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Jesús Villellas, William F. Morris and María B. García **Running head:** Stochastic LTRE across spatial scales Variation in stochastic demography between and within central and peripheral regions in a widespread short-lived herb Jesús Villellas^{1, 4}, William F. Morris^{2, 3, 5} and María B. García^{1, 6} ¹Instituto Pirenaico de Ecología (IPE-CSIC), Apdo. 13034, 50080 Zaragoza, Spain. Fax: 0034976716019. ²Biology Department, Duke University, Box 90338, Durham, North Carolina 27708-0338 USA. Present address: ³ Department of Ecology and Genetics, Uppsala University, Norbyvägen 18D, 752 36 Uppsala, Sweden. E-mail addresses: ⁴jesusvi@ipe.csic.es ⁵wfmorris@duke.edu ⁶mariab@ipe.csic.es

26 Abstract

27 Analyzing intraspecific variation in population dynamics in relation to 28 environmental factors is crucial to understand the current and future distributions of 29 plant species. Across ranges, peripheral populations are often expected to show lower 30 and more temporally variable vital rates than central populations, although it remains 31 unclear how much any differences in vital rates actually contribute to differences in 32 population growth rates. Moreover, few demographic studies accounting for 33 environmental stochasticity have been carried out both at continental and regional 34 scales. In this study we calculated stochastic growth rates in five central and six 35 northern peripheral populations of the widespread short-lived herb *Plantago coronopus* 36 along the Atlantic Coast in Europe. To evaluate at two spatial scales how mean values 37 and variability of vital rates (*i.e.* fecundity, recruitment, survival, growth and shrinkage) 38 contributed to the differences in stochastic growth rates, we performed Stochastic Life 39 Table Response Experiment analyses between and within central and peripheral regions. 40 Additionally, we searched for correlations between vital rate contributions and local 41 environmental conditions. Lower mean values and greater variability for some vital 42 rates in peripheral than in central populations had an overall negative but non-43 significant effect on the stochastic growth rates in the periphery. Different life cycle 44 components accounted for differences in population growth depending on spatial scale, 45 although recruitment was the vital rate with the highest influence both between and 46 within regions. Interestingly, the same pattern of differentiation among populations was 47 found within central and peripheral areas: in both regions, one group of populations 48 displayed positive contributions of growth and shrinkage and negative contributions of 49 recruitment and survival, the opposite pattern being found in the remaining populations. 50 These differences among populations within regions in vital rate contributions were

51	correlated with precipitation regime, whereas at the continental scale, differences in
52	contribution patterns were related to temperature. Altogether, our results show how
53	populations of <i>P. coronopus</i> exhibit life cycle differences that may enable it to persist in
54	locations with widely varying environmental conditions. This demographic flexibility
55	may help to explain the success of widespread plants across large and heterogeneous
56	ranges.
57	
58	Key words
59	Climatic conditions, comparative demography, compensatory shifts in vital rates,
60	core and marginal populations, intraspecific variation, latitudinal gradient, matrix
61	projection models, multiple spatial scales, Plantago coronopus, species distribution
62	limits, Stochastic LTRE
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76 Introduction

77	Peripheral populations have been predicted to show lower densities, lower
78	population growth rates, or higher demographic fluctuations than central populations,
79	due to hypothetically less suitable conditions and higher isolation (Brown 1984, Lawton
80	1993, Vucetich and Waite 2003). Though some studies found declining performance of
81	plant populations towards range edges (Carey et al. 1995, Nantel and Gagnon 1999,
82	Eckhart et al. 2011), others did not (Angert 2009, Eckstein et al. 2009, García et al.
83	2010, Doak and Morris 2010), and recent reviews have seriously challenged the validity
84	of these widely accepted predictions (Sagarin and Gaines 2002, Gaston 2009, Sexton et
85	al. 2009). There is actually no reason to expect that population performance will always
86	decrease towards the periphery, as the locations where peripheral populations occur may
87	simply be the ones where the environment is locally favorable for the species, even if
88	such locations are less common near the range limits (Holt and Keitt 2000, Lennon et al.
89	2002). In addition, while some studies have assessed the means and temporal variability
90	in vital rates and the stochastic population growth rates in central and marginal areas of
91	species' distributions (Angert 2009, Doak and Morris 2010, Eckhart et al. 2011), the
92	relative contributions of differences in vital rate means vs. standard deviations to
93	population growth rates across ranges have never been quantified.
94	Another set of studies has explored spatial variability in population dynamics
95	within limited areas of species' distributions in relation to varying environmental
96	conditions (van Groenendael and Slim 1988, Horvitz and Schemske 1995, Jongejans
97	and de Kroon 2005). However, few studies have examined variability both between and
98	within distinct regions (but see Menges and Dolan 1998, Jongejans et al. 2010), even
99	though the relative importance of different vital rates for population growth may change
100	across spatial scales (Jongejans et al. 2010). Determining which life cycle components

