15. A. Woolfe et al., PLoS Biol. 3, e7 (2005).
16. A. Siepel et al., Genome Res. 15, 1034 (2005).
17. L. Z. Holland et al., Genome Res. 18, 1100 (2008).
18. Materials and methods are available as supporting material on Science Online.
19. K. S. Pollard, M. J. Hubisz, K. R. Rosenbloom, A. Siepel, Genome Res. 20, 110 (2010).
20. International HapMap Consortium, Nature 449, 851 (2007).
21. G. Robertson et al., Nat. Methods 4, 651 (2007).
22. G. E. Crawford et al., Genome Res. 16, 123 (2006).
23. A. P. Boyle et al., Cell 132, 311 (2008).
24. A. Valouev et al., Nat. Methods 5, 829 (2008).
25. M. Ashburner et al., Nat. Genet. 25, 25 (2000).
26. C. Y. McLean et al., Nat. Biotechnol. 28, 495 (2010).
27. C. J. Bult, Nucleic Acids Res. 36, D724 (2008).
28. P. Wu et al., Int. J. Dev. Biol. 48, 249 (2004).

# Rapid Range Shifts of Species Associated with High Levels of Climate Warming

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The distributions of many terrestrial organisms are currently shifting in latitude or elevation in response to changing climate. Using a meta-analysis, we estimated that the distributions of species have recently shifted to higher elevations at a median rate of 11.0 meters per decade, and to higher latitudes at a median rate of 16.9 kilometers per decade. These rates are approximately two and three times faster than previously reported. The distances moved by species are greatest in studies showing the highest levels of warming, with average latitudinal shifts being generally sufficient to track temperature changes. However, individual species vary greatly in their rates of change, suggesting that the range shift of each species depends on multiple internal species traits and external drivers of change. Rapid average shifts derive from a wide diversity of responses by individual species.

Threats to global biodiversity from climate change (1-8) make it important to identify the rates at which species have already responded to recent warming. There is strong evidence that species have changed the timing of their life cycles during the year and that this is linked to annual and longer-term variations in temperature (9–12). Many species have also shifted their geographic distributions toward higher latitudes and elevations (13–17), but this evidence has previously fallen short of demonstrating a direct link between temperature change and range shifts; that is, greater range shifts have not been demonstrated for regions with the highest levels of warming.

We undertook a meta-analysis of available studies of latitudinal (Europe, North America, and Chile) and elevational (Europe, North America, Malaysia, and Marion Island) range shifts for a range of taxonomic groups (18) (table S1). We considered $N = 23$ taxonomic group × geographic region combinations for latitude, incorporating 764 individual species responses, and $N = 31$ taxonomic group × region combinations for elevation, representing 1367 species responses. For the purpose of analysis, the mean shift across all species of a given taxonomic group, in a given region, was taken to represent a single value (for example, plants in Switzerland or birds in New York State; table S1) (18).

The latitudinal analysis revealed that species have moved away from the Equator at a median rate of 16.9 km decade$^{-1}$ (mean = 17.6 km decade$^{-1}$, SE = 2.9, $N = 22$ species group × region combinations, one-sample $t$ test versus zero shift, $t = 6.10$, $P < 0.0001$). Weighting each study by the $\sqrt{}$(number of species) in the group × region combination gave a mean rate of 16.6 km decade$^{-1}$. For elevation, there was a median shift to higher elevations of 11.0 m uphill decade$^{-1}$ (mean = 12.2 m decade$^{-1}$, SE = 1.8, $N = 30$ species groups × regions, one-sample $t$ test versus zero shift, $t = 7.04$, $P < 0.0001$). Weighting elevation studies by $\sqrt{}$(number of species) gave a mean rate of uphill movement of 11.1 m decade$^{-1}$.

