

1 **Predicting the strength of urban-rural clines in a Mendelian polymorphism**
2 **along a latitudinal gradient**

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34 all authors.

35

36 **Abstract**

37 Cities are emerging as models for addressing the fundamental question of whether populations
38 evolve in parallel to similar environments. Here, we examine the environmental factors that drive
39 parallel evolutionary urban-rural clines in a Mendelian trait — the cyanogenic antiherbivore
40 defense of white clover (*Trifolium repens*). We sampled over 700 urban and rural clover
41 populations across 16 cities along a latitudinal transect in eastern North America. In each
42 population, we quantified the frequency of genotypes that produce hydrogen cyanide (HCN), and
43 in a subset of the cities we estimated the frequency of the alleles at the two genes (*CYP79D15*
44 and *Li*) that epistatically interact to produce HCN. We then tested the hypothesis that winter
45 environmental conditions cause the evolution of clines in HCN by comparing the strength of
46 clines among cities located along a gradient of winter temperatures and frost exposure. Overall,
47 half of the cities exhibited urban-rural clines in the frequency of HCN, whereby urban
48 populations evolved lower HCN frequencies. The weakest clines in HCN occurred in cities with
49 the lowest temperatures but greatest snowfall, supporting the hypothesis that snow buffers plants
50 against winter frost and constrains the formation of clines. By contrast, the strongest clines
51 occurred in the warmest cities where snow and frost are rare, suggesting that alternative selective
52 agents are maintaining clines in warmer cities. Additionally, some clines were driven by
53 evolution at only *CYP79D15*, consistent with stronger and more consistent selection on this locus
54 than on *Li*. Together, our results demonstrate that both the agents and targets of selection vary
55 across cities and highlight urban environments as large-scale models for disentangling the causes
56 of parallel evolution in nature.

57 **Impact Summary**

58 Understanding whether independent populations evolve in the same way (i.e., in parallel) when
59 subject to similar environments remains an important problem in evolutionary biology. Urban
60 environments are a model for addressing the extent of parallel evolution in nature due to their
61 convergent environments (e.g. heat islands, pollution, fragmentation), such that two distant cities
62 are often more similar to one another than either is to nearby nonurban habitats. In this paper, we
63 used white clover (*Trifolium repens*) as a model to study the drivers of parallel evolution in
64 response to urbanization. We collected >11,000 plants from urban and rural habitats across 16
65 cities in eastern North America to examine how cities influence the evolution of a Mendelian
66 polymorphism for an antiherbivore defense trait – hydrogen cyanide (HCN). This trait had
67 previously been shown to exhibit adaptive evolution to winter temperature gradients at
68 continental scales. Here we tested the hypothesis that winter environmental conditions cause
69 changes in the frequency of HCN between urban and rural habitats. We found that half of all
70 cities had lower frequency of HCN producing genotypes relative to rural habitats, demonstrating
71 that cities drive parallel losses of HCN in eastern North America. We then used environmental
72 data to understand why cities vary in the extent to which they drive reduction in HCN
73 frequencies. The warmest cities showed the greatest reductions in HCN frequencies in urban
74 habitats, while colder, snowier cities showed little change in HCN between urban and rural
75 habitats. This suggests that snow weakens the strength of natural selection against HCN in cities.
76 However, it additionally suggests alternative ecological or evolutionary mechanisms drive the
77 strong differences in HCN between urban and rural habitats in the warmest cities. Overall, our
78 work highlights urban environments as powerful, large-scale models for disentangling the causes
79 of parallel and non-parallel evolution in nature.

80 **Introduction**

81 The extent to which populations adapt in parallel to similar environmental conditions remains a
82 fundamental problem in evolutionary biology (Losos 2017; Bolnick et al. 2018). High levels of
83 genetic and phenotypic parallelism suggest that adaptive evolution is constrained, increasing our
84 confidence in predicting species' responses to similar conditions (Losos 2011). Despite
85 predictions that similar environments should select for similar alleles and phenotypes, the degree
86 of parallelism observed both within and among species is often imperfect (Bolnick et al. 2018).
87 Genetic constraints, genetic drift, and gene flow, among other processes, can all alter the amount
88 of parallelism among populations (Bolnick et al. 2018; Langerhans 2018). Replication is key to
89 disentangling the many causes and consequences of parallel evolution in nature, from
90 macroevolutionary (Schluter 2000) to microevolutionary scales (Lenski 2017), including
91 leveraging naturally repeated cases of adaption across habitat types (Steiner et al. 2009; Stuart et
92 al. 2017; Langerhans 2018).

93 Urban environments are emerging as models for investigating the causes of (non)parallel
94 (*sensu* Bolnick et al. 2018) evolution among natural populations (Rivkin et al. 2019). Cities tend
95 to share many biotic and abiotic environmental variables such as increased temperatures,
96 elevated pollution, greater habitat fragmentation, and altered structure and composition of
97 ecological communities (McKinney 2006), which can drive parallel adaptive evolution (Reid et
98 al. 2016; Winchell et al. 2016; Yakub and Tiffin 2016; Kern and Langerhans 2018).
99 Additionally, the commonly observed decreased size and increased isolation of urban
100 populations can drive parallel losses of genetic diversity within urban populations due to stronger
101 genetic drift and restricted gene flow (Munshi-South et al. 2016; Mueller et al. 2018). Despite the
102 many examples of parallel responses to urbanization, imperfect parallelism—wherein

103 phenotypes vary in the direction of evolutionary change between replicate urban and non-urban
104 populations—is also common (Thompson et al. 2016; Diamond et al. 2018), although the causes
105 of non-parallel responses to urbanization are poorly understood (Rivkin et al. 2019).

106 Recent work has used the globally-distributed plant, white clover (*Trifolium repens*) as a
107 model for examining parallel evolutionary responses to urbanization. Thompson *et al.* (2016)
108 documented repeated reductions in the frequency of HCN—a chemical plant defense against
109 herbivores — within urban populations across three of the four cities examined in northeastern
110 North America. Observational and experimental data show that HCN is predicted to be costly in
111 the presence of cold winter temperatures because the metabolic components of HCN reduce
112 tolerance to freezing (Daday 1954a, 1965; Kooyers et al. 2018). Consistent with this prediction,
113 correlational data suggest that reduced urban snow cover has led to the observed colder winter
114 ground temperatures in some cities relative to rural areas, which drives selection to reduce HCN
115 frequencies in cities (Thompson et al. 2016). The absence of a cline in one of the four previously
116 studied cities was explained by high urban snow depth in both urban and rural locations, which
117 was hypothesized to insulate plants against the damaging effects of frost (Thompson et al. 2016).
118 If urban-rural variation in snow depth is the only cause of urban-rural clines in cyanogenesis, this
119 leads to an explicitly testable prediction: cities lacking snow should lack urban-rural clines in
120 HCN. However, the two previous studies that have documented urban-rural cyanogenesis clines
121 only sampled northern cities where minimum winter temperatures are below freezing (Thompson
122 et al. 2016; Johnson et al. 2018), preventing a reliable test of the hypothesis that colder winter
123 conditions are the primary agent driving the evolution of urban clines in HCN. Sampling cities
124 that vary in winter temperature and frost exposure is required to understand the environmental
125 conditions under which we expect to find (non)parallel responses of HCN to urbanization.

