

1	Range shifting species reduce phylogenetic diversity in high latitude communities via
2	competition
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35	1.	Under anthropogenic climate change, many species are expanding their ranges to						
36		higher latitudes and altitudes, resulting in novel species interactions. The						
37		consequences of these range shifts for native species, patterns of local biodiversity,						
38		and community structure in high latitude ecosystems are largely unknown but critical						
39		to understand in light of widespread poleward expansions by many warm-adapted						
40		generalists.						
41	2.	Using niche modelling, phylogenetic methods, and field and laboratory studies, we						
42		investigated how colonisation of Scotland by a range expanding damselfly, Ischnura						
43		elegans, influences patterns of competition and niche shifts in native damselfly						
44		species, and changes in phylogenetic community structure.						
45	3.	Colonization by <i>I. elegans</i> was associated with reduced population density and niche						
46		shifts in the resident species least related to I. elegans (Lestes sponsa), reflecting						
47		enhanced competition. Furthermore, communities colonized by I. elegans exhibited						
48		phylogenetic underdispersion, reflecting patterns of relatedness and competition.						

49 4. Our results provide a novel example of a potentially general mechanism whereby
50 climate change-mediated range shifts can reduce phylogenetic diversity within high
51 latitude communities, if colonising species are typically competitively superior to
52 members of native communities that are least-closely-related to the coloniser.

53 <u>Key words:</u> Climate Change, Range Shifts, Competition, Community Assembly, Damselflies,
54 Odonata, Coexistence, Non-analog communities, thermal niche.

55 <u>Introduction</u>

56 Many species are shifting their ranges to higher elevations and latitudes in response to climate change (Parmesan & Yohe 2003; Hickling et al. 2005). However, rates of range shift 57 are not consistent across species (Hickling et al 2008), thus many ecological communities are 58 59 experiencing changes in composition in response to novel regional species pools (Moritz et 60 al. 2008; Telwala et al. 2013; Therry et al. 2016). Typically, high latitude communities which have not been colonised by range shifting species are simple, often containing several 61 62 endemic, keystone species with little local redundancy in ecosystem function (Gaston 2000; Willig, Kaufman & Stevens 2003). Such features make high latitude communities open to 63 64 invasions and colonization by range-expanding species (Lebouvier et al. 2011), but the general consequences of range expansions for high latitude community diversity are largely 65 unknown. Several recent, large-scale analyses suggest that regional (gamma) biodiversity will 66 67 continue to increase under climate change at high latitudes, which may also be reflected in increases in (alpha) diversity at the local community level (Menéndez et al. 2006; Thuiller et 68 al. 2011). However, other analyses suggest that colonizing species may typically outcompete 69 70 and replace native species at high latitudes (Alexander et al. 2015), resulting in irreversible species loss and biotic homogenization along latitudinal gradients (Dornelas et al. 2014). 71 Recent work also suggests that colonization by range-shifting species or invaders often 72 reduces phylogenetic diversity of impacted communities (Lessard et al. 2009; Selvi, Carrari 73

& Coppi 2016), but it is unknown whether or how this process results from patterns of
competition between colonizing and native species. Understanding of these underlying
mechanisms is critical in order to mitigate loss of phylogenetic diversity at high latitudes.
Biotic homogenization and reduced phylogenetic diversity could have severe consequences
for ecosystem function and future evolutionary potential for high latitude communities to
respond to future climatic stressors (Pio *et al.* 2014; Li *et al.* 2015).

80 Underlying processes affecting community phylogenetic diversity:

81 Two processes, environmental filtering and competition, are often invoked to explain the makeup of communities (Kraft et al. 2007). Environmental filtering represents the process 82 by which the environment acts as a "sieve", so that species with shared niche requirement or 83 84 environmental performances are expected to cluster together in space as they colonise shared habitats (Cavender-Bares et al. 2004; McGill et al. 2006; Kraft et al. 2007). Over an 85 environmental gradient, species with similar niche requirements will persist in shared locales 86 87 to form communities (Wiescher, Pearce-Duvet & Feener 2012; Laliberté, Turner & B.L. 88 2014). Inversely, competition may result in the exclusion of ecologically similar species from occupying the same geographic space, via limiting niche similarities between species (Cahill 89 90 et al., 2008, Darwin 1859). Species with similar functional or niche traits are typically expected to compete most strongly for resources, resulting in reduced densities or local 91 exclusion of all but the best performing (i.e., most competitive) species from each functional 92 group (Macarthur & Levins 1967). Under competitive exclusion, and in contrast to 93 environmental filtering, coexistence within a community is therefore often expected to arise 94 95 from interspecific variation in functional and niche traits (Macarthur & Levins 1967; Chesson 2000). In high-diversity regions, competition may determine coexistence within communities, 96 97 but if the number of potential competitors is limited, or if spatial environmental variation is

extreme, environmental filtering is often the dominant process. In most cases, these processes
act in tandem (Chesson 2000; Kraft *et al.* 2007).

These processes of filtering and competition are also influenced by the evolutionary 100 history of species that can potentially coexist. Because multiple traits contribute to an 101 individual or species' ecological niche (Kraft et al, 2015), niches are often less evolutionarily 102 labile than individual traits (Wiens et al. 2010). Thus traits which determine a species' 103 environmental niche tend to be conserved among closely related species (Wiens & Graham 104 2005; Wiens et al. 2010). Such phylogenetic niche conservation implies that community 105 assembly processes (such as colonisation of and persistence in a patch) based on niche 106 107 similarity or differences may generate phylogenetic structure within communities (Webb et al. 2002). If ecological niches are highly evolutionarily conserved among closely related taxa 108 within the regional species pool, and competition is an important factor limiting coexistence 109 110 within communities, phylogenetic overdispersion is expected to arise within communities (Webb et al., 2002). Phylogentic overdispersion occurs in this case because closely related 111 112 species, with shared community-based niches, are more likely to competitively exclude each other from limited resources and habitats (Burns & Strauss 2011; Violle et al. 2011; Peay, 113 Belisle & Fukami 2012). Alternatively, if niche traits are evolutionarily conserved but 114 environmental filtering is more important for ecological processes such as colonisation and 115 persistence, then phylogenetic underdispersion may define local community structure (Webb 116 et al., 2002). This is because, in the absence of strong competition, shared niches among 117 closely related taxa will cause them to cluster in resource and habit space (Cavender-Bares et 118 al. 2004). Under these general predictions, many studies have attempted to classify the 119 relative roles of competition versus environmental filtering as drivers of community 120 121 assembly, based on estimates of phylogenetic structure alone (Webb 2000; Lebrija-Trejos et

al. 2010). However, several key limitations of this approach make inferring the roles ofcompetition and environmental filtering from phylogenetic structure problematic.