A previous meta-analysis (14) of distribution changes analyzed individual species, rather than the averages of taxonomic groups × regions that we used, and also included data on latitudinal and elevational shifts in the same analysis (18). It concluded that ranges had shifted toward higher latitudes at 6.1 km decade$^{-1}$ and to higher elevations at 6.1 m decade$^{-1}$ (14), whereas the rates of range shift that we found were significantly greater [$N = 22$ species groups × regions, one-sample $t$ test versus 6.1 km decade$^{-1}$, $t = 3.99$, $P = 0.0007$ for latitude; $N = 30$ groups × regions, one-sample $t$ test versus 6.1 m decade$^{-1}$, $t = 3.49$, $P = 0.002$ for elevation (18)]. Our estimated mean rates are approximately three and two times higher than those in (14), for
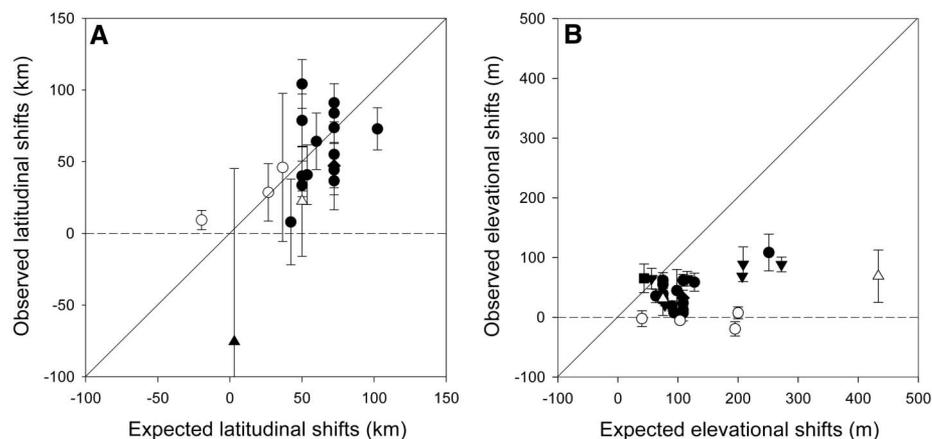
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**Fig. 1.** Relationship between observed and expected range shifts in response to climate change, for (**A**) latitude and (**B**) elevation. Points represent the mean responses (±SE) of species in a particular taxonomic group, in a given region. Positive values indicate shifts toward the pole and to higher elevations. Diagonals represent 1:1 lines, where expected and observed responses are equal. Open circles, birds; open triangles, mammals; solid circles, arthropods; solid inverted triangles, plants; solid square, herptiles; solid diamond, fish; solid triangle, mollusks.

latitude and elevation respectively, implying much greater responses of species to climate warming than previously reported (*18*). Most of the data we analyzed are from the temperate zone and from tropical mountains (table S1), where ecosystems are at least partly temperature-limited; different rates of change might be observed in moisture-limited ecosystems (*19*).

Published studies have shown nonrandom latitudinal and elevational changes (*1, 7, 13–17*) but have not previously demonstrated a statistical linkage between range shifts and levels of warming. We found that observed latitudinal and elevational shifts (the latter more weakly) have been significantly greater in studies with higher levels of warming (mean latitudinal shift versus average temperature increase; $N = 23$ species groups × regions, Pearson correlation coefficient ($r$) = 0.59, $P = 0.003$; mean elevational shift versus temperature increase; $N = 31$, $r = 0.37$, $P = 0.042$). Temperature gradients differ across the world, so a given level of warming leads to different expected range shifts of species in different regions (*20*), assuming that species track climate changes. To estimate the expected shifts, we calculated the distances in latitude (kilometers) and elevation (meters) that species in a given region would have been required to move to track temperature changes and thus to experience the same average temperature at the end of the recording period as encountered at the start (*18*) (table S1). We found that both observed latitudinal and elevation range shifts were correlated with predicted distances (Fig. 1A, $N = 20$ species groups × regions, $r = 0.65$, $P = 0.002$ for latitude; Fig. 1B, $N = 30$ groups × regions, $r = 0.39$, $P = 0.035$ for elevation), so our analyses directly link terrestrial range shifts to regional and study differences in the warming experienced.

Despite reports that many species lag behind climate change (*21–23*), nearly as many studies of observed latitudinal changes fall above as below the observed = expected line in Fig. 1A (9 points above, 11 below; $\chi^2 = 0.20$, 1 df, $P = 0.65$), suggesting that mean latitudinal shifts are not consistently lagging behind the climate. The lag in elevation response (Fig. 1B; 2 points above the 1:1 line, 28 below; $\chi^2 = 22.53$, 1 df, $P < 0.001$) is equally surprising because the required distances to track climate are much shorter than for latitudinal shifts (*20*). Real and apparent elevation lags may arise if suitable new conditions at higher elevations occur only in locations that cannot be reached easily (for example, on other mountain peaks), or they may reflect the topographic and microclimatic complexity of mountainous terrain [for example, cooler locations may be on poleward-facing slopes rather than higher (*24*)]; the need for finer-resolution analyses (*25*); and additional topographic, climatic, geological, and ecological constraints [for example, causing declines in cloud forest species (*26–28*)].

