**Appendix S1. Supplementary Methods.**

**Phylogenies used**

We used three time-calibrated molecular phylogenies to identify sister species and to estimate rates of change in climatic niches. First, we used the phylogeny of 1230 grass species from Edwards & Smith [13]. We then used two phylogenies of 3595 grass species from a subsequent study [2]. All three phylogenies were estimated using a combination of chloroplast and nuclear DNA sequences. The tree from Edwards & Smith [13] was dated using fossil phytolith data. The two trees from Spriggs *et al.* [2] were estimated using identical sets of chloroplast and nuclear sequences but they differed in which fossils were used for divergence-time estimation. Specifically, one tree (hereafter 2014-1) was dated using only macrofossils, whereas the other (2014-2) was dated using both macrofossils and fossil phytoliths [2]. Given that it is not clear which set of dates is correct, we ran all analyses on both of these trees.

**Selecting species**

We used the trees to select the sister species in which rates were estimated. Despite the large absolute size of these three phylogenies, their taxon sampling is still incomplete relative to the overall richness of the family, which includes over >11,000 species [2]. Limited species sampling risks excluding closely related species with divergent niches, which may cause underestimation of rates of climatic niche evolution [11]. To reduce this problem, we first selected only the youngest sister species pair in each genus. Second, we only selected sister species from genera in which multiple species (>2) were represented. Thirdly, we excluded species for which climatic data were not available [13]. Fourth, we excluded genera in which the most recently diverged species were part of a polytomy because it was unclear in these cases which species were actually sister taxa. Using these criteria, for the 2010 tree, we selected 85 species-pairs (170 species total), representing eight subfamilies (Aristidoideae, Bambusoideae, Chloridoideae, Danthonoideae, Ehrhartoideae, Micrairoideae, Panicoideae and Pooideae). Among the three trees, 155 species are unique to this tree. We selected 31 and 30 species pairs from Trees 2014-1 and 2014-2, respectively, representing seven subfamilies (Arundinoideae, Bambusoideae, Chloridoideae, Danthonoideae, Ehrhartoideae, Panicoideae, and Pooideae). Among these two trees, 2 pairs are unique to the 2014-1 tree and 3 pairs are unique to the tree 2014-2 (the few sister-species pairs selected that differed between the two 2014 trees differed because in a few genera the youngest species pairs differed because of differences in clade ages, even though the topologies were identical). Across all three phylogenies, 95 genera were represented. Many more taxa were represented in the phylogenies from 2014 and we were able to include genera that had too few species represented in the 2010 tree. However, we excluded genera from the 2014 trees in which the youngest species pair included a species for which we lacked climatic data.

**Climatic data**

Climatic and locality data were obtained from Edwards & Smith [13]. Those authors obtained their data from the Global Biodiversity Information Facility (GBIF) web portal (http://www.gbif.org/) for georeferenced specimens in herbaria and natural history collections, for a total of 1230 grass species. Across all species included in our analyses of all three trees, the median number of localities per species was 95.5, with a minimum of 10 and a maximum of 35,339. Climate data were at a spatial resolution of 10’ (18.5km at equator; [13]). We focused on four climatic variables: mean annual temperature (Bio1, MAT), maximum annual temperature (Bio 5, TMAX), minimum annual temperature (Bio6, TMIN), and mean annual precipitation (Bio12, MAP). Climatic and locality data for each species in the three trees are summarized in appendices S2–S7. Climatic data for each species for each variable were summarized based on the mean value across localities. However, we address whether results might be different using median values in the final section of this appendix (see below).