126 Because neutral processes can sometimes drive parallel phenotypic responses in nature
127 (Losos 2011; Bolnick et al. 2018), it is important to reject neutral explanations before inferring
128 that parallel selection has led to repeated adaptive differentiation. Population genetic simulations
129 suggests that although drift could theoretically cause consistent clines if cities experience more
130 drift (Santangelo et al. 2018a), empirical evidence from neutral microsatellite markers does not
131 support this demography, implying selection is the primary driver of clines. (Johnson et al. 2018;
132 Santangelo et al. 2018a), although three additional lines of evidence would help to distinguish
133 between the roles of selection and drift in generating phenotypic clines in HCN. First, although
134 the two-locus epistatic genetic architecture of HCN can lead to the evolution of clines due to drift
135 (Santangelo et al. 2018a), neutral processes are expected to cause allele frequencies to vary
136 randomly at the two underlying loci (Santangelo et al. 2018a). Thus, repeated clines in the same
137 direction at individual loci underlying HCN can only be explained by selection driving
138 differentiation of urban populations (Santangelo et al. 2018a). Second, an absence of clines in
139 warm cities without snow would be consistent with altered selection in urban environments
140 specifically caused by urban-rural gradients in snow depth and minimum winter ground
141 temperatures. Additionally, clines in cyanogenesis to environmental gradients across North
142 American have arisen via sorting of pre-existing and recurrent gene deletions at underlying loci
143 (*CYP79D15* and *Li*) rather than novel mutations, such that multiple deletion haplotypes segregate
144 at both loci in natural populations (Olsen et al. 2013; Kooyers and Olsen 2014; Olsen and Small
145 2018). The presence of multiple deletion haplotypes in both rural and urban populations would
146 strengthen our inference that cyanogenesis is the target of selection rather than specific genes
147 linked to the HCN loci; selection on linked genes are expected to lead to a single haplotype being
148 overrepresented in urban or rural populations.

149 Here, we combine sampling of over 11,000 white clover plants from 16 cities with
150 publicly available climate data to assess the environmental drivers underlying the evolution of
151 latitudinal and urban-rural clines in cyanogenesis across multiple cities in eastern North
152 America. We begin by assessing the environmental predictors of HCN frequencies along the
153 latitudinal gradient by asking: (1) What regional environmental factors predict mean HCN
154 frequencies within populations? Consistent with previous work (Daday 1954a, 1965, Kooyers
155 and Olsen 2012, 2013), we expected to observe lower HCN frequencies at more northern
156 latitudes due to lower winter temperatures. We then examine urban-rural clines in HCN across
157 16 cities to address the following questions: (2) How common are urban-rural clines among large
158 (> 2 million people) cities in eastern North America? (3) What regional environmental factors
159 predict the strength of clines in cyanogenesis? We predicted that we would observe the weakest
160 clines in cities with high minimum winter temperature (i.e., warm cities) and also in those with
161 high levels of snowfall due to weaker frost-mediated selection against HCN-producing
162 genotypes. (4) Are clines present at both genes underlying cyanogenesis? Repeated clines at
163 both loci underlying HCN would suggest that genetic drift does not cause urban-rural clines in
164 HCN and that selection specifically acts on the production of HCN, as opposed to alternative
165 functions of the individual loci. Finally, we ask: (5) Do urban populations show only a subset of
166 the variation in deletion haplotypes as rural populations? The presence of multiple or fewer
167 deletion haplotypes segregating in urban populations relative to rural populations would suggest
168 that selection favors acyanogenic genotypes directly, rather than linked sites. Our results
169 highlight urban environments as large-scale, replicated systems for addressing the ecological and
170 genetic underpinnings of (non)parallel evolutionary responses in nature.

171

172 **Materials and methods**

173 *Study system*

174 *Trifolium repens* (Fabaceae) is a perennial legume that reproduces clonally through the
175 production of stolons and sexually through self-incompatible, hermaphroditic flowers arranged
176 in dense inflorescences (Burdon 1983). Plants are typically found in grazed or mowed pastures,
177 lawns and meadows where they can maintain large dense populations (Burdon 1983). Native to
178 Eurasia, *T. repens* was introduced to temperate regions worldwide as a forage and nitrogen-
179 fixing crop (Burdon 1983; Kjærgaard 2003). Because of its long history of human-mediated
180 transport, white clover is found in cities all over the world, making it an ideal system for
181 studying patterns of parallel evolution in response to urbanization.

182 Many white clover populations are polymorphic for the production of hydrogen cyanide
183 (HCN), with cyanogenic (HCN present) and acyanogenic (HCN absent) cyanotypes co-occurring
184 (Daday 1958). The molecular and genetic basis at the individual loci underlying the production
185 of both metabolic components involved in HCN production was recently characterized (Olsen et
186 al. 2007, 2008, 2013; Olsen and Small 2018). The *Ac/ac* polymorphism is caused by deletions
187 overlapping the *CYP79D15* locus (hereafter *Ac*), which encodes the cytochrome P450 subunit
188 involved in the synthesis of cyanogenic glycosides (linamarin and lotaustralin) stored in the cell
189 vacuole (Olsen et al. 2008, 2013; Olsen and Small 2018). Plants require at least one functional
190 allele with dominant expression (i.e., *Ac*-) to produce cyanogenic glycosides. Similarly, the *Li/li*
191 polymorphism results from a deletion at the *Li* locus encoding the hydrolyzing enzyme
192 linamarase, which is stored in the cell wall (Kakes 1985); at least one dominant allele (i.e., *Li*-)
193 is required to produce linamarase. Thus, plants require a minimum of one dominant allele at each
194 locus to produce HCN (i.e., cyanotype *Ac*- *Li*-), which is released when cell damage causes

195 cyanogenic glycosides and linamarase to interact (Hughes 1991). If either locus is homozygous
196 for the recessive allele, then a plant lacks HCN and is said to be “acyanogenic” (i.e., cyanotypes
197 *Ac- lili*, *acac Li-*, *acac lili*).

198

199 *Sampling and HCN assays*

200

201 In May and June 2016, we sampled 15 plants from each of 15 to 45 populations (mean = ~38)
202 along urban-rural gradients in each of 12 cities in eastern U.S.A (Fig. 1). Power analyses
203 conducted by resampling the data from Thompson *et al.* (2016) showed that this sampling
204 scheme provides sufficient power to detect even the weakest statistically significant clines in
205 HCN (see supplemental text S2: “Power analyses for sampling design”, Fig. S1). We sampled
206 only large cities (240,000 < Human population size (city area) < 8,200,000; 151 < city area (km²)
207 < 2,300.) because these are likely to have the strongest environmental gradients associated with
208 urbanization. We additionally chose cities along a north-south latitudinal transect such that more
209 southern cities had less snow and warmer winter ground temperatures, which earlier research
210 suggested would weaken selection against HCN in urban environments, leading to weaker or
211 absent clines in southern cities (Thompson *et al.* 2016).

