $n = 5$) for site A and $127.04\,\mathrm{g\,m^{-2}}$ (s.e.m. = 10.14, $n = 5$) for site B. However, the coefficient of variation in B_{comm} was not significantly different between the two sites ($CV_{comm} = 27.06\%$ for site A and 31.92% for site B; $P > 0.05$). The values of CV_{comm} for these Inner Mongolia steppes are comparable to those for the North America grasslands (25–35%)[22,23], but much lower than those for semi-arid African grasslands (60–70%)[24]. Ecosystem stability, measured as the coefficient of variation in aboveground biomass[4,10], increased systematically from the species to the PFG to the community level (that is, $CV_{sp.} > CV_{PFG} > CV_{comm}$) for both site A ($F = 16.09$, $P < 0.0001$) and site B ($F = 13.71$, $P < 0.001$) (Fig. 2c). Such 'metastability' has been widely observed in complex hierarchical systems whose apparent stability hinges on the more transient dynamics of their components[25,26].

Were compensatory effects responsible for the increased stability at the community level? To address this question, we assumed that if an ecosystem in a changing environment had compensatory mechanisms, at least some of its major components (species or PFGs) would show negative correlations in terms of biomass production over time. At the species level, correlation analyses for 231 species pairs in site A and 120 pairs in site B showed that a negative correlation existed for 10 pairs in site A and 15 pairs in site B, whereas a positive correlation was found for 19 pairs in site A and 24 pairs in site B (Supplementary Information). Importantly, the negative correlation existed between dominant and sub-dominant species as well as between dominant and non-dominant species at both sites. In contrast, the positive correlation was found mainly between sub-dominant and non-dominant species or between non-
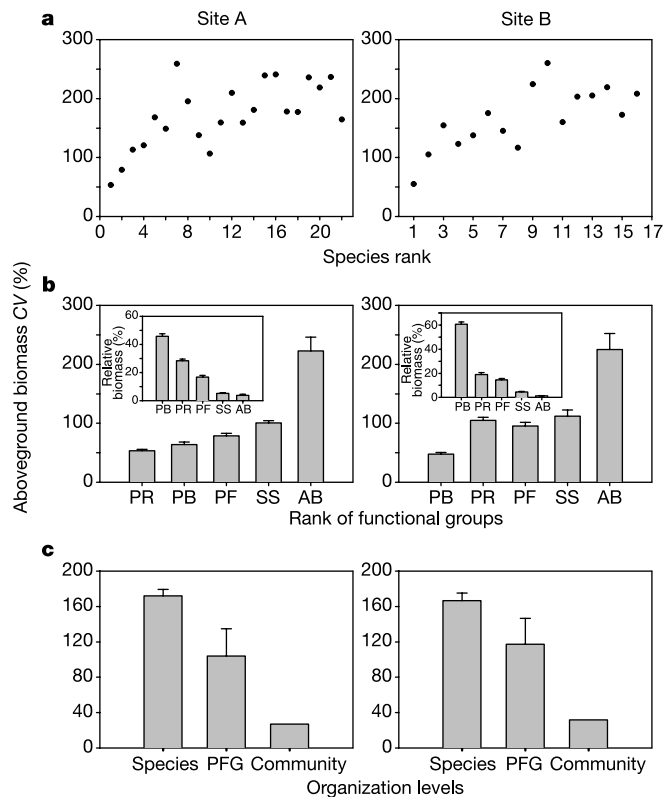