The limitations in determining community processes based on phylogenetic clustering 124 125 within the community are twofold. Firstly, contrasting with the traditional assumptions above, niche traits that determine competition within communities may not be the same traits 126 that are important for habitat filtering, and these traits may experience different levels of 127 phylogenetic conservatism (Silvertown et al. 2006; Pigot & Tobias 2013). Second, conserved 128 129 functional traits, which do not relate to niche occupancy but instead influence a species' competitive ability, may also result in phylogenetic underdispersion within communities 130 131 dominated by competitive processes (Mayfield & Levine 2010). More recent theory suggests that if functional traits that predict competitive abilities (e.g., body size, aggression levels, 132 boldness, or growth rates) are conserved, coexisting species will be those most similarly 133 134 matched in competitive ability and thus should be closely related, while distantly related species with lower competitive abilities values will be excluded (The Competitive Trait 135 136 Conservatism Hypothesis; Chesson, 2000; Mayfield & Levine, 2010). However, the relative 137 influence of competition on phylogenetic dispersion within communities has rarely been empirically tested (Mayfield & Levine 2010; Thuiller et al. 2011; Alsos et al. 2012). 138

139 *Range expansions and phylogenetic diversity of high latitude communities:*

Widespread range shifts under climate change create the ideal natural laboratory to
understand community assembly dynamics, because changes in the regional species pool are
observable over short spatial scales reflecting the colonisation process, where expanding,
range edge communities reflect most recent opportunities for coexistence. In Great Britain,
several members of the regional damselfly biota have been expanding northward or to greater
altitudes under climate change (Hickling *et al.* 2005). We examined patterns of species

coexistence in local damselfly guilds in Northeast Scotland with relationship to
environmental variables and opportunity for competition between established residents and
incoming, range expanding species.

Taking advantage of these well-documented range expansions among British 149 Odonata, we aim to improve understanding of community assembly processes under dynamic 150 regional changes in biodiversity, and to empirically investigate the merits of using 151 phylogenetic community structure to access community assembly processes. In particular we 152 aim to study these effects in a species-poor, high latitude community where the ecological 153 effects of individual range shifting species are likely to be profound. Recent range expansions 154 155 of potential competitors may pose a conservation risk to high-latitude endemics, compounding stressors due to climate change alone (Lancaster 2016). Thus understanding the 156 mechanisms that influence possible interactions between high-latitude residents and 157 cosmopolitan range shifting species is of high importance. To achieve our aims, we 158 investigated phylogenetic dispersion of species within colonized and uncolonized damselfly 159 160 communities, whether niche traits are phylogenetically conserved among incoming and resident species, and how patterns of niche shifts related to competition reflect the shared 161 evolutionary history of the species within this study. 162

163 <u>Materials and Methods</u>

164 <u>Study system</u>

Damselflies (Odonata: Zygoptera) are semi-aquatic, predatory insects, which exhibit strong intra- and interspecific competition at both larval (aquatic) and adult (terrestrial) life stages (Convey 1988; Worthen & Patrick 2004). Damselfly performance is highly limited by climate, with higher temperatures shown to increase growth rates (Corbet & May 2008; Nilsson-Ortman *et al.* 2013) and adult flight performance (Okuyama, Samejima & Tsubaki

2015). Higher temperatures are also correlated with increased damselfly population densities
in high-latitude habitats (Lancaster *et al.* 2015). Levels of interspecific aggression and direct
competition are also positively correlated with environmental temperature in damselfly
communities from high latitudes (Lancaster, Morrison & Fitt 2017).

The strong relationship between climate and competitive regimes in damselflies 174 makes dissecting patterns of coexistence easier to characterise than in many other guilds, 175 because both environmental filtering and competitive exclusion are strongly dependent on the 176 same set of (abiotic, thermal) conditions (Saito et al. 2016a). Furthermore, most damselfly 177 species in the UK are restricted to still water ponds and lakes, where they have the 178 179 opportunity to compete for thermally-preferred habitats at all stages of their life cycles (Cham et al., 2014). These shared ecological requirements mean that damselflies are often found in 180 dense guilds around still water ponds, which represent clearly defined, distinct habitat patches 181 182 (Wilson 1999; Sánchez-Herrera & Ware 2011). Diurnal patterns of flight with damselflies are also highly synchronised (Corbet & May 2008), allowing for accurate sampling of all species 183 184 within a community. For all of the above reasons, damselflies represent an ideal animal study system for studying coexistence mechanisms on a landscape scale. 185

186 Within our study area of Northeast Scotland (see below), there are six species of cooccuring damselflies, four of which are long-time residents of the region: Lestes sponsa 187 (Hansemann, 1823), Enallagma cyathigerum (Charpebtier, 1840), Pyrrhosoma nymphula 188 (Sulzer, 1776). These are common and widespread species across most of Great Britain as 189 well as much of Europe and Asia (Askew 1988). The northern relict species within Scotland 190 191 Coenagrion hastulatum (Charpentier, 1825) is also a long-time resident of the region. Two additional species are currently range expanding into or within the region: *Coenagrion puella* 192 (Linnaeus, 1758) and Ischnura elegans (Vander Linden, 1820). Ischnura elegans has recently 193 194 undergone a northwards range shift in Northeast Scotland, with a 143km northwards range

195 shift between 1985 and 1995, and is currently undergoing an altitudinal range shift to upland sites (Hickling et al., 2005; Cham et al., 2014), while C. puella has only recently started 196 colonising Scotland and is found only sporadically through our study area (Hickling et al., 197 198 2005; Cham et al., 2014). All of these species are members of the family Coenagrionidae (superfamily Coenagrionoidea) except for L. sponsa, which belongs to the somewhat 199 distantly related Lestidae (superfamily Lestoidea). Based on 97 occupied sites visited during 200 201 the summer breeding season across Northeast Scotland (see 'Field surveys', below), we identified 56 unique combinations of co-occurance among these 6 species, with no site 202 203 occupied by all 6 species.