101	have a higher influence on population performance is indeed one of the best ways to
102	analyze intraspecific demographic variation (Morris and Doak 2005). Unraveling the
103	spatial variability of the key processes shaping population dynamics and its possible
104	environmental drivers might help us to discern the causes of range limits (Eckhart et al.
105	2011), and may enable to project with greater precision the future distributions of
106	species (Keith et al. 2008, Lavergne et al. 2010).
107	Life Table Response Experiments (LTRE) are very useful in this context because
108	they allow us to evaluate how differences in vital rates contribute to differences in
109	growth rates among populations (Caswell 2001). In addition, this analysis can detect
110	differences in population dynamics even in situations of similar population growth
111	rates, if positive contributions of some life cycle components offset negative
112	contributions of other components. Indeed, compensatory changes in vital rates have
113	been already found among plant populations along environmental gradients (Jongejans
114	and de Kroon 2005, Elderd and Doak 2006, Doak and Morris 2010). Two
115	methodological advances have been incorporated into LTREs in recent studies: the
116	consideration of underlying vital rates, and the use of stochastic rather than
117	deterministic models (Caswell 2010, Davison et al. 2010, Jacquemyn et al. 2012). The
118	former provides more precise assessments of population dynamics because these rates
119	represent distinct biological processes better than projection matrix elements, which
120	may confound several of these processes (Franco and Silvertown 2004). In addition,
121	there is a growing recognition of the potential relevance of environmental stochasticity
122	for the fate of populations (Tuljapurkar et al. 2003; but see Buckley et al. 2010),
123	particularly for short-lived species (García et al. 2008, Morris et al. 2008), as temporal
124	variability generally leads to decreased long-term population growth (Lewontin and
125	Cohen 1969, Gillespie 1977). Stochastic LTREs (SLTRE), thus, constitute a valuable

tool to examine the contributions of both the average values and the variation in
underlying vital rates to the observed differences in stochastic growth rates (Davison et
al. 2010), a considerable advantage with respect to deterministic approaches when
analyzing strongly fluctuating vital rates. However, SLTREs have not yet been used to
compare stochastic demography between and within central and peripheral areas of
species' ranges.

132 In this study, we analyze intraspecific demographic variation in the widespread 133 short-lived herb *Plantago coronopus*, and apply SLTRE to assess the effects of 134 differences in vital rates between and within distinct regions of its distribution. Previous 135 studies have shown that populations of *P. coronopus* differ substantially in life history 136 and demography, both at local (Waite and Hutchings 1982, Braza et al. 2010, Braza and 137 García 2011) and continental scales (Villellas et al. 2012, Villellas and García 2012). 138 Across the species' latitudinal gradient, for example, central populations showed higher fecundity, whereas northern peripheral populations presented higher recruitment 139 140 (Villellas et al. 2012). However, no clear pattern emerged between central and 141 peripheral regions in temporal variability of vital rates, and it remains untested whether 142 differences among populations in mean performance and demographic variability result 143 in differences in long-term population growth rates. Even within regions, P. coronopus 144 is exposed to a variety of environments, which may trigger demographic variation at 145 different spatial scales. Identifying the environmental factors associated with variation 146 in population dynamics over time and across ranges is indeed crucial for understanding 147 plant demography (Holt and Keitt 2005, Buckley et al. 2010, Eckhart et al. 2011). 148 Here we present an integrative analysis of population dynamics of the widespread 149 short-lived herb P. coronopus, using a 4-yr demographic dataset from five central and 150 six northern peripheral populations. To our knowledge, this is the first study that

151 performs a SLTRE at different spatial scales in a nested fashion (continental and

regional), analyzing central and peripheral populations of a plant, and accounting for

sampling variation in the estimation of temporal demographic variability. First, we

- 154 tested whether peripheral populations had lower stochastic growth rates than central
- 155 populations, and examined how differences in vital rates means and fluctuations
- 156 between the center and the periphery contributed to differences in stochastic population
- 157 growth. Second, we tested whether the same vital rates were responsible for

158 demographic variation between and within regions. Third, we analyzed the relationship

159 between variation in population dynamics and variation in environmental conditions,

- 160 *i.e.*, climate, soil fertility, and intraspecific competition.
- 161

162 Methods

163 <u>Study species and populations</u>

164 Plantago coronopus L. (Plantaginaceae) is a common, short-lived herb present 165 from North Africa and the Iberian Peninsula to SW Asia. It also extends to North 166 Europe in a narrow strip along the Atlantic coast and the Baltic Sea, and along the 167 coasts of the United Kingdom (Hultén and Fries 1986). We chose the subspecies 168 *coronopus* (hereafter *P. coronopus*), which is the most common one throughout the 169 species' distribution. Plants have one or a few basal rosettes, and produce spikes with 170 wind-pollinated flowers when they reach reproductive stage (which they sometimes do 171 in their first year).