Figure 2 Coefficients of variation (CVs) in aboveground biomass at different organizational levels in the two study sites. **a**, Scatter-plots of species-level CVs against relative biomass-based species rank in which only common species were included.
b, Relationship between CVs of plant functional groups (PFGs) and relative biomass-based ranks of PFGs, with insets showing the average relative biomass values of PFGs in descending order. PR, perennial rhizome grass; PB, perennial bunchgrasses; PF, perennial forbs; SS, shrubs and semi-shrubs; and AB, annuals and biennials.
c, Comparison of average CVs at the species, PFG and community levels (means differ significantly at $P < 0.0001$ in both sites). Error bars in **b** and **c** represent s.e.m.
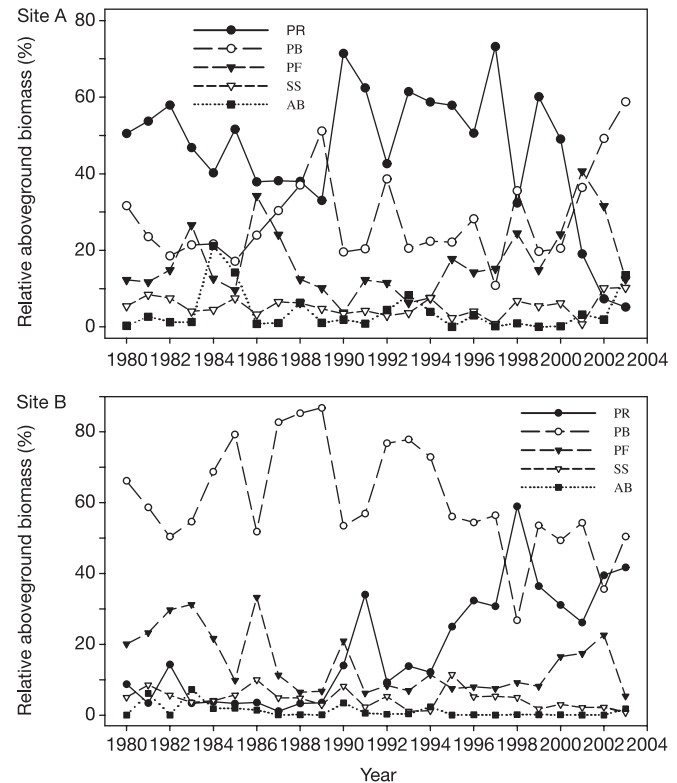

Figure 3 Time series of the relative aboveground biomass of plant functional groups from 1980 to 2003. Abbreviations are as in Fig. 2.

Table 1 **Correlation coefficients* between plant functional groups in terms of aboveground biomass**

Plant functional groups†	Site A		Site B	
	Correlation coefficient (r)	P	Correlation coefficient (r)	P
PR vs PB	−0.2673	0.0032	−0.4843	<0.0001
PR vs PF	−0.3019	0.0008	−0.3312	0.0002
PR vs SS	0.1648	0.0721	−0.2989	0.0010
PR vs AB	0.1616	0.0778	−0.3189	0.0004
PB vs PF	0.1297	0.1580	0.0747	0.4197
PB vs SS	0.2302	0.0114	0.2516	0.0058
PB vs AB	0.2668	0.0032	0.3001	0.0009
PF vs SS	0.0690	0.4537	0.0770	0.4050
PF vs AB	−0.2452	0.0069	0.2812	0.0020
SS vs AB	0.2233	0.0142	0.1587	0.0848

*Spearman's rank correlation coefficients.
†PR, perennial rhizome grass; PB, perennial bunchgrasses; PF, perennial forbs; SS, shrubs and semi-shrubs; and AB, annuals and biennials.

dominant species themselves. A similar trend was found at the PFG level. In site A, a negative correlation existed between PR and PB, between PR and PF, and between PF and AB, whereas a significant positive correlation was found between PB and SS, between PB and AB, and between SS and AB (Table 1). In site B, there was a significant negative correlation between PR and PB, PR and PF, PR and SS, and PR and AB, and a significant positive correlation between PB and SS, PB and AB, and PF and AB (Table 1 and Supplementary Information).

The observation that certain PFGs and species were negatively correlated suggests that compensatory effects may take place at both levels, but primarily among dominant components (that is, species and PFGs with high relative biomass). For example, the perennial rhizome grass, *Leymus chinensis*, alone made up 44.85% of B_{comm} in site A, and perennial bunchgrasses made up 61.6% of B_{comm} in site B (Fig. 3). Positive correlations at the species and PFG levels, a possible indication of the existence of complementary effects[4,6], could increase temporal ecosystem variation. Most species pairs (87.4% in site A and 67.5% in site B) did not show any statistically significant correlations in terms of biomass production. This may imply that at the species level a statistical averaging effect might have been operating. But because of the small relative biomass of the species or the PFGs involved (Fig. 3), these effects did not seem significant. The stabilizing effects of the compensatory interactions were also corroborated by the relatively high drought resistance and resilience of these steppe communities. The average value of drought resistance $((B_{drought} − B_{pre-drought})/B_{pre-drought})$ for five significantly drier years (1980, 1983, 1987, 1995 and 2000 when January–July precipitation was 50–80% of the mean) was −0.27 for site A and −0.22 for site B. These values were higher than those for species-rich ($\geq$11 species) experimental grassland plots in North America (about −0.35)[11]. The average values of ecosystem resilience ($B_{post-drought}/B_{pre-drought}$) for the five dry years were 1.19 for site A and 1.22 for site B, slightly higher than those for species-rich experimental grassland plots in North America (about 1.1)[11].