212 Sampling took place in three trips: trip one (May 16th to 23rd, 2016) involved collections
213 from Tampa and Jacksonville, FL, Atlanta, GA, and Charlotte, NC; trip 2 (June 5th to 11th, 2016)
214 from Norfolk, VA, Washington, D.C., and Baltimore, MD, and Philadelphia, PA; and trip 3
215 (June 15th to 20th) from Cleveland and Cincinnati, OH, Pittsburgh, PA, and Detroit, MI. In each
216 city, we targeted populations spaced at least 1 km apart. In each population, we recorded the
217 latitude and longitude coordinates and collected ~6 cm-long white clover stolons with three to

218 four intact leaves; stolons were at least 1.5 m apart to minimize sampling the same clonal
219 genotype. Stolons were placed in sandwich bags and kept on ice in a cooler until being brought
220 back to the lab where they were individually placed in 2 ml microcentrifuge tubes and stored at
221 -80°C until HCN phenotyping. In total, we collected and assayed 6,738 stolons from 459
222 populations across 12 cities. For all downstream analyses, we combined the data from the 12
223 cities described above with the 4 cities (Boston, MA, New York, NY, Toronto and Montréal,
224 CA) originally sampled by Thompson *et al.* (2016). In total, we analyzed urban-rural clines in
225 HCN using 11,908 plants from 721 populations across 16 cities.

226 We used Feigl-Anger assays to determine whether plants were cyanogenic or
227 acyanogenic (Feigl and Anger 1966; Gleadow *et al.* 2011), which uses a simple color change
228 reaction to determine the plant's phenotype. Briefly, we added a single mature leaf to wells in
229 96-well plates with 80 μL of sterile deionized water. Leaf samples were added to alternating
230 wells so that a single plate could accommodate 48 plant samples. The plates were frozen at
231 -80°C to facilitate cell-lysis and release of HCN, and upon removal we macerated the plant
232 tissue with pipette tips. We then covered the plate with Feigl-Anger test paper and incubated the
233 covered plate at 37°C for 3 hr. Cyanogenic individuals (i.e., *Ac- Li-*) produce a blue spot on the
234 filter paper above the well, whereas acyanogenic plants (i.e., *Ac- lili*, *acac Li-*, or *acac lili*)
235 produce no color change.

236 To assess whether clines were driven by changes in the frequency of HCN or clines at
237 either component gene (i.e. *Ac* or *Li*), we determined the frequency of *Ac* and *Li* for a subset of
238 the cities (Atlanta, Baltimore, Charlotte, Cleveland, Jacksonville, New York, Norfolk, and
239 Washington), which was combined with previously-collected allele frequency information for *Ac*
240 and *Li* for the city of Toronto (Thompson *et al.* 2016). For plants that tested negative for HCN,

241 we added either (1) 30 μ L of 10 mM exogenous cyanogenic glycosides (linamarin, Sigma-
242 Aldrich 68264) plus 50 μ L of ddH₂O or (2) 80 μ L of 0.2 EU / mL linamarase (LGC Standards
243 CDX-00012238-100). A positive reaction in (1) indicates a plant producing linamarase (i.e. *acac*
244 *Li*-); a positive reaction in (2) indicates a plant producing glycosides (i.e. *Ac*- *lili*); a negative
245 reaction in both indicates plants that do not produce glycosides nor linamarase (i.e. the double-
246 homozygous recessive genotype, *acac lili*). These assays have been previously confirmed
247 through PCR to reliably determine the cyanotype of individual *T. repens* genotypes (Olsen et al.
248 2007, 2008; Thompson and Johnson 2016). Due to the complete dominance of functional alleles
249 at both loci, we are unable to calculate the frequency of *Ac* or *Li* solely from the phenotyping
250 assays described above (e.g. *AcAc* and *Acac* are indistinguishable). We therefore used the marker
251 frequency (e.g. *Ac*-) to calculate the frequency of *Ac* and *Li* assuming Hardy-Weinberg
252 equilibrium ($p^2 + 2pq + q^2 = 1$), where q^2 represented the observed frequency of homozygous
253 recessive genotypes at *Ac* (i.e. *acac*) or *Li* (i.e. *lili*). While urban-rural HCN clines may not
254 always meet the assumptions of HWE (Johnson et al. 2018; Santangelo et al. 2018a), deviations
255 from HWE are not predicted to greatly impact inferred allele frequencies when homozygous
256 dominant and heterozygous individuals are phenotypically identical, as is the case for HCN
257 (Lachance 2009; Kooyers and Olsen 2013). Analyzing changes in the frequency of *Ac* and *Li* for
258 these nine cities allowed us to assess whether selection is targeting HCN specifically or
259 individual loci underlying HCN production.

260 To examine whether urban and rural populations varied in the frequency of deletion
261 haplotypes at *Ac* or *Li*, we used PCR with previously described forward-reverse primer pairs
262 (Olsen et al. 2014) to identify the relative size of deletions at both loci for individual plants. We
263 extracted total genomic DNA from each of 10 randomly-selected urban and rural plants ($n = 20$)

264 for each of seven cities (Table 1) using a standard CTAB-chloroform extraction method
265 (Agrawal et al. 2012). We chose these cities because they spanned the range of latitudes included
266 in our study, thus reducing potential impact of geographical variation on haplotype frequencies.
267 We included cities that varied in the presence (5 cities) and absence (2 cities) of clines in HCN.
268 We only extracted DNA from plants that were homozygous recessive at both loci (i.e. *acac lili*)
269 because these plants have at least one deletion haplotype at each locus. Each plant was amplified
270 with 6 different primer pairs (3 for each locus), designed to assay the approximate size of the
271 genomic deletion at each locus based on the presence/absence of PCR products (Kooyers and
272 Olsen 2014). Note that larger deletions are masked by smaller deletions when resolving
273 haplotypes on a gel, preventing us from estimating the true frequency of each deletion; we
274 therefore rely only the presence/absence of deletions in our analyses (see “Statistical analyses”
275 below). Using this approach, we were able to assign 88% and 78% of samples to previously
276 described *Li* (n = 4) and *Ac* (n = 2) deletion haplotypes, respectively. The remaining individuals
277 were either newly discovered haplotypes or individuals with intact *Li* and *Ac* genes, the latter
278 indicating either false negative phenotyping or false positive haplotyping assays (or the presence
279 of a silencer modifier locus). We focus our results on the haplotypes that aligned with those
280 previously described by Kooyers and Olsen (2014) to understand whether one
281 deletion haplotype versus multiple haplotypes were segregating in urban and rural populations in
282 cities across our latitudinal transect.

283

284 *Environmental data*

285 To examine the regional abiotic factors that predict the strength of clines in HCN, we retrieved
286 environmental data from publicly available databases. First, we retrieved the minimum winter

287 temperature (MWT, Bio6) — an important predictor of HCN frequencies (Daday 1965; Kooyers
288 and Olsen 2013) — and the maximum summer temperature (MST, Bio5) using the highest
289 resolution data (30 arc seconds; 1 km²) available from the BioClim database (version 1.4,
290 Hijmans et al. 2005). We additionally retrieved the average monthly precipitation (Precip) at 1
291 km² resolution from the same database. Next, we obtained the annual aridity index (AI), monthly
292 average potential evapotranspiration (mPET) and average annual potential evapotranspiration
293 (aPET) at 1 km² resolution from the Consortium for Spatial Information (CGIAR-CSI, Trabucco
294 and Zomer 2009). These three abiotic factors are known predictors of the frequency of HCN and
295 its component genes at the continental scale in North America, Europe and New Zealand
296 (Kooyers and Olsen 2013). BioClim and CGIAR datasets are provided as gridded raster layers,
297 from which we extracted the relevant data for all 721 populations using QGIS v. 3.2.3 (QGIS
298 Development Team 2018).