204 Field surveys

205 Data on damselfly communities throughout Northeast Scotland was obtained by surveying 97 occupied pond sites between 4th of May through 23rd of July 2014. This period 206 covers the peak flight times for all species studied, with I. elegans, P. nymphula, C. 207 208 hastulatum, C. puella and E. cyathigerum reaching peak adult density in mid-June, while L. 209 sponsa adult densities peak in mid-July (Cham et al., 2014), and L. sponsa emergence is highly synchronized in this period (Powney et al. 2014). Furthermore, L. sponsa peak 210 211 emergence occurs earlier in the northern extent of its range than in the south (Sniegula, Golab & Johansson 2016), leading to high interspecific convergence among of flight times among 212 all 6 coexisting species in our study area. Sites ranged from 56.37° to 57.68° Latitude, and -213 4.13° to -2.11° longitude, and elevation between 3m to 442m, thus covering a large spatial 214 extent and encompassing a range of climatic variation (table S1). Sites were selected to be as 215 216 similar to each other as possible across the region, and to exhibit mutual suitability for all colonizing and native species. For this reason we limited our surveys to permanent water 217 bodies with open, shallow bottoms and consistent varieties of emergent vegetation. 218 219 Temporary, flowing, or heavily-shaded water bodies, each of which only support a subset of

220 Scottish species, were avoided in our site selection procedure. We visited sites between 8:00am and 6:00pm, when the weather was warm with little or no rain, so that sites were 221 visited when the weather was favourable and all species of damselfly present would be 222 223 active. We recorded air temperatures during each of our site visits in order to quality control the density data (see below). Sites were surveyed by walking transects around the perimeter 224 of water bodies and capturing damselflies in timed catching bouts. Species present were 225 226 recorded and a proxy for the density of each species was calculated as the number of individuals of each species caught per minute of capture time; sites were visited multiple 227 228 times and the per species mean density was averaged over the study period. A species was assumed to not be present at significant density at a site if no individuals were observed 229 within 15 minutes of catching effort during the species' adult flight season, and return trips to 230 231 most ponds confirmed presumed absences. Co-occurrence at each site does not necessarily imply stable coexistence, as damselflies often exhibit metapopulation dynamics characterized 232 by frequent local extinction and recolonization events (Mcpeek, Brown & Apr 2000; 233 Gibbons, Reed & Chew 2002). Our study design does not encompass long-term dynamics, 234 and thus captures predictors of co-occurrence rather than stable coexistence. However, our 235 study design enables us to capture the dynamics of competitive interactions that are likely to 236 correlate with longer-term patterns of persistence or competitive displacement across the 237 region. 238

239 <u>Morphology</u>

Morphology has been shown to be a highly variable trait in damselflies, and shifts in morphology may represent either an evolutionary or plastic response to abiotic conditions or altered competitive regimes (Chaput-Bardy *et al.* 2010; Hassall 2013). Thus we investigated effects of climate and altered competitive regimes on body size. A subset of captured damselflies of each species from each site were brought back to lab to assess body size.

Individuals of *C. hastulatum*, which are locally endangered (Cham et al., 2014), were never 245 removed from the field. Scans of each damselfly were taken using an Epson Perfection V37 246 flatbed scanner, at a resolution of 600 DPI. From these scans, measurements were taken of 247 forewing length, abdomen length and width, thorax length and width and total body length 248 using ImageJ (Schneider, Rasband & Eliceiri 2012). Principal components analysis was 249 conducted in R v.3.0.2 (R core development team, 2008) to account for variation in size 250 251 across all morphological measurement (Gosden et al., 2011). The first principal component (PC1) accounted for 73.38% of variation in these measurements and was negatively 252 253 correlated with each. Given the negative relationship, and to make results easier to interpret, inverse PC1 was therefore used to estimate body size. 254

255 <u>Statistical analyses of climate and species interactions</u>

To identify patterns of competitive displacement from climatically favourable sites 256 arising between range-shifting (i.e., I. elegans) and resident species, we compared linear 257 258 models to explain the log(density) of each of the resident species, averaged over the season at 259 each site. Because mean annual temperature has been shown to be the best abiotic predictor of damselfly field densities (Lancaster et al. 2015), we included in these models an effect of 260 261 climate (georeferenced values of uncorrelated, biologically relevant climate variables from table S1: Hijmans et al. 2005), an effect of I. elegans presence, and all interactions between I. 262 elegans presence and temperature. The full model was compared against all reduced models 263 264 using linear models in the base stats package in R v.3.0.2 (R core development team, 2008). The best model was selected using the corrected Akaike Information Criterion (AICc; 265 Mazerolle 2015) (Table S2). C. puella and C. hastulatum were not found at sufficient 266 numbers of sites to include in these analyses. Given the high reliance of damselflies on 267 climate (see 'study system', above), a significant interaction suggests that the presence of *I*. 268 269 *elegans* modifies the ability of resident species to persist in preferred sites, and indicates that

270 competition may be an important driver of co-occurence patterns in recently colonised communities. In the absence of evidence for competition, environmental filtering processes 271 were investigated by examining patterns of niche overlap and coexistence between species 272 273 (see niche overlap, below). To determine whether site-specific densities were spatially autocorrelated within each species, we ran a Mantel test of species densities in the Ecodist 274 package for R (Goslee & Urban 2007). To determine if daily air temperatures (measured on 275 276 the day of capture) affected our local density estimates (via effects on individual activity levels and thus detectability), we ran mixed effect linear models in the lmerTest and lme4 277 278 packages for R (Kuznetsova et al., 2016) regressing daily density estimates on air 279 temperature measurements taken at the time when sampling occurred, and including a random effect for site, since most sites were visited on multiple occasions. 280

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282 <u>Phylogenetic community structure</u>

Phylogenetic reconstruction of Scottish damselfly evolutionary relationships was 283 obtained from Dumont, Vierstraete & Vanfleteren (2010) and Guan et al. (2013), with branch 284 lengths set to 1 because true branch lengths are unknown and are potentially unlikely to 285 accurately reflect rates of divergence in niche traits (Fig. 1). To estimate phylogenetic over-286 or under-dispersion at each site, phylogenetic relationships were used to construct a pairwise 287 phylogenetic distance matrix of all species within each site using the cophenetic() function in 288 the picante package for R (Kembel et al. 2010). Subsequently, mean pairwise distances were 289 290 calculated for each site, and compared to a null expectation using the ses.mpd() function, also in picante, where the null expectation was generated by randomizing shuffling tip labels on 291 292 the phylogeny 99 times. Where the observed phylogenetic dispersion of a site was greater than 90% of randomly-generated phylogenies for the site, we classified the site as 293

294 phylogenetically overdispersed. Similarly, we diagnosed phylogenetic underdispersion where the phylogenetic dispersion at a site was less than 90% of randomly generated phylogenies 295 for that site. If the phylogenetic dispersion of a site was similar to the middle 80% of 296 297 randomly-generated phylogenies for the site, we classified the site as evenly phylogentically dispersed. Due to conservative cutoffs for phylogenetic dispersion, we do not attempt to use 298 these data to draw rigorous conclusions about phylogenetic patterns at any particular site. 299 300 However, such conservative cutoffs give us an appropriate range of values to feed into further analysis. Sites with only one species present were classified as single species communities. 301 302 These categories were used in linear models to analyse the correlation between phylogenetic structure of communities and climate or the presence of *I. elegans*. 303