On the basis of a short-term (3 yr) field manipulative drought experiment with artificial grassland plots, it has been suggested that there is a potential trade-off between ecosystem production and stability with increasing species richness[10]. Our results indicate that plant communities in the Inner Mongolia grassland achieve high species richness, productivity and ecosystem stability simultaneously at the late successional stage[18,27,28] (Supplementary Information). These findings shed new light on the effects of precipitation fluctuations on the structure and functioning of the steppe ecosystems, and have important implications for understanding future impacts of climate change, and improving current grassland management practices. For example, as the precipitation regime and dry period pattern are altered, a shift in dominance of species and functional groups may occur. For restoring the vast areas of degraded grasslands in Inner Mongolia[29], it is important to establish and maintain grassland communities with a high diversity

of dominant species and functional groups, such that compensatory mechanisms can enhance long-term ecosystem productivity and stability in the face of eternal climatic fluctuations (Supplementary Information). □

Methods

Study sites and field sampling

The two study sites, each 500 m by 500 m, are the permanent field sites of the Inner Mongolia Grassland Ecosystem Research Station (IMGERS), located in the Xilin River Basin, Inner Mongolia Autonomous Region, China (116°42′ E, 43°38′ N) and administered by the Institute of Botany, the Chinese Academy of Sciences, Beijing. The growing season in the Inner Mongolia grassland runs from early April to late September for perennial plant species, whereas annual plants usually germinate in early July following the rains. Site A was dominated by a perennial rhizome grass, *Leymus chinensis*, whereas site B was dominated by a perennial bunchgrass, *Stipa grandis*. These two community types represent the most widely distributed grassland communities in the Eurasia steppe region[18,27,28,30], which is the largest contiguous grassland area in the world. Both sites have been fenced-off since 1979, preventing grazing by large animals. At the time of enclosure, both sites were considered to be in excellent condition, representative of undisturbed, climax steppe communities[28,30]. In 1980, site A and site B had 86 and 61 vascular plant species, respectively, and neither of them changed in species richness over the 24-yr period.

At each site, an east–west transect of 200 × 100 m was established with five equal-sized replicate blocks (40 × 100 m each). Aboveground biomass was sampled during 28–30 August each year by clipping all plants within a 1 × 1 m^2 quadrat that was randomly located within each block. All living vascular plants were sorted into species, dried and weighed. The dry mass of all plant species per quadrat averaged over the five blocks was used to estimate the aboveground community biomass. Because the standing crop of these steppe communities reached the annual peak at the end of August, our estimated community biomass approximated the aboveground net primary productivity of these ecosystems. All meteorological data were obtained from the weather stations of IMGERS.

Data analysis

Statistical analyses were performed using SAS version 8.0. Analysis of variance (ANOVA) and general linear models were used for analysis of variance. The coefficient of variation was calculated as: $CV = $ (standard deviation/mean) × 100. Spearman's rank correlation was used to analyse possible correlations among species and PFGs in terms of their aboveground biomass. Multiple regressions and backwards elimination were used to determine the effects of climatic variables on the total community biomass. At the species level, only commonly found species (that is, those present in at least 17 out of the 24 years) were considered. The biomass of the rare species excluded from the analysis was deemed trivial in relation to the total community biomass.

1. Naeem, S. & Li, S. Biodiversity enhances ecosystem reliability. *Nature* **390,** 507–509 (1997).
2. Yachi, S. & Loreau, M. Biodiversity and ecosystem productivity in a fluctuating environment: the insurance hypothesis. *Proc. Natl Acad. Sci. USA* **96,** 1463–1468 (1999).
3. Tilman, D. *et al.* The influence of functional diversity and composition on ecosystem processes. *Science* **277,** 1300–1302 (1997).
4. Tilman, D. The ecological consequences of changes in biodiversity: a search for general principles. *Ecology* **80,** 1455–1474 (1999).
5. Loreau, M. Biodiversity and ecosystem functioning: a mechanistic model. *Proc. Natl Acad. Sci. USA* **95,** 5632–5636 (1998).
6. Loreau, M. Biodiversity and ecosystem functioning: recent theoretical advances. *Oikos* **91,** 3–17 (2000).
7. McNaughton, S. J. Diversity and stability of ecological communities: A comment on the role of empiricism in ecology. *Am. Nat.* **111,** 515–525 (1977).
8. Givnish, T. J. Does diversity beget stability? *Nature* **371,** 113–114 (1994).
9. Huston, M. A. Hidden treatments in ecological experiments: re-evaluating the ecosystem function of biodiversity. *Oecologia* **110,** 449–460 (1997).
10. Pfisterer, A. B. & Schmid, B. Diversity-dependent production can decrease the stability of ecosystem functioning. *Nature* **416,** 84–86 (2002).
11. Tilman, D. & Downing, J. A. Biodiversity and stability in grasslands. *Nature* **367,** 363–365 (1994).