These four variables are standard descriptors of species climatic niches [11], including overall yearly temperature and precipitation and yearly temperature extremes. They include three variables that may be particularly important for assessing climate change impacts (i.e. maximum temperature, mean temperature, and yearly precipitation). These four variables are also the same ones used by Edwards & Smith [13] to characterize climatic niches of grass species. However, those authors also included temperature and precipitation seasonality, which we do not consider here. Seasonality variables have a less straightforward interpretation in terms of rates of change over time. Furthermore, we focused on annual precipitation instead of precipitation over shorter time periods (e.g. wettest or driest quarters). Annual precipitation is the primary variable that distinguishes different habitats (e.g. rainforest vs. desert), whereas the relevance of precipitation over shorter time periods is less clear.

We note that some of these climatic variables may be correlated in some cases. However, this is not problematic at all for our analyses or our conclusions. For example, the fact that we obtain similar results using all three temperature variables does not make our separate inferences from these variables incorrect. Instead, it shows that our conclusions are robust across different climatic variables. Most importantly, our analyses do not assume that these variables are uncorrelated.

Finally, we acknowledge that we have not established that these four climatic variables necessarily set the geographic range limits of the grass species considered here. In general, we expect the geographic range limits of each species to be set by multiple factors and variables, depending on the specific part of the geographic range considered (e.g. low vs. high elevational limits, low vs. high latitudinal limits, different longitudinal range limits). These factors may or may not include these four variables. Nevertheless, we anticipate that rapid and dramatic changes in one or more of these four variables might still cause local or global extinctions regardless (e.g. due to high temperatures, reduced precipitation, or related factors).

**Rates of climatic niche change**

For each species, we first estimated a rate of climatic niche change for each species, following Quintero & Wiens [11]. To do this, we found the best-fitting model of trait evolution for each climatic variable for each subfamily for each tree (see next paragraph). We then used this best-fitting model to reconstruct ancestral values of each climatic variable for the ancestor of each selected species pair in each subfamily. The niche shift associated with each species was then the difference between the species current value and the value in its ancestor. The rate of niche change was then the niche shift divided by the age of the ancestor.

Note that throughout the paper, we generally use the terms “niche change” and “niche shift” rather than “niche evolution,” given that we recognize that changes in climatic niches over time could be evolutionary (i.e. adaptation to new abiotic or biotic conditions), non-evolutionary (e.g. due to plastic shifts or changes in habitat availability), or some mixture of both. Although we use phylogenetic approaches to find the best-fitting reconstruction model, our final estimates of niche shifts and rates of change do not require that all changes in climatic niches in individual species must be evolutionary.

To find the best fitting model of change for each climatic variable in each subfamily, we used the R package *geiger* (version 2.0.3; [23]) to compare the AIC values of four models of change: white noise (WN; no phylogenetic signal, lambda = 0), Brownian Motion (BM; strong phylogenetic signal, lambda = 1), estimated lambda (EL, lambda between 0 and 1), and Ornstein-Uhlenbeck (OU; similar to a model of stasis or stabilizing selection). The model with the lowest AIC value was chosen. We then used the *ace* function in the R package *ape* (version 3.2; [24]) to reconstruct ancestral values for each variable for the best-fitting model. The *ace* function assumes a Brownian Motion model of evolution. If the OU, EL, or WN model was identified as the best-fitting, we first used the *rescale* function in *geiger* to transform the subfamily trees to have either OU branch lengths using the alpha parameter, EL branch lengths using the lambda parameter, or WN branch lengths using the sigsq argument recommended in *geiger* for this model (although this function simply makes branch lengths equal). Note that ancestral reconstructions would be problematic under the WN model, but this model was chosen very infrequently.

Prior to fitting models of trait evolution, the trees for each subfamily were pruned to include only those species for which climatic data were available. We also pruned species that were associated with polytomies, so that these polytomies did not impact the relative fit of different evolutionary models.

The fit of different models for each variable for each tree are presented in tables S2–S4. For all three trees, the best fitting model for the majority of variables and subfamilies was the EL model (>50%). The OU model was the best fitting model in about 25–32% of the total number of variables and subfamilies per tree, and the BM model in about 10% (but 0% for tree 2014-2). The WN model had the best fit in only 3–7%. Estimated rates under the best-fitting model are provided in tables S5–S7.