304 <u>Competitive trials</u>

To quantify thermal preference and competition between *I. elegans* and *L. sponsa*, 305 thermal preference trails were conducted in the laboratory using wild-captured damselflies in 306 307 2016. One hundred and three I. elegans and 108 L. sponsa from 7 sites (capture dates and 308 locations in Table S3) were assessed for their preferred basking site temperatures in a repeated measures design, where each individual was assessed for its thermal preferences 309 310 alone, and in the presence of an interspecific 'competitor'. Treatment order (alone vs. in competition with the other species) was randomised so that repeated exposure to the thermal 311 gradient would have no effect on the damselflies. Thermal preference was assessed by 312 placing the damselfly in a 60cm Tube with a thermal gradient from 60°C to 10°C, achieved 313 by heating the tube at one end using a heat lamp (100W, 50Hz Exoterra ceramic heat emitter) 314 315 and cooling the opposite end with ice (Fig. S1). Each damselfly was given 5 minutes to settle in their preferred position on the thermal gradient. The thermal environment where the 316 damselfly settled was measured by photographing the damselfly using a Flir Ex Series E6 317 318 thermal imaging camera and analysing the image using the Flir Tools software package

319 (v5.2.15, Flir systems.). For image analysis, the average temperature was taken of 5 point samples of the temperature surrounding the damselfly (Fig. S2). Points were randomly 320 selected ~5mm from the individual's thorax. Effects of competition were analysed in a 321 322 mixed-effects linear model where the dependent variable was resting site temperature, and fixed effects were included for species, treatment (alone or in competition), and the 323 interaction (species x treatment). Random effects were included to account for individual ID 324 325 (repeated measures) and for pair identity (because two individuals share a paired trial). The model was run in lme4 and lmerTest packages for R. 326

327 Environmental variables and niche model construction

Species distributions were modelled over the geographic extent of Scotland using a 328 329 maximum entropy habitat suitability model implemented in MaxEnt, version 3.3.3k (Phillips, Avenue & Park 2004) and executed through the Dismo package for R (Hijmans et al., 2014). 330 Each species' presence points were obtained from records downloaded from the Global 331 332 Biodiversity Information Facility (http://www.gbif.org), and Odonata records from The 333 British Dragonfly Society (BDS) accessed from the National Biodiversity Network (http://www.nbn.org.uk/), with duplicate records removed, leaving 2783 unique presence 334 335 records for I. elegans, 2485 for L. sponsa, 5470 for P. nymphula, 158 for C. hastulatum and 4667 for E. cyathigerum. Ten thousand randomly selected background points were used as 336 pseudo-absences in each model. The models were constrained to Scotland by using the 337 boundaries dataset available from the Office of National Statistics (Ordinance Survey, 2011). 338 Bioclim climate layers were sampled at 30 arcsecond resolution and clipped to the extent of 339 this region using the Raster package for R (Hijmans et al., 2013); these were used as 340 predictor variables in the models (Table S1). In the case that climatic predictor variables were 341 correlated at > 80% across species presence and background points, the variable considered 342 343 likely less important to damselfly biology was removed. The MaxEnt model was run 5 times

344 using default parameters, withholding a separate 20% of presence points for model testing on each model run. The final niche model for each species represented the average habitat 345 suitability's calculated across the five model runs. The full model (with all environmental 346 347 predictor variables) and stepwise-reduced models were compared using AICc, implemented in the ENMeval R package (Muscarella et al., 2016), with a Δ AICc of 2 denoting significant 348 differences between models. Model fit was also assessed by estimating the area under the 349 Receiver Operating Characteristic (ROC) curve (AUC), which estimates sensitivity versus 1 350 - specificity (positively identified known presences versus the false positive rate). AUC 351 352 values of 0.5 or less correspond to the model performing similarly or worse than random, while AUC values of 1 - a/2 (where a is the relative size of the true species range within the 353 study area) indicate a very good fit of the model to the data (Phillips et al. 2004). 354

355 <u>Phylogenetic analysis of niche overlap</u>

Pairwise overlap in habitat suitability of each species was calculated using the D 356 357 statistic (Warren, Glor & Turelli 2008) based on Schoeners D (Schoener & Schoener 1968), 358 in the Phyloclim package for R (Heibl & Calenge 2013). To test for phylogenetic signal in niche overlap, niche overlap was assessed for correlations with phylogenetic distances 359 360 between clades at each node of the phylogeny, using the age.range.correlation() tool from the Phyloclim package. The significance of niche overlap across the phylogeny of Scottish 361 damselflies was assessed using a Monte Carlo randomization procedure with 999 362 permutations of the overlap matrix, with α set to 0.05. 363

364 <u>Results</u>

Overall we sampled 4767 individual damselflies over 96 sites, of which *C. hastulatum* occurred at 12 sites with a mean density of 0.3 ± 0.48 damselflies per minute (dpm) (\pm amongsite standard deviation), *C. puella* at 15 sites with a mean density of 0.14 ± 0.19 dpm, *E*.

368	cyathigerum at 82 sites with a mean density of 0.63±1.22 dpm, <i>I. elegans</i> at 50 sites with a
369	mean density of 0.34±0.34 dpm, L. sponsa from 39 sites with a mean density of
370	0.88 ± 1.59 dpm, and <i>P. nymphula</i> from 65 sites with a mean density of 0.13 ± 0.1 dpm.
371	Spatial autocorrelation and abundance responses local to daily temperatures.
372	No species exhibited spatial autocorrelation for site densities except for <i>I. elegans</i> ,
373	where spatial autocorrelation likely reflects the ongoing range expansion process (spatial
374	autocorrelation for I. <i>elegans</i> , r=0.12, P=0.014; <i>L. sponsa</i> , r=0.01, P=0.39; <i>P. nymphula</i> , r =-
375	0.9, P=0.98; E. cyathigerum, r=0.02, P=0.31; C. hastulatum, r=0.02, P=0.34; C. puella,
376	r=0.04, P=0.21). Species densities calculated from individual capture bouts were uncorrelated
377	with the air temperature during these capture bouts, confirming that we selected days
378	characterised by favourable weather conditions for sampling, and thus that our density
379	estimates are not confounded by temperature-based detectability issues: I. elegans effect of
380	daily temperatures on daily density estimates, $Est = -0.005 \pm 0.063$, $t = -0.08$, $P = 0.94$; L.
381	<i>sponsa</i> Est=0.18±0.11, t=1.611,P=0.12; <i>C. hastulatum</i> Est=-0.34±0.21, t=-1.67, P=0.15; <i>E.</i>
382	<i>cyathigerum</i> Est=0.08± 0.05, t=1.54, P=0.13; <i>C. puella</i> Est= -0.27±0.17, t= -1.6, P=0.1;, <i>P.</i>
383	<i>nymphula</i> Est=0.08±0.049, t=1.75, P=0.09.