299 Finally, we obtained daily snow depth, snowfall, maximum temperature, and minimum
300 temperature for all cities for the years 1980 to 2015 from the National Oceanic and Atmospheric
301 Administration's National Centers for Environmental Information
302 (<https://www.ncdc.noaa.gov/cdo-web/datatools/selectlocation>). Importantly, these are regional
303 environmental data obtained from a single weather station for each city located at the nearest
304 international airport; thus, these data represent city-level abiotic conditions and not the
305 conditions extracted for each population.

306 Some filtering and processing of the environmental data was required prior to
307 downstream analyses. First, we took the mean MWT (°C), MST (°C), AI, and aPET across all
308 populations within a city to estimate the city-level minimum winter temperature, maximum
309 summer temperature, aridity, and annual potential evapotranspiration, respectively. Next, we

310 calculated an alternative measure of aridity, the soil moisture deficit (SMD), as the difference
311 between Precip and mPET. This measure of aridity can more reliably estimate regional aridity in
312 cases where both precipitation and PET are low (Thompson et al. 2014). We calculated SMD for
313 all months from May to September to represent the plant growing season, and again took the
314 mean of these measurements across all populations as our measure of city-level SMD. Finally,
315 we used NOAA's weather station data to estimate regional snow depth (cm), snowfall (cm), and
316 the number of days below zero with no snow cover, a measure of frost exposure that has been
317 previously associated with urban-rural clines in HCN (Thompson et al. 2016). To retrieve these
318 estimates, we first filtered the weather data to remove missing data and only included
319 observations from January and February as these are the coldest winter months in eastern North
320 America. We additionally removed observations from years where data was unavailable for both
321 January and February and eliminated months with fewer than 10 days of weather data. Following
322 filtering, we retained 31,005 weather observations, with a mean of 1937 observations per city
323 (Table S1). From these data, we calculated the mean snow depth, mean snowfall, and the number
324 of days below 0 °C with no snow cover (i.e. snow depth of 0 cm) and took the mean of these
325 measurements across all years as our estimates of regional winter conditions.

326

327 *Statistical analyses*

328

329 For brevity, we only briefly describe the statistical procedures used throughout the paper; a
330 detailed description of all analyses can be found in the supplementary materials (text S1:
331 "Detailed statistical analyses"). We first tested whether, on average, cities varied in mean HCN
332 frequencies and whether urbanization influenced HCN frequencies. To do this, we fit an

333 ANOVA using type III SS with within-population HCN frequencies as the response variable and
334 city, standardized distance to the urban center and the city \times distance interaction as predictors.
335 We used distance to the urban center as a measure of urbanization as this is highly correlated
336 with % impervious surface ($R^2 = 0.64$, Johnson et al. 2018) and sufficiently captures variation in
337 HCN frequencies across urban-rural gradients (Thompson et al. 2016; Johnson et al. 2018).
338 Because urban-rural transects varied in length, we scaled distance within cities between 0 (most
339 urban) and 1 (most rural). In our model, a significant effect of City suggests that mean HCN
340 frequencies vary across the 16 cities. A significant Distance term means that across all cities,
341 HCN frequencies vary in parallel across the urban-rural transect (i.e. parallel clines in HCN
342 frequencies), while a significant City \times Distance interaction indicates the strength or direction of
343 clines in HCN varies across cities. The significant effects of City and the City \times Distance
344 interaction in our model (see “Results”) justify an examination of the environmental predictors
345 of mean HCN frequencies and variation in the strength of clines across cities, respectively.

346 To assess the environmental predictors of mean HCN frequencies across cities along our
347 latitudinal gradient, we fit the following linear model: mean HCN frequency \sim PC1_{HCN} + # days
348 $< 0^\circ\text{C}$ with no snow + annual aridity index + soil moisture deficit, where PC1_{HCN} is a composite
349 axis generated via PCA that explained 90.2% of the variation in MST, MWT, summer
350 precipitation, annual PET, and snowfall, all of which were highly correlated and individually
351 significantly predicted variation in HCN frequencies. Lower values of PC1_{HCN} represented cities
352 with higher summer temperatures, higher minimum winter temperatures, higher summer
353 precipitation, greater potential evapotranspiration, and lower snowfall. We assessed significance
354 of model predictors using an AIC_c-based multi-model selection and averaging process.

355 Upon confirming that cities varied significantly in the strength of urban-rural phenotypic
356 clines using ANOVA, we used a similar approach to that described above to examine the
357 environmental predictors of the strength of urban-rural phenotypic clines in HCN. For each city,
358 we first fit a linear regression with the proportion of cyanogenic plants within each population as
359 the response variable and standardized distance to the urban center as the sole predictor. Note
360 that cities that showed significant changes in HCN frequency with distance (Table 1) were also
361 significant following Bonferroni correction of logistic regressions using data from individual
362 plants (i.e., 1 for HCN+, 0 for HCN-). We extracted the slope (i.e. β coefficient) from each
363 city's model as a measure of the strength of the clines and examined the environmental
364 predictors of cline strength by running the following model: $\beta \sim PC1_{slope}$, where $PC1_{slope}$ is a
365 composite axis generated via PCA that explains 92.8% of the variation in snow depth, snowfall,
366 MWT, and MST, all of which were highly correlated and on their own significantly predicted
367 variation in the strength of clines (see text S1). Cities with low values along $PC1_{slope}$ experience
368 little snow, higher minimum winter temperature, and higher maximum summer temperature.

369 We explored whether clines were present at each of the two loci underlying HCN. This
370 was done by fitting linear models in which the allele frequencies for the *Ac* and *Li* loci were
371 treated individually as a response variable in separate analyses, which was regressed against
372 standardized distance to the urban core as a predictor. Finally, to examine variation in deletion
373 haplotypes across urban and rural habitats, we used the raw counts of deletion haplotypes at each
374 locus to calculate Simpson's diversity index for deletions in urban and rural habitats for each
375 city, which accounts for both presence/absence and abundance of haplotypes in each population
376 when estimating diversity. We fit Simpson's diversity index as the response variable in a linear
377 model with habitat type (i.e. urban vs. rural) as the sole predictor such that a significant effect of

378 habitat suggested differences in deletion haplotype diversity among urban and rural habitats. All
379 analyses were performed in R v. 3.6.0 (R Core Team 2019).

380

381 **Results**

382

383 *Variation in HCN frequencies in cities along a latitudinal gradient*

384

385 The mean frequency of HCN varied across the 16 cities from 19% (New York) to 99% (Tampa)
386 (Effect of City: $F_{15,689} = 18.48$, $P < 0.001$, Table 1, Fig. 1, Fig. 2), with the highest frequencies at
387 the most southern latitudes (Fig. S2). The number of days $< 0^{\circ}\text{C}$ with no snow cover and PC1_{HCN}
388 together accounted for 94.1% of the variation in mean HCN frequencies among cities (Table S4).
389 Specifically, HCN frequencies decreased by 1.5% for every additional day below 0°C with no
390 snow cover ($\beta = -0.015$, $z = 8.77$, $P < 0.001$, Table S5, Fig. 3a), and by 6.4% for every unit
391 increase along PC1_{HCN} ($\beta = -0.064$, $z = 7.0$, $P < 0.001$, Table S5, Fig. 3b), suggesting HCN
392 frequencies decrease in colder, wetter environments that get more snow. Annual aridity index
393 was not significant predictor of mean HCN frequencies in our model ($P = 0.36$, Table S5) while
394 soil moisture deficit was not included in any top models following model selection and
395 averaging.