172 Plantago coronopus occurs in a variety of environmental conditions, regarding 173 climate, vegetation cover and soil fertility. The species is present both in coastal and 174 inland locations in the range center, where it may grow in dunes, shrublands or human-175 disturbed areas, and where populations present either annual or short-lived perennial

176 life-forms (Chater and Cartier 1976). Northern populations are rather restricted to the 177 coast, in seashore meadows and salt marshes, presenting a short-lived perennial life-178 form. For this work we selected 11 perennial populations along the Atlantic coast to 179 minimize habitat differences, as our focus was on the latitudinal range rather than the 180 coastal-to-inland axis. We monitored five central populations in sand dunes in Spain 181 and France, and six northern peripheral populations in coastal meadows in Denmark, 182 Sweden and Scotland (Appendix A). Central populations were Tarifa (T), Camposoto 183 (CA), Corrubedo (C), Traba (TB) and Pen Bron (F). Northern peripheral populations 184 were Helnaes (DH), Skallingen (DS), Glommen (SG), Torekov (ST), Aberdeen (EA) 185 and Skye (ES). Our study did not include southern peripheral populations (*i.e.*, in North 186 Africa). All study populations contained thousands or tens of thousands of individuals, 187 and appeared to be relatively stable in the long term (J. Villellas and M. B. García, 188 personal observation). Further information of populations can be found in Villellas et 189 al. (2012).

190 Data collection

191 We surveyed populations annually for 4 yr, yielding three annual transitions. All 192 populations were sampled from 2007 to 2010, except for population F (period 2003-193 2006). However, we verified that the average and the variance of climatic variables at 194 site F were similar in both sampling periods. In the first year, we established a number 195 of randomly distributed plots in each population. We censused and mapped all the 196 plants within plots each July (central populations) or August (peripheral populations), 197 when fruits had matured but before seed dispersal. In each population census, we 198 measured 100–400 individuals older than 1 yr that had been mapped in previous years. 199 For each plant, we recorded the number of leaves and inflorescences, and the length of 200 an average leaf and an average inflorescence. Plant size was later estimated as number

201 of leaves \times length of an average leaf, and seed production was estimated for

202 reproductive individuals as number of inflorescences × length of an average

203 inflorescence \times number of seeds per unit of inflorescence length (calculated with a

204 regression equation for each population). We also mapped each year all the new

205 seedlings within plots (hereafter "yearlings").

206 We collected 10-cm deep soil cores from all populations and measured the 207 percentage of organic matter content from the organic carbon (Heanes 1984). 208 Meteorological data were obtained from the Spanish National Meteorological Agency 209 (populations T and CA), MeteoGalicia (C and TB), MeteoFrance (F), Danish 210 Meteorological Institute (DH and DS), Swedish Meteorological and Hydrological Institute (SG and ST) and Met Office (EA and ES). We used information from 10-20 211 212 years within the last four decades (depending on the availability) from the nearest 213 meteorological station to each population (between 1 and 35 km away). We calculated 214 mean annual temperature (°C), mean annual precipitation (mm), and coefficient of 215 variation (CV) in annual and monthly precipitation. The first year of this study we also 216 estimated mean above-ground available area per individual (yearlings excluded) 217 calculating Voronoi polygons on the scanned maps of plots (hereafter "resource area"; 218 see also Villellas et al. 2012). We used resource area as an inverse proxy for 219 intraspecific competition.