Taxonomic differences are not consistent predictors of recent response rates. For example, birds seem to have responded least in terms of elevational shifts but had a slightly greater than expected latitudinal shift (Fig. 1). Much greater variation is associated with differences among species within a taxonomic group than between taxonomic groups (Fig. 2 and table S2). For latitudinal studies, on average 22% (average of $N = 23$ species groups × regions) of the species actually shifted in the opposite direction to that expected. Similarly, 25% of species shifted downhill rather than to higher elevations (average of $N = 29$ species groups × regions). Thus, despite an overall significant shift toward higher latitudes and elevations, which is greatest where the climate has warmed the most, and despite around three-quarters of species shifting poleward and to higher elevations, we found that species have exhibited a high diversity of range shifts in recent decades.

At least three processes are likely to generate the high diversity of range shifts among species: time delays in species' responses, individualistic physiological constraints, and alternative and interacting drivers of change. Species may lag behind climate change if they are habitat specialists or immobile species that cannot colonize across fragmented landscapes (*17, 21–23*), or if they possess other traits associated with low extinction or colonization rates (*29*). Species may also show individualistic physiological responses to different aspects of the climate, such as different sensitivities to maximum and minimum temperatures at critical times of their life cycles. These sensitivities will combine with variable wait times for different novel climatic extremes to take place (*30*). Species are also affected to different extents by nonclimatic factors and by multispecies interactions, which themselves depend on a diversity of environmental drivers (*21, 28*). For example, a species might retreat toward the Equator at its poleward margin if it contracts with habitat loss faster than it expands through climate warming; whereas the poleward range margin of a species that thrives in novel agricultural landscapes may spread at a rate exceeding that expected, were warming the sole driver.

We found that rates of latitudinal and elevational shifts are substantially greater than reported
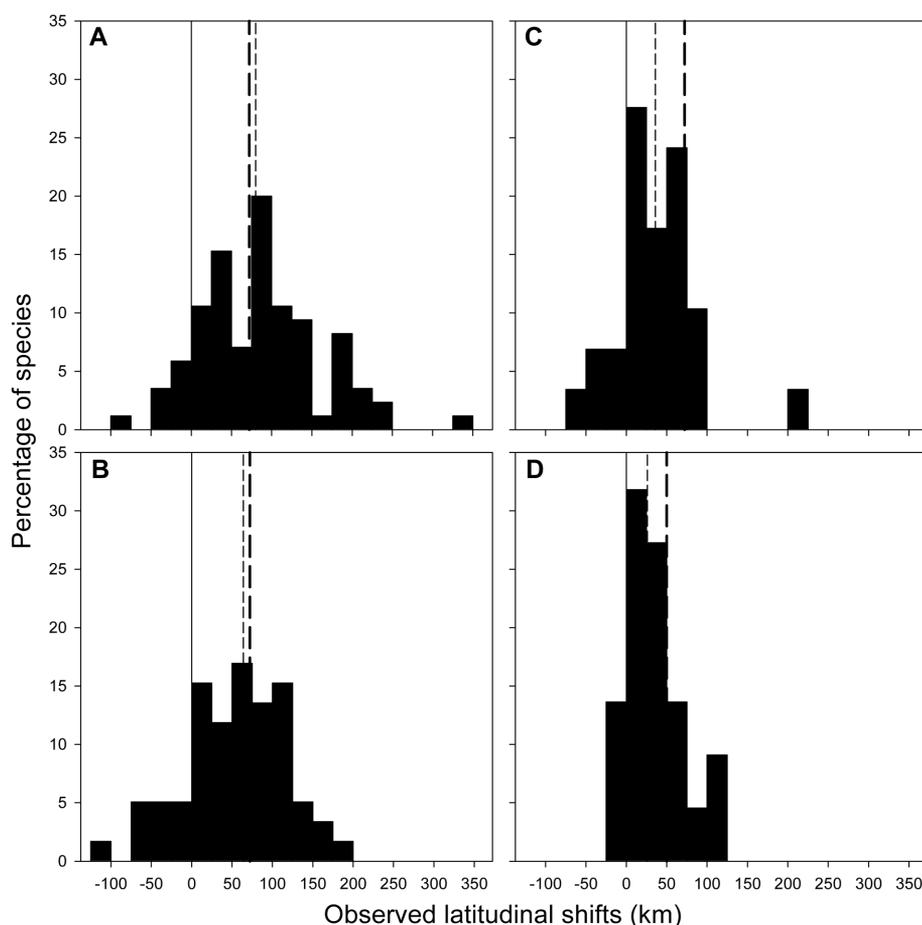