letters to nature

12. Brown, J. H., Whitham, T. G., Ernest, S. K. M. & Gehring, C. A. Complex species interactions and the dynamics of ecological systems: long-term experiments. *Science* **293**, 643–650 (2001).
13. Wardle, D. A., Bonner, K. I. & Barker, G. M. Stability of ecosystem properties in response to aboveground functional group richness and composition. *Oikos* **89**, 11–23 (2000).
14. McNaughton, S. J. Ecology of a grazing ecosystem: The Serengeti. *Ecol. Monogr.* **55**, 259–294 (1985).
15. McCann, K. S. The diversity–stability debate. *Nature* **405**, 228–233 (2000).
16. Huston, M. A. *et al.* No consistent effect of plant diversity on productivity. *Science* **289**, 1255 (2000).
17. Hooper, D. U. & Vitousek, P. M. The effects of plant composition and diversity on ecosystem processes. *Science* **277**, 1302–1305 (1997).
18. Chen, Z. Z. & Wang, S. P. *Typical Steppe Ecosystems of China* (Science, Beijing, 2000).
19. Chen, S. H., Zhang, H., Wang, L. Q., Zhanbula & Zhao, M. L. *Root Systems of Grassland Plants in Northern China* (Jilin Univ. Press, Chuangchun, 2001).
20. Inner Mongolia Grassland Ecosystem Research Station, Chen, Z. Z., Huang, D. H. & Zhang, H. F. *Research on Grassland Ecosystems* No. 1 112–131 (Science, Beijing, 1985).
21. Bai, Y. F. Influence of seasonal distribution of precipitation on primary productivity of *Stipa krylovii* community. *Acta Phytoecol. Sin.* **23**, 155–160 (1999).
22. Knapp, A. K. & Smith, M. D. Variation among biomes in temporal dynamics of aboveground primary production. *Science* **291**, 481–484 (2001).
23. Knapp, A. K. *et al.* Rainfall variability, carbon cycling and plant species diversity in a mesic grassland. *Science* **298**, 2202–2205 (2002).
24. O'Connor, T. G., Haines, L. M. & Snyman, H. A. Influence of precipitation and species composition on phytomass of a semi-arid African grassland. *J. Ecol.* **89**, 850–860 (2001).
25. Wu, J. & Levin, S. A. A spatial patch dynamic modeling approach to pattern and process in an annual grassland. *Ecol. Monogr.* **64**, 447–464 (1994).
26. Wu, J. & Loucks, O. L. From balance of nature to hierarchical patch dynamics: a paradigm shift in ecology. *Q. Rev. Biol.* **70**, 439–466 (1995).
27. Inner Mongolia Grassland Ecosystem Research Station, Li, B., Yong, S. P. & Li, Z. H. *Research on Grassland Ecosystem* No. 3 84–183 (Science, Beijing, 1988).
28. US National Research Council, Wu, J. & Loucks, O. L. *Grasslands and Grassland Sciences in Northern China* 67–84 (National Academy Press, Washington DC, 1992).
29. Tong, C., Wu, J., Yong, S. P., Yang, J. R. & Yong, W. Y. A landscape-scale assessment of steppe degradation in the Xilin River Basin, Inner Mongolia, China. *J. Arid Environ.* **59**, 133–149 (2004).
30. Inner Mongolia Grassland Ecosystem Research Station & Jiang, S. *Research on Grassland Ecosystem* No. 1 1–11 (Science, Beijing, 1985).