220

Projection matrices and stochastic growth rates

Individuals were classified into four stages based on age and size: one stage of yearlings (y) for plants younger than 1 yr, and three size stages (1, 2 and 3) for older plants. We used the same thresholds for size stages across populations in order to produce as even a distribution of individuals across stages as possible (see above for details on calculation of plant size, estimated from total leaf length): size ≤ 32 cm (stage

226 1), $32 < \text{size} \le 50 \text{ cm}$ (stage 2), and size > 50 cm (stage 3). For most populations and 227 years, sample sizes per size-based stage remained between 10 and 400 individuals, and 228 in the case of yearlings between 25 and 1500 individuals. To construct projection 229 matrices, we calculated 21 stage-specific vital rates for three annual transitions and 230 eleven populations, for a total of 33 matrices (Fig. 1; Appendix B). Vital rates were: 231 survival (s); probability of growing to any larger size class conditional on surviving (g); 232 probability of growing two size classes conditional on surviving and growing (k); 233 probability of shrinking to any smaller size class conditional on surviving and not 234 growing (r); probability of shrinking two size classes conditional on surviving and 235 shrinking (h); probability of reproducing (p); seed production conditional on reproducing (f); and recruitment, *i.e.* the proportion of seeds giving rise to yearlings the 236 following year (z). Recruitment was estimated on each plot as the number of yearlings 237 238 divided by the number of seeds produced in the previous year, and then averaged across plots, as recruitment from the seed bank is negligible in this species (Waite and 239 240 Hutchings 1979, R. Braza and M. B. García, unpublished data).

241 Raw estimates of vital rates vary annually due both to environmental variation and 242 to sampling variation (Gould and Nichols 1988). As our goal was to assess how much 243 true demographic variation due to environmental fluctuations contributes to population 244 differences in growth rates, we corrected the raw vital rate estimates for sampling error 245 with mixed models that contained only a random effect of year (cf. Altwegg et al. 2007, 246 Morris et al. 2011). Specifically, we corrected normally distributed vital rates (seed 247 production) using linear mixed models, and the other rates with generalized linear 248 mixed models, assuming binomial errors (*lme* and *lmer* procedures, packages *nlme* and 249 *lme4*, respectively; R Development Core Team 2011). This procedure produces annual 250 vital rate estimates that are "shrunken" toward the multi-year mean value in years with

251 low sample sizes. Accounting for sampling variation avoids overestimating the

contribution of the vital rates variabilities (Gould and Nichols 1988).

253 Following Caswell (2001), we calculated stochastic growth rates by projecting each population 50000 yr using random draws from the set of three annual matrices, 254 255 assuming identical and independent distribution. To calculate 95% confidence intervals 256 (CI) on stochastic growth rates, we generated 5000 bootstrap replicates for each 257 population and identified the 2.5th and 97.5th percentiles of the distribution of growth 258 rates. To test for differences in stochastic growth rates between central and peripheral 259 populations, we performed a Mann-Whitney test (wilcox.test procedure, package stats in 260 R) because we could not assume a normal distribution. 261 SLTRE analyses

262 To evaluate the contributions of the differences among populations in vital rates to 263 the differences in stochastic growth, we carried out SLTRE analyses (Davison et al. 2010), but based on underlying vital rates rather than matrix elements (Jacquemyn et al. 264 2012). We performed SLTREs between central and peripheral regions of P. coronopus 265 (hereafter SLTRE^b) and *within* both regions (hereafter SLTRE^w). In the central 266 SLTRE^w, we analyzed differences among the five central populations, comparing them 267 to a central reference population (CR); in the peripheral SLTRE^w, we compared the six 268 peripheral populations to a peripheral reference population (PR); in the SLTRE^b, we 269 270 compared CR and PR to a grand reference population (GR). To construct CR and PR 271 annual matrices, we averaged annual vital rates across central and peripheral 272 populations, respectively. To construct GR annual matrices, we averaged the mean 273 annual vital rates from CR and PR. For all the reference and study populations, we 274 calculated means and standard deviations of all vital rates across years (Davison et al. 275 2010). We then computed for each SLTRE the contribution of each vital rate's mean