396

397 *Environmental predictors of urban-rural clines in HCN frequencies*

398

399 On average, urbanization was associated with reduced HCN frequencies across cities, whereby
400 the main effect of standardized distance from the urban center was positively associated with the

401 frequency of HCN within *T. repens* populations (main effect of Distance, $F_{1,689} = 36.42$, $P <$
402 0.001 , Fig. 2). In a model with unstandardized distance as a predictor, this translated into an
403 average increase in HCN frequency of 0.3 % per km from the urban center. However, the
404 strength of urban-rural phenotypic clines in HCN varied across cities (Distance \times City
405 interaction: $F_{15,689} = 3.26$, $P < 0.001$, Table 1, Fig. 2). The strength of urban-rural clines
406 decreased with increasing values along PC1_{slope} ($R^2 = 28.4\%$, $\beta = -0.036$, $t_{13} = -2.27$, $P = 0.04$,
407 Table 2, Fig. 4), implying that the strongest clines occurred in the warmest environments and the
408 weakest clines occurred in regions of low temperature and high snowfall/depth.

409

410 *Clines at loci underlying HCN and deletion haplotype frequencies*

411

412 Of the 16 cities surveyed in this study, we assayed the genotype at the two underlying genes in
413 nine cities, six of which showed significant clines in HCN (Table 1). Of the six cities with
414 significant clines, three (Atlanta, Jacksonville, Toronto) showed significant linear clines at both
415 *Ac* and *Li*, three (New York, Norfolk, Washington) showed significant linear clines only at *Ac*,
416 whereas no cities had a significant linear cline only at *Li*. Significant clines at *Ac* and *Li* were
417 always in the same direction as clines in HCN (i.e., lower frequencies of the dominant alleles *Ac*
418 and *Li* in urban populations). None of the three cities that lacked a cline in HCN showed a cline
419 at either underlying gene.

420

421 All deletion haplotypes at *Ac* and *Li* identified previously in this system were found in
422 each city, and their relative frequencies did not vary for either locus between urban and rural
423 populations (fig. S3 and S4). Haplotype diversity (*Ac*: Simpson's $D_{\text{rural}} = 0.41$, $D_{\text{urban}} = 0.38$, $t_{11} =$
 -0.23 , $P = 0.82$; *Li*: Simpson's $D_{\text{rural}} = 0.60$, $D_{\text{urban}} = 0.52$, $t_{11} = -0.74$, $P = 0.47$) did not vary

424 across urban and rural habitats for either locus. Together, these results suggest that no specific
425 deletion haplotype is favored in urban habitats at either *Ac* or *Li* .

426

427 **Discussion**

428 We combined field sampling of white clover populations from large eastern North American
429 cities with environmental data to assess the environmental predictors of cyanogenesis on a
430 continental scale and of urban-rural gradients in HCN frequencies. Several key results are most
431 important to answering our research questions. As expected, HCN frequencies decreased
432 northward across the continent as frost exposure increased (question 1). Urban-rural
433 cyanogenesis clines occurred in half of the cities studied (question 2) and the strongest clines
434 occurred in the warmest environments (question 3). Clines in HCN were matched by clines at
435 one or both of the loci underlying HCN, and these clines were always in the same direction
436 (question 4). Finally, the diversity of deletion haplotypes among acyanogenic plants was
437 consistent across urban and rural populations of multiple cities (question 5). Together, these
438 results provide compelling evidence that selection is driving parallel evolution of cyanogenesis
439 clines across multiple large urban centers in North America, although regionally cold and snowy
440 climates dampen parallel responses of HCN to urbanization. Below, we discuss our results in the
441 context of the environmental drivers of HCN evolution at the scale of entire continents and
442 individual cities.

443

444 *Environmental predictors of HCN frequencies*

445 The cyanogenesis polymorphism has long served as a model for assessing the climatic drivers of
446 adaptation in natural populations. Pioneering work in the 1950's and 1960's identified cold

447 winter temperatures as key drivers of reduced HCN frequencies at northern latitudes and higher
448 altitudes (Daday 1954a,b, 1958, 1965). More recent work corroborated the finding that colder
449 environments have reduced cyanogenesis (Ganders 1990; Kooyers and Olsen 2012, 2013) and
450 additionally identified aridity as a correlate of HCN frequencies, with more HCN in drier
451 habitats due to selection favoring plants producing cyanogenic glucosides (*Ac*) (Kooyers and
452 Olsen 2013; Kooyers et al. 2014). Our results are consistent with previous work demonstrating a
453 cost to producing HCN or its metabolic components in frost-prone habitats (Daday 1954a, 1958,
454 1965; Ganders 1990; Kooyers and Olsen 2013; Kooyers et al. 2018): northern cities with lower
455 winter temperatures and greater frost exposure had reduced cyanogenesis than southern cities. In
456 contrast to previous work (Kooyers and Olsen 2013), we did not identify aridity as an important
457 predictor of mean HCN frequencies, possibly because the latitudinal transect sampled here
458 spanned a shallow aridity gradient (annual aridity index range: 0.84 – 1.22) and steeper gradients
459 may be necessary to detect aridity as an important correlate of HCN frequencies (e.g. New
460 Zealand cline, aridity index range: 0.5941– 4.8569, Kooyers and Olsen 2013).

461

462 *Urban-rural clines in cyanogenesis*

463 Although the repeated appearance of clines in different cities suggests that selection is acting on
464 HCN, population genetic simulations demonstrated that genetic drift can also generate similar
465 patterns (Santangelo et al. 2018a). Thus, the presence of repeated clines in HCN is insufficient
466 evidence for the role of selection to drive adaptation of urban populations. Two current lines of
467 evidence suggest a negligible role of genetic drift in driving urban HCN clines. First, observed
468 clines in HCN are substantially stronger than those expected under realistic gradients in the
469 strength of drift alone (Santangelo et al. 2018a), suggesting that other processes are additionally

470 contributing to the presence of clines. Second, recent population genetic analyses show no
471 increased strength of genetic drift in urban white clover populations, and clines are evolving
472 despite substantial gene flow between urban and nonurban populations, consistent with natural
473 selection driving local adaptation of urban populations (Johnson et al. 2018).

474 Two additional lines of evidence presented here solidify the role of selection rather than drift
475 in driving the formation urban-rural HCN clines. First, the presence of repeated clines in the
476 same direction at individual loci underlying HCN strongly implicates selection since genetic drift
477 is expected to drive random fluctuations in allele frequencies at a single locus (Santangelo et al.
478 2018a). Second, the negative relationship between the strength of clines and regional winter
479 conditions suggests that latitudinal variation in winter temperature and snow depth—or
480 something correlated with it—modulates the strength of selection along urban-rural gradients,
481 driving phenotypic clines in cyanogenesis. Additionally, the presence of clines at each individual
482 locus, and equivalent deletion haplotype diversity in urban and rural populations across multiple
483 cities, both suggest that selection favors acyanogenic plants rather than alternative biological
484 functions of individual loci or because of genes tightly linked to particular deletion haplotypes.