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Epigenetic regulation of translation reveals hidden genetic variation to produce complex traits

Heather L. True*, **Ilana Berlin** & **Susan L. Lindquist**

Whitehead Institute for Biomedical Research, Cambridge, Massachusetts 02142, USA

* Present address: Washington University Medical School, Department of Cell Biology and Physiology, St Louis, Missouri 63130, USA

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Phenotypic plasticity and the exposure of hidden genetic variation both affect the survival and evolution of new traits[1–3], but their contributing molecular mechanisms are largely unknown. A single factor, the yeast prion $[PSI^+]$, may exert a profound effect on both[4]. $[PSI^+]$ is a conserved, protein-based genetic element that is formed by a change in the conformation and function of the translation termination factor Sup35p[5], and is transmitted from mother to progeny. Curing cells of $[PSI^+]$ alters their survival in different growth conditions and produces a spectrum of phenotypes in different genetic backgrounds[4]. Here we show, by examining three plausible explanations for

this phenotypic diversity, that all traits tested involved $[PSI^+]$-mediated read-through of nonsense codons. Notably, the phenotypes analysed were genetically complex, and genetic re-assortment frequently converted $[PSI^+]$-dependent phenotypes to stable traits that persisted in the absence of $[PSI^+]$. Thus, $[PSI^+]$ provides a temporary survival advantage under diverse conditions, increasing the likelihood that new traits will become fixed by subsequent genetic change. As an epigenetic mechanism that globally affects the relationship between genotype and phenotype, $[PSI^+]$ expands the conceptual framework for phenotypic plasticity, provides a one-step mechanism for the acquisition of complex traits and affords a route to the genetic assimilation of initially transient epigenetic traits.

There are three possible explanations for the diversity of phenotypes that are produced when different $[PSI^+]$ strains are cured of the prion by growth on guanidine hydrochloride (GdHCl)[4]. Firstly, several yeast prions have now been identified[5] (and others probably exist)[6,7], each with different potential biological consequences. As growth on GdHCl cures all known naturally occurring prions in *Saccharomyces cerevisiae*, the diverse phenotypes we observed may have arisen from eliminating different combinations of prions present in different strains. Secondly, the reduction in translation–termination activity that is associated with $[PSI^+]$ may cause ribosomes to read through naturally occurring stop codons[8–10]. This could alter message stability and/or promote the translation of sequences that are prone to accumulating genetic variation, such as pseudogenes and $3'$ untranslated regions (see Supplementary Data and Supplementary Fig. 1). Thirdly, $[PSI^+]$ prion formation is accompanied by protein aggregation. Therefore, the acquisition and removal of such aggregates could have diverse effects on protein homeostasis and produce distinct phenotypes in different strains[11].

We systematically tested these hypotheses by creating three sets of strain derivatives in several different genetic backgrounds that uncoupled the effects of other prions (set one), translational read-through (set two) and protein aggregation (set three) (Supplementary Table 1). For set one, prions were cured by two different general methods that should eliminate most, if not all, prions (growth on GdHCl and deletion of Hsp104; ref. 5) or by two highly selective methods (mutating the prion-determining domain of the *SUP35* gene (NM) to eliminate $[PSI^+]$[12,13] and deleting the *RNQ1* gene to eliminate the other known prion present in some of the strains, $[RNQ^+]$[14]). For set two, we recreated the effects of translational read-through in cells that did not contain the prion ($[psi^-]$) either by introducing partial loss-of-function mutations into *SUP35*[15,16] or by introducing mutations that alter the stability of messenger RNAs containing nonsense codons ($\Delta upf1$, $\Delta ski7$)[17,18]. For set three, prion-like aggregates were recreated in a strain immune to their effects on translation termination. The strains were selectively cured of $[PSI^+]$ by chromosomal deletion of the prion-forming domain ($sup35^{\Delta NM}$) and NM–green fluorescent protein (GFP) was expressed from a strong promoter. We also created other strains that retained Sup35p prion aggregates but had efficient translation termination. This was accomplished by introducing a form of Sup35p that is immune to capture by $[PSI^+]$ aggregates (extra-chromosomal expression of *sup35C* (without NM)[12] or antisuppressor (ASU) *sup35* variants)[19].

The majority of the phenotypes tested proved to be a simple and direct consequence of $[PSI^+]$-mediated nonsense suppression (Table 1; Fig. 1; Supplementary Fig. 2; and data not shown). For example, resistance to 3 mM paraquat was greater in the $[PSI^+]$ derivative of strain 5V-H19 than in the $[psi^-]$ derivative (Fig. 1, centre). The $[psi^-]$ cells acquired resistance to paraquat in the absence of the prion when wild-type *SUP35* was replaced with a mutant that enhanced nonsense suppression ($sup35^{C653R}$). $[PSI^+]$ cells lost paraquat resistance when $[PSI^+]$ was selectively cured by deleting the prion-forming domain (ΔNM). Reducing nonsense