276	(C_m) and standard deviation (C_{sd}) . For each vital rate and study population, C_m was
277	calculated as $C_m = (x^P - x^R) \times S_m$, where x^P is the vital rate's mean in the study
278	population, x^{R} is the vital rate's mean in the corresponding reference population, and S_{m}
279	is the sensitivity of the reference population's stochastic growth rate to changes in the
280	vital rate's mean. Similarly, C_{sd} 's were calculated as $C_{sd} = (x^P - x^R) \times S_{sd}$, where the
281	x's are now vital rate standard deviations and S_{sd} is the stochastic sensitivity to changes
282	in vital rate's standard deviation. We calculated S_m and S_{sd} using the perturbation
283	method of Tuljapurkar et al. (2003) modified for vital rates (cf. Morris et al. 2006).
284	To facilitate interpretation we grouped the vital rate contributions into
285	contributions of five life cycle components: fecundity (C_m^{Fe} and C_{sd}^{Fe} , which contain the
286	sum of C_m and C_{sd} , respectively, of vital rates f and p), growth (C_m^{Gr} and C_{sd}^{Gr} , for rates g
287	and k), shrinkage (C_m^{Sh} and C_{sd}^{Sh} , for rates r and h), survival (C_m^{Su} and C_{sd}^{Su} , for rate s) and
288	recruitment (C_m^{Re} and C_{sd}^{Re} , for rate z). Then, we calculated across populations the
289	percentage contribution of means (% C_m) and standard deviations (% C_{sd}) for each life
290	cycle component, relative to the sum of absolute values of all contributions (Appendix
291	C).
292	Relationship between population dynamics and environmental factors
293	To test whether populations showing demographic differences also differed in
294	environmental conditions, we grouped them within central and peripheral areas
295	according to the pattern of vital rate contributions (see Results). Groups C1 (T, CA and
296	F) and C2 (C and TB) contained central populations, and groups P1 (DH, DS, ST and
297	EA) and P2 (SG and ES) contained peripheral populations. The environmental variables
298	analyzed were: mean annual temperature (hereafter "temperature"), mean annual
299	precipitation (hereafter "mean precipitation"), CV in monthly precipitation (hereafter

300	"precipitation variability"), soil organic matter content and resource area. CV in annual
301	precipitation was discarded due to its similarity to CV in monthly precipitation and its
302	lower correlation with demographic differences. To evaluate how the environmental
303	variables explained demographic differences among groups, we performed a Linear
304	Discriminant Analysis (<i>lda</i> procedure, package MASS in R). We tested the significance
305	of differences among groups regarding environmental variables with a Wilks' lambda
306	test (manova procedure, package stats in R).
307	
308	<u>Results</u>

309 <u>Stochastic growth rates</u>

310 Populations showed large differences in stochastic growth rate within regions,

311 ranging from 0.53 (population F) to 1.01 (C) in the central area and from 0.57 (DS) to

312 1.11 (ST) in the peripheral area (Fig. 2). For all populations, 95% confidence intervals

of growth rates were narrower than ± 0.01 . Nine of the 11 populations showed

314 stochastic growth rate values below one. We found no significant differences in

315 stochastic growth rates between central and peripheral populations (Mann-Whitney test;

316 W =15, P = 1).

317 <u>SLTRE analyses</u>

318 Stochastic sensitivities

319 For the three reference populations (GR, CR and PR), the vital rates' S_m were on

320 average *ca*. 10 times higher in absolute value than their corresponding S_{sd} values

321 (Appendix D, Fig. D1), indicating that the stochastic growth rate of these populations is

- 322 far more sensitive to the average than to temporal variability in performance. S_m was
- 323 positive for all rates except for the shrinkage rates r_2 , r_3 and h_3 . Most S_{sd} were instead
- 324 negative, showing that demographic fluctuations had an overall detrimental effect on

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325	population growth, although some vital rates, such as p_y and p_{3} , showed positive S_{sd} .
326	Recruitment was the vital rate with by far the highest S_m and S_{sd} in absolute value in the
327	three reference populations, followed by yearling vital rates (s_y , p_y and g_y). Differences
328	in vital rates' means and standard deviations between study populations and their
329	corresponding reference population are shown in Appendix D, Table D1.
330	Contributions of single vital rates
331	In all SLTRE analyses (both between and within central and peripheral regions),
332	C_m of vital rates was much larger than C_{sd} in absolute value (Appendix D, Figs. D2 and
333	D3), which indicates that temporal variability of vital rates played a much smaller role
334	than mean values in explaining spatial variability in stochastic population growth rates.
335	Recruitment was always the rate with the highest C_m (Appendix D, Fig. D2). In
336	addition, yearlings showed higher C_m than other stages in survival (s) and growth rates
337	(g, k) , whereas in fecundity rates (f, p) the highest C_m corresponded either to stage 3 or
338	to yearlings. There was less consistency among the three SLTREs regarding C_{sd} of vital
339	rates, although recruitment and yearling survival tended to show the highest values in
340	all three analyses (Appendix D, Fig. D3).
341	Contributions of life cycle components
342	In the SLTRE ^b , fecundity and recruitment showed by far the largest percentage
343	contribution of mean values, and shrinkage the lowest (Fig. 3a). In CR, $%C_m^{Fe}$ was
344	positive and $\% C_m^{\text{Re}}$ was negative, and the net contribution of mean values was slightly
345	positive, whereas in PR the opposite pattern was found. The net contribution of standard
346	deviation values was positive in CR and negative in PR, recruitment making the largest
347	contribution (Fig. 3d). The percentage contributions of the variabilities of the other life
348	cycle components were smaller due to low sensitivities in the case of growth (Appendix

349 D, Fig. D1), and to opposition between positive and negative contributions in survival350 and fecundity (results not shown).