To assess whether niche rate estimates were robust to different models of evolution, we also reconstructed ancestral values and estimated past and future rates of change under the BM, OU, and EL models for all trees and subfamilies. Rates of niche change were broadly similar under different models. Estimated rates for all species under all models are provided in appendix S8. Most importantly, under all evolutionary models, the mean niche rates were consistently >10,000 fold slower than rates of projected climate change under the median model of projected change, for all four climatic variables.

We note that our choice of fitting different models to different subfamilies for each variable allowed for some heterogeneity in evolutionary models across the phylogeny of grasses. Alternatively, we could have allowed for even more heterogeneity by performing model selection separately for each genus. However, some genera had relatively few species with climatic data, which would have made this problematic. Moreover, the choice of models had relatively little impact on the estimated rates (appendix S8). This makes intuitive sense, since the rate should be determined largely by the differences in climatic niche differences between sister species (i.e. sister species with very similar climatic niches will have low rates) and by the age of these species. In contrast, the specific model used to reconstruct the values of ancestral species should have very limited impact.

These analyses did not utilize reconstructions of paleoclimates to estimate rates of climatic niche change in extant species. Even though it is possible to obtain data on climate at certain points in the relatively recent past, it is far more difficult to tell where exactly a particular extant species occurred during those time points. Therefore, it is difficult to use paleoclimate data to estimate niche shifts, without extensive distributional data from fossils for extant species. We acknowledge that there have been rapid climatic changes in the geologically recent past (i.e. Pleistocene climatic cycles of cooling and warming). We assume that if species responded to these changes through rapid niche shifts, there should be some signature of these changes in terms of climatic differences among closely related extant species. On the other hand, if species responded primarily through local extinctions and range shifts, then we assume that their climatic niche values will be similar between sister species, and that they will show relatively low rates of climatic niche evolution. Most importantly, the fact that there were rapid climatic oscillations in the past does not by itself show that species underwent rapid niche shifts.

A related topic is the potential relationship between climatic niche shifts and speciation. Importantly, our methodology does not assume that climatic niche shifts happen only at speciation. In fact, there are several possible relationships between climate and speciation. First, climatic niche shifts between populations could drive speciation (e.g. [25, 26]), but there could still be subsequent divergence in their climatic niches after speciation. Second, similarity between species’ climatic niches might actually drive speciation instead (speciation through climatic niche conservatism [26, 27]). This occurs when a species range is bisected by a barrier of unsuitable climatic conditions that the species is unable to adapt to, leading to allopatry between sets of populations [27], potentially followed by the evolution of reproductive isolation through various mechanisms (e.g. Dobzhansky-Mueller incompatibilities [28]). In this case, most observed climatic niche divergence between sister species would presumably occur after speciation. Third, speciation might be completely unrelated to climate (for example, due to polyploidy, pollinator shifts, or geographic barriers that are unrelated to climate [28]). Again, in this case, climatic niche divergence between sister species would presumably occur after their speciation. In summary, the analyses presented here on rates of climatic niche change do not assume any particular relationship between climate and speciation.