485 Environmental heterogeneity among ‘replicate’ environments can reduce the extent of
486 parallel evolution (Stuart et al. 2017). Previous work in white clover identified colder winter
487 temperatures in urban populations as a putative mechanism driving reduced HCN frequencies in
488 urban environments, which was alleviated in cities with high snowfall (Thompson et al. 2016).
489 Based on this earlier work, we predicted the weakest clines in cities with high mean winter
490 temperature or high snowfall due to the absence of frost-mediated selection against HCN in these
491 cities. Consistent with this prediction, cities with high snowfall (i.e. high values along $PC1_{\text{slope}}$)
492 had the weakest clines, potentially due to snow buffering plants from frigid temperatures and

493 weakening frost-mediated selection against HCN-producing genotypes. However, the strongest
494 clines occurred in the warmest cities (i.e. low values along $PC1_{\text{slope}}$), contrary to our predictions.
495 Importantly, this provides no information about whether lower winter temperatures in cities is an
496 important selective agent; urban frost may still be important in frost-prone cities with shallower
497 urban-rural gradients in snow depth, as suggested by currently available data (Thompson et al.
498 2016). However, this does suggest that alternative mechanisms must drive the evolution of clines
499 in warmer cities where frost is uncommon. Indeed Atlanta, which gets little snow (mean snowfall
500 = 0.07 cm/year) and is relatively warm throughout the winter months (average minimum winter
501 temperature = -0.43 °C) contained the strongest phenotypic cline in HCN observed in any city to
502 date ($\beta = 0.36$, Table 1).

503 The stronger clines in warmer cities suggests that regional temperature modulates the
504 strength of selection along urban-rural clines in some cities. Given that cyanogenesis functions as
505 an antiherbivore defense (Dirzo and Harper 1982; Thompson and Johnson 2016; Santangelo et
506 al. 2018b), some clines may be explained by differential herbivory among urban and rural
507 populations if urbanization reduces herbivore damage (Raupp et al. 2010; Moreira et al. 2019).
508 Although previous experimental work found a negligible role of herbivory as a driver of urban
509 clines in HCN (Thompson et al. 2016), this work was performed in a single northern city
510 (Toronto). Since herbivory often increases with warmer temperatures (Lemoine et al. 2014), the
511 role of herbivory in generating urban-rural clines in HCN may be more important in warmer,
512 southern cities. Additional work quantifying the strength of clover-herbivore interactions, and
513 biotic interactions more generally, in these cities is needed. Alternatively, recent experimental
514 data suggests a cost to producing the metabolic components of HCN in stressful environments,
515 especially for cyanogenic glucosides (Kooyers et al. 2018). If environmental stressors are

516 stronger in cities (e.g. frost, salinity, pollution, etc.), costs involved in the production of the
517 metabolic components of HCN may result in selection against these genes and lower frequencies
518 in urban populations. Consistent with this hypothesis, some urban-rural clines in HCN were
519 mirrored only by clines at *Ac*, suggesting selection may be acting on this locus due to its greater
520 metabolic costs (Kooyers et al. 2018).

521

522 *Conclusions and future directions*

523 We have demonstrated the repeated evolution of urban-rural cyanogenesis clines across eastern
524 North American cities. A major goal for future work in this system entails distinguishing among
525 the targets of selection across replicate clines (i.e., *HCN* vs. *Ac*. vs. *Li*) and disentangling the
526 numerous ecological (e.g., environmental factors) and evolutionary (e.g., selection, drift) drivers
527 of (non)parallel responses of HCN to urbanization. This work will require quantifying a broad
528 array of environmental factors at a finer-scale (e.g. population-level) in cities spanning all
529 continents. White clover is a natural model for understanding how cities drive parallel evolution
530 on a global scale due to its ubiquity across the globe and ease of sampling and phenotyping. Such
531 work would advance our understanding of how cities influence the evolution of populations in
532 our own backyards, and further cement the utility of cities as useful models for understanding the
533 causes and consequences of parallel evolution in nature.

534

535 **References**

- 536
- 537 Agrawal, A. A., A. P. Hastings, M. T. J. Johnson, J. L. Maron, and J. Salminen. 2012. Insect
538 herbivores drive real-time ecological and evolutionary change in plant populations. *Science*.
539 338:113–116.
- 540 Bolnick, D. I., R. D. H. Barrett, K. B. Oke, D. J. Rennison, and Y. E. Stuart. 2018. (Non) Parallel
541 Evolution. *Annu. Rev. Ecol. Evol. Syst.* 303–330.
- 542 Burdon, J. J. 1983. Biological flora of the British Isles: *Trifolium repens* L. *J. Ecol.* 71:307–330.
- 543 Daday, H. 1954a. Gene frequencies in wild populations of *Trifolium repens* I. Distribution by
544 latitude. *Heredity.* 8:61–78.
- 545 Daday, H. 1954b. Gene frequencies in wild populations of *Trifolium repens* II. Distribution by
546 altitude. *Heredity.* 8:377–384.
- 547 Daday, H. 1958. Gene frequencies in wild populations of *Trifolium repens* L III. World
548 distribution. *Heredity.* 12:169–184.
- 549 Daday, H. 1965. Gene frequencies in wild populations of *Trifolium repens* L IV. Mechanism of
550 natural selection. *Heredity.* 20:355–365.
- 551 Diamond, S. E., L. D. Chick, A. Perez, S. A. Strickler, and R. A. Martin. 2018. Evolution of
552 thermal tolerance and its fitness consequences: parallel and non-parallel responses to urban
553 heat islands across three cities. *Proc. R. Soc. B Biol. Sci.* 285:20180036.
- 554 Dirzo, R., and J. L. Harper. 1982. Experimental studies on slug-plant interactions: III .
555 differences in the acceptability of individual plants of *Trifolium repens* to slugs and snails.
556 *J. Ecol.* 70:101–117.
- 557 Feigl, F., and V. Anger. 1966. Replacement of benzidine by copper ethylacetoacetate and tetra
558 base as spot-test reagent for hydrogen cyanide and cyanogen. *Anal.* 91:282–284.
- 559 Ganders, F. R. 1990. Altitudinal clines for cyanogenesis in introduced populations of white
560 clover. *Heredity.* 64:387–390.
- 561 Gleadow, R., N. Bjarnholt, K. Jørgensen, J. Fox, and R. Miller. 2011. Research methods in plant
562 science, Vol. 1. Pp. 283–310 in S. S. Narwal, L. Szajdak, and D. A. Sampietro, eds. Soil
563 allelochemicals. Studium Press, Houston.
- 564 Hijmans, R. J., S. E. Cameron, J. L. Parra, P. G. Jones, and A. Jarvis. 2005. Very high resolution
565 interpolated climate surfaces for global land areas. *Int. J. Climatol.* 25:1965–1978.
- 566 Hughes, M. A. 1991. The Cyanogenic Polymorphism in *Trifolium repens* L (White Clover).
567 *Heredity.* 66:105–115.
- 568 Johnson, M. T. J., C. Prasad, M. Lavoignat, and H. S. Saini. 2018. Contrasting the effects of
569 natural selection, genetic drift and gene flow on urban evolution in white clover (*Trifolium*
570 *repens*). *Proc. R. Soc. B Biol. Sci.* 285:20181019.
- 571 Kakes, P. 1985. Linamarase and other fl-glucosidases are present in the cell walls of *Trifolium*
572 *repens* L. leaves. *Planta* 166:156–160.
- 573 Kern, E. M. A., and R. B. Langerhans. 2018. Urbanization drives contemporary evolution in
574 stream fish. *Glob. Chang. Biol.* 1–13.
- 575 Kjærsgaard, T. 2003. A plant that changed the world: the rise and fall of clover 1000-2000.
576 *Landsc. Res.* 28:41–49.
- 577 Kooyers, N. J., L. R. Gage, A. Al-Lozi, and K. M. Olsen. 2014. Aridity shapes cyanogenesis
578 cline evolution in white clover (*Trifolium repens* L.). *Mol. Ecol.* 23:1053–1070.
- 579 Kooyers, N. J., B. Hartman Bakken, M. C. Ungerer, and K. M. Olsen. 2018. Freeze-induced
580 cyanide toxicity does not maintain the cyanogenesis polymorphism in white clover