384 Species interactions and climate

Ischnura elegans density was best explained by a model including only mean annual
temperature (Table S2), although the correlation was not significant (effect of
bio1=0.55±0.35, t=1.58, P=0.12). For *L. sponsa*, the best model included the interaction
between mean annual temperature and *I. elegans* presence/absence (Table S2). This
interaction effect was a significant predictor of *L. sponsa* densities in the model (effect of
bio1 x *I. elegans* presence=-0.21±0.084, t=-2.55, p=0.016; Fig. 2a). In the absence of *I. elegans*, *L. sponsa* densities were positively correlated with mean annual temperature.

However, where *I. elegans* was present, *L. sponsa* density no longer correlated with climate. Furthermore, where both of these species co-occurred, densities of *I. elegans* were negatively associated with *L. sponsa* densities (estimate =-0.683 \pm 0.28, t =-2.43, *P*=0.03; Fig. 2b). *I. elegans* presence or absence did not influence body sizes of any of the other species.

Ischnura elegans presence did not show clear-cut patterns of influence on any other 396 species' densities: For *P. nymphula*, *I. elegans* presence and temperature each improve the 397 model fit in comparison to an intercept-only model explaining P. nymphula densities (Table 398 S2), but these effects are non-significant, and likely reflect that fact that the P. nymphula 399 range, while largely congruent with the range of *I. elegans*, extends to cooler, higher 400 401 elevation sites within our study region (Cham et al. 2014). For E. cyathigerum, a model which included both mean annual temperature and I. elegans presence/absence (but not the 402 interaction) best explained local densities (Table S2). Enallagma cyathigerum densities were 403 404 positively associated with *I. elegans* presence, (effect of *I. elegans* presence = 0.89 ± 0.38 , t=2.32, P=0.02) and the model also contained a slightly negative but highly non-significant, 405 406 residual effect of mean annual temperature (P=0.93). Although I. elegans presence is weakly 407 correlated with mean annual temperature across our sites, these models did not suffer from collinearity of these effects. No climate variable other than mean annual temperature (bio1) 408 409 affected the site-specific densities of any species.

410 Effects of *I. elegans* presence on *L. sponsa* morphology and thermal preferences

411 Complementarily to our density data, the presence of *I. elegans* at a site was 412 correlated with larger body sizes in *L. sponsa*, in a model that included a covariate for climate 413 and a random effect for site and date (effect of mean annual temperature on *L. sponsa* body 414 size= 1.6 ± 1.27 , df=23.59, t=-2.68, P=0.21; effect of *I. elegans* presence on *L. sponsa* body 415 size= -66.85 ± 22.53 , t=-2.97, p=0.007; Fig. 2c). Similarly, thermal preferences were

416 influenced by competition in ways that are complementary to our density and morphology

417 results. The effect of species x treatment (alone or in competition) on thermal site selection in

the laboratory was: Est= 1.97 ± 1.14 , df=104.19, t=1.72, P=0.04 using a 1-tailed hypothesis test

- 419 to predict that the presence of *I. elegans* would shift *L. sponsa* to cooler preferred
- 420 temperatures; Fig. 3). As predicted, where *I. elegans* was introduced to trials, *L. sponsa* shifts
- 421 to cooler position in comparison to when *L. sponsa* is allowed to thermoregulate alone.

422 <u>Phylogenetic community structure</u>

423 Consistent with a decline in *L. sponsa* densities at warmer sites where *I. elegans* is present, 424 warmer sites within our study region exhibited significantly higher levels of phylogenetic 425 underdispersion than cooler sites within this region (effect of mean annual temperature on 426 phylogenetic underdispersion= 13.29 ± 2.52 , t=5.27, P <0.01, Fig 4a). In a separate but 427 complementary model, phylogenetic underdispersion was also significantly predicted by the 428 presence of *I. elegans* at a site (9.98 ± 1.39 ,t=7.19,p<0.001, Fig. 4b).

429 <u>Niche similarity and phylogenetic signal</u>

Variable importance and AUC values for each species' best fit Maxent niche model are 430 presented in table S4. In all cases, the full model (containing all uncorrelated predictor 431 variables) was the best fit, with the lowest AICc. Although individual niche models for each 432 species vary in the relative importance of different climatic variables (Table S4, Fig. 5a), 433 pairwise niche overlap (measured using D; Warren et al. 2008) illustrated that most species 434 occupy similar niche space. I. elegans, E. cyathigerum, L. sponsa and P. nymuphula showed 435 436 pairwise overlap values between 0.81 and 0.92 (Fig 5b). Only C. hastulatum and to a lesser extent C. puella accounted for the majority of niche differences, with C. hastulatum 437 demonstrating pairwise overlap values between 0.18–0.25 for all other species (Fig. 5b), 438 439 while C. puella demonstrated values between 0.18-0.65 with all species (Fig. 5b). These

patterns of niche similarity showed no phylogenetic signal across the 6 species (f=0.33,
p=0.66). To identify if lack of signal was caused by the relatively large niche differences
between the closely related habitat specialist species *C. hastulatum* and *C. puella*, the analysis
was repeated with *C. hastulatum* and *C. puella* removed. Again no significant phylogenetic
signal was observed (f=0.3, p= 0.6).