**Future rates of climate change**

We determined the rate of future climate change for each species for each variable based on the difference between the “current” climatic value (i.e. the mean values from 1950 to 2000; Hijmans *et al.* [14]), and the projected values in 2070. We calculated the average difference between current climate across localities for each species, and then divided by the difference between these two time periods. However, determining the projected values was not straightforward, given the many different potential scenarios for future change. Therefore, we first determined a range of climate scenarios to represent future climate conditions, including those involving minimal change, maximum change, and an intermediate level of change. To determine this range, we arbitrarily selected two temperate grass species (one New World, one Old World) and two tropical grass species (again, one New World and Old World) to represent different regions across the world, and compared the mean values across localities for each species for 32 different future climate projections. Based on these values, we determined which projections tended to yield the smallest, largest, and intermediate levels of change (relative to current conditions) across all four species. Specifically, from among the species in tree of Edwards & Smith [13], we selected two species with temperate distributions (*Zizania aquatica* from 33 locations in the southern US and *Danthonia alpina* from 19 locations in Austria, Eastern Europe and the Mediterranean) and two species with tropical distributions (*Eriachne triseta* from 95 locations in Australia and southeast Asia, and *Rhipidocladum pittieri* from 33 locations in Central America and Mexico). We then focused on four different greenhouse gas scenarios (representative concentration pathways; RCP26, RCP45, RCP60, RCP85) and eight standard global climate models, chosen because climatic data were available from the WorldClim database for all four RCPs (ACCESS 1-0, AC; BCC-CSM1-1, BC; CCSM4, CC; HadGEM2-CC, HG; HadGEM2-ES, HE; IPSL-CM5A-LR, IP; MIROC5, MC; MRI-CGCM3, MG) for a total of 32 possible climate scenarios. All climatic data were downloaded from the WorldClim database, Version 1.4 (release 3; [14]). We extracted data from each climatic variable for each species at 30 arc-second (~1 km) spatial resolution (CMIP5 30-seconds) for 2070 (representing the average from 2061–2080) under each of the 32 climate scenarios. To identify the projections that yielded the minimum, maximum, and median levels of climate change across all 32 projections, we calculated the mean difference between current climate values and climate values under each of the 32 future projections at each locality. We then selected the projections that most frequently predicted the minimum, median, and maximum levels of climate change. Across the four chosen species and three temperature variables (MAT, TMAX, TMIN), HE-RCP85 most frequently predicted the maximum level of change (7 times out of a possible 12), MG-RCP26 most frequently predicted the minimum level of change (6/12) and BC-RCP60 most frequently predicted the median level of change (5/12). The climate scenarios that most frequently predicted the maximum, minimum, and median levels of change in mean annual precipitation were MC-RCP45 (2 out of 4 species), HE-RCP60 (2 out of 4 species) and MC-RCP26 (2 out of 4 species), respectively. Future rates of climate change were estimated as the mean difference between current and projected climate conditions at each locality for each species, divided by 95 years. The estimates of current climate values span from 1950-2000, and so 95 years is the difference between the midpoint of 1950-2000 (1975) and 2070. Estimated rates for all species under all projections are provided in appendix S8.

**Niche rates and species ages**

We also tested whether rates of niche change were faster in younger species (as in [11]). We first performed a Shapiro-Wilk test of normality on all variables (species ages and niche rates on all trees). All variables initially failed this test (*p*<0.05, rejecting the null hypothesis of normality). All variables were ln-transformed and then retested. For pairs of variables that were normally distributed after ln-tranformation, we used ordinary-least squares regression. For pairs in which one or more variables were still non-normally distributed, we used a non-parametric test (Spearman’s rank correlation). Results are presented in electronic supplementary materials, table S8. All tests were conducted in R. We acknowledge that we did not perform a phylogenetic comparative test of these relationships, but the ages and rates of individual, terminal species should not be a shared property of clades that requires phylogenetic correction.

**Non-native localities**

Our analyses assumed that the locality and associated climatic data of Edwards & Smith [13] were valid and adequately vetted. However, those authors did not mention the potential impact of non-native localities on their data. We therefore tested whether there were any non-native localities in their dataset in the ranges of the focal species of our study (those for which rates of climatic niche change were estimated). We also evaluated whether the inclusion or exclusion of non-native localities (and species with non-native localities) might impact our conclusions.

First, we identified those species with one or more non-native localities. To do this, we identified the continents on which each focal species occurs and identified the continents that comprise the native range from the World Checklist of Poaceae [29]. For each of the 225 focal species in our dataset, we determined the continents on which the minimum and maximum latitudes and longitudes occurred, as these should represent the extremes of their species distributions. We identified species with non-native localities if their minimum or maximum coordinates occurred on a continent that was not part of their native range, as determined by the World Checklist [28]. The continent on which each georeferenced locality occurred was identified using the R packages *rworldmap* [30] and *sp* [31]. We compared each locality to the World Checklist to identify the non-native localities and removed them. The mean value for each climatic variable for each species was then recalculated using only localities from the native range.