351	In the SLTRE ^w analyses, recruitment had in general the largest percentage
352	contributions of mean values (Fig. 3b, c). Two differentiated groups of populations
353	emerged both in the central and peripheral areas: in three central populations (T, CA
354	and F; group C1) and four peripheral populations (DH, DS, ST and EA; group P1),
355	$%C_m^{Gr}$ and $%C_m^{Sh}$ were generally positive, and $%C_m^{Re}$ and $%C_m^{Su}$ were negative; the
356	remaining two central (C and TB; group C2) and two peripheral populations (SG and
357	ES; group P2) generally showed the opposite pattern (with a few exceptions with
358	respect to growth or survival). Equivalent patterns of differentiation among populations
359	in life cycle components were thus found within both regions. Survival, fecundity and
360	recruitment showed the largest percentage contributions of variability (Fig. 3e, f).
361	Population dynamics and environmental factors
362	In the Linear Discriminant Analysis, temperature loaded most strongly on the first
363	axis, which explained 92 % of the differences in environmental conditions among the
364	four groups identified in Figure 3, followed by soil organic matter, precipitation
365	variability and resource area (Fig. 4, Appendix E). The second axis explained 7 % of the
366	spatial variation, and was mainly determined by mean precipitation and to a lesser
367	extent by precipitation variability. Central populations (groups C1 and C2)
368	differentiated from peripheral populations (groups P1 and P2) along the first axis,
369	showing higher temperatures and lower soil organic matter. Groups of populations that
370	were defined within regions on the basis of demographic performance were instead
371	separated along the second axis: populations from groups C1 and P1 showed lower
372	mean precipitation and higher precipitation variability than populations from groups C2

and P2. Differences among groups regarding the environmental variables under study were significant (Wilks' lambda = 0.10, $F_5 = 9.38$, P = 0.014).

375

376 Discussion

377 In our study across the European latitudinal range of the widespread Plantago 378 coronopus, we found large intraspecific variation in stochastic demography both at 379 continental and regional scales. Despite that variation, we can formulate some general 380 patterns. Some vital rates showed lower mean values and greater variability in 381 peripheral than in central populations, but led to no significant differences in stochastic 382 growth rates between regions. Although different life cycle components accounted for differences in population dynamics depending on spatial scale, recruitment was the vital 383 384 rate with the highest contribution both between and within central and peripheral 385 regions. Our results also showed that demographic variation among populations seemed to be related with differences in temperature at the continental scale, whereas it was 386 387 correlated with variation in precipitation regime within both central and peripheral 388 areas. 389 Variation in population dynamics across spatial scales

390 We found no significant differences in stochastic growth rates between central and 391 peripheral populations, which contrasts with classical predictions of a generalized 392 reduction in population performance in the range periphery (Lawton 1993, Lesica and 393 Allendorf 1995). Other recent studies have failed to find decreased growth rates towards 394 range margins, using both deterministic (Stokes et al. 2004, Kluth and Bruelheide 2005, 395 Eckstein et al. 2009) and stochastic approaches (Angert 2009, Doak and Morris 2010, 396 García et al. 2010). Indeed, although multiple studies have shown reduced values in 397 some demographic parameters at range edges, such as density or some vital rates (e.g.

Carey et al. 1995, García et al. 2000, Tremblay et al. 2002), few have reported a worse

399 overall performance in terms of population growth rates (Nantel and Gagnon 1999,

400 Angert 2009, Eckhart et al. 2011).

401 Irrespective of their position, most populations in our study showed stochastic 402 growth rates lower than one, which deserves some attention. Deviation from 403 equilibrium in population growth is indeed typical of short-lived plants (García et al 404 2008). Populations of *P. coronopus* can be relatively transient in space (J. Villellas and 405 M. B. García, *personal observation*), such that plant patches that established and grew 406 in a certain year may decline following a perturbation, or invasion of more competitive 407 taxa in the following years. However, the species may compensate for such declines by spreading to nearby sites within the same locations. Thus, although permanent plots are 408 409 often set up in places where plants are relatively dense, the situation can change over 410 years for short-lived species, given the large fluctuations in local populations they 411 commonly experience (Glazier 1986). Buckley et al. (2010) also referred to the potential 412 problems of choosing "good sites" within populations at the beginning of demographic 413 studies.