- 581 (*Trifolium repens*). *Am. J. Bot.* 105:1224–1231.
- 582 Kooyers, N. J., and K. M. Olsen. 2014. Adaptive cyanogenesis clines evolve recurrently through
583 geographical sorting of existing gene deletions. *J. Evol. Biol.* 27:2554–2558.
- 584 Kooyers, N. J., and K. M. Olsen. 2012. Rapid evolution of an adaptive cyanogenesis cline in
585 introduced North American white clover (*Trifolium repens* L.). *Mol. Ecol.* 21:2455–2468.
- 586 Kooyers, N. J., and K. M. Olsen. 2013. Searching for the bull’s eye: agents and targets of
587 selection vary among geographically disparate cyanogenesis clines in white clover
588 (*Trifolium repens* L.). *Heredity.* 111:495–504.
- 589 Lachance, J. 2009. Detecting selection-induced departures from Hardy-Weinberg proportions.
590 *Genet. Sel. Evol.* 41:1–6.
- 591 Langerhans, R. B. 2018. Predictability and parallelism of multitrait adaptation. *J. Hered.* 109:59–
592 70.
- 593 Lemoine, N. P., D. E. Burkepile, and J. D. Parker. 2014. Variable effects of temperature on
594 insect herbivory. *PeerJ* 2:e376.
- 595 Lenski, R. E. 2017. Convergence and divergence in a long-term experiment with bacteria. *Am.*
596 *Nat.* 190:S57–S68.
- 597 Losos, J. B. 2011. Convergence, adaptation, and constraint. *Evolution.* 65:1827–1840.
- 598 Losos, J. B. 2017. *Improbable destinies: Fate, chance, and the future of evolution.* Riverhead
599 books, New York, NY.
- 600 McKinney, M. L. 2006. Urbanization as a major cause of biotic homogenization. *Biol. Conserv.*
601 127:247–260.
- 602 Moreira, X., L. Abdala-roberts, J. C. Berny, F. Covelo, R. De Mata, M. Francisco, B. Hardwick,
603 R. M. Pires, T. Roslin, D. S. Schigel, P. J. G. Jan, B. G. H. Timmermans, L. J. A. Van Dijk,
604 B. Castagneyrol, and A. J. M. Tack. 2019. Impacts of urbanization on insect herbivory and
605 plant defences in oak trees. *Oikos* 128:113–123.
- 606 Mueller, J., K. Heiner, S. Boerno, J. Tella, M. Carrete, and B. Kempnaers. 2018. Evolution of
607 genomic variation in the burrowing owl in response to recent colonization of urban areas.
608 *Proc. R. Soc. B Biol. Sci.* 285:20180206.
- 609 Munshi-South, J., C. P. Zolnik, and S. E. Harris. 2016. Population genomics of the
610 Anthropocene: urbanization is negatively associated with genome-wide variation in white-
611 footed mouse populations. *Evol. Appl.* 9:546–564.
- 612 Olsen, K. M., S.-C. Hsu, and L. L. Small. 2008. Evidence on the molecular basis of the *Ac/ac*
613 adaptive cyanogenesis polymorphism in white clover (*Trifolium repens* L.). *Genetics*
614 179:517–26.
- 615 Olsen, K. M., N. J. Kooyers, and L. L. Small. 2014. Adaptive gains through repeated gene loss:
616 parallel evolution of cyanogenesis polymorphisms in the genus *Trifolium* (Fabaceae).
617 *Philos. Trans. R. Soc. B Biol. Sci.* 369:20130347–20130347.
- 618 Olsen, K. M., N. J. Kooyers, and L. L. Small. 2013. Recurrent gene deletions and the evolution
619 of adaptive cyanogenesis polymorphisms in white clover (*Trifolium repens* L.). *Mol. Ecol.*
620 22:724–738.
- 621 Olsen, K. M., and L. L. Small. 2018. Micro- and macroevolutionary adaptation through repeated
622 loss of a complete metabolic pathway. *New Phytol.* 219:757–766.
- 623 Olsen, K. M., B. L. Sutherland, and L. L. Small. 2007. Molecular evolution of the *Li/li* chemical
624 defence polymorphism in white clover (*Trifolium repens* L.). *Mol. Ecol.* 16:4180–4193.
- 625 QGIS Development Team. 2018. QGIS geographic information system.
- 626 R Core Team. 2019. R: A language and environment for statistical computing. Vienna, Austria.