A total of 102 species had one or more non-native localities. Data for these species are summarized in appendix S9, and the climatic data for each native locality for each species are given in appendix S10. For many species, the impact of removing non-native localities on the mean values for climatic variables was minor (appendix S9). For example, for 49 species, the raw mean values for all three temperature variables were within 1°C of the means when non-native localities were removed. Other species showed somewhat larger differences, and seven species had no localities in their native ranges. On average, the absolute value of the mean absolute differences between climatic values for the native and non-native ranges were: MAT = 1.207 °C, TMAX = 1.367 °C, TMIN = 1.680 °C, and MAP = 114.118 mm/year. Furthermore, species means before and after removing non-native localities were strongly correlated among the 102 species with one or more non-native localities: MAT: r2 = 0.816, TMAX: r2 = 0.791; TMIN: r2 = 0.785; MAP: r2 = 0.838 (all P < 0.0001), using ordinary least-squares regression.

Finally, we evaluated the impact of removing species with non-native localities on our comparison of rates of niche change and future climate change (tables S10–S16). For these comparisons we focused on the intermediate projections of future climate change (table S10). We first removed all species that had any non-native localities, and then estimated the mean difference in rates of future niche change and climate change for the remaining species (roughly 50% of the original set of species for each tree). This was done separately for each of the three trees (tables S11, S13, S15). We also evaluated the impact of removing only those species that showed more substantial differences in mean climatic values after removing non-native localities (roughly 25% of the original set of species; tables S12, S14, S16). Specifically, these species had a difference in mean values of one or more temperature variables of 1°C or more (before and after removing non-native localities).

The results (table S10) show that the differences between niche rates and rates of future climate change are generally similar in magnitude after excluding species with any or some non-native localities. Importantly, removing species with non-native localities can increase or decrease the difference in rates, depending on the climatic variable, the tree, and whether some or all species with non-native localities are removed. All four variables show increases in some cases, and decreases in others. Based on these results, we conclude that the large differences in rates are not simply an artifact of including some non-native localities.

Note that an alternative approach would be to find and delete all non-native localities in all species (>1,200) and then re-do every analysis in the study. However, these analyses (table S10) suggest that doing so would not change the major conclusions of our study.

**Summarizing within-species variation**

The analyses described above were all based on summarizing variation within species based on the mean value across localities, following standard practice [11, 14]. We also tested whether the mean values for species might be skewed by extreme values at some localities, such that mean values did not reflect overall species values. Therefore, we tested whether there was a tight relationship between the mean and median values among species. This was tested separately for each variable and for the set of species in each of the three trees.

We first tested whether each variable fit a normal distribution before deciding the exact test to apply to address the relationship between mean and median values. Median and mean values for all climatic variables initially failed the Shapiro-Wilk test for normality for the species from the 2010 tree. MAP also failed for the species from the 2014-1 and 2014-2 trees. Variables that failed were ln-transformed and tested again, with all climatic variables still failing for the species of the 2010 tree. Therefore results presented here are either ordinary-least squares (OLS) regressions on MAT, TMAX and TMIN for the 2014 trees, OLS after ln-transforming MAP for both 2014 trees, or from a non-parametric test (Spearman’s rank correlation; SR).

The results (table S17) show extremely tight relationships between mean and values across species, for all four variables and all three datasets (SR: rho = 0.93–0.95; OLS: *r*2 = 0.98–0.99). Therefore, we infer that our main results would not change using median values instead of mean values, and that our main results are not simply an artifact of skewed values due to localities with extreme values within species.

**Additional references (not in main text)**

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