414 Numerous studies to date have analyzed temporal variability in vital rates across 415 ranges, with contrasting results. A previous study with *P. coronopus* showed higher 416 temporal variability in peripheral than in central populations in some life cycle 417 components, such as recruitment, and lower fluctuations in others, such as fecundity, 418 but differences were not statistically significant (Villellas et al. 2012). Studies with 419 other plant taxa showed higher temporal variability in vital rates in peripheral 420 populations (Nantel and Gagnon 1999, Vucetich and Waite 2003, Gerst et al. 2011), in 421 central populations (Kluth and Bruelheide 2005), or failed to find any clear pattern 422 (Angert 2009). However, to our knowledge, this is the first study that quantifies the real

423 effect on population growth rates of such differences across ranges, discounting as well 424 for sampling variation to reduce the implicit overestimation of temporal variability. In 425 *P. coronopus*, the overall effect of temporal variability was slightly negative for the 426 population growth of peripheral populations, and originated almost exclusively from 427 differences in recruitment variability. The contribution of variation in other life cycle 428 components was negligible due to low sensitivity values or opposition between positive 429 and negative contributions.

430 In all the SLTREs performed, vital rate means showed in general higher 431 sensitivities and greater contributions to differences in population growth rates than did 432 temporal variability, as expected (Davison et al. 2010, Jacquemyn et al. 2012). 433 However, the net contribution of the mean values of all vital rates together was lower 434 than that of the standard deviations in three populations in the within-region SLTREs 435 (central TB, and peripheral DS and SG; Fig. 3). In these populations, positive and 436 negative contributions of mean vital rates cancelled each other, whereas contributions of 437 standard deviations did not. This result highlights the importance of considering 438 stochasticity, and not only mean performance, when assessing demographic differences 439 among populations (Gillespie 1977, Tuljapurkar et al. 2003, Davison et al. 2010). 440 Previous studies in *P. coronopus* had already suggested a key role of recruitment 441 (Waite 1984, Braza and García 2011). Our analyses of sensitivities and contributions 442 showed that, irrespective of the spatial scale of comparison, recruitment was indeed the 443 most relevant vital rate for stochastic population growth. The importance of the early 444 stages in the life cycle of *P. coronopus* was further confirmed by the high sensitivities 445 and contributions of vital rates (e.g. survival) of newly recruited yearlings. Similar 446 results were found in the short-lived congener P. lanceolata (van Groenendael and Slim 447 1988) and in other short-lived perennials (Pico et al. 2003, García et al. 2008, Davison

448 et al. 2010), whereas population dynamics in the longer-lived congener *P. media* were 449 more influenced by survival of the oldest stages (Eriksson and Eriksson 2000). 450 Despite a consistently high relevance of recruitment for the population dynamics of *P. coronopus*, we found that the set of life cycle components contributed in distinct 451 452 ways to differences in population growth rates depending on the spatial scale of 453 analysis. At continental scale, the present work confirmed previous findings (Villellas et 454 al. 2012) that fecundity (higher in central populations) and recruitment (higher in 455 peripheral locations) underlie demographic differences between the core and the 456 northern edge of the species' range. Within central and peripheral regions, in contrast, 457 there was a more balanced contribution of different life cycle components: recruitment showed the highest contribution, but growth, survival and fecundity were also relevant. 458 459 Similarly, Jongejans et al. (2010) found in three perennial plants that, although a single 460 vital rate was the most important for differences in deterministic population growth 461 rates both between and within regions, the role of the remaining vital rates varied across 462 scales. Changes in the relative importance of vital rates can also be found among nearby populations (Morris and Doak 2005), which indicates that the importance of life cycle 463 464 components may vary within plant taxa even at small spatial scales. 465 The role of environmental conditions in life cycle variation 466 Differences in population dynamics across the range of *P. coronopus* are better 467 understood when accounting for variation in environmental conditions. In the central-468 peripheral comparison, demographic differences seem to be correlated with 469 temperature, and secondarily with other factors such as soil conditions or precipitation, 470 although direct causal relationships are difficult to establish. Within central and 471 peripheral areas, in contrast, demographic differences were clearly associated with 472 precipitation regime: in both regions, populations with positive contributions of