- 627 URL <https://www.R-project.org/>
628 Raupp, M. J., P. M. Shrewsbury, and D. Herms. 2010. Ecology of herbivorous arthropods in
629 urban landscapes. *Annu. Rev. Entomol.* 55:19–38.
- 630 Reid, N. M., D. A. Proestou, B. W. Clark, W. C. Warren, J. K. Colbourne, J. R. Shaw, S. I.
631 Karchner, M. E. Hahn, D. Nacci, M. F. Oleksiak, D. L. Crawford, and A. Whitehead. 2016.
632 The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild
633 fish. *Science.* 354:1305 LP-1308.
- 634 Rivkin, L. R., J. S. Santangelo, M. Alberti, M. F. J. Aronson, C. W. de Keyzer, S. E. Diamond,
635 M.-J. Fortin, L. J. Frazee, A. J. Gorton, A. P. Hendry, Y. Liu, J. B. Losos, J. S. MacIvor, R.
636 A. Martin, M. McDonnell, L. S. Miles, J. Munshi-South, R. Ness, A. E. M. Newman, M. R.
637 Stothart, P. Theodorou, K. A. Thompson, B. C. Verrelli, A. Whitehead, K. M. Winchell,
638 and M. T. J. Johnson. 2019. A roadmap for urban evolutionary ecology. *Evol. Appl.*
639 12:384–398.
- 640 Santangelo, J. S., M. T. J. Johnson, and R. W. Ness. 2018a. Modern spandrels: the roles of
641 genetic drift, gene flow and natural selection in the evolution of parallel clines. *Proc. R.*
642 *Soc. B Biol. Sci.* 285:20180230.
- 643 Santangelo, J. S., K. A. Thompson, and M. T. J. Johnson. 2018b. Herbivores and plant defenses
644 affect selection on plant reproductive traits more strongly than pollinators. *J. Evol. Biol.*
645 32:4–18.
- 646 Schluter, D. 2000. *The ecology of adaptive radiation.* Oxford University Press, Oxford, UK.
- 647 Steiner, C. C., H. Römpler, L. M. Boettger, T. Schöneberg, and H. E. Hoekstra. 2009. The
648 genetic basis of phenotypic convergence in beach mice: Similar pigment patterns but
649 different genes. *Mol. Biol. Evol.* 26:35–45.
- 650 Stuart, Y. E., T. Veen, J. N. Weber, D. Hanson, M. Ravinet, B. K. Lohman, C. J. Thompson, T.
651 Tasneem, A. Doggett, R. Izen, N. Ahmed, R. D. H. Barrett, A. P. Hendry, C. L. Peichel, and
652 D. I. Bolnick. 2017. Contrasting effects of environment and genetics generate a continuum
653 of parallel evolution. *Nat. Ecol. Evol.* 1:1–7.
- 654 Thompson, K. A., B. C. Husband, and H. Maherali. 2014. Climatic niche differences between
655 diploid and tetraploid cytotypes of *Chamerion angustifolium* (Onagraceae). *Am. J. Bot.*
656 101:1868–1875.
- 657 Thompson, K. A., and M. T. J. Johnson. 2016. Antiherbivore defenses alter natural selection on
658 plant reproductive traits. *Evolution.* 70:796–810.
- 659 Thompson, K. A., M. Renaudin, and M. T. J. Johnson. 2016. Urbanization drives the evolution
660 of parallel clines in plant populations. *Proc. R. Soc. B Biol. Sci.* 283:20162180.
- 661 Trabucco, A., and R. J. Zomer. 2009. Global aridity index (global-aridity) and global potential
662 evapo-transpiration (global-PET) geospatial database.
- 663 Winchell, K. M., R. G. Reynolds, S. R. Prado-Irwin, A. R. Puente-Rolón, and L. J. Revell. 2016.
664 Phenotypic shifts in urban areas in the tropical lizard *Anolis cristatellus*. *Evolution.*
665 70:1009–1022.
- 666 Yakub, M., and P. Tiffin. 2016. Living in the city: urban environments shape the evolution of a
667 native annual plant. *Glob. Chang. Biol.* 23:2082–2089.
- 668

669 **Tables**

670

671 **Table 1:** Beta coefficients (i.e. slope) and *P*-values from linear models testing the change in the frequency of HCN, *Ac*, or *Li* with
 672 increasing distance (standardized) from the urban center for each of 16 cities. Also shown are the total number of populations and
 673 plants sampled in each city, and whether deletion haplotypes were identified in urban and rural population of that city. Bolded terms
 674 represent linear clines that were significant at *P* < 0.05. Grey boxes represent cities where we did not quantify the frequency at the
 675 genes underlying HCN.

City	# populations	# plants	Haplotype	β_{HCN}	β_{Ac}	β_{Li}
Atlanta	45	654	Y	0.362***	0.263**	0.161[‡]*
Baltimore	39	584	Y	0.031	0.065	0.031
Boston	44	876	N	0.119*	—	—
Charlotte	40	589	N	0.070 [‡]	-0.077	0.003 [‡]
Cincinnati	40	588	N	0.035	—	—
Cleveland	40	594	Y	0.093	0.067	0.019
Detroit	40	593	N	0.052	—	—
Jacksonville	35	500	Y	0.272[‡]***	0.202**	0.292[‡]*
Montreal	49	969	N	-0.057	—	—
New York	48	946	Y	0.145*	0.204*	0.033
Norfolk	40	585	Y	0.337***	0.358***	0.038
Philadelphia	40	588	N	-0.031	—	—
Pittsburgh	40	590	N	0.069	—	—
Tampa [†]	15	215	N	-0.029	—	—
Toronto [□]	121	2379	N	0.283***	0.218**	0.271***
Washington, D.C.	45	658	Y	0.175*	0.326**	0.062 [‡]

676

Significance of β values: **P* < 0.05; ***P* < 0.01, ****P* < 0.001

677

[‡] Cities were better fit by a quadratic model (see online supplementary text: “Assessing the fit on non-linear clines”) and showed a significant non-linear change in the frequency of HCN, *Ac*, or *Li* with increasing distance from the urban center.

678

679

[†] Tampa was excluded from the analysis testing the environmental predictors of the strength of clines since it was functionally fixed for HCN (Fig. 1).

680

[□] Number of populations and plants for Toronto reflects the total across three urban-rural transects. The coefficients and *P*-values here are from a model that

681

includes all populations along all three transects since all three transects showed significant clinal variation when analyzed independently (Thompson *et al.* 2016)

682 **Figure legends**

683

684 **Figure 1:** Map of 16 cities from which we sampled white clover populations along urban-rural
685 transects. Pie charts represent the mean frequency of HCN (black = HCN+, white = HCN-) for
686 each city when averaged across all populations along the transect. Map color depicts the gradient
687 in the minimum winter temperature (MWT, °C) taken from BioClim.

688

689 **Figure 2:** Urban-rural clines in the frequency of HCN within populations of *Trifolium repens*
690 across 16 cities in eastern North America. The frequency of HCN within *T. repens* population is
691 plotted against the standardized distance from the urban center. Solid lines represent linear
692 regressions from cities where the phenotypic cline in HCN was significant at $P < 0.05$, whereas
693 dashed lines are cities that lack significant clinal variation. The thick black line represents the
694 main effect of standardized distance on HCN frequencies, averaged across all cities.

695

696 **Figure 3:** Mean HCN frequency was influenced by (a) the number of days below 0 °C with no
697 snow cover — a measure of frost exposure — and (b) PC1_{HCN}, a component axis accounting for
698 90.2 % of the variation in maximum summer temperature (°C, Bio5), minimum winter
699 temperature (°C, Bio6), annual potential evapotranspiration (mm), monthly summer precipitation
700 (mm), and snowfall (cm) (inset in (b)). City labels are slightly jittered to avoid overlap, if
701 necessary. Cities with low values along PC1_{HCN} have high summer temperatures, high minimum
702 winter temperatures, high summer precipitation and potential evapotranspiration, and low
703 snowfall, whereas cities with high values along PC1_{HCN} have the opposite. (City abbreviations:
704 Jacksonville (Jax); Tampa (Tpa); Atlanta (Atl); Norfolk (Nor); Charlotte (Clt); Toronto (Tor);
705 Montréal (Mtl); Detroit (Det); Washington D.C. (DC); Cleveland (Clv); New York (NY);
706 Pittsburgh (Pgh); Boston (Bos); Baltimore (Blt); Cincinnati (Cin); Philadelphia (Phl)).

707

708 **Figure 4:** The strength of urban-rural clines in HCN was influenced by PC1_{Slope}, a composite
709 axis that accounts for 92.8% of the variation in minimum winter temperature (°C, bio6),
710 maximum summer temperature (°C, bio5), snowfall (cm), and snow depth (cm). City labels are
711 slightly jittered to avoid overlap, if necessary. Bolded cities show significant linear changes in
712 HCN along urbanization gradients. Cities with low values along PC1_{Slope} have little snow and
713 higher minimum winter and maximum summer temperatures, whereas cities with high values
714 along PC1_{Slope} have the opposite. City abbreviations are the same as in Fig. 3.

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