**Fig. 2.** Observed latitudinal shifts of the northern range boundaries of species within four exemplar taxonomic groups, studied over 25 years in Britain. (**A**) Spiders (85 species), (**B**) ground beetles (59 species), (**C**) butterflies (29 species), and (**D**) grasshoppers and allies (22 species). Positive latitudinal shifts indicate movement toward the north (pole); negative values indicate shifts toward the south (Equator). The solid line shows zero shift, the short-dashed line indicates the median observed shift, and the long-dashed line indicates the predicted range shift.

in a previous meta-analysis, and increase with the level of warming. We conclude that average rates of latitudinal distribution change match those expected on the basis of average temperature change, but that variation is so great within taxonomic groups that more detailed physiological, ecological and environmental data are required to provide specific prognoses for individual species.

### References and Notes

1. J. A. Pounds, M. P. L. Fogden, J. H. Campbell, *Nature* **398**, 611 (1999).
2. S. E. Williams, E. E. Bolitho, S. Fox, *Proc. Biol. Sci.* **270**, 1887 (2003).
3. C. D. Thomas *et al.*, *Nature* **427**, 145 (2004).
4. A. Fischlin *et al.*, in *Climate Change 2007: Impacts, Adaptation and Vulnerability. Contribution of Working Group II to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change*, M. L. Parry, O. F. Canziani, J. P. Palutikof, P. J. van der Linden, C. E. Hanson, Eds. (Cambridge Univ. Press, Cambridge, 2007), pp. 211–272.
5. K. E. Carpenter *et al.*, *Science* **321**, 560 (2008).
6. C. H. Sekercioglu, S. H. Schneider, J. P. Fay, S. R. Loarie, *Conserv. Biol.* **22**, 140 (2008).
7. C. J. Raxworthy *et al.*, *Glob. Change Biol.* **14**, 1703 (2008).
8. B. Sinervo *et al.*, *Science* **328**, 894 (2010).
9. A. Menzel *et al.*, *Glob. Change Biol.* **12**, 1969 (2006).
10. C. Rosenzweig *et al.*, *Nature* **453**, 353 (2008).
11. T. L. Root, D. P. MacMynowski, M. D. Mastrandrea, S. H. Schneider, *Proc. Natl. Acad. Sci. U.S.A.* **102**, 7465 (2005).
12. S. J. Thackeray *et al.*, *Glob. Change Biol.* **16**, 3304 (2010).
13. C. Parmesan *et al.*, *Nature* **399**, 579 (1999).
14. C. Parmesan, G. Yohe, *Nature* **421**, 37 (2003).
15. R. Hickling, D. B. Roy, J. K. Hill, R. Fox, C. D. Thomas, *Glob. Change Biol.* **12**, 450 (2006).
16. C. Rosenzweig *et al.*, in *Climate Change 2007: Impacts, Adaptation and Vulnerability. Contribution of Working Group II to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change*, M. L. Parry, O. F. Canziani, J. P. Palut., P. J. van der Linden, C. E. Hanson, Eds. (Cambridge University Press, Cambridge, 2007), pp. 79–131.
17. C. D. Thomas, *Divers. Distrib.* **16**, 488 (2010).
18. Materials and methods are available as supporting material on *Science* Online.
19. W. Foden *et al.*, *Divers. Distrib.* **13**, 645 (2007).
20. S. R. Loarie *et al.*, *Nature* **462**, 1052 (2009).
21. M. S. Warren *et al.*, *Nature* **414**, 65 (2001).
22. R. Menéndez *et al.*, *Proc. Biol. Sci.* **273**, 1465 (2006).
23. R. Nathan *et al.*, *Ecol. Lett.* **14**, 211 (2011).
24. A. J. Suggitt *et al.*, *Oikos* **120**, 1 (2011).
25. C. D. Thomas, A. M. A. Franco, J. K. Hill, *Trends Ecol. Evol.* **21**, 415 (2006).
26. A. E. Pounds *et al.*, *Nature* **439**, 161 (2006).
27. I.-C. Chen *et al.*, *Glob. Ecol. Biogeogr.* **20**, 34 (2011).
28. G. Forero-Medina, L. Joppa, S. L. Pimm, *Conserv. Biol.* **25**, 163 (2011).
29. A. L. Angert *et al.*, *Ecol. Lett.* **14**, 677 (2011).
30. D. R. Easterling *et al.*, *Science* **289**, 2068 (2000).