445 <u>Discussion</u>

We show that relatively novel encounters between a range expanding species (I. 446 elegans) and a relatively distantly-related species within the native damselfly guild (L. 447 sponsa) can generate patterns of phylogenetic underdispersion within high-latitude 448 communities. Phylogenetic underdispersion occurs because L. sponsa is displaced from 449 450 thermally-favourable habitats by I. elegans, resulting in lower population densities. Because the other members of the native damselfly guild are much more closely related to I. elegans 451 than is L. sponsa, invasion by I. elegans reduces the overall breadth of phylogenetic 452 453 representation within these damselfly guilds. This result supports recent conceptual advances 454 suggesting that patterns of competitive exclusion may be common between distantly related species, if traits related to competitive abilities are more strongly phylogenetically conserved 455 456 than niche traits (Mayfield & Levine 2010). Species' competitive abilities are important predictors of successful range shifts and establishment in novel communities under climate 457 change (Alexander, Diez & Levine 2015), and novel communities produced by 458 environmental change may be subject to high levels of competition (Lancaster et al. 2017). 459 Our results suggest that clades with conserved competitive abilities, such as *Coenagrionid* 460 461 damselflies, may typically dominate novel communities under changing climates, resulting in the loss of phylogenetic diversity, particularly at high latitudes where species richness is low, 462 so the loss of even a single species can significantly impact phylogenetic diversity. 463 464 Furthermore, our results demonstrate that the processes driving under- and over-dispersion

within communities are more complex than classically expected, raising questions about theutility of phylogenetic signal as a proxy for describing community assembly processes.

467 <u>Evidence for partial competitive displacement</u>

We show evidence for incipient competitive displacement of L. sponsa by the range-468 expanding *I. elegans*, where *L. sponsa* is the least related species to *I. elegans* within the 469 470 regional species pool (Figs. 1, 2a&b, 3). Evidence in support of this includes: (i) L. sponsa and I. elegans inhabit strongly convergent climatic niche space (Fig. 5a&b). (ii) L. sponsa 471 population densities exhibit a negative relationship with *I. elegans* density (Fig 2C). (iii) In 472 the absence of *I. elegans* at a site, *L. sponsa* density is positively correlated with mean annual 473 temperature, but the presence of *I. elegans* disrupts this relationship (Fig. 2b), suggesting that 474 475 I. elegans displaces L. sponsa from preferred (warmer) sites. (iv) L. sponsa has undergone a morphological shift (to larger body sizes) where I. elegans is present (Fig. 2b). (v) L. sponsa 476 shifts its thermal preference to cooler temperatures when in competition with *I. elegans* (Fig. 477 478 3).

Patterns of partial competitive displacement between the two least-related species 479 within a guild is consistent with the expectations of the competitive trait conservation 480 481 hypothesis (Chesson 2000; Mayfield & Levine 2010). Given that L. sponsa population densities positively correlate to mean annual temperature, but only in the absence of I. 482 elegans, it is unlikely that environmental filtering is the primary causal factor explaining the 483 negative relationship between L. sponsa density and I. elegans density. Moreover, thermal 484 485 preference trials demonstrate competitive displacement of L. sponsa from their preferred thermal regimes in response to the presence of *I. elegans*. This result suggests that 486 487 behavioural traits, such as aggressive behaviour, might act as the mechanism of competition. At present we lack sufficient evidence to conclude this is the competitive mechanism, 488

although competition for basking sites via aggressive behaviour has been observed in larger
territorial odonata species (Lefevre & Muehter 2004; Worthen & Patrick 2004; Byers &
Eason 2009). Moreover, it is unlikely that there is only one mechanism by which *I. elegans*and *L. sponsa* compete, as the adult stage represents a relatively short (but critical) period of
interaction between these two species. A major component of co-occurrence between these
species is during aquatic larval development (see below).

495 The consequence of competition for *L. sponsa* is further reflected in changes in *L*. sponsa body size where I. elegans is present (Fig. 2c). Competition has widely been 496 demonstrated to result in increased size in invertebrates (Plaistow & Siva-Jothy 1996; Vande 497 498 Velde & Van Dyck 2013), though the drivers of this morphological shift in this case are unknown. A plastic or evolved response is equally plausible in explaining this result. Slower 499 growth rates through reduced food availability have been shown to delay damselfly 500 501 emergence, but emergence occurred at a larger size (Pickup, J. and Thompson 1990). Alternatively, competitive interactions have been shown to select for larger body size, which 502 503 may evolve because they improve competitive ability or facilitate niche divergence from the 504 invader (Plaistow & Siva-Jothy 1996; Vande Velde & Van Dyck 2013). These alternative hypotheses are currently indistinguishable, because the behavioural or resource-use basis for 505 506 competition between *I. elegans* and *L. sponsa* is unknown. The interactions may revolve around indirect competition for food resources during larval development or reduced adult 507 fitness through direct, competitive interactions (McPeek, Grace & Richardson 2001). The fact 508 that competition appears to be most intense at warmer sites (Fig. 2a) suggests that the I. 509 elegans are less competitively dominant at colder sites, or that both species compete most 510 intensively over preferred thermal niches or thermally-mediated resources. 511

512 Lancaster *et al.*(2017) have previously demonstrated that *I. elegans* exhibits
513 increased aggression under experimental warming treatments, suggesting that further

514 warming at high latitudes could compound the effects of invasions to destabilise high latitude communities (Lancaster et al. 2017). Furthermore, Lancaster et al. (2017) demonstrated that 515 I. elegans is competitively well-matched with E. cyathigerum, in terms of larval competitive 516 517 behaviours, at current water temperatures (these species exhibit highly congruous numbers of aggressive behaviours in laboratory trials to assess interspecific larval competition under 518 different temperature regimes). That I. elegans and E. cyathigerum are 1) well-matched 519 520 competitively, 2) closely related phylogenetically, and 3) highly likely to co-occur at sites across NE Scotland (see results section), further supports our conclusions that the 521 522 Competition-Relatedness hypothesis is a good explanation for drivers of community assembly in high latitude damselfly communities. Under this mechanism, *I. elegans* and *E.* 523 cyathigerum co-occur readily, following the expansion of I. elegans into the area, due to their 524 525 phylogenetically conserved competitive behaviours—in other words, neither can exclude the other. However, as temperatures continue to warm at high latitudes, this balance may shift 526 (Lancaster et al. 2017). 527

528 <u>Temporal dynamics and future directions in our field research</u>

A time lag between the colonisation of an antagonistic species in a population and the 529 530 point at which species displacement become pronounced can radically influence interpretation of how species interact during range shifts. Understanding this temporal lag 531 therefore represents an important avenue for future research. Anecdotally, our data may also 532 suggests that the effect of I. elegans presence on L. sponsa densities has a temporal 533 component (Fig. 2b). Points circled in green represent sites at the very leading edge of I. 534 535 elegans' range, and the point circled in blue represents a newly-created pond (within the last 5 years). At these sites, although *I. elegans* is present, patterns of *L. sponsa* densities are 536 similar to those observed at sites in the absence of I. elegans. This suggests a temporal lag 537 538 between I. elegans' initial colonisation to a site, and the subsequent decline of L. sponsa.