473	recruitment and survival, and negative contributions of growth and shrinkage (groups
474	C2 and P2) showed higher and more constant precipitation, whereas populations with
475	the opposite demographic pattern (groups C1 and P1) showed lower and more variable
476	rainfall. These differences among populations seem to be reflected in additional
477	demographic and morphological parameters analyzed elsewhere, as populations from
478	wetter locations present higher densities and lower plant sizes than populations from
479	drier sites (Villellas et al. 2012). Higher densities in wetter locations are likely the result
480	of high recruitment. In turn, a negative effect of higher intraspecific competition on
481	plant growth would result in lower plant sizes. Individual plant growth is indeed lower
482	on average (and shrinkage higher) in these wetter sites.
483	The effects of environmental conditions on demography across distribution ranges
484	seem to vary among taxa, and results from other studies differ from those presented here
485	for P. coronopus. Among populations of the widespread Stipa capillata, for example,
486	differences in plant performance are driven by climate in core areas and by soil
487	conditions in the northwestern periphery (Wagner et al. 2011). In Silene regia, regional
488	differences in population growth rates seem to respond in part to differences in the
489	frequency of summer droughts, although variation in fire regime has an overall higher
490	effect across the species' range (Menges and Dolan 1998). In the context of global
491	change, studies such as these that relate demography and environmental conditions at
492	different spatial scales may become powerful tools to assess current and future
493	population performance throughout species' distributions (Jongejans et al. 2010).
494	To conclude, the large variation found in the life cycle of <i>P. coronopus</i> did not
495	lead to diminished performance of any group of populations across the species' range as
496	measured by stochastic growth rates. Instead, compensatory changes in vital rates
497	among populations allow life cycle adjustments to regional and local environmental

498	conditions. Similar shifts in the role of vital rates have been also documented among
499	populations of other plant species along environmental or geographical gradients
500	(Elderd and Doak 2006, Doak and Morris 2010). This flexibility in the life cycle
501	appears to be common in widespread plants, and would explain the success of these taxa
502	across large and environmentally heterogeneous ranges. Further research would be
503	needed to determine whether the demographic differences we have observed across the
504	range reflect phenotypic plasticity vs. local adaptation in response to spatially varying
505	selection on life history traits.
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716 **Figure legends**

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718	Figure 1 Projection matrix (a) and life cycle (b) of <i>Plantago coronopus</i> , with
719	transitions between stages of one year (t) and the next $(t+1)$. Individuals were classified
720	into four classes: yearlings (y) and three size classes (1, 2 and 3). Vital rates, with
721	subindices according to classes, correspond to: survival (s); probability of growing to
722	any larger size class conditional on surviving (g) ; probability of growing two size
723	classes conditional on surviving and growing (k) ; probability of shrinking to any smaller
724	size class conditional on surviving and not growing (r) ; probability of shrinking two
725	size classes conditional on surviving and shrinking (h) ; probability of reproducing (p) ;
726	seed production conditional on reproducing (f); and recruitment, <i>i.e.</i> the proportion of
727	seeds giving rise to yearlings the following year (z) . All life cycle transitions were
728	recorded in this study, but only the calculation of those starting from class 2 is detailed
729	in b), for clarity.
730	
731	Figure 2 Stochastic growth rates in central (black circles) and peripheral (white
732	circles) populations of Plantago coronopus. Confidence intervals are too small to be
733	shown (see Results). Dotted line corresponds to stochastic growth rate of one.
734	
735	Figure 3 Percentage contributions of differences in mean values (% C_m) and
736	standard deviation values (% C_{sd}) of vital rates of <i>Plantago coronopus</i> , grouped into life
737	cycle components: survival, growth, recruitment, fecundity and shrinkage. Results from
738	the SLTRE between central and peripheral regions (a, d), and from the SLTRE within
739	central (b, e) and within peripheral (c, f) regions. Percentage contributions may be
740	positive or negative, but the sum of absolute values of % C_m and % C_{sd} of all life cycle

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741	components must be 100 for each population. In b) and c), the dashed line separates
742	groups of populations (C1, C2, P1 and P2) with different patterns in contributions. Note
743	the difference in scale in Y-axis between top and bottom graphics. See Methods for
744	population acronyms.
745	
746	Figure 4 Canonical correlations of environmental variables from the Linear
747	Discriminant Analysis in Plantago coronopus, indicating their contribution to the first
748	and second discriminant function (arrows). Variables are mean annual temperature (tm),
749	mean annual precipitation (pm), coefficient of variation in monthly precipitation
750	(pmcv), soil organic matter content (som) and resource area as an inverse proxy for
751	intraspecific competition (area). The position of populations (see Methods for
752	population acronyms) according to their corresponding group centroids is also shown.
753	Note the separation among groups of populations (C1, C2, P1 and P2) between regions
754	(left-right) and within regions (top-bottom).
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Figure 2



Figure 3



Figure 4