# Aneuploidy Drives Genomic Instability in Yeast

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Aneuploidy decreases cellular fitness, yet it is also associated with cancer, a disease of enhanced proliferative capacity. To investigate one mechanism by which aneuploidy could contribute to tumorigenesis, we examined the effects of aneuploidy on genomic stability. We analyzed 13 budding yeast strains that carry extra copies of single chromosomes and found that all aneuploid strains exhibited one or more forms of genomic instability. Most strains displayed increased chromosome loss and mitotic recombination, as well as defective DNA damage repair. Aneuploid fission yeast strains also exhibited defects in mitotic recombination. Aneuploidy-induced genomic instability could facilitate the development of genetic alterations that drive malignant growth in cancer.

Whole-chromosome aneuploidy—or a karyotype that is not a multiple of the haploid complement—is found in greater than 90% of human tumors and may contribute to cancer development (*1*, *2*). It has been suggested that aneuploidy increases genomic instability, which could accelerate the acquisition of growth-promoting genetic alterations (*1*, *3*). However, whereas aneuploidy is a result of genomic instability, there is at present limited evidence as to whether genomic instability can be a consequence of aneuploidy itself. To test this possibility directly, we assayed chromosome segregation fidelity in 13 haploid strains of *Saccharomyces cerevisiae* that carry additional copies of single yeast chromosomes (*4*). These aneuploid strains (henceforth disomes) display impaired proliferation and sensitivity to conditions that interfere with protein homeostasis (*4*, *5*). We measured the segregation fidelity of a yeast artificial chromosome (YAC) containing human DNA and found that the rate of chromosome missegregation was increased in 9 out of 13 disomic strains relative to a euploid control (Fig. 1A). The increase ranged from 1.7-fold to 3.3-fold, comparable to the fold increase observed in strains lacking the kinetochore components Chl4 or Mcm21. Consistent with chromosome segregation defects, 8 out of 13 disomic strains displayed impaired proliferation on plates containing the microtubule poison benomyl, including a majority of the strains that had increased rates of YAC loss (Fig. 1B).

Chromosome missegregation can result from defects in chromosome attachment to the mitotic spindle or from problems in DNA replication or repair. Defects in any of these processes delay mitosis by stabilizing the anaphase inhibitor Pds1 (securin) (*6*). Five out of five disomes (disomes V, VIII, XI, XV, and XVI) exhibited delayed degradation of Pds1 relative to wild type after release from a pheromone-induced $G_1$ arrest (Fig. 1C and fig. S1). Defective chromosome biorientation delays anaphase through the mitotic checkpoint component Mad2 (*6*). Deletion of *MAD2* had no effect on Pds1 persistence in four disomes, but eliminated this persistence in disome V cells (fig. S1). Disome V also delayed Pds1 degradation after release from a mitotic arrest induced by the microtubule poison nocodazole, which demonstrated that this strain exhibits a biorientation defect. Disome XVI, which displayed Mad2-independent stabilization of Pds1, recovered from nocodazole with wild-type kinetics (fig. S2). Thus, Pds1 persistence results predominantly from Mad2-independent defects in genome replication and/or repair (see below).

We next investigated whether aneuploidy could affect the rate of forward mutation. Disomes V, VIII, X, and XIV displayed an increased mutation rate at two independent loci, whereas disome IV displayed an increased mutation rate at *CAN1* but not at *URA3* (Fig. 2A). The fold increase ranged from 2.2-fold to 7.1-fold, less than the 9.5-fold and 12-fold increases observed in a recombination-deficient *rad51Δ* mutant and a mismatch repair–deficient *msh2Δ* mutant, respectively. Additionally, in an assay for microsatellite instability, we found that disomes VIII and XVI displayed increased instability in a poly(GT) tract (fig. S3), which demonstrated that aneuploidy can enhance both simple sequence instability and forward mutagenesis.

To define the mechanism underlying the increased mutation rate in aneuploid cells, we

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