However, given that only 5 ponds in our dataset exhibit this potential lagged effect, the
evidence for this is at present is only suggestive. The importance of time lags in competitive
displacement, while widely suggested by other researchers (Jackson & Sax 2010), bears
further investigation in our study system before firm conclusions can be drawn.

543

Niche Overlap and Environmental Filtering

Niche overlap among all 6 species exhibited no phylogenetic patterns. Instead, most 544 species exhibited strongly overlapping climatic niche space, with the exception of C. 545 hastulatum and C. puella (Fig. 5a & 5b). This is unsurprising given that these species 546 represent a guild, using similar resources at similar sites across Scotland. Strong overlap in 547 niche space among each of the interacting species means that environmental filtering based 548 549 on niche requirements is unlikely to be observed (see also Siepielski et al. 2010). The maintenance of a similar niche across a broad phylogenetic scale within damselflies is 550 consistent with earlier studies showing that speciation in damselflies is rarely linked to niche 551 552 divergence (McPeek et al. 2000; Wellenreuther & Sánchez-Guillén 2015). Our results extend 553 these previous findings by demonstrating that, like speciation, competitive displacements in damselflies is also unrelated to levels of niche divergence. The general lack of niche 554 divergence among damselfly species makes this a particularly good system to demonstrate 555 Mayfield and Levine's (2010) hypothesis for how the phylogenetic conservation of traits such 556 as competitive behaviours can produce phylogenetic clustering within communities in the 557 absence of niche trait variation (see also Saito et al. 2016). 558

559 <u>Phylogenetic patterns</u>

562

560 Our observed shift in phylogenetic structure within communities as a result of 561 competition (Fig 3A and 3B) has two major implications. Firstly, from a

methodological/theoretical perspective, it raises the issue of whether the use of phylogenetic

563 structure can be used as a method for ascertaining community assembly processes (Webb 2000; Lessard et al. 2009; Lebrija-Trejos et al. 2010). Secondly, reduced phylogenetic 564 diversity as a result of climate change-driven range shifts poses a conservation issue. 565 566 Declines in phylogenetic diversity may be common in regions affected by increased competition from invasive species (Lessard et al. 2009), and these diversity losses may be 567 exacerbated under further climatic warming (Willis et al. 2008; Zhang et al. 2015). Because 568 569 conservation of phylogenetic diversity is critical for maintaining high levels of biodiversity 570 into the future (Barker 2002), range shifts within regional species pools characterized by 571 conserved competitive abilities may pose a particularly urgent concern, particularly for high latitude ecosystems, which are strongly affected by this colonisation process. Little is known 572 about the factors underpinning range shifts in animals (Angert et al. 2011; Comte & 573 574 Grenouillet 2013), so we do not know the extent to which species prone to range shifting generally tend to express conserved (i.e., inherited) competitive abilities. 575

576 <u>Implications</u>

577 We find that a climate change-mediated expansion of a warm-adapted, generalist species, *I. elegans*, to a relatively species-poor, high latitude community results in partial 578 579 competitive displacement of the weakest competitor, L. sponsa, resulting in loss of phylogenetic diversity at higher latitudes. Typically, high latitude and high elevation 580 communities exhibit low species diversity, with overrepresentation by endemic or relict 581 species which are locally adapted and exhibit small geographic ranges. Climate change is 582 facilitating the colonization of warm-adapted, widespread generalist species into these 583 584 communities for the first time, and it is critical to understand how these colonization events alter high latitude community structure and diversity, despite the fact that low levels of native 585 species diversity in these environments can reduce the power of community-phylogenetic 586 587 analyses.

588 Our results highlight the importance of evaluating the relative degrees of both niche conservatism and competitive trait conservatism in regional species pools before inferring 589 ecological processes from phylogenetic patterns. Furthermore, our study raises the possibility 590 591 that competitive trait conservatism may generally be more an important factor in driving community assembly during periods of ecological instability, such as during range 592 expansions, than for stable species pools that have adapted in situ to their potential 593 competitors, although this hypothesis remains to be formally tested. Thus competitive 594 displacements or wholesale exclusion by invading or range shifting species may commonly 595 596 reduce phylogenetic diversity of the invaded community by this mechanism, particularly where ecological niches are similar among native and range-shifting species. 597 Acknowledgements: 598 We thank Heather Bodie and Debbie Young for assistance in the field, and local landowners 599 for permissions to study and sample damselflies on their land. Brad Duthie provided helpful 600 601 comments on an earlier version of this ms. The project was supported by a NERC DTP fellowship to RF and a start-up grant to LL provided by the U. of Aberdeen. 602 603 Data All data used in this study have been deposited in Dryad data repository DOI: 604 10.5061/dryad.kp89j 605 References 606

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813 814	Figure legends:
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813814815816	Figure legends: Figure 1. Phylogeny of Scottish damselfly species constructed using phylogenies from
 813 814 815 816 817 	Figure legends: Figure 1. Phylogeny of Scottish damselfly species constructed using phylogenies from
 813 814 815 816 817 	Figure legends: Figure 1. Phylogeny of Scottish damselfly species constructed using phylogenies from Dumont, Vierstraete & Vanfleteren (2010) and Guan et al. (2013), with branch lengths set to
 813 814 815 816 817 818 	Figure legends: Figure 1. Phylogeny of Scottish damselfly species constructed using phylogenies from Dumont, Vierstraete & Vanfleteren (2010) and Guan et al. (2013), with branch lengths set to 1.
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 813 814 815 816 817 818 819 820 821 822 	 Figure legends: Figure 1. Phylogeny of Scottish damselfly species constructed using phylogenies from Dumont, Vierstraete & Vanfleteren (2010) and Guan et al. (2013), with branch lengths set to 1. Figure 2. Effects of <i>Ischnua elegans</i> on <i>Lestes sponsa</i> within communities. 2a. <i>Lestes sponsa</i> density is positively correlated with mean annual temperature at sites where <i>I. elegans</i> is absent, but not where <i>I. elegans</i> is present (effect of biol x <i>I. elegans</i> presence =-0.21±0.084, t =-2.55, p=0.016) Green circles represent sites at
 813 814 815 816 817 818 819 820 821 822 823 	 Figure legends: Figure 1. Phylogeny of Scottish damselfly species constructed using phylogenies from Dumont, Vierstraete & Vanfleteren (2010) and Guan et al. (2013), with branch lengths set to 1. Figure 2. Effects of <i>Ischnua elegans</i> on <i>Lestes sponsa</i> within communities. 2a. <i>Lestes sponsa</i> density is positively correlated with mean annual temperature at sites where <i>I. elegans</i> is absent, but not where <i>I. elegans</i> is present (effect of biol x <i>I. elegans</i> presence =-0.21±0.084, t =-2.55, p=0.016) Green circles represent sites at the current expansion front for <i>L elegans</i> and blue circles represent ponds less than 5

824	years old. Thus, at all circled sites, the species have only recently co-occurred, and the
825	competitive displacement effect observed at other sites may not have yet developed.
826	2b. L. sponsa density is negatively correlated to densities of the invading competitor
827	<i>I. elegans</i> . The effect line represents the linear regression effect:-0.683 \pm 0.28, r ² =0.24
828	$F_{1,19}$ =5.89, t =-2.43, P=0.03.
829	2c. Lestes sponsa body size at sites where Ischnura elegans is present and absent,
830	where body size has been derived from principal components analysis of multiple
831	morphometric measurements (I. elegans presence on L. sponsa body size=-
832	264.52±7.174, t =-3.4238, p <0.001).
833	
834	Figure 3. Thermal preferences of Ischnura elegans and Lestes sponsa in the presence and
835	absence of each other. Error bars depict standard errors.
836	Figure 4. Predictors of phylogenetic structure within Scottish damselfly communities. 4a.
837	Communities are more phylogenetically underdispersed at warmer sites (assessed via mean
838	annual temperature at the site), where letters indicate significant differences. 4b. Effect of <i>I</i> .
839	elegans presence vs. absence on patterns of within-community phylogenetic dispersion.
840	Figure 5. Niche modelling of all damselfly species found in the study region.
841	5a. Habitat suitability of each damselfly species using MaxEnt niche modelling.
842	5b. Pairwise niche overlap scores given as Schoeners D (Warren et al. 2008).
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921 Figure 5



	lschnura elegans	Lestes sponsa	Pyrrhosoma nymphula	Coenagrion hastulatum	Coenagrion puella	Enallagma cyathigerum
Ischnura elegans	NA	0.87	0.82	0.22	0.65	0.87
Lestes sponsa		NA	0.87	0.26	0.61	0.91
Pyrrhosoma nymphula			NA	0.23	0.52	0.92
Coenagrion				NA	0.18	0.23
hastulatum						
Coenagrion					NA	0.57
puella						
Enallagma						NA
cyathigerum						

Supplementary material for: Range shifting species reduce phylogenetic diversity in high latitude communities via competition Robert Fitt^{1*}, Lesley T. Lancaster¹ 1. Institute of Biological and Environmental Sciences, The University of Aberdeen, Aberdeen, United Kingdom. *Corresponding author: r01rnf13@abdn.ac.uk. Table S1. Variation in georeferenced climate variables across the study sites in northeast Scotland. Climatic values for each site were bioclimatic variables obtained from (Hijmans et

939 al., 2005).

Clim	atic variables	Maximum value	Minimum Value
Bio1	Mean annual temperature	4.8°C	8.2°C
Bio2	Mean diurnal Range	7°C	7.3°C
Bio3	Iscothermality	3	3.9
Bio4	Temperature seasonality	400.9	548.4
Bio8	Mean temperature of wettest Quarter	0.2°C	11.6°C
Bio9	Mean temperature of driest quarter	3.6°C	10.3°C
Bio10	Mean Temperature of Warmest	10.9°C	14.6°C

	Quarter		
Bio15	Precipitation	14	26
	Seasonality		
Bio18	Precipitation	174mm	270mm
	of Warmest		
	Quarter		

941 Table S2. AICc scores for the different	t models predictir	ng site-specific	density of each
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942 species. A ΛAICc of greater than 2 was assumed to be significantly different.

Model				
	Lestes sponsa	Ischnura elegans	Pyrrhosuma nymphula	Enellagma cyathigerum
~1	153.2	178.9	188.6	266.9
~I.elegan	152.1	-	183.9	362.5
presence/absence				
(I.E)				
~Bio1	150.7	167.2	182.6	256.4
~I.E+Bio1	147.5	-	182.3	253.0
~I.E*Bio1	142.9	-	183.6	255.0

943

944 Table S3

945 Sites and dates of damselfly capture for thermal preference trials

Site	Latitude	Longitude		Dates visited	
31	56 38.880	-2 46.185	18/07/2016		
34	57 4.133	-2 30.245	18/07/2016		
51	57 11.174	-3 50.224	07/07/2016	21/07/2016	
84	56 44.537	-2 57.551	05/07/2016	13/07/2016	18/07/2016
87	56 32.503	-2 37.293	13/07/2016	18/07/2016	
90	57 31.311	-3 12.473	07/07/2016	21/07/2016	
91	57 40.562	-3 7.647	07/07/2016	21/07/2016	

946

Table S4. Permutation importance of climatic predictor variables included within best-fit
niche models for each species. AUC from ROC analysis scores are given to assess the fit of
each model to the data. More widespread species tend to have lower AUC values for a given
model quality; AUC > 0.5 indicates a better-than-random fit to the data. The variable with the
highest permutation importance for each species is depicted in bold.

Clin	Climatic variables		Permutation importance					
_		I.elegan s	L.sponsa	C.puella	C.hastulatum	P.nymphula	E.cyathigeru m	
Bio1	Mean annual temperature	54	11.9	30.8	1.5	14.6	12.3	
Bio2	Mean diurnal Range	11	12.1	30	36.2	16.9	9.4	
Bio3	Iscothermality	2.7	7.7	0.9	3	9.8	1	
Bio4	Temperature seasonality	1.5	6.2	13	2.9	1.9	6.9	
Bio8	Mean temperature of wettest Quarter	0.3	2.2	2.4	0.8	0.4	5.5	
Bio9	Mean temperature of driest quarter	0.5	0.7	0.4	0.2	0.4	0.6	
Bio10	Mean Temperature of Warmest Quarter	15.5	40.4	8.7	0.1	10.4	32.8	
Bio15	Precipitation Seasonality	9.1	6.7	10.2	1.1	28.4	15	
Bio18	Precipitation of Warmest Quarter	5.4	12.1	3.7	54.2	17.2	16.6	
AUC		0.739±0 .009	0.703±0 .009	0.873±0 .01	0.977±0.012	0.646±0.02	0.666±0.01	

958 Figure S1:

959 Depiction of the thermal gradient of used for thermal preference trials, where temperature

960 decreased gradually from ~60°C to ~10°C over 1 metre.

H Barre	~27.4 [℃] 51.3	
		T (
2	-Y-	
		7.0

- 964 Figure S2:
- 965 Example of a thermal image of where a damselfly settled within the thermal gradient. Circles
- 966 represent locations around the damselfly where environmental temperature was recorded.



